

**IDENTIFICATION AND REMEDIATION OF STUDENT  
DIFFICULTIES WITH QUANTITATIVE GENETICS**

By

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For my dad – I know you would have been proud of me!

For my mum, Laurence, Sam and Georgie

Without your love and support this project would never have been completed.

## PREFACE


The research described in this thesis was carried out in the Discipline of Genetics, School of Biochemistry, Genetics, Microbiology and Plant Pathology, University of KwaZulu-Natal, (Pietermaritzburg campus), from January 2002 to December 2005 under the supervision of Professor Trevor Anderson.

These studies represent original work by the author and have not been otherwise submitted in any other form for any degree or diploma to any other University. Where use has been made of the work of others, it has been duly acknowledged in the text.



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## ABSTRACT

Genetics has been identified as a subject area which many students find difficult to comprehend. The researcher, who is also a lecturer at the University of KwaZulu-Natal, had noted over a number of years that students find the field of quantitative genetics particularly challenging. The aim of this investigation was two-fold. Firstly, during the diagnostic phase of the investigation, to obtain empirical evidence on the nature of difficulties and alternative conceptions that may be experienced by some students in the context of quantitative genetics. Secondly, to develop, implement and assess an intervention during the remediation phase of the study which could address the identified difficulties and alternative conceptions.

The research was conducted from a human constructivist perspective using an action research approach. A mixed-method, pragmatic paradigm was employed. The study was conducted at the University of KwaZulu-Natal over four years and involved third-year students studying introductory modules in quantitative genetics. Empirical evidence of students' conceptual frameworks, student difficulties and alternative conceptions was obtained during the diagnostic phase using five research instruments. These included: free-response probes, multiple-choice diagnostic tests, student-generated concept maps, a word association study and student interviews. Data were collected, at the start and completion of the modules, to ascertain the status of students' prior knowledge (*prior knowledge concepts*), and what they had learnt during the teaching of the module (*quantitative genetics concepts*).

Student-generated concept maps and student interviews were used to determine whether students were able to integrate their knowledge and link key concepts of quantitative genetics. This initial analysis indicated that many students had difficulty integrating their knowledge of *variance* and *heritability*, and could not apply their knowledge of quantitative genetics to the solution of practical problems.

Multiple-choice diagnostic tests and interviews with selected students were used to gather data on student difficulties and alternative conceptions. The results suggested that students held five primary difficulties or alternative conceptions with respect to *prior knowledge concepts*: (1) confusion between the terms variation and variance; (2) inappropriate association of heterozygosity with variation in a population; (3) inappropriate association of variation with change; (4) inappropriate association of equilibrium with inbred populations and with values of zero and one; and, (5) difficulty relating descriptive statistics to graphs of a normal distribution. Furthermore, three major difficulties were detected with respect to students understanding of *quantitative genetics concepts*: (1) students frequently confused individual and population measures such as breeding value and heritability; (2) students confused the terms heritability and inheritance; and, (3) students were not able to link descriptive statistics such as variance and heritability to



histograms. Students found the concepts of variance and heritability to be particularly challenging. A synthesis of the results obtained from the diagnostic phase indicated that many of the difficulties and alternative conceptions noted were due to confusion between certain terms and topics and that students had difficulty with the construction and interpretation of histograms. These results were used to develop a model of the possible source of students' difficulties. It was hypothesized and found that the sequence in which concepts are introduced to students at many South African universities could be responsible for difficulties and alternative conceptions identified during the study, particularly the inappropriate association of terms or topics.

An intervention was developed to address the identified difficulties and alternative conceptions. This intervention consisted of a series of computer-based tutorials and concept mapping exercises. The intervention was then implemented throughout a third-year introductory module in quantitative genetics. The effectiveness of the intervention was assessed using the multiple-choice diagnostic tests and interview protocols developed during the diagnostic phase. The knowledge of the student group who participated in the intervention (test group) was compared against a student group from the previous year that had only been exposed to conventional teaching strategies (control group). t-tests, an analysis of covariance and a regression analysis all indicated that the intervention had been effective. Furthermore, an inductive analysis of the student responses indicated that most students' understanding of the concepts of *variance*, *heritability* and histograms was greatly improved.

The concept maps generated by students during the remediation phase, and data from the student interviews, provided an indication of the nature and extent of the conceptual change which had occurred during the teaching of the module. The results showed that most of the conceptual change could be classified as conceptual development or conceptual capture and not conceptual exchange. Furthermore, it seemed that conceptual change had occurred when considered from an epistemological, ontological and affective perspective, with most students indicating that they felt they had benefited from all aspects of the intervention.

The findings of this research strongly suggest an urgent need to redesign quantitative genetics course curricula. Cognisance should be taken of both the sequence and the manner in which key concepts are taught in order to enhance students' understanding of this highly cognitively demanding area of genetics.

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## CHAPTER 1

### CONTEXT AND AIMS OF THE INVESTIGATION

The first chapter of this thesis provides an overview of the investigation conducted and describes the context of the study, focussing on the problems, which motivated the research.

#### 1.1 OVERVIEW OF THE THESIS

This thesis describes a four-year investigation that was conducted to investigate tertiary students' difficulty in the understanding of foundational concepts in quantitative genetics and possible ways to address these problems. The investigation employed an action research approach where I was both the researcher and the lecturer of the modules concerned. The investigation was performed in two phases; a diagnostic phase and a remediation phase. The diagnostic phase aimed to empirically assess students' conceptual frameworks and to establish which concepts students found most difficult, as well as the nature of specific alternative conceptions held by the students. This component of the investigation was conducted over a three-year period during which data were collected from different groups of third-year genetics students taking introductory modules in quantitative genetics. Five instruments were used to gather relevant data, (1) free-response probes, (2) multiple-choice diagnostic tests, (3) student-generated concept maps, (4) a word association study and (5) interviews with selected students. Data were collected both at the commencement of the modules, to ascertain the status of students' knowledge prior to the teaching of the principles of quantitative genetics, as well as at the completion of the modules, to determine the conceptions of students that had been acquired during the teaching process.

The remediation phase involved developing and evaluating a system of teaching aimed at improving the level of students' understanding of certain concepts found during the diagnostic phase to be problematic, such as variance and heritability. Thirty-seven third-year genetics students participated in the remediation phase of the investigation. Data on students' understanding of relevant concepts were gathered both before and after the

intervention, using the diagnostic multiple-choice tests and interview protocols developed during the first part of this investigation. In addition, the conceptual change which occurred during the teaching of the module was monitored using student-generated concept maps. Students' attitudes towards both the module content and the teaching strategy were also evaluated using a survey-style questionnaire.

## 1.2 SIGNIFICANCE OF GENETICS IN THE 21<sup>ST</sup> CENTURY

The scientific community has recently celebrated the 50-year anniversary of the announcement by Francis Crick and James Watson that they had discovered "the secret of life" when they unravelled the structure of DNA (Watson and Crick 1953). It has been stated that this, and the many subsequent scientific discoveries in genetics, have altered the manner in which we all understand life (Plomin and Walker 2003).

In the 21<sup>st</sup> century we are all affected by genetics in some manner. Consider the modern world's latest and largest natural disaster, the Tsunami that hit South East Asia in December 2004: forensic science, including DNA testing, allowed for the identification of thousands of bodies. The identification of these bodies was broadcast all over the world and was able to give much needed closure to many families who had lost loved ones. Genetics plays a role not only in forensic studies and criminal investigations, but also in medicine and the treatment of diseases, the conservation of endangered species, the study of evolution, as well as, and perhaps most importantly, in the provision of food to feed an ever-growing human population (Snustad and Simmons 2003).

Understanding of the mechanisms involved with DNA structure and replication, and thus the transmission of inherited characteristics from one generation to the next, has allowed the creation of scientifically bred, higher yielding varieties of commodities such as rice, wheat and maize (Snustad and Simmons 2003). In this way, overall food production in developing countries has largely been able to keep pace with population growth. Despite these demonstrable achievements in developing countries, over 800 million people live a life of permanent or intermittent hunger and are chronically undernourished. Simply exporting more food from the industrialised countries is not a solution as market economies are notoriously ineffective in achieving equitable distribution of benefits (Madeley 2002). These arguments point to the need for an agricultural revolution that is both more productive and more "green" in terms of conserving natural resources and the environment. This can be achieved by a combination of ecological approaches to sustainable agriculture; greater participation by farmers in agricultural analysis, design and

research; and the greater application of modern breeding methods directed towards the needs of the poor in developing countries (Madeley 2002).

Genetics has been described as the science of heredity and variation (Sturtevant and Beadle 1962) with the subdiscipline of quantitative genetics being the study of characteristics which vary in a continuous manner; quantitatively rather than qualitatively (Falconer and Mackay 1996). This field of quantitative genetics is arguably one of the most important areas of genetics as it has far reaching practical applications. These include not only the understanding and treatment of diseases such as HIV, cancer and heart disease, but also the understanding of the inheritance of most characteristics of economic importance, for example crop yield and disease resistance (Podlich and Cooper 1998).

As a result of public interest and the demands for increased food production, the genetics departments of universities such as the University of KwaZulu-Natal in South Africa, have shown dramatic increases in student numbers in recent years. It is therefore imperative that such academic institutions are able to ensure that young scientists are well educated in the exciting field of genetics, especially in developing countries such as South Africa.

### **1.3 STATEMENT OF THE PROBLEM WHICH MOTIVATED THE RESEARCH**

The author of this thesis has been teaching modules in quantitative genetics, at the University of KwaZulu-Natal, South Africa, for eight years and has become very aware that many students find these modules more difficult than those of other content areas. Literature describing such problems world-wide is reviewed in the next section. Cooper (1998) suggests that students' difficulties in this subdiscipline may primarily be because mathematical frameworks are used to represent biological concepts, which may create a barrier to meaningful learning. In this regard, I have noticed that students seem to have great difficulty with the mathematical and statistical components of the modules, which leads to a perception, on the part of many students, that they cannot cope with the underlying genetic principles. Very often this perception leads to students losing interest in the course and resorting to rote-learning of relevant definitions and equations in an attempt to pass. The precise nature of students' unscientific ideas and alternative conceptions of concepts in quantitative genetics, and the reasons for their occurrence, in an international or local context, have not previously been empirically established and reported in the literature. The diagnostic phase of this investigation therefore aimed to gather empirical data on students' understanding of this important area of genetics.

The observation that students are unable to learn quantitative genetics in a meaningful manner may be further exacerbated by the current status of education in many South African schools where students, like those around the world, are inclined to practice a system of rote-learning. Therefore a system of undergraduate teaching which recognises the problems experienced by students and which helps students develop appropriate skills, organize new knowledge and change existing knowledge, is required to aid in addressing the shortage of suitably qualified geneticists in developing countries. The remediation phase of this investigation thus involved the development and evaluation of teaching strategies aimed at assisting students to learn in a meaningful manner and thereby develop a sound understanding of the principles of quantitative genetics.

## **1.4 LITERATURE REVIEW OF STUDENT DIFFICULTIES AND ALTERNATIVE CONCEPTIONS APPLICABLE TO THIS INVESTIGATION**

### **1.4.1 Classification of student difficulties, alternate conceptions and the genetics focus area**

The proliferation of research into student conceptions in science has resulted in the use of numerous terms to describe the difficulty students may experience with a subject area and the possible existence of alternative conceptions (Cho *et al.* 1985; Abimbola 1988; Wandersee *et al.* 1994). In the subject area of genetics, Cho *et al.* (1985) clearly discriminates between studies into the reasons for students' difficulties with genetics and the existence of alternative conceptions, which was also the position adopted by the author of this thesis. For the purposes of this thesis it was thus deemed necessary to clarify the author's preferred understanding and usage of relevant terminology.

#### **(a) Nature of student difficulties**

Literature investigating student difficulties in genetics (Radford and Bird-Stewart 1982; Bahar *et al.* 1999) implied the application of the word "difficulties" as being consistent with the Oxford Dictionary (1964) definition, where something is perceived as being difficult if it "requires much effort or skill" or is something that is "not easy". In this thesis a "student difficulty" thus refers to an idea or collection of ideas, the mastery of which requires a great deal of effort on the part of most of the students concerned.

#### **(b) Nature of alternative conceptions**

It has become increasingly clear to both teachers and researchers in science education that students can never be considered blank slates beginning with zero knowledge and

awaiting the receipt of current scientific understanding (Gilbert *et al.* 1982; Novak 1993). However, many of the ideas which students bring to the classroom are erroneous from a scientific point of view (Eylon and Linn 1988; Fisher and Moody 2000; Cakiroglu and Boone 2002). A number of names have been suggested for such conceptions. These primarily include the term “alternative conceptions”, or “misconceptions” denoting student understanding of scientific concepts that are not aligned with the current understanding of scientists (Wandersee *et al.* 1994; Anderson *et al.* 2002). The term “alternative conception”, however, is currently the preferred term for conceptions requiring a cognitive transformation to the accepted scientific view, as intellectual respect is conferred to the student holding the conception (Wandersee *et al.* 1994). In addition, other names have been introduced to describe the ideas students bring to the classroom, such as “naïve ideas”, “pre-scientific ideas” and “preconceptions”. These terms refer to ideas which are less negative than “alternative conceptions” as these conceptions may more easily be built on and modified using appropriate instructional strategies (Wandersee *et al.* 1994; Fisher and Moody 2000). If prior ideas are in partial agreement with accepted scientific theories and may be extended and modified to align with currently accepted scientific conceptions, they may act as “anchors” for future learning. This type of conception is sometimes referred to as an “anchoring conception” (Clement *et al.* 1989). The notion of “missing conceptions” also exists, indicating that students lack any conception of a particular idea (Hackling and Treagust 1984). The proposal of the terms “critical conceptions”, “critical propositions”, “protoconcepts”, “critical concepts” or “critical barriers” have all been suggested to refer to conceptions, knowledge of which is required for the learning of higher level topics (Driver 1989; Trowbridge and Wandersee 1994; Pearsall *et al.* 1997; Fisher and Moody 2000). As suggested by Abimbola (1988) the term “alternative conception” will be used in this thesis when referring to students’ ideas which are not compatible with a scientifically accepted view and “alternative conceptual framework” will refer to the organisation and relationships between students’ alternative ideas of concepts, rather than the ideas themselves.

Wandersee *et al.* (1994) reviewed more than 3000 studies of alternative conceptions in science and summarised the key claims made by researchers regarding this type of conception.

- Learners come to formal instruction with many alternative conceptions regarding natural objects and events.
- Alternative conceptions occur in all sexes, races and ability levels.
- Alternative conceptions are often those that were previously accepted as scientifically correct by early scientists in that they are logical conclusions drawn from limited data.
- Alternative conceptions arise from personal experiences.

- Alternative conceptions are often tenacious and resistant to change as they are very plausible to the student.
- Many teachers hold the same alternative conceptions as their students.
- Prior knowledge may interact with new knowledge presented during formal instruction in inexplicable ways leading to unwanted learning outcomes.
- Instructional strategies that encourage conceptual change are required for replacing a resistant alternative conception with a scientifically accepted idea. Consequently, teachers and researchers must possess in-depth pedagogical content knowledge that is useful for the teaching of that topic.

**(c) Nature of genetics**

The science of genetics has evolved dramatically over the last 50 years and currently embraces the foundational subject areas of (1) cytogenetics, (2) molecular genetics and (3) transmission or Mendelian genetics. Cytogenetics is primarily concerned with the structure of genetic material as well as the processes of cell division and the segregation of alleles during gamete formation. Molecular genetics, at a foundational level, considers the processes of DNA replication, transcription and translation. As such the basis of cytogenetics and molecular genetics is the structure and function of genetic material as well as the processes involved in cell division and gene expression. In contrast, transmission genetics considers the physical expression of a trait and the manner in which genotypes and their resultant phenotypes may be predicted. Transmission genetics is dependent on an understanding of the mathematical principles of probability as well as the use of abstract algebraic symbols and complex terminology. A sound understanding of all three of these foundational subject areas is required before students can learn the applied or advanced subject areas such as bioinformatics, immunogenetics, pharmacogenetics, population genetics, evolution, plant breeding, animal breeding and quantitative genetics.

Quantitative genetics is an area of genetics which focuses on the inheritance of traits whose phenotypic appearance is determined by many genes at different loci and numerous environmental factors (Falconer and Mackay 1996). This multifactorial nature of the inheritance of quantitative traits means that statistical principles are required to quantify the variation in the phenotypic appearance of characteristics observed in populations (Bourdon 2000). Consequently, an understanding of the inheritance of quantitative traits is dependent on the foundational principles of transmission genetics as well as elementary statistics.

The review of the literature presented in this chapter, therefore, addresses relevant publications on student difficulties and alternative conceptions which have been documented in the disciplines of genetics, with particular reference to transmission

genetics and statistics, and discusses their potential influence on students' understanding of quantitative genetics.

#### **1.4.2 Nature and source of student difficulties in genetics**

Genetics is a central component of school and university curricula worldwide, as it is important to the understanding of biology and the impact of the biological sciences on society (Browning and Lehman 1988). Many research studies on the perceived difficulty of topics covered in school and university-level biology modules, have revealed that genetics was identified, by both students and examiners, as an area of maximum difficulty (Johnstone and Mahmoud 1980; Cho *et al.* 1985; Bahar *et al.* 1999a; Martinez-Gracia and Gil-Quilez 2003). Unfortunately, if students regard a topic as difficult their ability and willingness to learn are subsequently affected (Johnstone and Mahmoud 1980; Bahar *et al.* 1999a).

As quantitative genetics is dependent on an understanding of complex terminology, mathematical principles and a working knowledge of the segregation of alleles during meiosis (the cause of variation in populations), the factors identified by previous research as causes of student difficulties may also be applicable to those observed by the researcher in quantitative genetics. Table 1.1 provides details of the primary difficulties which have been documented in the literature regarding the discipline of genetics and the possible implications thereof for students' understanding of quantitative genetics. The studies cited in the table involved both high school and undergraduate students in England, Scotland, Germany, Australia, the U.S.A. and Southern Africa. Furthermore, in some of the cited studies, relevant textbooks and the wording of examination questions were studied in order to ascertain the causes of students' difficulties in genetics. The results of such studies imply that students experience similar difficulties worldwide and that students in a South African context may well experience comparable problems when studying genetics. (Details of the context of the various studies cited are given in Appendix 1 on page 287).



**Table 1.1: Student difficulties observed in foundational genetics and the implications thereof for quantitative genetics.**

Issue	Nature of difficulty	Example	Source of difficulty	Implications for this investigation
Terminology	Confusion between terms.	Allele, gene, chromatid and chromosome (Longden 1982; Pashley 1994; Moletsane and Sanders 1995; Bahar <i>et al.</i> 1999a; Lewis <i>et al.</i> 2000; Lewis 2004).	Genetics has a large, complex and precise language and the incorrect use of terminology prevents the accurate exchange of ideas (Bahar <i>et al.</i> 1999a).	Students may confuse terms such as variation, variance, inheritance and heritability.
	Confusion between look-alike and sound-alike words.	Homologue, homologous, homozygote and homozygous (Bahar <i>et al.</i> 1999a).		
Mathematical nature of genetics	Genetic ratios are often viewed as deterministic and not probabilistic (Cho <i>et al.</i> 1985).	The rigid teaching of the 3:1 ratio produced from a monohybrid cross (Mertens 1992).	The rigid teaching of ratios is detrimental to students' understanding of the role of chance in the process of inheritance (Hackling and Treagust 1984).	Students may expect precise phenotypic ratios for a particular trait in a population. However, due to the random nature of inheritance and the existence of evolutionary forces, this will almost certainly not be the case.
		The Hardy-Weinberg principle (Radford and Bird-Stewart 1982; Mertens 1992).	Principles such as this are necessary for the understanding of evolutionary theory (Radford and Bird-Stewart 1982; Mertens 1992).	
Differentiation between the processes of growth and inheritance, mitosis and meiosis	Lack of understanding the segregation of genes and chromosomes during meiosis.	Gametes contain both of the genes at a locus and both of the chromosomes from the parents body cells (Hackling and Treagust 1984; Browning and Lehman 1988).	An understanding of meiosis impacts on students' ability to solve monohybrid and dihybrid crosses (Browning and Lehman 1988).	Students may be unable to solve applied problems in quantitative genetics.
		Students seldom connect the process of meiosis and the use of punnet squares (Cavallo 1996).	Punnet squares may be used without thinking of the probabilistic nature of meiosis (Cho <i>et al.</i> 1985).	

A number of potential sources have been postulated for various learning difficulties experienced by certain genetics students (Longden 1982; Radford and Bird-Stewart 1982). These include teacher factors, student factors, the syllabus and time constraints, textbooks, terminology and the mathematical and abstract nature of many concepts in genetics, all of which may also be applicable to this investigation.

**(a) Teacher factors**

Some high school teachers, who teach certain topics in genetics, lack confidence and competence in these topics, and themselves hold a variety of alternative conceptions. In addition, they are unable to recognise the relevance of genetics to the curriculum (Longden 1982; Cakiroglu and Boone 2002). Furthermore, it is thought that the type of questions posed in examinations may perpetuate certain errors made by students (Radford and Bird-Stewart 1982). It is also possible that some teachers construct test and examination questions with the aim of simply grading the students and not necessarily to evaluate or ensure a clear understanding of key concepts.

**(b) Student factors**

It is important to note that students are not always able to integrate new knowledge with existing ideas and to thereby learn in a meaningful manner. As the principles of quantitative genetics are founded on other foundational modules such as transmission genetics, mathematics and statistics, students must be able to understand the basic principles of these modules before they can learn the more applied concepts. An added problem is that many students do not reach a sufficient level of attainment in these foundational modules. This level of attainment may include conceptual knowledge as well as certain skills (Longden 1982).

**(c) Syllabus and time constraints**

The syllabus and the sequence in which concepts are introduced may also hinder student learning (Eylon and Linn 1988). For example, Mendel's Laws are usually presented in historical order and therefore require students to have a simultaneous grasp of the ideas of segregation, diploidy and dominance (Radford and Bird-Stewart 1982). In addition, most introductory modules in genetics do not consider topics such as the genetics of continuously varying traits (quantitative inheritance). This is a serious omission as most traits of importance to the human population are of this kind (Radford and Bird-Stewart 1982). Students may thus hold the perception that the genetics content they learn is of no practical value (Mertens 1992).

Mitosis and meiosis are often taught one after the other and many students become confused between these two processes (Hackling and Treagust 1984). In particular, many

students lack an understanding of the segregation of genes and chromosomes during meiosis. 72% of the undergraduate students taking a biology module at Purdue University in the U.S.A (Browning and Lehman 1988) and 48% of the high school students studied in Perth Australia (Hackling and Treagust 1984) thought that gametes contain both genes at a locus and both chromosomes from the parent's body cells. Furthermore, Cavallo (1996) in an investigation on 189 10<sup>th</sup>-grade biology high school students in the U.S.A., found that students were seldom able to connect the process of meiosis and the use of punnet squares, with only 2% of students showing a meaningful understanding. Almost half the students, 44% illustrated a lack of any understanding and 11% gave rote-learned responses. This lack of understanding of the segregation of alleles during meiosis may impact on students' understanding of the mechanism by which variation is produced in offspring generations, an important focus of the present investigation. As quantitative genetics is primarily the study of phenotypic variation in populations, this type of difficulty may have repercussions on students' ability to learn in a meaningful manner in this advanced area of genetics.

#### **(d) Terminology**

Genetics has a large, complex and precise language in order to allow for the accurate exchange of ideas (Longden 1982; Bahar *et al.* 1999a). Some researchers have suggested that this complex terminology has lead to confusion between the terms gene, allele, chromatid and chromosome (Longden 1982; Pashley 1994; Moletsane and Sanders 1995; Lewis *et al.* 2000; Lewis 2004). In a study of first year university students' understanding of concepts in genetics, Sanders *et al.* (1997) observed that students struggled with the vocabulary used in genetics and that some students confused the terms "mitosis" and "meiosis". It must also be noted that in an African context where second language students are taught genetics in English, their use of everyday English words is not always accurate. For example, Sanders and Sebego (1995) found, in a study of over 300 high school students in Botswana, that the words, "weak" and "less" were sometimes used as synonyms. In addition, the cultural background of students has been shown to influence students' views of certain biological concepts such as inheritance. Furthermore, confusion between look-alike and sound-alike words such as homologue, homologous, homozygote and homozygous has been documented (Bahar *et al.* 1999a).

#### **(e) Textbooks**

Textbooks have been identified as the origin of many difficulties and alternative conceptions as they are used as major sources of information (Cho *et al.* 1985; Martinez-Gracia and Gil-Quilez 2003) and students tend to rely on them and believe what they read

in textbooks (Barrass 1984). Some reasons for confusion which may arise from the use of textbooks may be:

- The illogical sequence in which topics are introduced.

Concepts such as meiosis and genetics are frequently treated separately in textbooks so that the relationships between them is not clearly emphasised (Cho *et al.* 1985). A similar situation occurs in the areas of population and quantitative genetics where these two topics are placed in separate chapters or even separate books (Cooper 1998). From an experts point of view there are a number of clear distinctions between the two areas, whilst for the novice these distinctions will be difficult to understand and may contribute to learning difficulties (Cooper 1998).

- Incorrect use of terminology.

In many textbooks ambiguous and incorrect use of genetic terminology is encountered. For example, the terms "allele" and "gene" are often used interchangeably (Radford and Bird-Stewart 1982; Cho *et al.* 1985; Journet 1986; Pearson and Hughes 1988). Pearson and Hughes (1988) also noted the use of different terms to incorrectly refer to the same concept, for example, "no dominance" and codominance", which are totally different forms of dominance, where the heterozygote is distinct from either of the homozygotes. In addition, symbols are often not used consistently by teachers and textbook writers (Bahar *et al.* 1999a). An example of this is that the symbols "A" and "BV" are both used to symbolise the breeding value of an individual in some quantitative genetics textbooks.

- Instructional format.

Regrettably, textbooks and current methods of instruction tend to emphasize the ability to generate correct answers through memorisation and not the exploration of questions using critical thought processes (Stewart 1988; Johnson and Stewart 1990). As a consequence textbooks urgently require critical revision to encourage meaningful learning and to thereby facilitate understanding of genetics in the 21<sup>st</sup> century (Martinez-Gracia and Gil-Quilez 2003).

**(f) Mathematical and abstract nature of genetics**

Transmission, population and quantitative genetics, all characterized by their dependence on numerical measurements, require a certain level of numeracy and a more analytical approach than other aspects of biology (Radford and Bird-Stewart 1982; Mertens 1992; Bahar *et al.* 1999a; Ortiz *et al.* 2000). A dislike of mathematics and a fear of incompetence regarding the mathematical components of some fields of genetics may therefore impair the ability of certain students to learn (Longden 1982; Browning and Lehman 1988). In both the United Kingdom and United States of America, mathematics is viewed by many

students as a series of disconnected, standard procedures which may simply be memorised. However, memorisation of procedures is insufficient if situations require a decision about which procedures should be used. An inability to do this leads to failure and thus a fear of ineptitude (Boaler 2002). Journet (1986: 478) suggests that students have difficulty with population genetics and the Hardy-Weinberg principle because of a "lack of understanding of the mathematics of probability and the symbolism of binomial expansion." As quantitative genetics is traditionally taught in terms of mathematical models and equations are used to define certain principles, Cooper (1998) also identified the reliance of quantitative genetics on a mathematical framework as a barrier to successful learning outcomes in this field.

Some genetics students view genetic ratios as deterministic and not probabilistic (Cho *et al.* 1985). This may be due to the rigid teaching of the 3:1 ratio produced from a monohybrid cross when there is complete dominance (Mertens 1992) which detracts from students' understanding of chance in the process of inheritance. For example, Hackling and Treagust (1984) found that 27% of the high school students which they interviewed thought that three-quarters of the children from any  $F_1$  cross will show the dominant phenotype. Only 8% of these students understood the role played by chance in the process of fertilization. Similarly, Browning and Lehman (1988) when analysing undergraduate students' problem-solving performance, found that 27% of the students in their study assumed that, when considering a single locus there would always be a 3:1 phenotypic ratio irrespective of the allele frequencies of the population under consideration.

Topics in genetics exist on three different levels, the MACRO level of observations of morphological traits of living things, the SUB-MICRO level of genes and alleles and the SYMBOLIC level where concepts are represented by symbols and mathematical equations. Students, unlike experts in the field, initially find it extremely difficult to operate on all three levels, and in particular have difficulty with the complex and precise symbolic representation and language used in genetics (Longden 1982; Bahar *et al.* 1999a). Similarly, Lawson *et al.* (2000) described three types of scientific concepts: *descriptive*, which can be observed (e.g. an organism), *hypothetical*, which cannot be observed due to time constraints (e.g. evolution) and *theoretical* which are abstract in nature (e.g. gene). These researchers point out that the more concrete concepts should be introduced first to students, followed by hypothetical and finally theoretical concepts; a procedure very seldom followed. This is of particular importance as it has been postulated by some researchers that, as discussed by Journet (1986), up to 50% of introductory biology students are concrete-operational thinkers. As such these students are not able to comprehend abstract symbolism and may respond by resorting to a method of rote-

learning. These students may consequently show limited understanding of subject areas such as quantitative genetics.

Along with investigations into student difficulties with genetics, numerous research studies have been conducted to investigate and identify specific alternative conceptions which may be held by students studying foundational principles of genetics. Particular attention will be given to the area of transmission or Mendelian genetics as it is most applicable to this investigation (also see Section 1.4.1).

### 1.4.3 Alternative Conceptions in Genetics

Numerous studies on the presence of alternative conceptions in the physical sciences have been conducted. However, research in the biological sciences is still emerging (Driver 1989; Duit 2004). Wandersee *et al.* (1994) describe much of the literature on studies in the biological sciences as being focused on four subject areas: concepts of life, animals and plants, the human body and reproduction, genetics and evolution. In the field of genetics the emphasis of research into the presence of alternative conceptions has focused on students' knowledge of the rules and patterns of inheritance (transmission genetics) and subsequently the structures, processes and mechanisms of inheritance (cytogenetics and molecular genetics) and evolutionary genetics (Lewis 2004).

In the area of cytogenetics and molecular genetics, studies such as those conducted by Hackling and Treagust (1984) and Lewis (2004) found incidences of 65% and 59% respectively, of the conception that cells only contain the information they require to perform their function. This alternative conception illustrates that these students did not associate mitosis with growth and that they have a limited understanding of gene regulation. In addition, Lewis *et al.* (2000) found that 25% of the 482 school children between the ages of 14 and 16 believed that genes only occurred in certain tissues such as reproductive organs and the blood. Furthermore, some students have thought that chromosomes are either male or female (Lewis 2004). From a South African perspective, Moletsane and Sanders (1995) found that out of 185 first-year university students studying Biology at the University of the Witwatersrand, only 19% illustrated a sound understanding of chromosomes, whilst one fifth and one third illustrated a meaningful understanding of chromatids and homologous chromosomes, respectively. However, a review of the literature suggests that studies of this type have limited influence on students' understanding of quantitative genetics.

Numerous studies of students' understanding of the applied field of evolution have been conducted. This is because evolution is considered a cornerstone in the science of biology

and is seen to provide a unifying framework for most biological knowledge (Keown 1988; Soderberg and Price 2003). Numerous alternative conceptions regarding the process of evolution and particularly natural selection, have been identified (Brumby 1984; Greene 1990; Anderson *et al.* 2002) in both high school and university students and the concept of natural selection and its role in evolution has been identified as being difficult for students to understand (Desmastes *et al.* 1995). The primary difficulties are: firstly, that evolution is a single, gradual process and not both a random process that generates variation as well as a non-random process of survival where genetic variation is decreased primarily by natural selection. Secondly, some students hold a typological view of populations in that they do not consider the variation between individuals in a population and where they tend to think an entire species or population changes because of some need. This conception was found by Greene (1990) in 48% of undergraduate students taking a biology module at an American university. Thirdly, evolution is seen as a change in the traits of individuals themselves and not the relative proportions among individuals (Brumby 1984; Greene 1990; Alters and Nelson 2003; Soderberg and Price 2003). Furthermore, a Lamarckian view on the inheritance of acquired characteristics was held by most of the 150 1<sup>st</sup> year medical students at an Australian university (Brumby 1984) and by 21% of high school students (Lawson and Thompson 1988) and 17% of a total of 322 undergraduate students answering questions on natural selection (Greene 1990). With regard to another evolutionary force, that of mutation, Cho *et al.* (1985) found that all three of the textbooks under investigation referred to mutations as being rare, harmful and recessive, an inappropriate conception subsequently held by many students. Notwithstanding the fact that evolution is concerned with changes in allele frequencies over time, student difficulties in this area are not considered as relevant to quantitative genetics. This is because natural selection, for example, is a result of an interaction between the phenotypes of individuals and their environments. In contrast, artificial selection, as discussed in this thesis, is a methodology purposefully employed to alter the mean phenotypic value of an entire population, thereby improving the performance of individuals under specific environmental conditions. The other evolutionary forces of mutation, migration and genetic drift have no bearing on the concepts under investigation in this study.

When considering students' understanding of transmission genetics, many alternative conceptions concerning the nature and inheritance of genes have been found in various student groups. For example, 38% of high school pupils interviewed in the U.S.A considered dominant alleles to be more powerful than recessive alleles (Hackling and Treagust 1984). Furthermore, some students cannot understand that different forms of genes (alleles) explain the occurrence of different forms of a trait, they do not think of a gene in terms of information used to program the development of a given feature (Hackling and Treagust 1984; Lewis *et al.* 2000). In addition, students in both England and Germany

held the conception that genes and traits are equivalent and that inheritance of a trait is due to the transfer of unchanged features (traits or genes) between generations. In fact, 73% of these students did not understand the mechanism of inheritance (Lewis 2004). This may be due to a comparison with everyday experiences of receiving goods intact (inheriting goods) from an older generation (Lewis 2004). Regrettably, this conception that genes and characteristics are equivalent may lead students to think of the genotype and phenotype as acting on the same level thereby avoiding the abstract nature of a genotype (Lewis 2004) That some students consider genotypes and phenotypes to be equivalent was evident in a study conducted at a university in the U.S.A. where 37% of the 135 undergraduate students confused these concepts (Browning and Lehman 1988). These perceptions could most certainly interfere with students understanding of quantitative inheritance where the phenotype is determined by both genes and the environment.

Of particular interest is that the two primary mechanisms of inheritance, qualitative and quantitative inheritance, are frequently not fully understood by students. For example, some students equate differences between individuals for continuously varying traits (quantitative traits) with environmental influences and discontinuous variation purely with genetic differences (Radford and Bird-Stewart 1982). Moreover, few students understand that many genes can influence one trait. This lack of awareness of polygenic inheritance is undesirable as many important human traits are inherited in a quantitative manner (Hackling and Treagust 1984; Plomin and Walker 2003). It seems that very little research has been conducted on students' understanding of concepts in the area of quantitative genetics, a component of genetics which should receive attention as it considers the causes of the continuous variation observed in most economically important traits.

Notwithstanding the limited research that has been conducted in the area of the quantitative inheritance of traits, numerous investigations have been conducted in statistics with particular reference to students understanding of variation (Hammerman and Rubin 2004); the cornerstone of quantitative genetics (Radford and Bird-Stewart 1982).

#### **1.4.4 Student difficulties with statistics: their cause and possible impact on the learning of quantitative genetics**

The teaching and learning of statistics has pervaded all levels of education (Broers 2002). A possible reason for this is that in almost every discipline, especially one such as quantitative genetics, the ability to understand, interpret and critically evaluate research findings is an essential core skill (Mills 2002). It is because all characteristics and



processes vary that there is a need for statistics and a need to deal with variation. This is achieved through numerical measurements and the analysis of the resultant data for any patterns that may exist (Meletiou-Mavrotheris and Lee 2002). Variation or variability is therefore a fundamental component of statistics theory and practice (Ben-Zvi 2004; Ben-Zvi and Garfield 2004; Garfield and Ben-Zvi 2005; Pfannkuch 2005). Consequently, many authors believe that variation should be emphasized at all levels of statistics instruction, from the earliest grades through to university (Ballman 1997; Garfield and Ben-Zvi 2005; Makar and Confrey 2005) as uncertainty is a characteristic of reality (Meletiou-Mavrotheris and Lee 2002). However, the concept of variation has been found to be notoriously difficult for students to understand (Hammerman and Rubin 2004; Garfield and Ben-Zvi 2005).

Batanero *et al.* (1994) gave some possible reasons for the difficulties encountered when teaching statistics. These include the requirement of proportional reasoning, which students find difficult, the existence of false intuitions and a distaste for statistics because it, like mathematics, has been taught in an abstract and formal way. Furthermore, it has been postulated that some difficulties may be due, in part to the instructional neglect of the core concept of variation (Meletiou 2000) and the lack of understanding of graphical distributions (DelMas and Liu 2005; Makar and Confrey 2005). The causes of students' difficulties with statistics, including recommendations for overcoming these difficulties are summarised in Table 1.2.

Table 1.2 indicates that a statistics curriculum with a focus on graphical literacy and with variation at its core may help students studying applied courses, such as quantitative genetics, which depend on an understanding of concepts of random variation. Therefore, it is thought that concepts such as variation of a single random outcome, the difference between large and small sample size variation, and the properties of a normal distribution curve, should be covered in an introductory statistics course (Ballman 1997). A study conducted during an introductory statistics module at a university in the United States, with variation at its core, confirmed this view as the majority of these students not only emphasized measures of centre, but also took the overall spread of the data into account and demonstrated a sound understanding of the standard deviation (Meletiou-Mavrotheris and Lee 2002).

Table 1.2: Sources of student difficulties in statistics.

Cause of difficulty	Problem observed	Implications	Suggested improvements
The “formalist” method of teaching in science, particularly mathematics.	A perceived detachment from any real context and a reliance on axioms and principles and not on understanding (Meletiou 2000; Broers 2002; Garfield 2002; Makar and Confrey 2005).	This has led to the view that statistics is simply a branch of mathematics which requires the memorisation of formulas and procedures (Meletiou-Mavrotheris and Lee 2002). However, knowledge of a computational rule does not mean that there is any level of conceptual understanding (Bakker 2004; Hammerman and Rubin 2004). In fact it may inhibit the acquisition of further conceptual knowledge (Batanero <i>et al.</i> 1994).	Statistical education should move away from a mathematical and probabilistic approach, to a constructive one where the students collect their own data, create their own models of variation, produce graphical displays and design their own experiments (Ballman 1997; Tappin 2000).
People often consider the population as a whole when making judgements on the probability of an event.	Students show no sensitivity to sample size (Tversky and Kahneman 1974). People tend to believe that things should ultimately balance out to better represent the population distribution (Tversky and Kahneman 1974; Garfield 2002).	Students hold a perception of pattern in essentially random data. An example of this would be an individual with a moderately high breeding value for a particular characteristic. If this individual has a string of inferior progeny, people will tend to think the next offspring must be better.	Statistics must be taught in context for it to have any true meaning for students (Meletiou-Mavrotheris and Lee 2002; Garfield and Ben-Zvi 2005; Makar and Confrey 2005).
A propensity to think of individual cases rather than groups of individuals (Konold <i>et al.</i> 1997; Bakker 2004; Hammerman and Rubin 2004; Makar and Confrey 2005).	An inability to understand population measures such as the mean and measures of central tendency such as the standard deviation. These are difficult for students to understand as being representative of the entire data set (Bakker 2004; Hammerman and Rubin 2004).	The conceptual move from seeing data as individuals to recognising that grouped data has properties that do not apply to individuals is required for students to understand population statistics such as the mean and variance of a population.	Students must have a personal experience of variation (Konold 1995). A curriculum with variation at its core would facilitate the understanding of population statistics (Meletiou-Mavrotheris and Lee 2002).

<p>Students measure the spread of data independently of a reference point, for example, the mean (Loosen <i>et al.</i> 1985; Ben-Zvi 2004).</p>	<p>Students understanding of <i>measures of variation</i>, such as the standard deviation, are determined <b>only</b> by the ability to calculate the value using a particular procedure (DelMas and Liu 2005) or as a characteristic shape in a distribution (Bakker 2004; Makar and Confrey 2005).</p>	<p>In order for students to have some meaningful understanding of the standard deviation they must perceive that a histogram depicts one variable and the frequency of its possible values, understand the concept of a mean as well as the idea of values deviating from the mean (DelMas and Liu 2005).</p>	<p>Graphical distributions should be used to provide a visual structure with which students are able to conceive the aggregate features of data sets (Bakker 2004; Pfannkuch 2005) such as measures of centre and variation (Ben-Zvi 2004). For example, the idea of middle clumps, “hills” or “bumps” can be used by students in developing a sense of average (Bakker 2004; Ben-Zvi 2004). The distribution should also provide a visual representation of the variation in a data set (Makar and Confrey 2005).</p>
<p>Many students cannot relate variation to graphical representations, such as histograms.</p>	<p>Students perceive histograms as displays of raw data where each bar stands for an individual value. In addition, students may also interpret histograms as two-variable scatterplots (Meletiou and Lee 2002; Lee and Meletiou-Mavrotheris 2003).</p>	<p>Some students when shown two histograms, judge the relative variation by the variation in the heights of bars – the “bumpiness” of the graph (Meletiou and Lee 2002; Lee and Meletiou-Mavrotheris 2003; DelMas and Liu 2005) rather than the density of data around the mean.</p>	<p>The interpretation of graphical representations requires a degree of diagrammatic reasoning (Bakker 2004) and a level of “graphical literacy” where students are familiar with the signs and symbols used (Roth 2002). Teaching strategies which address the graphical understanding of students is required.</p>
<p>The neglect of the identification of variation and uncertainty and the recognition that a sample is never totally representative of the population from which it was selected (Biehler 1997; Meletiou-Mavrotheris and Lee 2002).</p>	<p>The majority of research has focused on students’ understanding of the study of centres and randomness at the expense of variability (Loosen <i>et al.</i> 1985; Batanero <i>et al.</i> 1997). A reason for the focus on the study of the understanding of centres may have been because centres are used to predict what will happen in the future and to make comparisons between groups. The incorporation of variation into these predictions may have been thought to confound people’s ability to make the required comparisons and predictions (Shaughnessy 1997).</p>	<p>Knowledge of such measures of variation enables the interpretation of research results (DelMas and Liu 2005) and the ability to comprehend applied areas of statistics such as quantitative genetics.</p>	<p>A statistics curriculum with variation at its core may therefore help students studying applied courses, such as quantitative genetics, which depend on an understanding of concepts of random variation. Therefore, concepts such as variation of a single random outcome, the difference between large and small sample size variation and the properties of a normal distribution should be covered in an introductory statistics course (Ballman 1997).</p>



The aspects of variation that students taking a module in quantitative genetics need to be aware of include: that variation is present in any population, graphical representations may be used to visualise variation, summary statistics may be utilised to describe populations and it may be necessary to partition the variation inherent in populations in order to make comparisons between populations. The manner in which these factors impact on students' understanding of the quantitative inheritance of many traits is summarised in Table 1.3.

**Table 1.3: Importance of variation in a quantitative genetics curriculum.**

Aspect of variation	Relevance to quantitative genetics
Variation is omnipresent; it is everywhere and in everything. This variation is what makes it difficult to make predictions. It is sometimes difficult to determine all the causes of variation (Wild and Pfannkuch 1999).	The phenotypic variance of a trait is made up of variation due to genetic effects and environmentally induced variation (Falconer and Mackay 1996). Variation is also introduced by data collection; errors of measurement, random sampling and accidentally introduced variation. By examining the variables it may be possible to explain the reasons for the different sources of variation (Garfield and Ben-Zvi 2005).
Graphical representations of data show visually how things vary, and different numerical summaries indicate the aggregate features of the data, such as variability and centre which may be represented by the standard deviation and mean respectively (Garfield and Ben-Zvi 2005).	Students must understand why traits inherited in a quantitative manner are normally distributed. In addition they must understand that the ability to alter the mean of a population in a breeding programme is dependent on the standard deviation of the population under consideration.
Summary statistics may be more effectively used to make comparisons between data sets than individual data points (Garfield and Ben-Zvi 2005).	Breeders need to make comparisons not only between individuals but also between populations.
In normal distributions, knowledge of the standard deviation allows the estimation of the percentage of individuals within one, two or three standard deviations of the mean (Garfield and Ben-Zvi 2005).	This is crucial to quantifying what percentage of the population has a phenotype of interest.
There is variation in chance events and it is sometimes possible to link the variability in samples to variability in outcomes, thereby making predictions (Garfield and Ben-Zvi 2005).	In quantitative genetics it may be possible to predict the type of offspring that may be produced by a certain individual from knowledge of its breeding value (Bourdon 2000).
Statistics may provide some means of partitioning and understanding the variation inherent in any population (Wild and Pfannkuch 1999; Garfield and Ben-Zvi 2005).	Such a statistic used in quantitative genetics is the heritability of a trait which aids in the partitioning of the genetic and environmental sources of variation (Falconer and Mackay 1996).

### **1.4.5 Concluding remarks**

The literature indicates that many students experience difficulty with numerous concepts in the disciplines of genetics and statistics and may develop certain alternative conceptions. Furthermore, it is evident that many of the problems which students have been shown to experience in these disciplines may impact on their understanding of the foundational principles of quantitative genetics.

## **1.5 RESEARCH AIMS**

In response to the many documented conceptual and reasoning difficulties students encounter with statistics, in particular variation, there has, in the last decade, been a move towards changing the manner in which statistical concepts are taught and presented to facilitate a deeper understanding (Meletiou 2000). Unfortunately, this drive to gather empirical evidence of student difficulties, in order to devise more effective teaching strategies, has not extended sufficiently to the application of statistics and the concept of variation in quantitative genetics, with only limited research being done in this area (Cooper 1998). This investigation thus aimed to fill this void in the research literature by determining the difficulties and alternative conceptions experienced by students in the area of quantitative genetics and developing and evaluating teaching strategies to overcome these difficulties.

The diagnostic phase of the research aimed to assess the status of students' conceptual frameworks and to empirically establish third-year South African university students' difficulties with, and alternative conceptions about, introductory principles of quantitative genetics, with particular reference to the concepts of variance and heritability. For this purpose valid, reliable diagnostic tools were developed to ascertain the knowledge held by students at the beginning and the completion of a module in quantitative genetics.

The remediation phase of the research aimed to develop and assess teaching and learning strategies that could be employed to address students' alternative conceptions and graphical reasoning difficulties in an introductory module of quantitative genetics.

## **1.6 RESEARCH QUESTIONS**

The following research questions were asked during the diagnostic phase of the investigation:

1. What is the nature and extent of students' integrated knowledge and their ability to link key concepts of quantitative genetics?
2. Which concepts in quantitative genetics do students find difficult?
3. What is the nature of the difficulties experienced by students taking a module in quantitative genetics?
4. What are the possible source(s) of students' difficulties with quantitative genetics?

The remediation phase of the investigation aimed to answer the following questions:

5. What is an appropriate intervention strategy for use in a quantitative genetics module?
6. To what extent did the intervention assist students in the understanding of quantitative genetics?
7. What was the nature of the conceptual change which occurred during the module?

## **1.7 SUMMARY OF THE RESEARCH STRATEGY USED IN THIS INVESTIGATION**

A brief overview of the research strategy employed in this investigation is presented here. Comprehensive details of the methodology used are given in Chapters 3, 6, 7 and 8.

### **1.7.1 The diagnostic phase**

Five methods of data collection were used in this component of the investigation to answer the research questions. These were: student-generated concept maps, free-response probes, multiple-choice diagnostic tests, a word association study and interviews with selected students. More detail is given in Chapter 3.

**To answer research question 1:** Students were asked to draw concept maps at the commencement of the module and after the teaching of the majority of the module content in order to ascertain whether they were able to integrate their knowledge of quantitative genetics. Semi-structured interviews with selected students were conducted to further validate the findings from the student-generated concept maps. These results are presented in Chapter 4.

**To answer research question 2:** Written free-response probes were given to students to gather preliminary data on possible alternative conceptions held by students and to ascertain where they had difficulty understanding concepts. A process of inductive analysis of the answers given by students to the free-response probes was performed as described by McMillan and Schumacher (1993). Thereafter two multiple-choice diagnostic tests were developed using the protocol set out by Treagust (1988). The first multiple-choice diagnostic test was designed to evaluate students' knowledge on entry to a third-year module on quantitative genetics and the second the understanding of students at the completion of the module. Data gathered from students' answers given on the multiple-choice diagnostic tests was used to create a description of the difficulties and alternative conceptions held by students. The incidence and relative level of difficulty of each of the concepts probed was then determined. These results are presented in Chapter 5.

**To answer research question 3:** An inductive analysis of the reasons given by students for their answer choice on the multiple-choice diagnostic tests, the results of a word association study and interviews with selected students were used to determine the *nature* of the difficulties and alternative conceptions held by students. The results of this component of the investigation are given in Chapter 5.

**To answer research question 4:** All of the data gathered using the five research instruments were used in the construction of a model of the possible sources of students alternative conceptions using the protocol set out by Justi and Gilbert (2002). The model is given in Chapter 5.

### 1.7.2 The remediation phase

The intervention that was developed consisted of two teaching tools namely, computer-based tutorials and concept mapping, with the aim of determining whether it was possible to prevent or remediate the previously identified student difficulties with and, alternative conceptions about, quantitative genetics.

**To answer research question 5:** An intervention was developed and designed based on the results of the diagnostic phase as well as what the literature indicated to be requirements for effective teaching and learning of a discipline such as quantitative genetics. The intervention consisted of computer-based tutorials that were developed with the aim of assisting students to “visualise” key statistics used in quantitative genetics, namely variance and heritability, in the form of graphical representations. In addition, students were required to construct a series of concept maps during the teaching of the module.

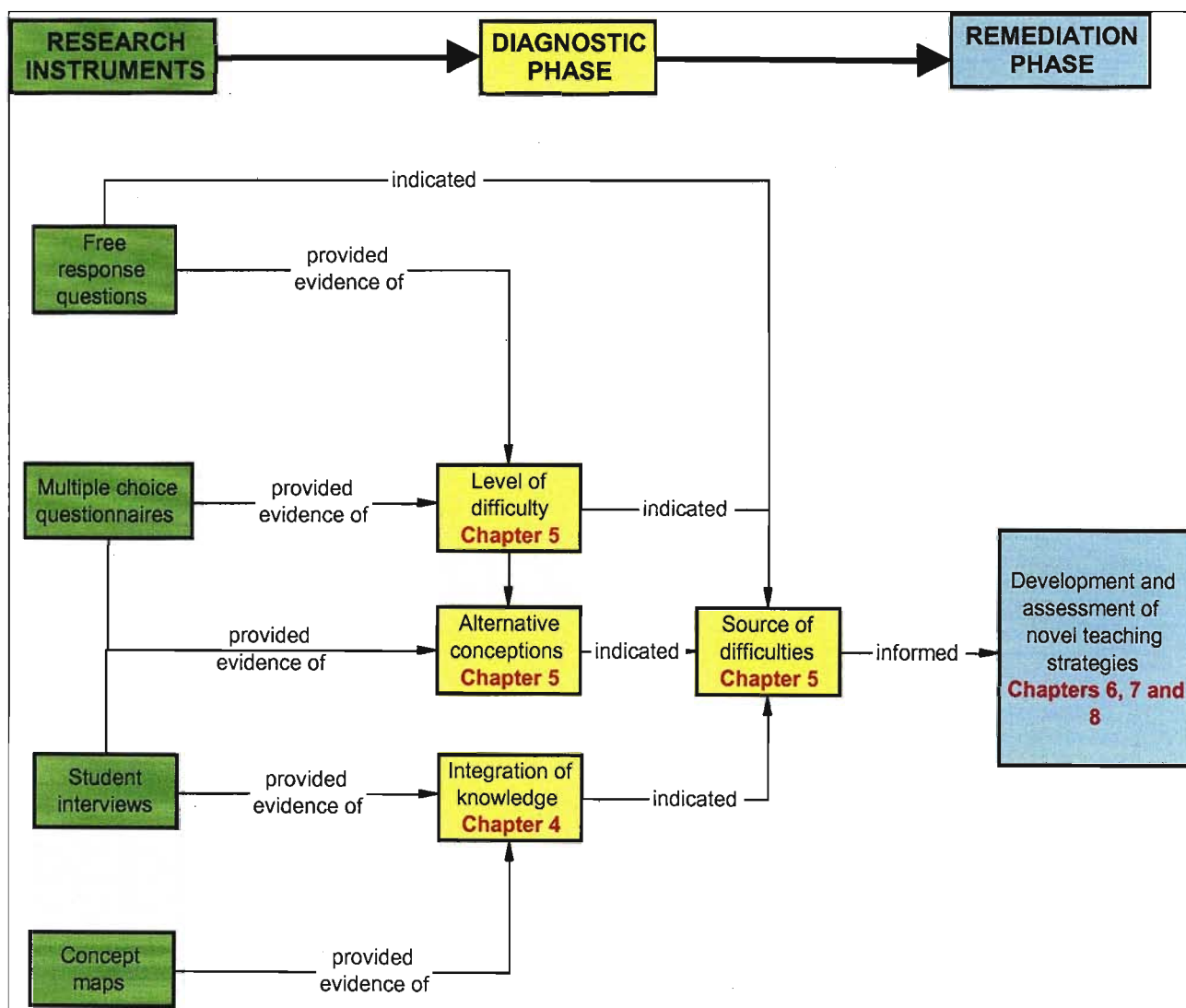
**To answer research question 6:** The diagnostic multiple-choice tests and interview protocols, developed during the diagnostic phase, were used to evaluate the effectiveness of the intervention.

**To answer research question 7:** Students were required to construct a series of concept maps using *Inspiration software* (1997) during the course of the module. These student-generated concept maps were used to monitor any epistemological and ontological conceptual change that occurred during the teaching of the module. Attitudinal questionnaires completed by the students provided information on any affective changes which occurred during the teaching process.

The development and design of the intervention employed is discussed in Chapter 6 and the results thereof are presented in Chapters 7 and 8.

An overview of the research instruments used in this investigation and the results obtained in the two phases of the research is given in Figure 1.1.





**Figure 1.1:** Diagram illustrating the instruments used in the process of data collection and the nature of the results obtained during this investigation.

## CHAPTER 2

# THEORETICAL, METHODOLOGICAL AND RESEARCH FRAMEWORKS OF THE INVESTIGATION

This chapter discusses the theories which underpin this investigation. The Oxford dictionary defines a theory as “an idea or set of ideas put forward to describe something”. The theories that are thus discussed in this chapter are: (1) a theory of learning to explain the occurrence of student difficulties and alternative conceptions, (2) the theory of quantitative genetics, the subject under investigation, (3) the theory of action research, the methodological framework and (4) the research paradigm or approach followed in this investigation.

### 2.1 THEORETICAL FRAMEWORK OF LEARNING: CONSTRUCTIVISM

A theoretical framework may be described as “an organising model for the research questions or hypotheses and for the data collection procedure” (Creswell 2003). A theoretical framework provides a theoretical lens or perspective through which an investigation may be viewed. A theoretical framework makes the assumptions made in the investigation implicit, assists in understanding the problem addressed in the research and why it occurs, provides a structure for the research questions, the research design chosen and the interpretation of the results. In this investigation, the theory of constructivism was seen to provide an appropriate theoretical framework to explain the occurrence of student difficulties and alternative conceptions in the field of quantitative genetics. The theoretical framework used in the design of the intervention (remediation phase) is discussed in Chapter 6.

#### 2.1.1 Historical perspective on the development of constructivism

For a large proportion of the 20<sup>th</sup> century, the study of education was founded upon the behaviourist theory of learning (Shuell 1987). Central to this theory was that

learning was the direct result of a stimulus (S) from the environment producing a response (R) from the organism. Repetition of the stimulus was then assumed to become associated with a particular response and thus learning took place (von Glasersfeld 1989; Novak 1993). However, psychologists later began to question the soundness of the behaviourist theory as a basis for learning as it could not explain how learners construct knowledge. In particular, the theory could not account for the idiosyncratic nature of knowledge construction (von Glasersfeld 1989; Novak 1993). Consequently, the constructivist view of learning was founded, based on the epistemology of the interpretive or *Verstehen* tradition (Driver and Oldham 1986). In contrast to previous learning theories, this tradition focused on the meanings constructed by individuals during their attempt to make sense of the world (Driver and Bell 1986).

Constructivism is in direct conflict with the traditional behaviourist theory in that the learning process is considered to be far more than merely a series of passive automatic responses to external factors (Driver and Bell 1986; Driver and Oldham 1986; Shuell 1987). According to the constructivist perspective that is based on the research of school psychologist, Kelly, which was published in 1955, individuals actively and continuously reflect on their own unique experiences and thereby construct an idiosyncratic understanding of the world we live in (Gilbert *et al.* 1982; Driver 1989). In this way humans create their own mental models which they utilise to make sense of new experiences. Learning, as seen from a constructivist viewpoint, can therefore be defined as the revision and modification of one's conceptual frameworks to accommodate new experiences (Driver 1989; von Glasersfeld 1989; Mintzes and Wandersee 1998).

A founder of constructivist theory, Jean Piaget, proved to have a remarkable influence on science education with his theory of "genetic epistemology", a stage theory of cognitive development (Eylon and Linn 1988). He described the reasoning of children under approximately twelve years of age as being governed by concrete, observable phenomena. He postulated that a qualitative shift in the way learning occurred happened sometime during adolescence where individuals became capable of abstract or formal thought (Eylon and Linn 1988). Piaget's research led him to understand that learning is a biological process characterised by successive periods of assimilation, accommodation and equilibrium (von Glasersfeld 1989). However, he primarily emphasized general cognitive functions and did not take into account differences between individuals due to differences in context and prior knowledge (Mintzes and Wandersee 1998).

Following the work of Piaget, Bruner (1960) proposed that learning takes place in a spiral fashion, with learners constantly building on their prior knowledge. Furthermore, he proposed that science should be taught as a process of engaging students in active scientific inquiry where students ask questions, make observations and develop conclusions. In this way science could not be accepted as a series of empirical, literal and irrevocable truths (Mintzes and Wandersee 1998). The work of Kelly, published in a book entitled *The Psychology of Personal Constructs* viewed learning as a process which built on an existing grid of personal constructs (see Cohen *et al.* 2000 for an overview). Neither of these researchers however, recognised that the acquisition of knowledge may involve not only the building on of new ideas to existing ideas, but also the reorganisation and replacement of previously held conceptions. In addition, they did not emphasize the presence of concepts and propositional frameworks which may exist in the cognitive structure.

Ausubel's cognitive assimilation theory (1968) had a profound influence on our understanding of the influence of what a learner already knows on future learning. He proposed that *meaningful learning* occurs when new ideas are incorporated into students' cognitive frameworks in a systematic fashion and where the process of rote-learning is not utilised. Three criteria must be met before meaningful learning can take place:

- The material must have potential meaning to the learner and not be, for example, a list of symbols;
- The learner must possess relevant concepts on which to anchor new ideas; and,
- The learner must actively incorporate knowledge in a systematic and meaningful way.

According to Ausubel (1968) if these criteria are not met then the learner may resort to rote learning; the accumulation of isolated propositions rather than a hierarchical framework of knowledge. This in turn may lead to a poor retention of knowledge and the inability to retrieve ideas in order to solve novel problems.

Novak (1971) stated that much of Ausubel's theory of meaningful learning can be explained by what he called subsumption. Pearsall *et al.* (1997) explain that *subsumption* is the linking of new, specific ideas to more general existing propositions thereby leading to a gradual increase in domain specific knowledge. Furthermore, according to Novak (1971), Ausubel postulated that *obliterative subsumption* may take place where learning significantly modifies existing general propositional knowledge. *Superordinate learning* then occurs when more general,

inclusive and powerful concepts are acquired that override existing ideas in a students' framework. This type of learning has been described as "paradigm shifts" (Novak 1977; Mintzes and Wandersee 1998).

Two further ideas developed by Ausubel are useful for describing changes that occur during meaningful learning. The first is *progressive differentiation*, which is the gradual elaboration and clarification of the meaning of concepts that occur during subsumption and superordinate learning (Novak 1977; Pearsall *et al.* 1997). Progressive differentiation results in learning occurring at higher hierarchical levels in the mind of the learner and the development of highly dendritic knowledge structures. The second is *integrative reconciliation* which involves the learner forming cross connections between concepts and identifying similarities and differences between concepts (Novak 1971, 1977; Pearsall *et al.* 1997; Mintzes and Wandersee 1998).

The importance of the affective facet associated with meaningful learning was highlighted by von Glasersfeld when he expounded his ideas on radical constructivism. von Glasersfeld viewed science as merely a world of idealised abstractions. Furthermore, social interaction is thought to aid in the synthesis of personal knowledge. Accordingly, von Glasersfeld advocates that teachers should have an understanding of how their students view the world, the students' alternative conceptions and what they already know, before they can influence their future learning (von Glasersfeld 1989, 1992). For example, each learner may have a different meaning, based on his own experience, for a particular word. As learning is based on words, this will influence all future interpretations of a concept. The teacher must thus be able to change, add to, or reinforce what students already perceive to be correct to promote meaningful learning (von Glasersfeld 1989, 1992; Tobin and Tippins 1993).

In line with the thinking behind von Glasersfeld's theory, Lave and Wenger (1991) developed a theory of situated learning. In this case, learning is seen as a result of the interrelationships between the person, their culture, language and the context in which new material is presented. It is postulated that each person's knowledge of a concept continually evolves every time it is used in novel situations and contexts (Brown *et al.* 1989). Therefore a practice of cognitive apprenticeship whereby teachers introduce students to novel ideas or contexts by making their knowledge explicit and assisting students in attempting a task before empowering them to work independently, is thought to provide a means of promoting meaningful learning (Collins *et al.* 1991). During the process of cognitive apprenticeship students are guided and supported out of their "comfort zone" or "zone of competence" (referred to



by Vygotsky as the “Zone of Proximal Development”) thereby building on their existing knowledge (Bockarie 2002).

Novak’s view of constructivism, termed *human constructivism*, attempted to marry all of the above-mentioned theories. Novak (1993) states “knowledge has structure, a history of creation and affective connotations”. This view is however, principally influenced by the work of Ausubel in that Human Constructivism, advocates the theory of meaningful learning, including the ideas of subsumption and superordinate learning. Furthermore, Novak concurs that the ideal product of learning should be a highly hierarchical, branched, interconnected set of cohesive concepts which form the cognitive framework of an individual. However, Novak expands and improves on Ausubel’s theory by integrating the knowledge derived from Ausubel’s cognitive theory of learning as well as from an expansive epistemology, with a set of valuable tools that can be used by science educators and knowledge builders to promote meaningful learning (Mintzes and Wandersee 1998). In this regard, knowledge of the difficulties experienced by students is deemed necessary for informing the manner in which a subject should be taught. It is logical to assume that teachers should thus have knowledge of what makes learning of certain topics easy or difficult as well as conceptions that students bring with them to the classroom. This is one aspect of what is known as pedagogical content knowledge (Shulman 1986).

### **2.1.2 Influence of constructivist ideas on the interpretation of research conducted in genetics education**

The current information explosion has made it impossible to teach or learn all of the knowledge contained within any discipline. In fact, many students may later be required to understand and apply knowledge which had not yet been discovered during their formative years. It has thus been said that the most critical educational task of current society must be to teach students a set of basic procedural skills, primarily problem-solving skills (Smith and Good 1984; Slack and Stewart 1990; Georghiades 2004a). Consequently, increasing the problem-solving abilities of students has become a major focus of mathematics and science educators (Stewart 1982, 1988) who consider that situating the conceptual knowledge of a discipline within the context of problem solving allows students the opportunity to develop a highly structured understanding of the conceptual knowledge of the discipline, general and domain-specific problem-solving strategies as well as insights into the intellectual nature of the discipline (Stewart 1988; Hafner and Stewart 1995; Stewart and Rudolph 2001). The investigations that have been conducted in the field of

genetics education therefore include research into the teaching and learning of the structure and content of genetics, as well as research which has focused on students ability to solve problems in a genetics context (Eylon and Linn 1988; Lewis 2004). The manner in which the notions behind constructivism have influenced research in the discipline of genetics is summarised in Table 2.1. (Further details of the research studies cited in Table 2.1 are provided in Appendix 2 on page 293.)

The research literature (Table 2.1) thus indicates that: (1) the ability to think in terms of abstract ideas (formal thinking) is necessary for successful problem-solving in genetics, (2) students actively involved in their own learning are better able to develop sound conceptual and procedural knowledge, (3) students must possess relevant concepts on which to anchor new ideas and they must choose to incorporate knowledge in a systematic and meaningful manner and, (4) knowledge is an idiosyncratic, hierarchically organised framework of concepts that are interrelated in the mind of the individual. As the human constructivist view of constructivism embraces all of these principles, it was considered an appropriate theoretical framework for this investigation into students' understanding of quantitative genetics and is discussed more fully below.

Table 2.1: The influence of constructivism on the interpretation of research in genetics education.

Constructivist ideas of Leading Theorists	Relevant research findings in genetics education	Implications for the teaching and learning of genetics
<p><b>Jean Piaget: Stage Theory of Genetic Epistemology</b></p> <p>Students at a certain cognitive level of development cannot understand concepts that require formal reasoning abilities achieved only at later stages of development.</p>	<p>Researchers working within this theoretical framework have concluded that formal thought processes such as combinatorial reasoning, propositional logic and the use of probabilistic reasoning, not found in concrete-operational students, are all necessary for the understanding of the underlying principles of genetics and the ability to effectively solve many types of genetics problems (Gipson <i>et al.</i> 1989). Furthermore, Lawson and Thompson (1988) postulated that whereas students capable of formal reasoning are able to reflect on a naïve conception which they may possess, and replace that conception with a scientifically accepted view, students at the concrete-operational stage will retain both views.</p> <p>Smith and Suthern Sims (1992) argue that formal reasoning abilities are not an absolute necessity but rather are merely conducive to successful problem solving in genetics. These researchers believe that formal-operational students are more easily able to perceive “theoretical” or abstract concepts such as a gene and an allele, than concrete-operational students who are only able to relate to more physical and observable entities such as a trait, a phenotype and a chromosome.</p>	<p>Concrete operational students retain two contradictory ideas, the use of which will be largely unpredictable and based on irrelevant problem cues, possibly causing some misconceptions in the biological sciences. In addition, concrete-operational students may be unable to connect the information learnt in two different, but linked, fields of study, such as population and quantitative genetics, and are often therefore incapable of finding solutions to problems in these subject areas (Lawson and Thompson 1988; Cooper 1998).</p> <p>With the aid of perceptual props, such as illustrations, diagrams and models, even concrete-operational students may be assisted in the task of problem solving in genetics (Smith and Suthern Sims 1992). However, in the fields of population and quantitative genetics, the frequency of various allelic forms of a gene in the gene pool, for example, have to be abstracted using formal symbols. Furthermore, mathematical logic is frequently required for higher-order operations such as multiplication. In these circumstances, formal thought may therefore be deemed a requirement for successful problem solving in these sub-disciplines of genetics (Smith and Suthern Sims 1992).</p>
<p><b>Jerome Bruner: Discovery or Active Learning</b></p> <p>Because learners construct new ideas based on their current knowledge, science should be taught as a process of active inquiry.</p>	<p>Numerous researchers have made use of problem solving software in the instruction of high school pupils where the students were encouraged to solve problems from effects to causes (phenotypes to genotypes). Whilst attempting to solve this type of problem it was not possible for the students to automatically apply algorithms, but they had to propose a hypothesis and apply diverse resolution strategies. In the process of model revision the students thus had to evoke a previous model, test the model and then evaluate their findings. Thereafter the model had to be continually revised until the students felt that it fitted the data (Slack and Stewart 1989; Johnson and Stewart 1990; Hafner and Stewart 1995; Finkel 1996; Johnson and Stewart 2002). This form of learning was shown to enhance the problem-solving abilities of students.</p>	<p>Successful problem solving is encouraged by strategies which detect anomalous data by using existing models as templates, the revision of the existing models to account for the anomalous data and then the assessment of the model revisions in relation to their ability to explain the phenomena under consideration (Hafner and Stewart 1995; Johnson and Stewart 2002). During the process of this form of problem-solving students use their metacognitive knowledge whilst keeping track of their progress and planning what they intend to do next as they discuss their findings with peers (Finkel 1996).</p> <p>Stewart and Hafner (1991) proposed that students should be encouraged to learn how to generate data, for example how to choose parents to produce certain offspring. Furthermore, that students' should recognise that all models have constraints. Finally that students should be shown that models may be correlated as they share certain components, for example pleiotrophy and epistasis. Models may also be linked so as to produce a larger model. An example is the elaboration of the initial model of one gene determining one trait, to the idea of many different genes determining the phenotype of a particular trait; quantitative inheritance (Stewart and Hafner 1991).</p>



Constructivist ideas of Leading Theorists	Relevant research findings in genetics education	Implications for the teaching and learning of genetics
<p><b>David Ausubel: Meaningful learning</b></p> <p>The material to be learned must have potential meaning to the learner and not be, for example, a list of symbols. The learner must possess relevant concepts on which to anchor new ideas.</p> <p>The learner must choose to incorporate knowledge in a non-arbitrary, non-verbatim manner.</p>	<p>Students can never be considered blank slates beginning with zero knowledge and awaiting the receipt of current scientific understanding (Gilbert <i>et al.</i> 1982; Novak 1993). Many of the ideas which students bring to the classroom are erroneous from a scientific point of view and are termed alternative conceptions (Eylon and Linn 1988; Fisher and Moody 2000; Cakiroglu and Boone 2002). Research findings of alternative conceptions in genetics are summarised in table 1.2.</p> <p>Meaningful learning orientation (whether students approach learning in a meaningful manner) and reasoning ability have been found to be positively related to student understanding (conceptual knowledge) and problem solving ability (procedural knowledge) (Cavallo and Schafer 1994; Cavallo 1996). Furthermore, research has ascertained that knowledge which is acquired by a process of rote learning cannot be used in problem solving and is quickly forgotten (Novak 1977).</p> <p>Stewart (1983) conducted an investigation on 27 high school biology students in the United States of America with the aim of describing the specific steps (procedural knowledge) that biology students use when solving basic cause-effect Mendelian problems. Surprisingly, the researchers found that although many students could solve the various problems, acting merely as information processors, following certain algorithms, they had very limited understanding of the conceptual knowledge of genetics.</p>	<p>The implications of this type of research are presented in table 1.2.</p> <p>These results imply that there are two different aspects of knowledge which are required for understanding genetics, firstly, whether students approach learning in a meaningful manner (meaningful learning orientation) or practice a system of rote learning and secondly, whether the students are capable of formal or concrete reasoning (Cavallo 1996). It is important to note that whereas aptitude is considered a fixed variable, both meaningful learning orientation and reasoning ability are variables which can be developed and improved in students (Cavallo 1996). Thus learning of scientific principles may not be restricted by the aptitude of a student, but rather by the manner in which they learn (Cavallo and Schafer 1994).</p> <p>Marinez Aznar (2005) confirmed that the reproduction of an algorithm (a form of rote learning) does not mean that the student understands the knowledge involved. Therefore, as cause-effect problems can usually be solved algorithmically they do little to promote conceptual learning (Stewart 1988).</p>
<p><b>Josef Novak: Human constructivism</b></p> <p>Knowledge is an idiosyncratic, hierarchically organised framework of concepts that are interrelated.</p>	<p>Smith and Good (1984) found that successful problem solvers possessed large “chunks” of functional information which was organised in a hierarchical fashion. Further research into the problem-solving behaviour of individuals indicated that successful problem solvers took time to engage in qualitative planning and used a reasoned analytical strategy with a knowledge development approach (Smith and Good 1984; Simmons and Lunetta 1993; Thompson and Stewart 2003).</p>	<p>Good problem solvers are able to link salient information, whereas weak problem solvers cannot link or integrate related ideas (Eylon and Linn 1988).</p> <p>Slack and Stewart (1989, 1990) suggest that students require a bigger picture of genetics where certain conceptual relationships are clarified. For example, the relationships between the concepts of a gene, an allele, a trait and variation need to be made explicit. This is necessary as students often refer to a trait when they mean variations of a trait. They need to think of a trait as a variable concept determined by different allelic forms of genes. Furthermore, the researchers suggest that qualitative thinking should be encouraged.</p>

### **2.1.3 Human Constructivism: A theoretical framework for this investigation**

The human constructivist view of learning was developed by Josef Novak with the aim of creating a “theory of education”, the principles of which could be used to guide researchers in education (Novak 1998). In this regard, Novak (1993) ascertained that the psychological process by which professionals in a field assemble new knowledge and the cognitive processes that facilitate the creation of new meaning in a novice learner are fundamentally the same. The foundation for this assertion is that all individuals construct meanings out of experiences through the formation of associations between novel concepts and those that are already part of an individual’s existing cognitive structure. According to adherents of human constructivist notions, the creation of new knowledge, in the form of an elaborate set of language symbol systems is uniquely human and is one of the most significant adaptations of humans as a species; hence the term Human Constructivism (Novak 1993; Mintzes and Wandersee 1998). Accordingly, a discipline such as mathematics is simply a result of human activity and a tool to help humans to make sense of the world (Confrey 1990). However, notwithstanding the conformity of the process of knowledge assimilation, Human Constructivists assert that no two individuals can construct exactly the same meanings even when shown the same objects or events. Furthermore, Novak (1993) postulated that as a consequence of the innumerable different manifestations of inter-concept relationships held by different individuals, each individual will possess his or her own idiosyncratic conceptual hierarchy of concepts.

As a consequence of the idiosyncrasy of the human cognitive structure, knowledge as held by each individual cannot be faithfully conveyed between teachers and students. The process of learning has the potential to occur only because of a sufficiently shared commonality between the cognitive frameworks of different individuals. As explained by Bockarie (2002), Vygotsky viewed teaching and learning as being integrated processes where students are actively involved in their own learning and where language facilitates the interactions between teachers and their students. Thus language and the ideas which teachers and students have in common, allow for communication, discussion, enhancement and even the modification of meanings. Education can then be seen as an endeavour to ‘bridge’ the differences in meaning among people with teachers acting as mediators (Mintzes and Wandersee 1998). Furthermore, Human Constructivists acknowledge that learners are capable of conceptual change and suggest that teachers have a responsibility to extend the boundaries of students’ knowledge, obviously within the

reasonable margins of the learners' capability (Novak 1993; Mintzes and Wandersee 1998).

The investigation described in this thesis has been conducted from a concept learning perspective. This has been explained by Eylon and Linn (1988) as a perspective where the focus is on knowledge content and structure and where prior knowledge is recognised as being central to further learning. Accordingly, the theory of Human Constructivism has been chosen as the theoretical framework of this investigation as it is based on the premise that meaningful learning is seen to occur when knowledge is incorporated into an individual's cognitive structure in a non-arbitrary, non-verbatim, substantive manner and when a deliberate effort is made to link new knowledge to higher order, more inclusive concepts (Pearsall *et al.* 1997). Learning was therefore assumed to be related to experiences with objects or events and that there must be an affective commitment to relate new and previously held knowledge. Furthermore, the theory of Human Constructivism was applicable as it focuses on the process whereby concepts are understood, which involves the acquisition or modification of concepts and concept relationships, thereby providing insight into students' conceptual change over time. In addition, the theory accounts for the almost infinite number of permutations of concept-concept relationships that give rise to the great variation we see in individual conceptual frameworks. Furthermore, language is recognised to play an important role in the human acquisition of meanings for concepts (Novak 1993). The relevance of the principles of human constructivism to this investigation is presented in Table 2.2.

**Table 2.2: Relevance of Human Constructivism to this investigation.**

Human constructivist principle	Relevance to this investigation
Human constructivism is a theory of learning and an epistemology of knowledge construction.	It provides a framework for the determination of alternative conceptions held by students and the development and evaluation of tools which could be used to promote conceptual change.
Knowledge is idiosyncratic.	Students may hold different conceptions of the same idea, some of which are erroneous from a scientific point of view. This investigation aimed to determine the nature of these conceptions.
Knowledge is built up slowly by a process of assimilation to form a hierarchically organised framework of interrelated concepts. Radical restructuring of knowledge may also occur, resulting in conceptual change.	The status of students' knowledge on entry to a module (their prior knowledge) was ascertained so that its influence on the subsequent learning of concepts in quantitative genetics could be monitored. The hierarchal assimilation of knowledge over time was evaluated using student-generated concept maps.
Knowledge is not a transmission of ideas about real world objects or events that can be faithfully communicated from one person to another or something to be gained thorough direct observation.	This is particularly true of concepts in quantitative genetics which are abstract in nature.
The construction of a framework of conceptual knowledge requires the active connection of new to existing knowledge and testing it against ones perceptions of real world objects, events and knowledge constructed by others.	An understanding of the foundational principles of statistics and genetics, and the relationships between them, is required for an understanding of concepts in quantitative genetics.
Concept meanings are constructed using language and symbols.	The terminology of genetics is highly complex and symbols are extensively used. This may influence the ability of students to learn.
Teaching approaches should involve active participation, intensive interaction and thoughtful reflection.	Computer-assisted learning encouraged the active participation of students in their own learning. Concept mapping was used as a metacognitive tool.
The focus of education should be on quality not quantity and understanding, not memorisation.	The key concepts of variance and heritability, students understanding and the teaching thereof, were the focus of this investigation.

## 2.2 THEORETICAL FRAMEWORK OF SUBJECT AREA: QUANTITATIVE GENETICS

Students' ability to learn in a meaningful manner has been widely researched in many subject areas. This investigation aimed to specifically investigate student difficulties and alternative conceptions in the area of introductory quantitative genetics. The scientific concepts of quantitative genetics therefore represent the theoretical phenomena through which the learning process was viewed in this investigation.

### 2.2.1 Course content of modules used in this investigation

Two modules taught by the researcher at the University of KwaZulu-Natal incorporate all the key components of introductory quantitative genetics and were considered suitable for addressing the proposed research questions. These modules were *Introduction to Quantitative Genetics* (Genetics 332), a third year module taught during the first semester and *Introduction to Animal Breeding* (Genetics 350), a third year module taught during the second semester.

An introductory module in quantitative genetics taught at the University of KwaZulu-Natal would include the following:

- An introduction to quantitative inheritance and its relationship to Mendelian genetics;

In this regard, students are made aware that unlike traits inherited in a Mendelian manner, quantitative traits are affected by many genes. Furthermore, students learn that the expression of these traits is highly variable and when a frequency distribution of the phenotypic values is constructed, a continuous, normal distribution results;

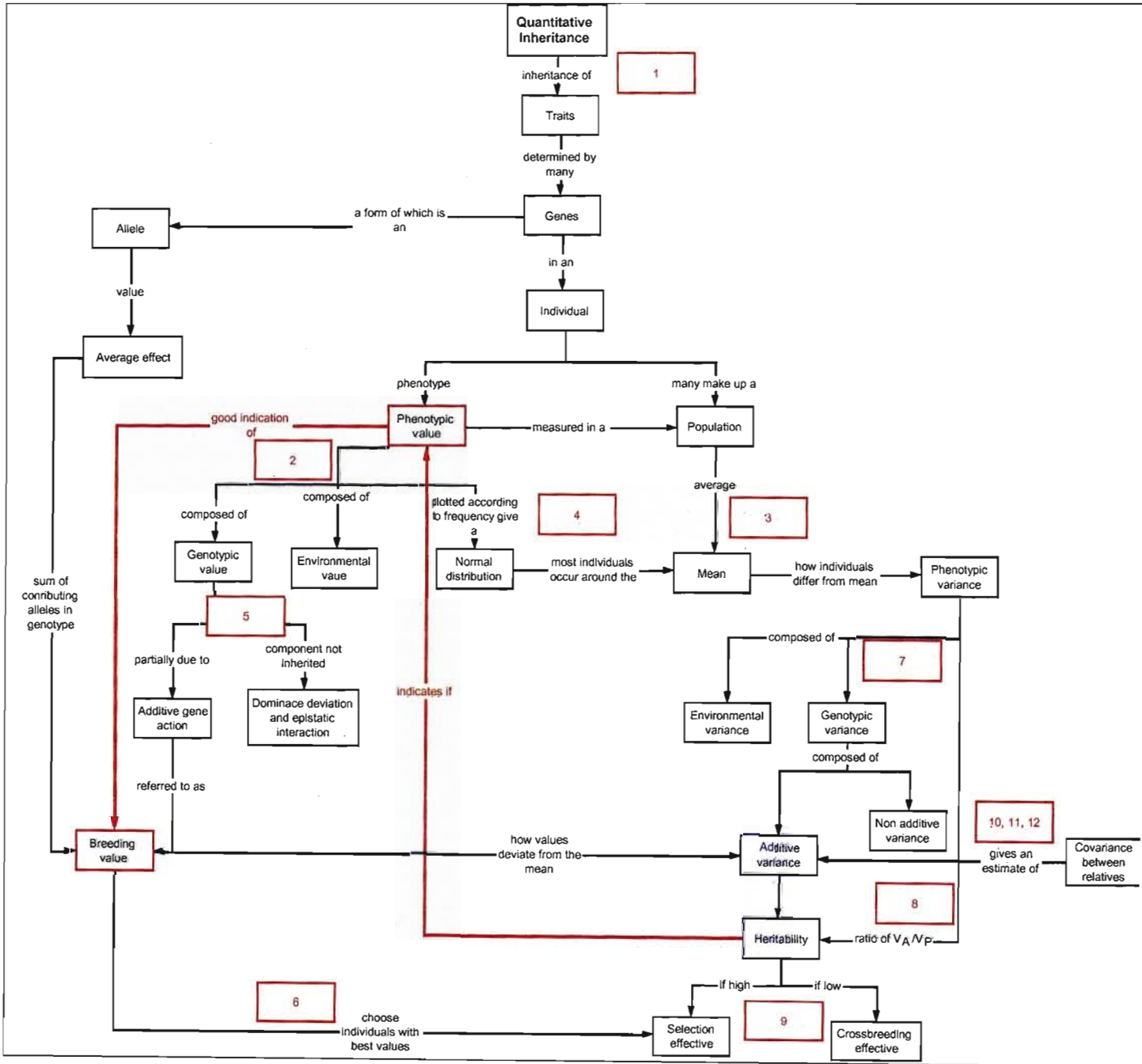
- The composition of the phenotypic value of individuals;
- The composition of the phenotypic variance of a population;
- The calculation of the additive variance from the resemblance between groups of relatives;

In this regard students learn that relatives “share” or carry the same form of certain alleles and that consequently relatives resemble one another. Students further learn that this degree of resemblance may be quantified in terms of the covariance, the covariance being directly proportional to the additive variance.

- The calculation and meaning of heritability; and;
- The application of heritability in the determination of an appropriate breeding strategy.

A concept map prepared by the researcher which indicates the relationships between the primary concepts taught in a quantitative genetics module at the University of KwaZulu-Natal is given in Figure 2.1. The concept map highlights how the values associated with individuals are linked to population parameters by statistics such as the mean and variance. The concept map (pathway highlighted in red) further shows that notwithstanding the fact that heritability is a population measure, it does nevertheless indicate the relationship between certain characteristics of individuals as well as the selection of an appropriate breeding strategy.





The pathway highlighted in blue shows how the statistic heritability is calculated.

The pathway highlighted in red indicates the central role of the concept of heritability and its applications.

**Figure 2.1: Concept map highlighting the relationships between key concepts taught in a typical introductory module of quantitative genetics.**

**(a) Differences between qualitative and quantitative inheritance**

Introductory modules of genetics, worldwide, traditionally begin with a consideration of the inheritance of traits such as the presence or absence of horns in cattle, which are determined by single genes. This type of inheritance is commonly referred to as “Mendelian” or “qualitative inheritance”. The study of traits inherited in a Mendelian manner is relatively straight forward as a single gene gives rise to only a limited number of genotypes and to discrete phenotypic classes. It is thus usually possible to infer the genotypes of individuals from their appearance (phenotype) thereby identifying those with a desirable genetic makeup (Snustad and Simmons 2003).

In contrast, the appearances of traits, such as yield or weight, which are inherited in a quantitative manner, are determined by many different genes in an individual. In addition, the expression of these traits is also influenced by the environment (Lynch and Walsh 1998). For example, in the case of crop yield, the phenotypic value of an individual (its yield) would not only be determined by genes at numerous loci, but also by temperature, soil fertility and other environmental factors. Quantitative traits are therefore multifactorial, producing a wide range of phenotypes in the population, so that it is difficult to discriminate one phenotypic class from another (Falconer and Mackay 1996). Consequently, if the phenotypic values of a trait, like yield of a particular crop, are represented graphically as a frequency distribution, a continuous normal distribution results. When considering such traits it is thus not possible to infer the genotype of an individual from its phenotypic appearance.

The study of quantitative traits is of paramount importance to plant and animal breeders as it is these traits that are related to economically important production traits such as yield and fertility. However, the multifactorial nature of quantitatively inherited traits is problematic for breeders as it is generally not possible to identify genetically superior individuals from their appearance; the genotype cannot be inferred from the phenotype. Therefore, the inheritance of these traits cannot be studied using classical Mendelian methods (Snustad and Simmons 2003). As a result, extensive statistical methodology has been developed for the study and utilisation of these traits in breeding programmes.

**(b) Quantitative inheritance: values associated with individuals**

The aim of any plant or animal breeder is to improve or alter the mean value of a population for traits of economic importance. The reason for this is that most individuals in a population will have phenotypic values that are close to the mean value. A breeder will thus aim to improve the value of the majority of individuals in a

population and not just a select few (Bourdon 2000). The simplest breeding strategy is that of individual selection where genetically superior individuals are chosen to be the parents of the next generation based on their own phenotypic values. If successful these genetically superior individuals will contain desirable genes that will be passed onto the next generation, thereby improving the population mean of the next generation (Bourdon 2000). However, the problem with quantitative traits is that the phenotypic value (P) of an individual is not always a good indication of their genetic merit as the phenotypic value is composed of a genetic component (G) and a component due to the effect of the environment (E). The composition of the phenotypic value may be represented by the following equation, given in Figure 2.2.

<b>P = G + E</b>	
<b>P:</b>	The phenotypic value, e.g. a performance record. This value is directly measurable.
<b>G:</b>	The genotypic value, i.e., the effect of an individual's genes, singly and in combination. It is the value of an individual's genes to its own performance and is not directly measurable.
<b>E:</b>	The environmental value. This value includes all non-genetic factors affecting the performance of a trait and is not directly measurable

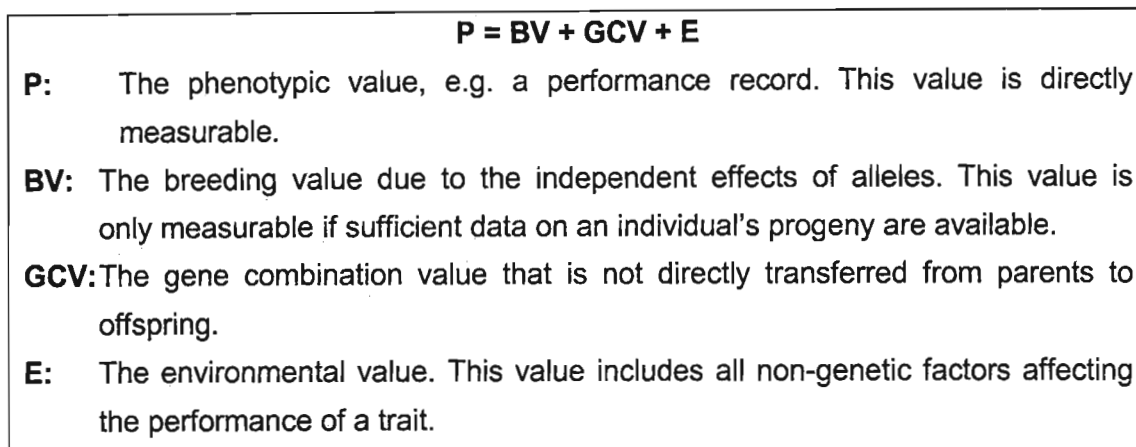
**Figure 2.2: Composition of the phenotypic value of individuals, when considering a quantitative trait.**

Individuals may thus have desirable phenotypic values merely due to a positive environmental effect and not an advantageous genetic makeup. For example, a person may be slim not because of their genetic make-up, but because they watch what they eat. It is therefore not possible to use the method of individual selection for traits that are largely influenced by the environment as the phenotype of individuals will not act as a reliable guide to the genetic makeup of the individuals. In such cases, it will not be possible to identify genetically superior individuals to be the parents of the next generation.

An added complication is that not all of the genotypic value is heritable. The breeding value of an individual (BV) is interpreted to be that part of the genotypic value that is due to the independent effects of alleles that are transferred from parents to offspring. The remainder of the genotypic value (GCV: gene combination value) is due to the effects of genes in combination including, dominance (allelic interactions at one locus) and epistasis (allelic interactions between loci). These effects are broken up and reformed each generation and are thus not directly transmitted from



parents to offspring (Bourdon 2000). A more detailed description of the phenotypic value of an individual is thus given by the model in Figure 2.3 (Bourdon 2000).

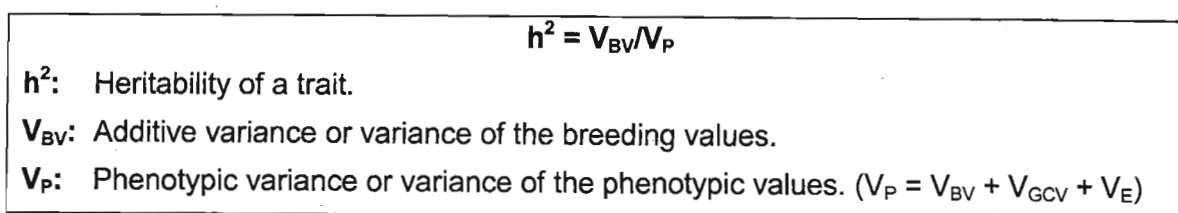


**Figure 2.3: Detailed description of the phenotypic value of an individual when considering a quantitative trait**

Breeders are therefore more specifically interested in the breeding value of individuals as this will indicate the type of offspring which they are likely to produce on average. As it is not possible to directly infer the breeding value of individuals from their phenotypic values, a statistic termed "heritability" is used to indicate the relative contributions of the different genetic components and the environment. The heritability of a trait informs breeders whether, on average, the phenotypic values of individuals may be used to infer their breeding values (Lynch and Walsh 1998).

**(c) Quantitative inheritance: heritability a population statistic**

Heritability is calculated as the proportion of additive genetic variance (variance of the breeding values,  $V_{BV}$ ), to the total phenotypic variance ( $V_P$ ) (Falconer and Mackay 1996). The phenotypic variance may be calculated directly from the phenotypic values of individuals in the population under consideration. However, the additive genetic variance must be calculated from information on the degree of resemblance between groups of relatives (Lynch and Walsh 1998). The narrow sense heritability is therefore calculated as indicated in Figure 2.4.



**Figure 2.4: Calculation of heritability**

The heritability of a trait therefore indicates to what extent the **differences** that are observed in individual performances are due to inheritance of the independent additive effects of the alleles of genes that are passed from parents to offspring. The heritability thus measures the proportion of differences in phenotypic values for a trait that are attributable to differences in the breeding values for the trait (Lynch and Walsh 1998). It answers the question “Are the differences that we observe in performance, primarily due to differences between the breeding values of individuals in a population or are they due to the environment?” If the breeding values in a population vary in the same manner as the phenotypic values (heritability estimate close to one) then it may be further inferred that the phenotypic values must be similar to the breeding values. In such cases, the phenotypic value can be used to **ESTIMATE** the breeding value of an **individual within that population** as,  $h^2 P = BV$  (Falconer and Mackay 1996).

Heritability is therefore a measure of the strength of the relationship between the phenotypic values and the breeding values for a trait in a population. As such, the heritability measures the degree to which offspring can be expected to resemble their parents for a trait. When a trait is highly heritable, the performance of individuals reveal a lot about their breeding values i.e., the expected performance of their offspring. A trait with a high heritability predicts that high performing parents will have high performing progeny and low performing parents will produce low performing progeny. Consequently, for traits with high heritabilities it will be possible to identify individuals with the most desirable genetic makeup to be parents of the next generation. In such cases, individual selection will then be an effective breeding strategy (Bourdon 2000). In contrast, traits with a low heritability such as fertility will show a poor response to individual selection (Lynch and Walsh 1998). This is because the phenotypic value may largely be determined by environmental effects, such as the individual's health and nutritional regime. These traits may, however, also be improved by utilising mating systems such as inbreeding and crossbreeding (Bourdon 2000).

It must be noted that as the environmental and genetic effects will differ between populations, the heritability estimate for a trait is not fixed and will vary between populations. Heritability estimates will thus change according to the genetic variation in a population and the environment in which the population occurs.

Heritability may be considered the key concept in quantitative genetics as knowledge of the heritability of traits is not only used to decide upon the most appropriate breeding strategy for a trait in a population (Falconer and Mackay 1996), but is also

useful from an evolutionary point of view, when considering traits such as disease resistance, as it indicates how fast a population may change. From a medical perspective, many life threatening diseases, such as heart disease, are quantitative traits and the heritability estimate for the disease, indicates the relative influence of genetics and the environment. This is essential information when developing treatment options (Snustad and Simmons 2003).

### **2.3 METHODOLOGICAL FRAMEWORK FOR THE RESEARCH PROCESS: ACTION RESEARCH**

Historically, action research has been described as being participatory, collaborative and democratic in nature, with teachers focusing on the improvement of their own practice and not that of others. It was thus seen as a form of professional development and not as a means of adding to the theoretical knowledge base (Weston 1998). However, the term is currently more broadly used to refer to research which *may* involve collaboration, but which can be purely for personal purposes and which can also contribute towards scientific theory (Gall *et al.* 2003). Stenhouse (1979), cited by Cohen *et al.* (2000: 227), thus suggests that “action research should contribute not only to practice but to a theory of education and teaching which is accessible to other teachers”.

Cohen *et al.* (2000) described action research as a process whereby a researcher studies a problem in a scientific manner in an attempt to evaluate, improve and steer decision making in practice. The research is carried out by those who are affected by the problem to be addressed (participatory) and is conducted in a local context (contextualised). In the present investigation, the researcher studied her students' understanding of quantitative genetics with the ultimate aim of improving her own teaching practice. In addition, it was hoped that the research would provide empirical evidence of the success of certain teaching strategies that could be used by other teachers in the field of quantitative genetics.

The aims of action research are two-fold; to increase knowledge and to improve practice (Cohen *et al.* 2000). The knowledge gained from this study was in the form of empirical evidence of student difficulties with quantitative genetics (Chapters 4 and 5). The improvement of practice included the development and assessment of novel teaching and remediation strategies in an attempt to prevent or correct the identified difficulties (Chapters 6 and 7). As Wadsworth (1998) suggests, action, research, theory and practice are dependent on one another. In this investigation action was

taken as a consequence of knowledge gained and knowledge was seen to be required to solve problems encountered. As Cohen *et al.* (2000), Duit and Treagust (2003) and Gall *et al.* (2003) note research frequently fails to impact on practice. In this investigation action research was considered as an appropriate methodology as it aimed to bridge the gap between research and practice.

Cohen *et al.* (2000) stated that action research may be used to evaluate:

1. *The use of innovative teaching methods;*

In this investigation a novel approach to teaching quantitative genetics was developed which included the use of concept mapping and computer-assisted learning (Chapter 7);

2. *The effectiveness of applying an integrated approach to teaching and learning;*

An integrated approach was developed which included the use of formal lectures, group work and computer-assisted learning (Chapter 7);

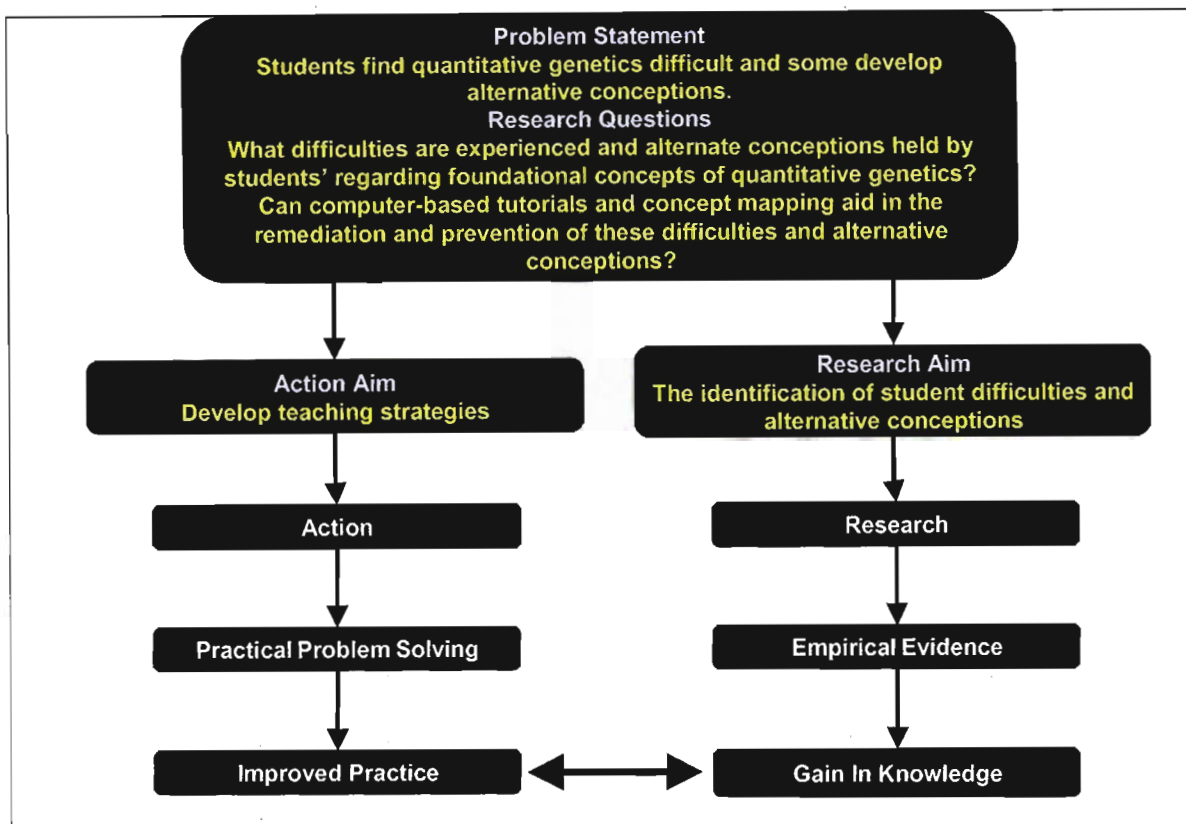
3. *Alternative methods of student assessment;*

Examples of alternative methods of assessment developed in the investigation included student-generated concept maps and multiple-choice diagnostic tests (Chapters 4, 5 and 7); and;

4. *Student attitudes to different teaching methods.*

In this investigation interviews with students, as well as diagnostic tests, shed light on attitudes towards novel teaching strategies (Chapter 7).

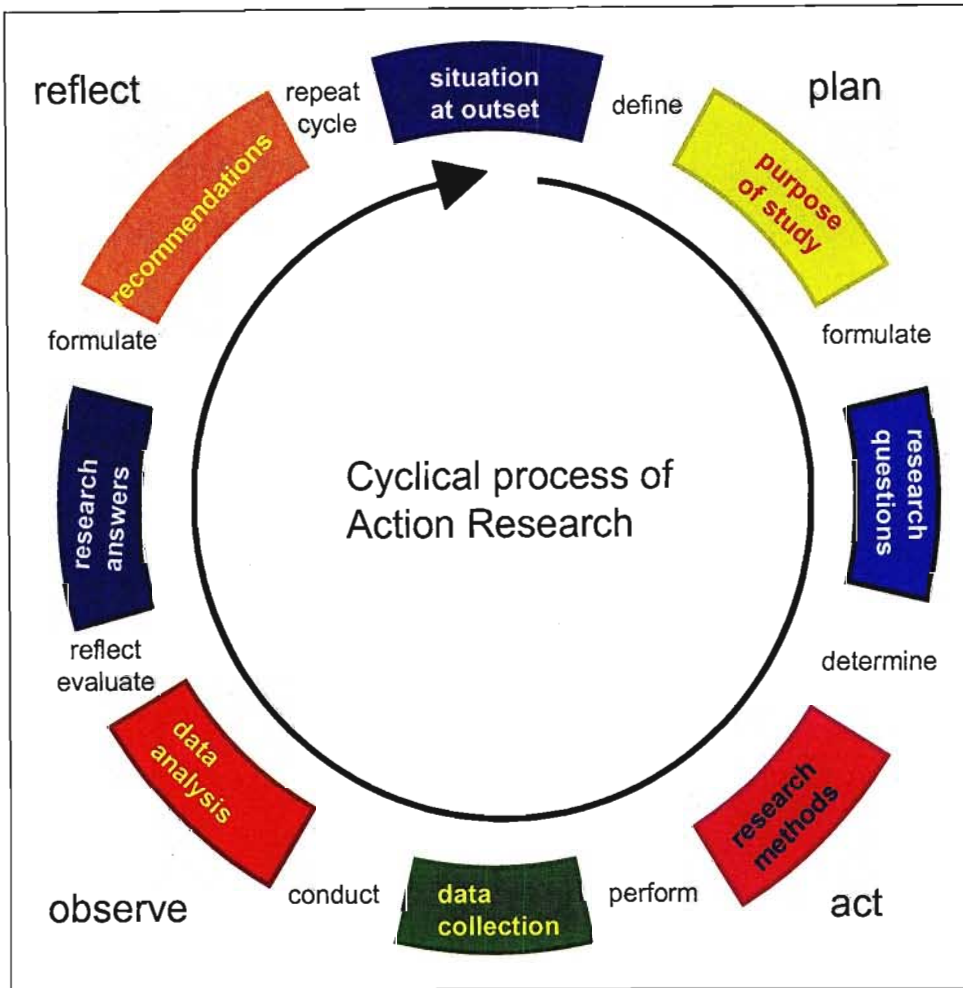
The relationships between the action and research components of the study are illustrated in Figure 2.5. Figure 2.5 highlights how, as suggested by Cohen *et al.* (2000), the research component of this investigation consisted of research planning, data collection, analysis of empirical evidence and evaluation of the results obtained, with an aim of expanding the scientific knowledge base of student difficulties in quantitative genetics. In contrast, the action component of the investigation consisted of planning of lectures and tutorials, implementation of practice, observation and reflection, with the aim of solving particular problems and reforming teaching practice.



**Figure 2.5: Representation of the inter-connected nature of the processes of research and action undertaken during this investigation**

The self-reflective cycle of the research process is illustrated in Figure 2.6. As is evident in Figure 2.6, action research is iterative in nature and involves repeated cycles of planning, action, observation and reflection or evaluation (Wadsworth 1998). The planning stage involves an analysis of the situation and the determination of the aims, research questions, methods of data collection and analysis. Thereafter the data are collected and analysed. The critical process of evaluation and reflection then occurs, during which answers to the research questions are found and recommendations for improvements made. This information may then lead to further cycles of research (Cohen *et al.* 2000; Gall *et al.* 2003).





**Figure 2.6: Cyclical process of action research.**

Action research, referred to by Gall *et al.* (2003) as “responsive action research”, typically involves two definite phases of research. The first phase is the diagnostic phase where problems are analysed and hypotheses developed. The second phase is a therapeutic stage where the hypotheses are tested using a consciously directed intervention (Cohen *et al.* 2000). The initial phase or diagnostic phase of this investigation involved the identification of specific difficulties experienced by students in the field of quantitative genetics (Chapters 4 and 5). The second research phase was then therapeutic in that teaching strategies were devised and tested to ascertain whether it was possible to prevent or remediate student difficulties with quantitative genetics (Chapter 7). It should be noted that within the diagnostic phase of the research certain stages were repeated several times, in an iterative manner in order to validate the research findings.

Gall *et al.* (2003) point out that a primary advantage of action research is that it allows the justification of educational work to others in the scientific community. They

claimed that one may justify the claims made by action research by showing that the evidence (data) was gathered in a scientific manner and that the analysis of the evidence was carried out as a process of critical reflection. However, during the process of critical reflection, the researcher has to always be aware of her own values, attitudes, perceptions, opinions, actions and feelings which would inevitably feed back into the situation under study, a precaution noted by Wadsworth (1998).

## 2.4 RESEARCH PARADIGM

A paradigm is described by Lincoln and Guba (1984) as a set of beliefs and their associated methods. Historically, there have been two established paradigms, namely the qualitative and quantitative paradigms.

Researchers within a quantitative method of inquiry believe in the scientific method (Creswell 2003) and strive for “objectivity, measurability and predictability” (Cohen *et al.* 2000: 28). This implies that the philosophical view held by such researchers is positivist in nature. Cohen *et al.* (2000: 8) claimed that positivism limits “inquiry and belief to what can be firmly established” and it thus abandons “metaphysical and speculative attempts to gain knowledge by reason alone”. Research within this paradigm thus focuses on measuring variables and determining the statistical relationship between them (Reeves and Hedberg 2003). Quantitative research usually begins with a hypothesis which researchers then attempt to verify or refute (Gall *et al.* 2003).

The qualitative paradigm, in contrast, is characterised by post-positivist beliefs which are “grounded in the assumption that features of the social environment are constructed as interpretations by individuals and that these interpretations tend to be transitory and situational” (Gall *et al.* 2003: 23). Proponents of a post-positivist view acknowledge the subjectivity of their research findings (Creswell 2003) and tend to use interpretative methodologies (Cohen *et al.* 2000). Subsequently, researchers within this paradigm investigate people in a particular context (Cohen *et al.* 2000) and use a process of inductive analysis of open-ended questions (Creswell 2003), the interpretations of which are expressed verbally (McMillan and Schumacher 1993).

A pragmatic perspective is more flexible than either the quantitative or qualitative paradigms, as within this paradigm the problem and not the methods are viewed to be of primary importance (Creswell 2003; Reeves and Hedberg 2003). As Cohen *et*

*al.* (2000: 73) stated: "the purposes of the research determine the methodology and design of the research process". In many instances it may then be deemed appropriate to use both quantitative and qualitative methods of data collection and analysis (Reeves and Hedberg 2003). Researchers within this paradigm recognise that attempting to gather data on a problem from multiple perspectives, making use of triangulation, may be beneficial and improve the validity and reliability of the research findings (Creswell 2003). In this way bias inherent in one method can balance or neutralise errors and bias from other methods (Reeves and Hedberg 2003). The characteristics of the three paradigms, as proposed by McMillan and Schumacher (1993), Cohen *et al.* (2000), Reeves and Hedberg (2001), Creswell (2003) and Gall *et al.* (2003) are tabulated in Table 2.3.

In this research the aim was firstly to gather empirical evidence of student difficulties and alternative conceptions and secondly to find practical solutions on how to overcome these difficulties. It was deemed appropriate to use a mixed-method, pragmatic approach to address these problems in their particular context (see Figure 1.1). During the diagnostic phase of the investigation, different methods were used sequentially to gather data on the problem. Initially free-response questions, which were open-ended in nature and analysed inductively, gave preliminary information on the nature of the problem and allowed the difficulties to be grouped into broad categories. Thereafter a multiple-choice questionnaire was developed to gather quantitative, more generalisable data on the difficulties and alternative conceptions. In addition, student-generated concept maps were analysed in a qualitative and quantitative manner to determine the level of integration of students' knowledge of quantitative genetics. Interviews with selected students enabled the researcher to further probe certain issues and gather qualitative data on the exact nature of the difficulties and the reasoning of students.

The remediation phase of the investigation used both qualitative and quantitative methods concurrently. The multiple-choice diagnostic tests were analysed quantitatively to determine the effectiveness of the computer-based tutorials. In addition, student-generated concept maps were analysed qualitatively and quantitatively to determine the extent of conceptual change that occurred during the teaching of the module. Survey-style diagnostic tests provided attitudinal data. In addition, interviews with selected students added depth to the data gathered from the other research methods and helped improve validity of the results.



**Table 2.3: Characteristics of the three paradigms.**

	<b>Quantitative</b>	<b>Qualitative</b>	<b>Pragmatic</b>
<b>Philosophical approach</b>	Positivist	Post-positivist or constructivist	Pragmatic
<b>Basis of inquiry</b>	Theory or a hypothesis	Data	Problem
<b>Typical strategy of inquiry</b>	Experimental	Narrative or ethnographic	Mixed methods
<b>Form of reasoning employed</b>	Deductive	Inductive	Both
<b>Nature of research</b>	Objective	Subjective	Both objective and subjective
<b>Research design</b>	Pre-determined	Emergent	Largely pre-determined but flexible
<b>Generalisability of results</b>	Yes	Limited to context of study	May be limited to context of study
<b>Sample</b>	Populations or random samples representative of populations.	Case studies and small samples.	Both
<b>Research methods employed and data collected</b>	Normative, using closed-ended questions. Numeric measurements of attitudes and aptitudes of students.	Interpretative using open-ended questions. Verbal data e.g. from interviews with students.	Both approaches used sequentially or concurrently.
<b>Data analysis</b>	Statistical methods	Analytical induction	Both

## CHAPTER 3

### DIAGNOSTIC PHASE: METHODOLOGY EMPLOYED

#### 3.1 DESCRIPTION OF STUDY GROUPS

The following three student groups, studying different modules at the University of KwaZulu-Natal, were used during the diagnostic phase of this investigation. The students were typically aged between 19 and 21 years of age and were completing an undergraduate science degree. Most students were majoring in genetics and as such were required to complete a module which included introductory aspects of quantitative genetics. The students who participated did not necessarily complete all of the three modules discussed below. However, it is important to note that students taking any of these modules must have completed modules in introductory genetics, mathematics and statistics at a tertiary level.

1. *Introduction to Population Genetics; Genetics 230.*

At the University of KwaZulu-Natal this module directly precedes modules in quantitative genetics. It was thus assumed that on completion of this module the status of students' knowledge would be the same as at the start of the quantitative genetics module; it would indicate the status of students' prior knowledge.

2. *Introduction to Quantitative Genetics; Genetics 332.*

Genetics 332 is a comprehensive module which covers all of the foundational concepts of quantitative genetics, including those discussed in section 2.2.1. Students taking this module were thus used to gather data on the status of students' preconceptions at the start of the module, as well as their conceptions after having been exposed to the principles of quantitative genetics.

3. *Introduction to Animal Genetics; Genetics 350.*

Genetics 350 is an applied module which is primarily concerned with animal breeding. As such, students taking this module are taught all the fundamental principles of quantitative genetics. These students were therefore able to supply further data on students' difficulties and alternative conceptions regarding quantitative genetics.

The diagnostic phase of the investigation was conducted over a three-year period. The number of students who were registered for each of the modules, the module used, the methodology employed, and the research questions addressed are summarised in Table 3.1.

**Table 3.1: Composition of study groups, methodology employed and research questions addressed.**

Year of study	Number of students	Genetics Module	Methods employed	Research Questions
2002 Semester 1	14	332	Free-response probes. Student-generated concept maps. Student interviews.	1,2,3,4
2002 Semester 2	40	230	Multiple-choice diagnostic tests.	2,3,4
2003 Semester 1	22	332	Multiple-choice diagnostic tests. Student interviews.	2,3,4
2003 Semester 2	29	350	Multiple-choice diagnostic tests. Student interviews.	2,3,4
2004 Semester 1	32	332	Multiple-choice diagnostic tests. Student interviews.	2,3,4

The researcher only had access to students taking modules at the University of KwaZulu-Natal, and the size of the classes dictated the sample size. Although the sample size was relatively small, the four different methods of data collection used enabled the identification of a wide range of student difficulties. In addition, data were collected over a three-year time period, which increased the reliability of the data.

In order to address the ethical issues of using students in this action research project, students were informed of the nature of the project and asked to sign an indemnity form in which they agreed to participate in the study. The students were assured that their identity would remain confidential, that they could withdraw from the study at any time and that the results of the study would not affect their grades in any way. It should also be noted that all data collected from students was stored and presented in a de-identified manner. All students consented to participate in the study. A copy of the document which the students were asked to sign is provided in Appendix 3 on page 297.

### 3.2 RESEARCH INSTRUMENTS

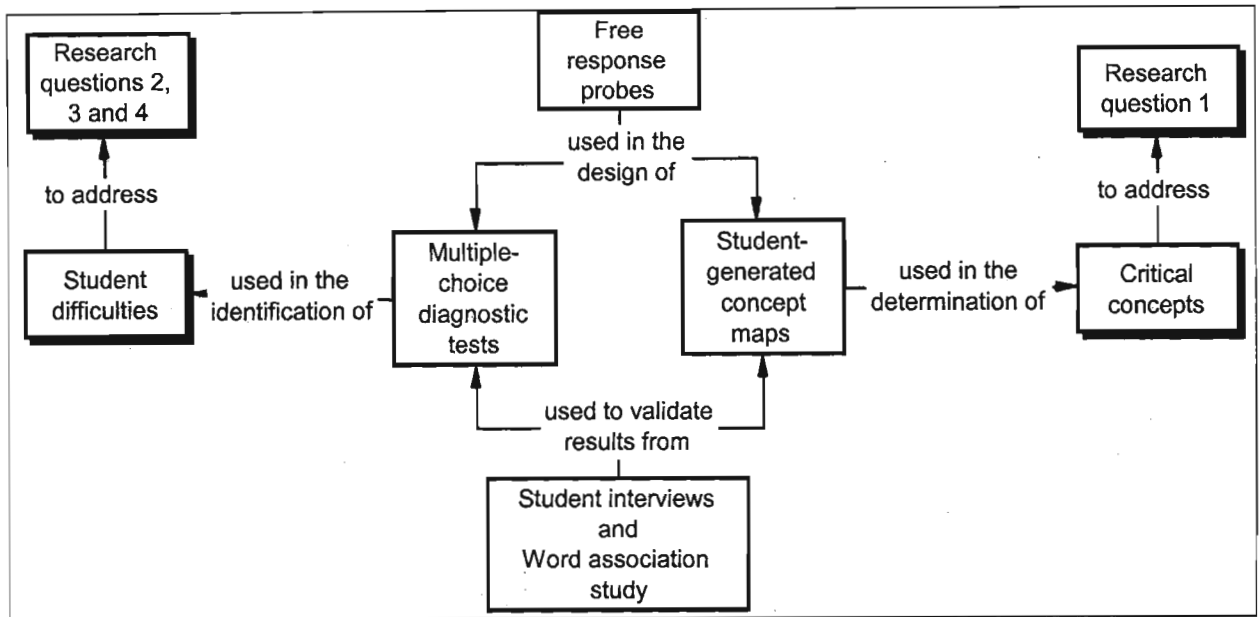
The diagnostic phase of the investigation aimed to address Research Questions 1, 2, 3 and 4. These questions assessed the status of students' conceptual frameworks

and their ability to integrate their knowledge of quantitative genetics. Furthermore, the investigation sought to identify and determine the nature of students' difficulties with the subject of quantitative genetics and to document any alternative conceptions held by students.

Initially three instruments were planned to be used to obtain data in this study. These included free-response written probes, multiple-choice diagnostic tests and semi-structured interviews. However, whilst planning this research project and considering what teaching and learning tools could be utilised in the therapeutic phase of the investigation, a review of the literature indicated to the researcher that concept mapping could be used as a tool to promote meaningful learning. She then decided to introduce the technique of concept mapping into one of her quantitative genetics modules in order to ascertain whether students are able to effectively use this learning tool to integrate their knowledge. Whilst looking through some of the student-generated concept maps it became clear to the researcher that the students' concept maps could be used to assess students' conceptual frameworks and their ability to integrate their knowledge of quantitative genetics. Thus, student-generated concept maps were included as a fourth research instrument.

A fifth research instrument was introduced later in the investigation once students' conceptual frameworks had been assessed and student difficulties and alternative conceptions had initially been identified. At this point in the research process the source(s) of student difficulties was being considered and a synthesis of the results from the multiple-choice diagnostic tests and student interviews indicated that students may be inappropriately associating certain terms and topics. A word association study was therefore conducted to add support to the findings from these research instruments. The manner in which the word association study was conducted is discussed in Section 3.3.

An illustration of the relationship between the five research instruments which were used to address each Research Question is given in Figure 3.1. The free-response probes were used to facilitate the design of the multiple-choice diagnostic tests and in the identification of conceptual relationships that needed to be explored in student-generated concept maps. The student-generated concepts maps were used in the assessment of students' conceptual frameworks thereby addressing Research Question 1. The multiple-choice diagnostic tests were used in the determination of student difficulties and alternative conceptions held by some students. The student interviews and word association study were used to validate the findings of the other research instruments when addressing Research Questions 2, 3 and 4.



**Figure 3.1: Relationships between the four research instruments used to address the Research Questions.**

### 3.2.1 Free-response probes

#### (a) Description of and rationale behind design of probes

Free-response probes are open-ended in nature and allow students to freely express their conceptual understanding, without any restriction (McMillan and Schumacher 1993). In contrast to multiple-choice diagnostic tests this form of questioning does not limit students' answers to particular pre-determined responses (Cohen *et al.* 2000). This type of probe was used to gather preliminary empirical evidence of the concepts that students found most difficult to understand with regard to the discipline of quantitative genetics. Such probes were also used to inform the design of multiple-choice diagnostic tests and the selection of concepts for inclusion in student-generated concept maps.

#### (b) Development and implementation of probes

Probes were developed based on the previous teaching experience of the researcher and addressed topics students in previous years perceived to be difficult. Different sets of free-response written probes were given to students taking the Genetics 332 module in 2002 (see Table 3.1). The first set of questions addressed students' prior knowledge on entry to the module. The other sets of questions were given to the



students to complete during the teaching of the module. Questions addressed students' understanding of statistical concepts such as *variance* and *covariance*, genetic concepts such as the *average effect of a gene* and *heritability*, and graphical representations such as histograms. Selected examples of free-response questions given to students at different times during the module are given in Figure 3.2. (The answers to the questions which allowed the identification of standard difficulties and alternative conceptions are given in Appendices 4 and 5, as they were later used in the multiple-choice diagnostic tests.)

- Why is it important, for a breeder, to have variation in a population and to be able to measure it?
- When does the variance of a distribution of phenotypes equal zero?
- Assessment of quantitative traits requires statistical procedures. Why is this so?
- Why are most quantitative traits normally distributed?
- What is the average effect of a gene? Why is this concept so important?
- When considering quantitative traits, what is implied when additive gene action is referred to?
- How may correlations between relatives be used by the quantitative geneticist in the improvement of populations?
- Why is it that close relatives tend to have similar performance in highly heritable traits but not in lowly heritable ones?
- The assumption is often made that if a trait is highly heritable, breeding values are necessarily high. What is wrong with this thinking?

**Figure 3.2: Selected examples of the free-response probes given to students at different times during the module.**

**(c) Analysis of probe data**

Inductive analysis, whereby categories and patterns emerge from the data (Lincoln and Guba 1984; McMillan and Schumacher 1993), was conducted on the student answers. During the analysis, topics of perceived difficulty were identified and categorised, using a method of coding as described by Cohen *et al.* (2000). Scientifically incorrect categories of answers given by students were then used as distractors in the development of the multiple-choice diagnostic tests (see Section 3.2.3). Students' answers or responses were also analysed in order to identify possible gaps in their conceptual frameworks. These data informed which concepts students would be asked to include in their concept maps (see Section 3.2.2).

### 3.2.2 Student-generated concept maps

#### (a) *Description of concept maps*

Concept maps are metacognitive tools that capture, organise and represent an individual's knowledge, encourage reflection, and enable evaluation of students' knowledge, thereby supporting a human constructivist approach to learning science (Heinze-Fry and Novak 1990; Okebukola 1992; Trowbridge and Wandersee 1994; Novak 1996; Trowbridge and Wandersee 1998; Wandersee 2000).

A concept map is a two-dimensional, hierarchical display of concepts, linked by lines labelled with linking words (Trowbridge and Wandersee 1998; Fisher 2000). They are often read from the top superordinate concept downwards, with the hierarchical structure mimicking the storage of knowledge in the brain (Wandersee 2000), although some have the main concept in the centre and radiate outwards. Although not all concept maps are hierarchical in nature, as some domains are not hierarchical themselves (Ruiz-Primo and Shavelson 1996; Schau and Mattern 1997; Nicoll 2001; Van Zele 2004), the most general concepts are usually presented near the top of the map (Freeman and Jessup 2004).

The concepts referred to may be defined as ideas with which individuals think (Wandersee 2000) and are designated on the map by a label (Novak 1996). Wandersee (2000) identifies four types of concepts. *Object concepts* which are nouns that refer to concrete objects such as "chair" or "cell"; *event concepts* which involve concepts arranged spatially and temporally like "meiosis"; *property concepts* which are adjectives like "dominant" and *constructs* which refer to higher order concepts with no real tangible referent in the world, like "gradient", "variance" and "heritability" (Wandersee 2000). *Object concepts* are the easiest concepts to understand because they are concrete, whilst *constructs*, because they are abstract, are often more difficult to understand.

Because concept maps are a condensed form of information, Wandersee (1990) pointed out that they include only the most important concepts in a topic and leave out all extraneous words. They are usually expressed as noun-centred ideas (Fisher *et al.* 2000). These noun-centred ideas represent concepts, which are linked by verbs or "linking words" (Heinze-Fry and Novak, 1990) to form propositions (Wandersee 2000). These linkages or relationships between concepts are more difficult for



students to grasp than the concepts themselves (Fisher *et al.* 2000). However, these links between concepts have been shown, by educational researchers, to enhance the anchorage and stability of concepts in the conceptual frameworks of students (Heinze-Fry and Novak 1990). Concept maps generally also include examples, generated by students, which serve to anchor new knowledge, not only with prior knowledge, but with examples with which a student can identify (Wandersee 1990; Trowbridge and Wandersee 1994, 1998).

**(b) Rationale behind the use of concept maps**

One reason for the inability of students to learn new concepts effectively is that in order to reason with their knowledge students must be able to access their propositional knowledge from their knowledge networks. If their connected knowledge is inadequate, they will be unsuccessful in adding new knowledge to their existing knowledge (Schau and Mattern 1997). Research question 1 addressed the determination of the status of students' conceptual frameworks and whether students were able to integrate their knowledge of the principles of quantitative genetics.

A highly sensitive tool that may be used to measure the integration of students' knowledge is that of concept mapping. The reason for this is that a concept map generated by a student can give a clear indication of the conceptual framework of the student at that time (Wallace and Mintzes 1990) and assist in the identification of concepts which are important to the understanding of a field of science. Furthermore, successive concept maps constructed by students can indicate the evolution of the student's knowledge during the teaching of any science module (Novak 1996).

Assessment of students' cognitive frameworks may be conducted and students may be ranked relative to one another (Ruiz-Primo 2000). This type of assessment may be regarded as more objective, for assessment purposes, than reading from a student's open response answer (Van Zele 2004) and better than multiple-choice tests which encourage rote learning (Novak 2003). Therefore, student-generated concept maps, constructed at different stages in the module, were used in this investigation to identify whether students could integrate their knowledge. Furthermore, as concept mapping not only aids students in gaining insight into their existing knowledge and its relevance to any new concepts, student-generated concept maps may also help in the detection of any alternative conceptions that the student may hold (Novak and Musonda 1991; Novak 1996; Pinto and Ziets 1997; Trowbridge and Wandersee 1998; McClure *et al.* 1999; Fisher and Moody 2000). This is particularly advantageous as one reason why alternative conceptions are so

difficult to remediate is that it is not always clear which elements in an individual's cognitive framework require alteration or addition of concepts and propositions (Novak 1996). During the analysis of the student-generated concept maps, care was thus taken to note any alternative conceptions held by students.

Martin *et al.* (2000) used student-generated concept maps to evaluate the conceptual change which occurred in a university-level module in marine biology in the U.S.A. These researchers found that some students did not make the connection between certain concepts. They named these missing relationships "conceptual gaps" and proposed that these gaps were indicative of concepts that may be critical to the learning of higher order concepts; *critical concepts*. In a further study on 173 students' understanding of the atom, conducted by Van Zele (2004), at a university in Belgium, it was also noted that students "left out" some relationships, regarded by experts in the field to be related, in their concept maps. These missing relationships were then thought to reveal only partial understanding of the subject area by these students (Van Zele 2004). Trowbridge and Wandersee (1994) also used student-generated concept maps to determine whether *critical junctures* were revealed in a university level course on evolution. However, in this case, the presence of a *critical juncture* was determined by students' selection of the superordinate concept among the terms provided for inclusion in the concept maps. A *critical juncture* was proposed to be present at stages in the module where students were confused about the choice of the superordinate concept.

The presence of incorrect linkages, missing concepts, the choice of the superordinate concept, and the inappropriate use of examples, are all indicators of a lack of integration of knowledge and the presence of alternative conceptions that may be held by students (Trowbridge and Wandersee 1998). Concept maps may thus indicate areas where understanding is lacking, and where relationships have not been seen by the student. In this investigation, the presence of missing relationships (links) and where the student-generated concept maps appeared fragmented or disconnected, were assumed to represent conceptual gaps in students' knowledge. The consistent presence of **missing or incorrect** links among class members regarding **one** concept and the subsequent inability of the students concerned to apply their knowledge was then thought to be indicative of a concept which may be crucial for the learning of higher order concepts.

A primary advantage of student-generated concept maps is that they are seen to represent, at least partially, the students' cognitive structures (Roth and

Roychoudhury 1993), which was important in this study. However, it must be stressed that the cognitive demand on the students, both from a verbal and a spatial-visual perspective, was extremely high. This was viewed, as suggested by Schau and Mattern (1997), as a potential problem for lower-achieving students or students whose first language was not that used in a classroom setting.

**(c) Implementation of concept maps**

Students were trained in the technique of concept mapping as well as the terminology relevant to the process of concept mapping. The students' were taught that concept mapping involves the following processes (Dorough 1997):

- Select a topic for mapping.
- Find a suitable written description about the topic. This could be an important text, passage, lecture notes, or laboratory background material.
- Underline key words or phrases; including objects and events (concepts).
- Rank the list of concepts from the most abstract and inclusive to the most concrete and specific.
- Group the concepts according to two criteria: concepts that function at a similar level of abstraction and concepts that interrelate closely.
- Arrange the concepts as a two-dimensional array analogous to a road map.
- Link related concepts with lines and label each line with a word or phrase that explains the relationship between concepts.
- Add examples wherever possible.
- Revise and redraw until they are as simple as possible without overlapping lines.

There is an enormous amount of variation in concept mapping techniques, particularly in the extent of the directions given to students before they start the task. At the one extreme, students are not given any concepts, connections between concepts, or any map structure. At the other extreme, students may be given some concepts or linkages and asked to fill in the blank parts of a skeleton map. The task demands imposed by the low direction tasks are higher than for the high-direction tasks and the low direction tasks better reflect a student's connected understanding (Ruiz-Primo 2000). In this study students were provided with a list of concepts to be included in the concept map, so as to probe the level of students' connected understanding between specific concepts. Each student was asked to construct two concept maps: (1) at the beginning of the *Introduction to Quantitative Genetics* module in order to gather data on the prior knowledge of students and (2) at the end of the module to determine how the cognitive frameworks of the students had developed during the formal teaching of the fundamental principles of quantitative

genetics. These student-generated concept maps were utilised to determine the level of integration of students' knowledge, thereby addressing Research Question 1.

**(d) Analysis of concept map data**

Student-generated concept maps may be evaluated using either quantitative or qualitative methods (Nicoll 2001). Quantitative assessment methods vary, but usually involve giving marks for the scientific validity of propositions, the labelling of links, the hierarchical structure and the presence of important cross-links (Dorough 1997; Trowbridge and Wandersee 1998; Wandersee 2000). Maps may therefore be used to assess propositional knowledge (knowing what something is), procedural knowledge (knowing how to do something) and strategic knowledge (knowing when, which and why specific knowledge is applied in a particular context). Different scoring systems have been proposed (Ruiz-Primo 2000). These included the following:

- a) Proposition accuracy score – the total sum of the accuracy of each proposition in a student's map assessed on a predetermined scale.
- b) Saliency score – the proportion of valid propositions out of all the propositions in the student's map.
- c) Convergence score – the proportion of accurate propositions in the student's map out of the total possible valid propositions in an expert's map. This seems to be the most efficient indicator of students' connected understanding (Ruiz-Primo *et al.* 2001).

The above-mentioned quantitative approach to assessing concept maps has been criticised for simply assigning one value to each map thereby not recognising the scope and depth of a student's knowledge (Van Zele 2004). Scoring criteria that focus on the accuracy of *all* propositions is thus deemed preferable to those that only count the number of certain map components (Ruiz-Primo and Shavelson 1996; Rice *et al.* 1998; McClure *et al.* 1999). In contrast, a qualitative approach examines all the links, including invalid links, revealing a substantial amount of information regarding the thought processes that lead to the student's understanding of a topic, including any alternative conceptions the students may hold (Novak and Musonda 1991; Kinchin 2001; Van Zele 2004). Furthermore, missing relationships reveal that only partial understanding has been achieved (Van Zele 2004). Thus, in this study it was deemed preferable to use a qualitative method of assessment.

One form of qualitative assessment, as proposed by Kinchin (2001), may divide concept maps based on their gross morphology into the broad categories of, for



example, spokes, chains and nets. A spoke has one central concept with other secondary concepts radiating out from it. However, none of the secondary concepts are linked. A spoke thus shows no hierarchy and little integration of concepts. A chain is depicted by a series of concepts each linked only to the next concept in the chain. A chain thus illustrates many levels but no complex interactions. In contrast, a net shows numerous levels, with complex interactions and a high degree of map integrity. This type of map can more easily support reorganisation and addition of new information than maps of the spoke or chain type (Kinchin 2001). All of the student-generated concept maps in this investigation were initially categorised as being of the spoke, chain or net type in order to obtain some idea of whether students' knowledge was well integrated or if gaps in their conceptual frameworks were evident.

Thereafter, the protocol of Nicoll (2001) was used to assess and code the links on the student-generated concept maps. This method focuses on the propositional knowledge contained in the links, the stability of student's knowledge and the complexity of the links; thus yielding information about the student's knowledge structures and how they learn information. The stability and complexity of the links were identified in the following way:

- The first level of analysis evaluated the accuracy of the link. The links were coded as *correct* (coded as 1), *incorrect* (coded as 2) or *missing* (coded as 3).
- The second level of analysis evaluated how confident the students appeared to be with their answers. Two categories were identified: *Defined* (coded as i), where the student was sure of the knowledge, and *emerging* (coded as ii).
- The final level of analysis looked at the complexity of the student's conceptual framework. The links previously identified as correct were further categorised as: *an example* (coded as a), *a fundamental fact* (coded as b) or *a link explained by other links* (coded as c).

The first level of analysis was primarily used to address Research Question 1 as the consistent presence of **missing or incorrect** links among class members regarding one concept and the subsequent inability of the students concerned to apply their knowledge was thought to be indicative of an inability to integrate their knowledge.

As the researcher had noted during her teaching experience that the important concepts of variance and heritability seemed to be difficult for many students to

understand, she paid particular attention to these concepts. Thus, when assessing the maps of students' foundational knowledge, at the start of the module, attention was directed at the following:

- Whether students illustrated an understanding of the statistic of variance by effectively linking this concept to the concept of the mean of a population.
- Whether students could connect statistical concepts with those of quantitative genetics.
- Whether students linked the concept of variance to concept of frequency distributions or histograms.

When assessing the maps of students knowledge of concepts in quantitative genetics, at the end of the module, particular attention was directed at the following:

- Whether students could differentiate between values and variances in the context of quantitative genetics.
- Whether students understood the connection between variance and heritability.
- Whether students could apply the concept of heritability i.e. the relationship between heritability and the selection of a particular breeding strategy.

### 3.2.3 Multiple-choice diagnostic tests

#### (a) *Description and rationale for selection of diagnostic tests*

Numerous benefits have been proposed for the use of multiple-choice diagnostic tests as diagnostic instruments, when compared with alternatives like interviewing. These include the ease and timeous collection of data (Gall *et al.* 1996), that the students may remain anonymous (McMillan and Schumacher 1993), that data may be gathered from many students simultaneously, that inarticulate students are not discriminated against and that the answers given are easy to categorise (Cohen *et al.* 2000).

The limitations of multiple-choice diagnostic tests are that the items included may not cover all relevant issues (Cohen *et al.* 2000) and that it is not possible to deeply probe students' beliefs, as would be the case with interviews (Gall *et al.* 2003). In

addition students may guess answers. They have a 50% chance of guessing correctly if there are only two options given, as was the case with some items in this investigation. In an attempt to overcome these limitations multiple-choice diagnostic tests which additionally required a reason for the student's choice of answer, as proposed by Treagust (1988), were developed for the identification of the conceptual and reasoning difficulties experienced by students. The part of the question which asked for a reason for the answer choice provided qualitative evidence of the nature of the conceptions and served to reinforce the choice made by the student. The items in the multiple-choice diagnostic instruments were specifically designed to provide empirical, quantitative evidence of student difficulties and to identify and describe the nature of any difficulties and alternative conceptions in the limited and clearly defined area of quantitative genetics, thereby answering Research Questions 2 and 3.

As proposed by Treagust (1988), the multiple-choice nature of the diagnostic tests enabled the lecturer to timeously and easily identify possible areas of difficulty and to immediately address potential misunderstandings. Furthermore, the research findings could be readily used by the lecturer for the improvement of her teaching practices, thereby promoting the practical implementation of research findings.

**(b) Development of the diagnostic tests**

Two multiple-choice diagnostic tests were developed, the first probing students' knowledge of concepts that they had previously learnt about in modules such as mathematics, statistics and introductory genetics (*prior knowledge concepts*) and the second their understanding of concepts in quantitative genetics at the completion of the quantitative genetics module (*quantitative genetics concepts*). This was deemed necessary as it was thought that students' knowledge of *prior knowledge concepts* may influence their understanding of *quantitative genetics concepts*. The following protocol proposed by Treagust (1988) was utilised:

- Propositional statements were identified for the curriculum covered in a typical introductory quantitative genetics module.
- A concept map was constructed to enable the researcher to consider the relationships between concepts taught in the pertinent module (Figure 2.1 on page 37).
- The propositional statements were related to the concept map to ensure that there was a representative covering of concepts and propositional statements for the topics under investigation.



- The propositional statements and concept map were validated by two specialists in the content area who were asked to check for accuracy and relevance of the content.
- The preparation of the multiple-choice diagnostic tests began during the first semester of 2002 when information on students' alternative conceptions was obtained from the semi-focused free-response probes given to students taking *Introduction to Quantitative Genetics*. Inductive analysis of the answers given to the free-response questions enabled the categorisation of the different student difficulties.
- Items of a multiple-choice nature were then written for each category of perceived difficulty. Each item was based on a limited number of propositional statements and addressed difficulties and alternative conceptions encountered in the free-response probes, previous class tests and from the literature. Each multiple-choice item was followed by a space for the student to give or write the reason why a particular option was chosen. The content validity of each of the items was established by two senior genetics lecturers who checked to see that the items were properly constructed, were relevant to the module under investigation, and that the answers given for each item were accurate.

**(c) Implementation of diagnostic tests**

The diagnostic component of the research process consisted of the following three phases (Summarised in Figure 3.2):

- *Phase 1: Preparation of the multiple-choice diagnostic tests*

The "prior knowledge" diagnostic test was given to students completing the module; *Introduction to Population Genetics* in 2002. This module immediately precedes the *Introduction to Quantitative Genetics* module and therefore the status of students' knowledge on completion of this module was deemed representative of their knowledge at the start of the next module; students' understanding of prior knowledge concepts was probed. Analysis of the data from these students enabled the researcher not only to gather data on difficulties and alternative conceptions held by students on entry to a module in quantitative genetics, but also to ascertain whether the layout of the questionnaire and the style of questioning were appropriate. No problems in this regard were detected.

- *Phase 2: Administration of the multiple-choice diagnostic tests*

In line with the process of action research, repeated cycles of planning, action, observation and reflection occurred during 2003. During the first semester of 2003

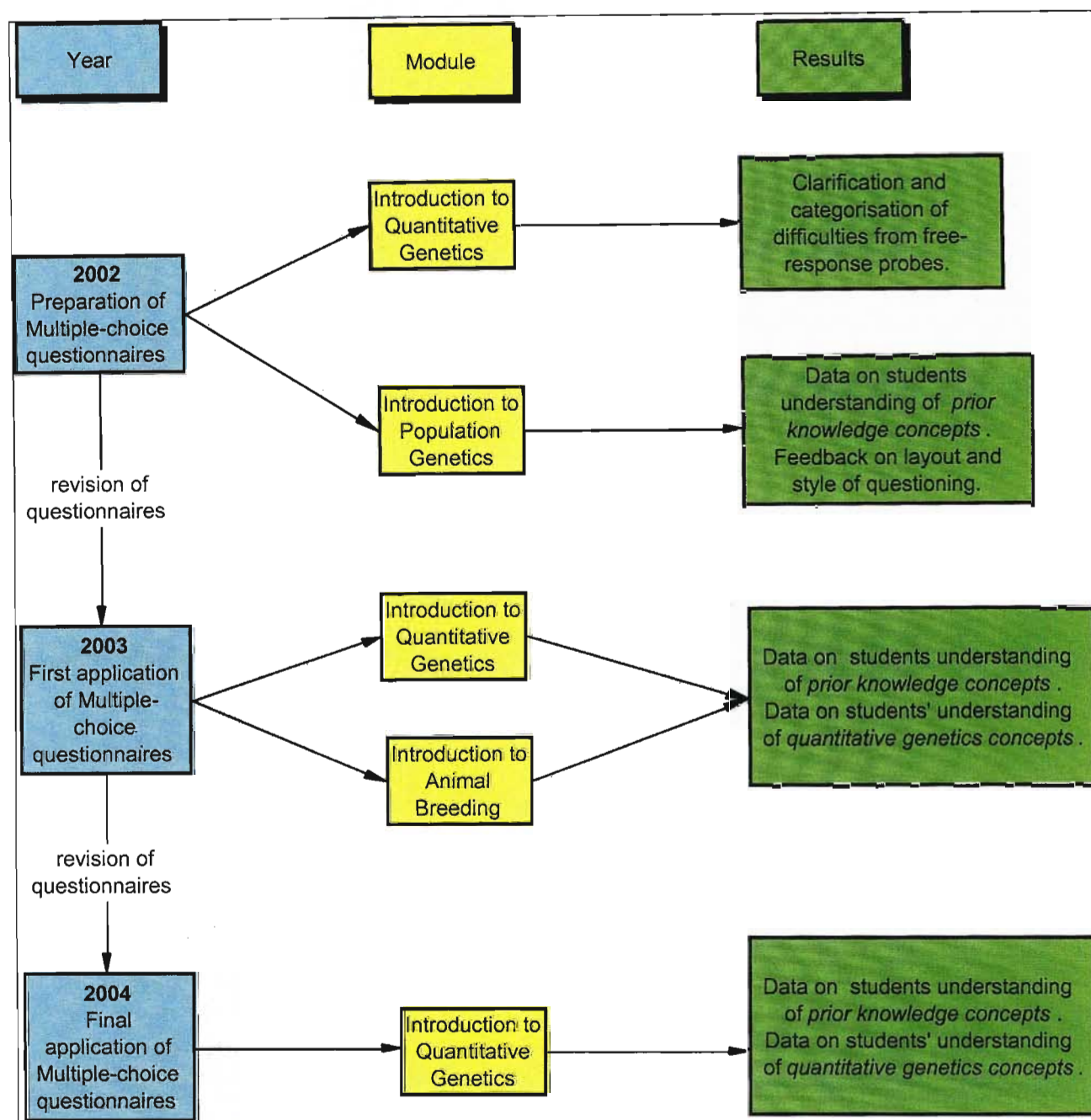
the prior knowledge diagnostic test and post-teaching diagnostic tests were both given to the *Introduction to Quantitative Genetics* class. After analysis of these data, questions were added to address previously unidentified alternative conceptions which emerged from the students' answers, items which did not yield meaningful data were omitted and items were re-worded where necessary. The revised post-teaching diagnostic test was then given to the *Introduction to Animal Breeding* class during the second semester. Further information on students' difficulties and alternative conceptions regarding concepts in quantitative genetics was then obtained. Subsequently, the diagnostic test was revised where necessary.

- *Phase 3: Final application of the multiple-choice diagnostic tests*

During the first semester of 2004 the final versions of the prior knowledge and post-teaching diagnostic tests were given to students registered for the Introduction to Quantitative Genetics module. This was the third iteration for each of the diagnostic tests and yielded the last set of data on students' alternative conceptions. The data from all three iterations were then synthesized and analysed.

Face validity of probes was assessed by three experts; one geneticist, one plant breeder and one statistician. The four-level framework of (Grayson *et al.* 2001) was used to classify each difficulty according to the amount of knowledge available on each difficulty. The factors which were taken into account to ensure research rigor are discussed in more detail in Section 3.4.

The final versions of the prior knowledge diagnostic test and post-teaching diagnostic test, as well as the propositional statements applicable to these diagnostic tests, are provided in Appendices 4 (page 296) and 5 (page 301) respectively. The reader will note that some of the questions in the diagnostic tests remained of the free-response style. This was to ensure that any ideas held by the students regarding the concepts probed could be identified.



**Figure 3.3:** The procedure used to develop the multiple-choice diagnostic tests.

**(d) Analysis of multiple-choice diagnostic test data**

The multiple-choice instruments were initially analysed inductively (Lincoln and Guba 1984) to identify the various difficulties and alternative conceptions held by students. Thereafter the frequency of each alternative conception was calculated. In addition, the Rasch model (Rasch 1980) was used to determine the relative difficulty of each test item as well as the validity and reliability of the data.

- *Inductive analysis*

Inductive analysis, as proposed by Lincoln and Guba (1984), of the reasons given for the answer choices of the multiple-choice diagnostic tests was conducted to reveal categories of student difficulties that emerged from the data (McMillan and Schumacher 1993). Each item was initially analysed individually. The reasons given for student answers were then compared to identify similarities and distinctions between categories and to discover patterns in the data. Groups of difficulties and alternative conceptions within different categories were then documented, thereby addressing Research Question 2. Thereafter, the data as a whole were considered and a synthesis of all the difficulties and alternative conceptions conducted to produce a comprehensive overview of the nature of students' knowledge, thereby addressing Research Question 3.

- *Calculation of frequency counts*

To determine the prevalence of each difficulty and alternative conception in each student group frequency counts were conducted.

- *Determination of relative difficulty, reliability and validity of test items*

The Rasch Model (Rasch 1980) was utilized for the analysis of test data to determine the relative difficulty of test items (to answer Research Question 2) and to evaluate the multiple-choice instrument's reliability and validity. The Rasch model is useful in research in human sciences as it transforms raw data into abstract, interval scales. The equality of intervals is achieved through log transformations of the raw data and abstraction is accomplished through probability equations. In addition, the Rasch model provides the necessary objectivity for the construction of a scale that separates the distribution of the attributes being measured from the persons under investigation (Bond and Fox 2001).

The value of the model lies in its ability to take non-linear raw score test data and to convert them into linear measures (Bond and Fox 2001). This is deemed necessary as it is erroneous to assume that a score of, for example,  $\frac{8}{10}$  is exactly twice as good as a score of  $\frac{4}{10}$ . In reality there may be groups of questions which are substantially easier for most students to answer, with a considerable increase in difficulty to another group of items. Thus the assumption of linearity of raw score data will only hold if the difficulty gaps between each of items are equal, and that the items span the entire range of the trait being measured.



Bond and Fox (2001) explained that the Rasch model is based on the formula:

$$\ln(B_n - D_i) = P(B_n - D_i)/1 - P(B_n - D_i) \text{ where:}$$

$B_n$  = ability of the person (on that trait)

$D_i$  = difficulty of the item

$P$  represents probability, and thus  $P(B_n - D_i)$  expresses the relationship between student "n" interacting with test item "i".

The model takes into account the difficulty of the items and the level of understanding of the students. An assumption of the model is that a student who attempts to answer an item exactly at his or her level of ability has a 50% chance ( $P = 0.5$ ) of correctly answering that item. In that case  $B_n$  and  $D_i$  are equal. In contrast, when  $B_n$  is large (a high ability person) and  $D_i$  is small (an easy item), then the probability of that person getting that item correct is greater than 50%.

The model simultaneously estimates both the overall understanding of each student, based on their overall performance, and the difficulty of each item, using the same metric. Both of these measures are estimated on a logit scale and each of the estimates has a degree of error associated with it (Bond and Fox 2001). The *Winsteps software* (2003) used in this investigation then illustrates the relationships between the overall performance of each person and the item difficulty in a person-item map. Each item and person is located on the map along the logit scale according to its estimated value; students with positive values being more able and items with positive values being more difficult (Bond and Fox 2001).

*Fit statistics* were used to identify persons and items that behaved in an idiosyncratic manner. These fit statistics identified whether students were behaving in an usual manner, for example, providing answers that were deliberately misleading or students that may have been guessing. Data from such students could then be excluded from the analysis, thereby improving the accuracy of the results. Similarly, fit statistics were generated for all items and were used to identify whether there were items on the test that were unexpectedly missed by some capable students or correctly answered by poorly performing students. Items which elicited such behaviour on the part of test takers could then be monitored and removed from the test if necessary, as advised by Bond and Fox (2001). The *Winsteps software* provided a *misfit index* for each person and item; if the index was above +3 or below -3 the student or item was considered as a "misfit" and eliminated from the analysis.

The *person indices* generated for the prior knowledge diagnostic test ranged from -2.36 to +2.39, and from -1.22 to +0.39 for the post-teaching questionnaire, well within the acceptable range, indicating that all students answered in a predictable fashion. The *item indices* generated ranged from -1.1 to +1.9 and from -1.22 to +0.39 for the prior knowledge and post-teaching diagnostic tests respectively, indicating that all of the test items appeared to provide a good measurement of the concept under investigation, suggesting a high level of content as well as construct validity.

Traditionally reliability estimates of test instruments are made by calculating a Cronbach alpha. However, in this study the Rasch model was used to determine an *item separation reliability index*. Item separation refers to the designation of item placement along a hierarchy and whether this placement will differ across other samples. Of advantage is that measurement error is adjusted for, as raw scores are not used in the calculation of the reliability index and the reliability term is not sample-specific (it does not depend upon the group of students completing a survey). A high item separation reliability index thus indicates that the placement of items along the continuum would be highly stable regardless of which sample of students took the test (Bond and Fox 2001). The estimates of the item separation reliability index values for the prior knowledge and post-teaching diagnostic tests, based on the Rasch model as implemented in the *Winsteps software* (2003), were 0.8 and 0.79 respectively. These estimates indicate that the order of item difficulty would remain unchanged if the same tests were given to another similar group of students.

Based on the estimates of the item separation reliability indices it is concluded that valid and reliable diagnostic instruments were developed for the assessment of the knowledge required by students' on entry to and after completion of, a module in quantitative genetics.

### 3.2.4 Interviews

#### (a) *Description and rationale for using interviews*

The benefits of conducting interviews with students are numerous. The interview process is flexible and adaptable (McMillan and Schumacher 1993) creating the opportunity to probe the motivation and reasoning of students (Cohen *et al.* 2000). Furthermore, as the interviewer has the opportunity to build up a rapport with the interviewee, it may be possible to gather in-depth data on the nature of student difficulties and alternative conceptions, a situation not possible when using written forms of questioning (Gall *et al.* 2003).

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The limitations of interviews are that they are time-consuming to conduct and analyse (McMillan and Schumacher 1993) and it is thus usually only possible to obtain data from fewer students in a particular time, compared with administering pen-and-paper instruments (Cohen *et al.* 2000). Furthermore, it must be recognised that the manner in which the interviewer interprets the responses given during the interview is subjective (Gall *et al.* 2003), the interviewer may ask leading questions and the interviewee may become uncomfortable and feel that the interviewer expects certain answers (McMillan and Schumacher 1993).

Due to the fact that interviews allow the interviewer to probe for the ability of students to integrate their knowledge and student difficulties and alternative conceptions in detail, the pen-and-paper tests were used as a method of obtaining information on the entire class, whilst the interviews with selected students were used to gain further insight into the conceptions and conceptual frameworks held by students. Thus, the interviews with selected students provided in-depth, qualitative data to validate the findings of the student-generated concept maps and multiple-choice diagnostic tests, as is commonly the case (Cohen *et al.* 2000). The researcher felt this was necessary as, especially in the use of multiple-choice diagnostic tests, the options given by the researcher may have led students to apparently show a conception that they did not actually hold. In addition, students' responses may have been based on what they thought was expected of them, rather than their own ideas, a problem which Duit *et al.* (1996) warned about. Interviews with selected students also enabled the researcher to probe more deeply into the identified difficulties, alternative conceptions and conceptual frameworks of students in an attempt to ascertain the possible nature and source(s) of the difficulties.

The interview protocols used in this study were semi-structured, that is, they consisted of a series of structured questions, but allowed for further unplanned in-depth probing of students' conceptual knowledge and methods of reasoning if the need arose, a benefit pointed out by Gall *et al.* (2003). Therefore, although the topics were selected in advance of the interview, the sequence and wording of the questions could be altered during the interview process. This allowed for systematic data collection within a relaxed and conversational atmosphere, as noted by Cohen *et al.* (2000).



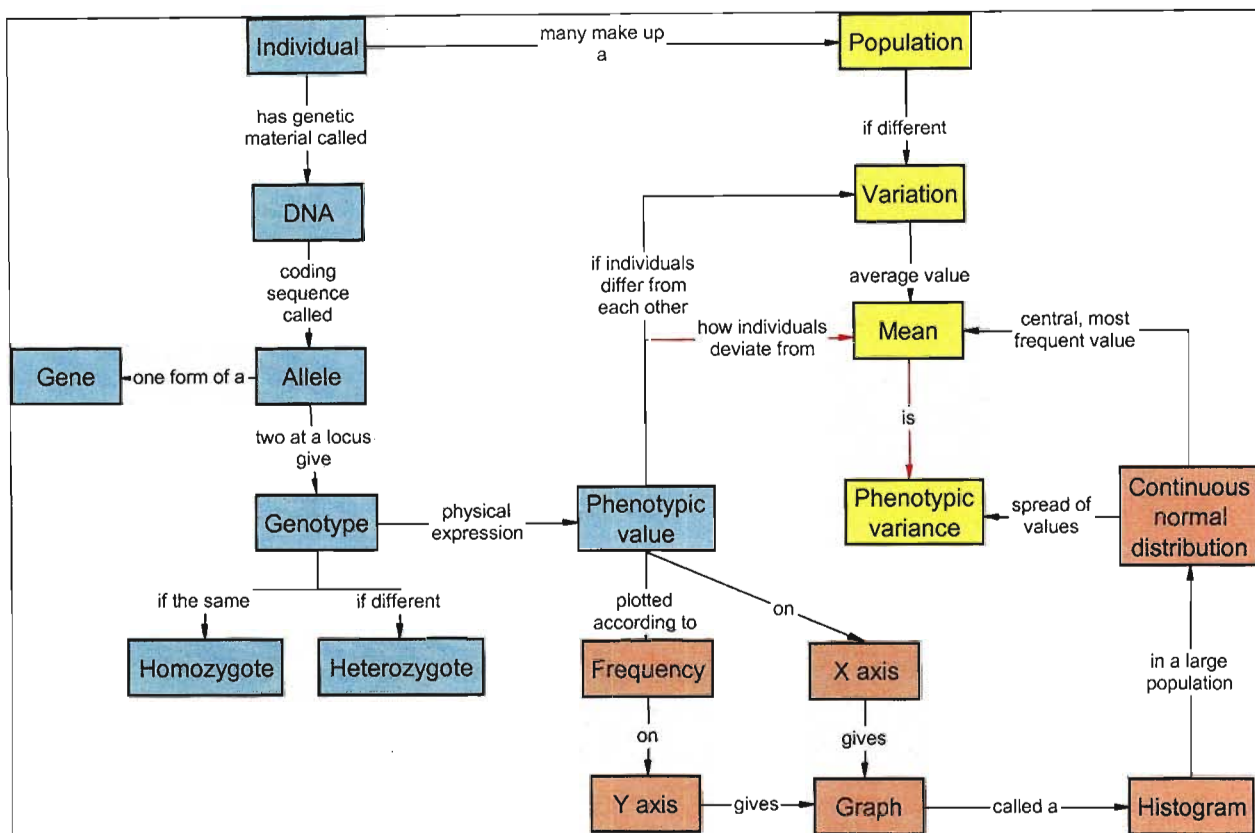
**(b) Development of the interview protocols**

Two interview protocols were developed. The first was used whilst interviewing students at the start of the module to ascertain students understanding of *prior knowledge concepts*, and the second at the completion of the module to ascertain their knowledge of *quantitative genetics concepts* that they had learnt during the teaching of the module.

The following protocol of Novak and Gowin (1984) was used as a basis for the development of the interview protocols.

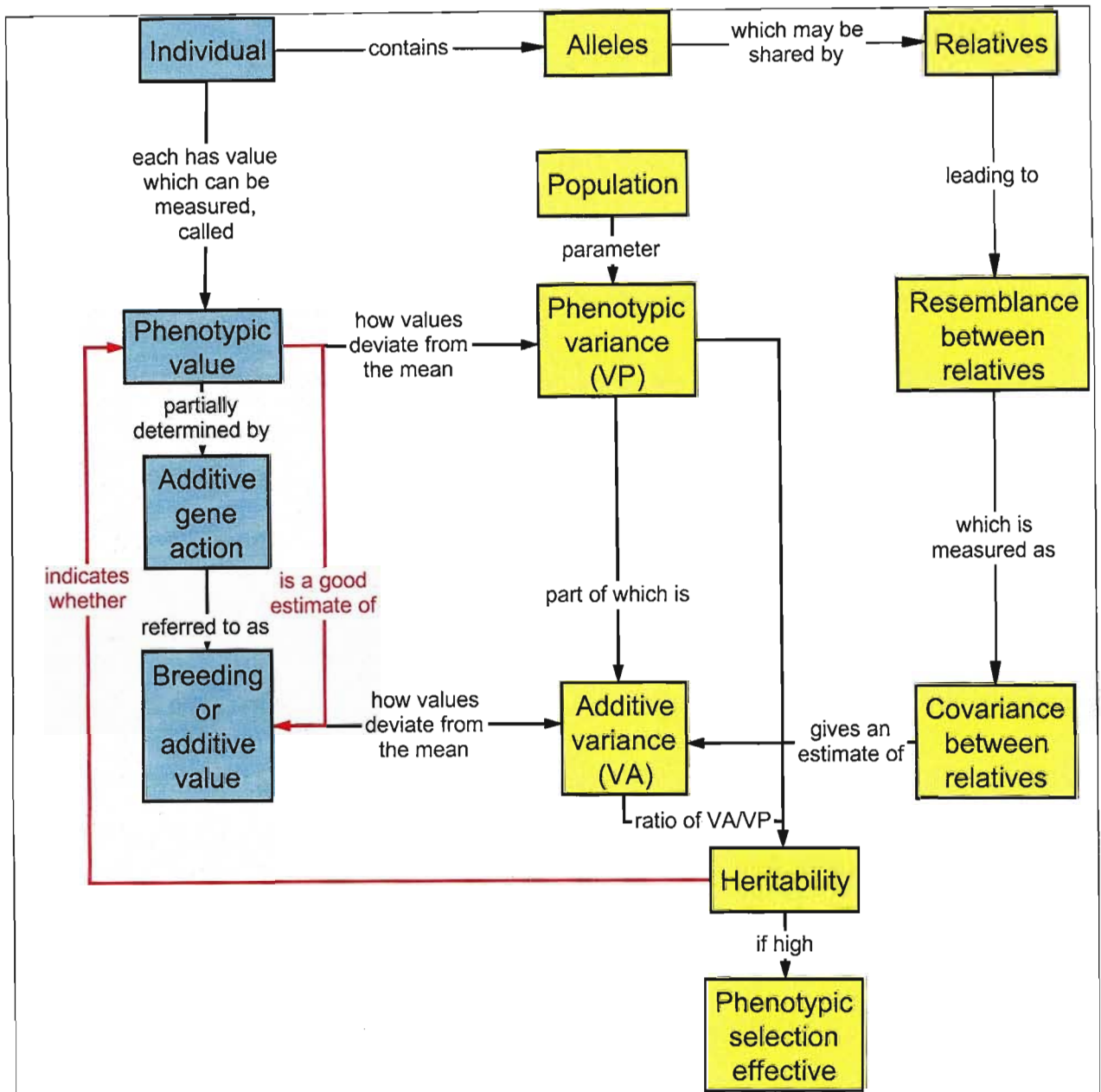
- Two lists of concepts considered by the lecturer/researcher to be important for an understanding of the topics under consideration were compiled. The first included all the *prior knowledge concepts*. The second included the *quantitative genetics concepts*.
- Two concept maps were constructed by the lecturer/researcher, in order to identify key relationships between concepts. The first concept map (Figure 3.4) contained all the *prior knowledge concepts*. The second concept map included the *quantitative genetics concepts* that students should have mastered by the end of the module (Figure 3.5).
- The concepts maps were validated by two senior genetics lecturers, who checked for face validity (discussed in detail in section 3.4).
- The concept maps were used to construct a series of propositional knowledge statements representing the scientifically correct information for the content covered in the concept maps.
- The interview questions were then designed, using the propositional knowledge statements and knowledge of concepts which students' find difficult, so as to probe for any difficulties and alternative conceptions, invalid propositions and gaps in the students' cognitive structures. The prior-knowledge and post-teaching interview protocols are presented in Appendix 6 (page 309).

In Figure 3.3 the concepts in blue represent foundational genetics concepts, those in yellow are concepts associated with populations and the concepts in red represent those associated with graphical representations. The pathway outlined in red illustrates the relationship between the phenotypic values and the variance; the variance is a value which indicates how individuals, on average, deviate from the mean.



**Figure 3.4: Concept map of *prior knowledge concepts* that was used in the development of the interview protocol used at the start of the module and for the analysis of interview transcripts.**

When considering Figure 3.5 the concepts shown in blue are concepts associated with individuals and those in yellow are concepts associated with populations. The pathway highlighted in red illustrates that the heritability value associated with a trait may be used to indicate whether, on average, the phenotypic values of individuals in the population are good indicators of their breeding values.



**Figure 3.5:** Concept map of *quantitative genetics concepts* that was used in the development of the interview protocol used at the completion of the module and for the analysis of interview transcripts.

### (c) Conducting the interviews

A small group of students was interviewed both at the start and the completion of the module. As suggested by Cohen *et al.* (2000), an atmosphere in which the student felt secure and able to talk freely was initially established. The interviewer also made an effort to appear interested and agreeable and to use everyday language and clearly stated questions. The interviews started with general questions, which most students could answer, so as to put the students at ease. Care was taken to avoid positive or negative feedback so as not to direct the students, but to always be

encouraging, as advised by Gall *et al.* (2003). In addition, the researcher gave the students sufficient time to answer a question before moving on. When students said that they did not know an answer, thereby indicating that their cognitive structure may not be well integrated, the question was re-worded before moving onto the next question. The length of the interview was kept to 30 minutes per student so as to avoid fatigue or frustration on the behalf of the student. The interviews closed with a discussion on the student's feelings about the module in general. The interviews all ended on a positive note. The interviews were all audio-taped and transcribed. This ensured that the interview transcript was a reliable record of the interview and allowed the interviewer to concentrate on the answers given by the students during the interview process without having to take notes.

**(d) Analysis of interview data**

The transcribed interviews were analysed, by listing the difficulties and alternative conceptions as well as the valid propositions held by students. Quotes from the interview transcripts were then extracted, where applicable, to add to the results obtained from the multiple-choice diagnostic tests.

Whilst investigating the level of integration of students' knowledge of quantitative genetics, the listed difficulties and alternative conceptions and valid propositional statements were used to design a concept map of the conceptions and propositional knowledge statements of each of the students interviewed, as advised by Novak and Gowin (1984). These researcher-generated concept maps constructed from interview data allowed the researcher to reduce a lengthy interview transcript into a one page illustration of the cognitive structure of a student (Novak and Musonda 1991; Novak 2003). These were then compared to Figures 3.5 or 3.6, in order to identify conceptual relationships that students generally found most difficult or areas where students showed fragmented knowledge or evidence of alternative conceptions, a method suggested by Novak and Gowin (1984). The propositional knowledge contained in the links of the map was then coded using the protocol suggested by Nicoll (2001) (see section 3.2.2, on the analysis of concept maps) to indicate the stability of the students' knowledge and the level of complexity of the links, thereby yielding valuable information on students' knowledge structures and how they learn.

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### **3.3 MODEL CONSTRUCTION OF THE SOURCE(S) OF ALTERNATIVE CONCEPTIONS IN QUANTITATIVE GENETICS**

#### **3.3.1 Description and rationale for model construction**

The ultimate aim of any action research project is the improvement of practice. This investigation thus aimed not only to identify student difficulties with quantitative genetics, but also to develop teaching strategies which could address these difficulties. However, before such teaching strategies could be formulated, an understanding of the possible source(s) of student difficulties was required. Consequently, a model of the possible source(s) of students' alternative conceptions was constructed using the modelling framework of Justi and Gilbert (2002). This model addressed Research Question 4. An outline of the modelling framework used by the researcher in this investigation is depicted in Figure 3.6. As is evident from this figure, the modelling process is cyclical in nature, with constant revision of the model taking place after various thought experiments, as well as empirical tests. These thought experiments involved the comparison of the proposed model with empirical data on difficulties and alternative conceptions held by students as revealed by the multiple-choice diagnostic tests, student interviews and a word association study.

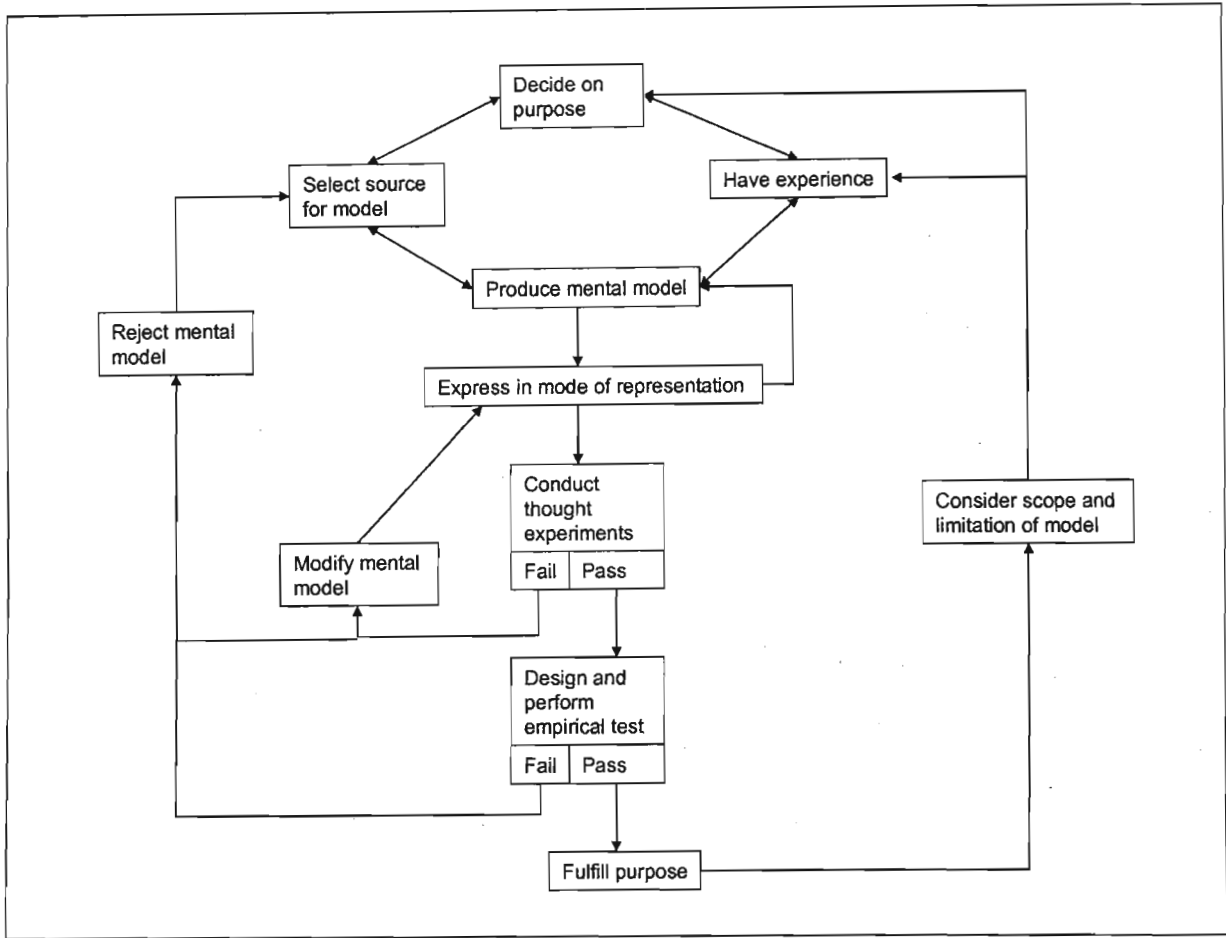


Figure 3.6: The modelling framework as proposed by Justi and Gilbert (2002).

### 3.3.2 Model development

The process involved in the development of the model of the possible source(s) of students' difficulties and alternative conceptions in quantitative genetics, based on the modelling framework as proposed by Justi and Gilbert (2002) is outlined in Figure 3.7.



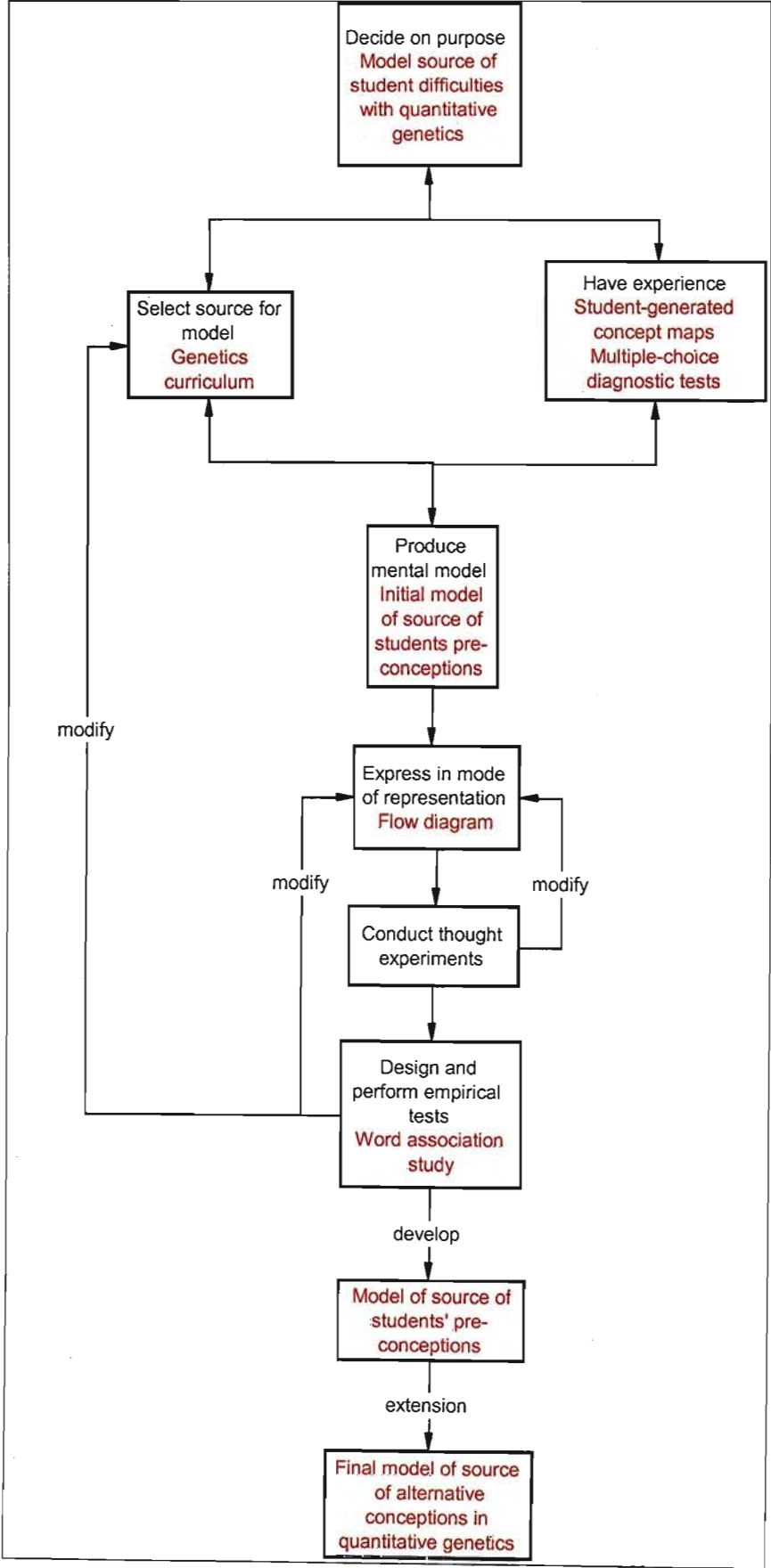


Figure 3.7: Application of the modelling process (Justi and Gilbert 2002).



The following steps were followed in the construction of the model, as depicted in Figure 3.7:

- A possible source of alternative conceptions held by students was hypothesized based on the prior teaching experience of the researcher as well as from data from student-generated concept maps, multiple-choice diagnostic tests and student interviews conducted prior to the start of the quantitative genetics modules. The genetic curriculum and the sequence in which concepts are introduced to students were postulated as a possible source of alternative conceptions held by students. It was further thought that some difficulties and alternative conceptions may be due to the association of certain words and concepts by some students;
- An *initial mental model* was constructed of the possible source of difficulties and alternative conceptions regarding students' understanding of *prior knowledge concepts*;
- The *initial mental model* was then expressed in the form of a flow diagram, called the *initial model*;
- The data was re-examined, using the data from all of the research instruments, in order to test the validity of the *initial model*;
- The *initial model* was further modified to account for any shortcomings;
- A word association study as proposed by Bahar *et al.* (1999b) was carried out to obtain empirical evidence to support the proposed *initial model* as a means of investigating the cognitive structure of students. This was performed as the researcher suspected that the students were inappropriately associating various ideas. Students were asked to write down any words that they associated with the concepts of equilibrium, mean, inbreeding and heterozygosity which are some foundational genetics concepts. The students were given 10 seconds to write down a list of up to 10 words for each stimulus word. The word association test was used to determine which concepts were most closely situated in students' cognitive frameworks. Only 10 seconds were allowed for each response as according to the semantic relatedness effect, concepts close together in a hierarchy are retrieved more quickly and thus represent a close association. The students' answers were then compiled and the words students most frequently associated with the stimulus words noted.
- The *initial model* was modified to account for the additional information obtained from the word association test. This then represented the *working model*;

- The *working model* was accepted as adequate in fulfilling its purpose of depicting the source of difficulties and alternative conceptions regarding students understanding of *prior knowledge concepts*;
- Data from student-generated concept maps, multiple-choice diagnostic tests and interviews conducted at the completion of the quantitative genetics modules were analysed in order to extend the *working model* to account for difficulties and alternative conceptions held by students regarding *quantitative genetics concepts*, thereby producing the *final model*.

### 3.4 RESEARCH RIGOUR

The following procedures were followed to improve the rigour of the research process.

- All diagnostic tests were face-validated by at least one expert in the field at the University of KwaZulu-Natal. Face validity refers to whether the content of the test is relevant to what is being probed (McMillan and Schumacher 1993). The questions used in the free-response diagnostic tests, the multiple-choice diagnostic tests and the interview guides were all face-validated. Table 3.3 specifies what the expert checked for when validating the various research instruments.

**Table 3.2: Aspects of the diagnostic tests that were checked by the expert.**

Aspects checked by the expert	Free-response diagnostic tests	Multiple-choice diagnostic tests	Interview protocols
Was the wording of the questions clear and easy for students to understand?	Yes	Yes	Yes
Were the instructions clear, unambiguous and easy for students to understand?	Yes	Yes	Yes
Did the questions address the topic under investigation?	Yes	Yes	Yes
Were the diagnostic tests short enough to hold the attention of the respondents?	Yes	Yes	Yes

- 
- The data analysis of all the research instruments was verified by an expert at the University of KwaZulu-Natal. This was an attempt to improve the reliability of the analysis, and to ensure that any subjectivity on behalf of the researcher was identified and rectified.
  - Data analysis techniques were both qualitative and quantitative in nature, thereby approaching the problem from more than one perspective.
  - A variety of research instruments was used to address each research question. The results from all the research instruments were then compiled and the consistency of the results verified (convergent validity). The researcher thus made use of the technique of triangulation.
  - The Rasch model as implemented in the *Winsteps software* (2003) was used to verify the content and construct validity and reliability of the multiple-choice diagnostic tests (Section 3.2, page number 65).
  - The interview transcripts were audio-taped and transcribed to ensure a complete and accurate verbal record of the interviews conducted.
  - Although the instruments were not “piloted” as such, the multiple-choice diagnostic tests and interview protocols were used over three years with at least three student groups, and were continually improved and revised when necessary. This was done to account for any problems in the style of questioning, to omit redundant questions and to add questions on areas of difficulty which became apparent during the investigation.
  - The four-level framework proposed by Grayson *et al.* (2001) was used to classify the alternative conceptions and student difficulties that were identified according to the amount of information available on the nature of each difficulty. The framework classifies *unanticipated difficulties* (difficulties which arise unexpectedly during data analysis) as being on level 1, *suspected difficulties* (based on the researchers teaching experience) on level 2, *partially established difficulties* (at least one investigation has been conducted where the difficulty has been noted), on level 3 and *established difficulties* (the difficulty has been noted in numerous investigations and in various contexts) on level 4. In this investigation all difficulties were initially classified as level 2 as they were merely suspected by the researcher from her teaching experience or were identified from the free-response probes. By the end of the investigation, however, the multiple-choice diagnostic tests had been repeatedly administered over 3 years to 4 student groups and interviews had been conducted over 3 years with 3 groups of students. This process served to confirm the reliability of the findings regarding the nature of each difficulty. All the difficulties are thus currently regarded as being all level 3, the highest

possible level attainable in this type of investigation. For the difficulties to be classified at level 4 the investigation would have to be conducted in multiple contexts.

### **3.5 CONCLUDING REMARKS**

Chapter 3 has outlined the methodology employed and the rationale behind the choice of instruments used in the diagnostic phase of this investigation. As discussed in Sections 2.3 and 2.4, this action research investigation has been conducted from a pragmatic point of view, using the mixed-methods paradigm, where the problem concerned determined the choice of instruments used to gather data. In presenting the methods used in this phase of the investigation care has been taken to highlight that the research process was conducted as rigorously as possible.

Chapters 4 and 5 give the results obtained from addressing the Research Questions of the diagnostic phase and provide a discussion on the relevance of these findings.

## CHAPTER 4

# STUDENTS' CONCEPTUAL FRAMEWORKS IN QUANTITATIVE GENETICS

**Research question 1:**

What is the nature and extent of students' integrated knowledge and their ability to link key concepts of quantitative genetics?

### 4.1 INTRODUCTION

In line with a human constructivist view of learning, Novak (1998) claimed that individuals construct knowledge through a process of forming unique associations between novel concepts and those which are already part of their conceptual frameworks. The ideal result of meaningful learning, as proposed by Ausubel (1968) and Novak (1993), may thus be viewed as an interconnected set of related concepts in the conceptual frameworks of individuals. If students' connected knowledge is inadequate then students may be unable to effectively add new knowledge to their existing knowledge (Schau and Mattern 1997). As this investigation was conducted from a human constructivist perspective, an initial analysis of the conceptual frameworks of students taking a module in quantitative genetics was undertaken. The aim of this component of the investigation was to determine the nature and extent of integration of students' knowledge and their ability to link key concepts in the field of quantitative genetics.

Based on the researcher's previous teaching experience, she proposed that students' required knowledge of two key concepts before they could fully understand the field of quantitative genetics. The first concept that was proposed as being central to students' understanding was that of *variance*. The reason for this is that a firm grasp of the meaning of variance is required before students are fully able to understand:

- The relevance of the normal distribution of phenotypic values produced by most quantitative traits. Students must comprehend that variance indicates



the spread of individual values from the mean value. In addition, they must realise that genetic variation is essential before change can occur in a population. For example, when practicing individual selection, there must be an opportunity for the breeder to select individuals with values that are much better or worse than the mean value in order for progress to be made.

- That the phenotypic variance is partitioned into various components, one of which being the additive variance, or variance of the breeding values of individuals in the population.
- That heritability is calculated as the ratio of two variances and not as the ratio of two individual values. (A detailed description is given in section 2.2.4).

The second concept that the researcher ascertained may be central to students' understanding of quantitative genetics was that of *heritability*. If students do not understand that heritability is an applied genetics statistic that enables one to determine whether, on average, the observed values of individuals indicate what the phenotypic values of the majority of their offspring are expected to be, then they may be unable to use the statistic in any application.

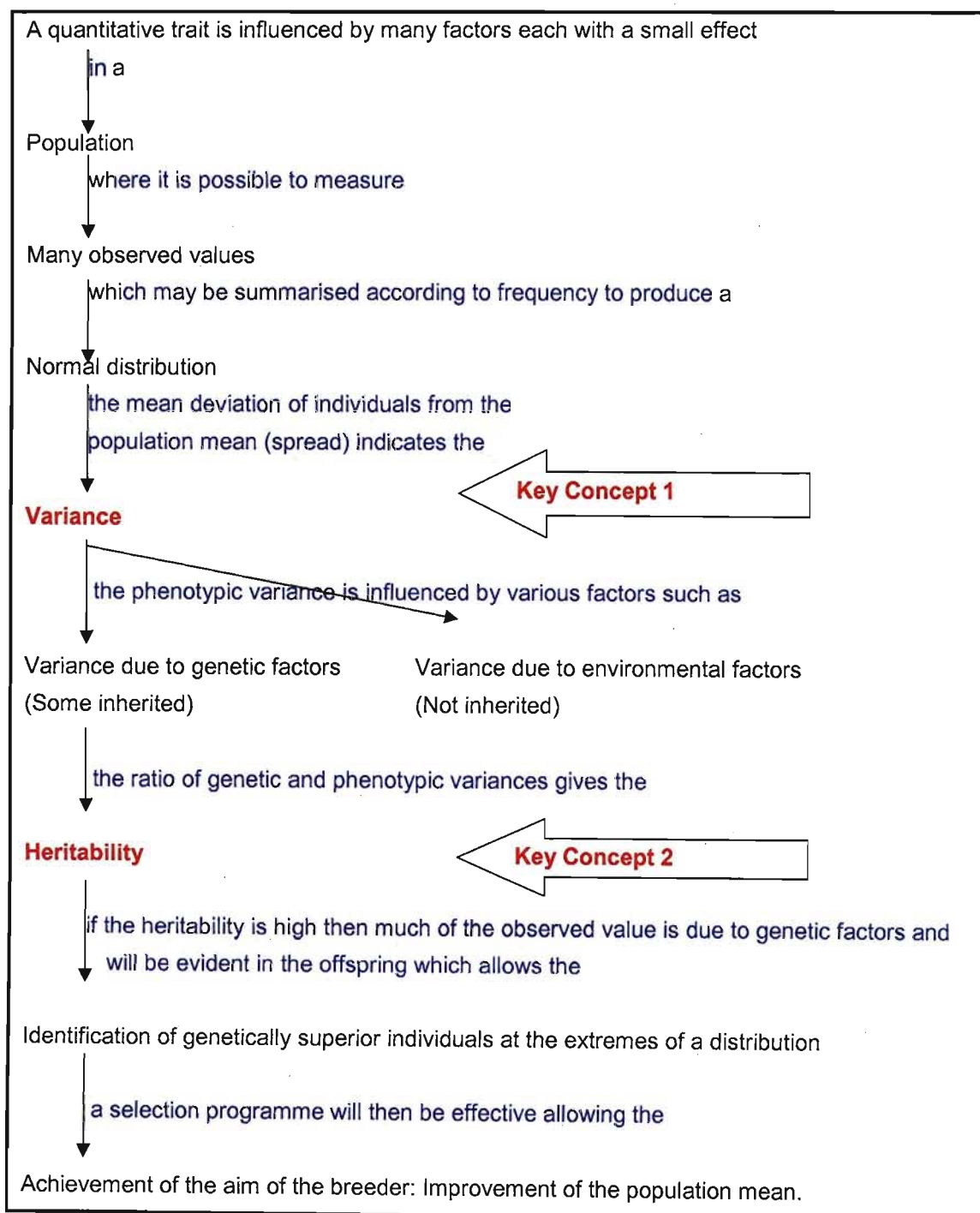
A representation of when the concepts of variance and heritability were taught in the quantitative genetics module described in this component of the investigation is depicted in the form of a flow diagram (Figure 4.1). Figure 4.1 illustrates the *sequence* in which the researcher proposed that students obtain knowledge of certain concepts. Variance is shown as the first important or key concept that students must have a meaningful understanding of, followed by the concept of heritability.

As described in Section 3.2.2 on page 55 concept mapping is a highly sensitive tool which can be used to give an indication of students' conceptual frameworks at any one point in time (Wallace and Mintzes 1990). Consequently, concept maps generated by the students and by the researcher were used as a tool for analysing the conceptual frameworks of students. During the analysis of the concept maps constructed in this investigation, students' integrated understanding of the concepts of variance and heritability was assessed by whether they were able to make meaningful connections to these concepts. Thus, the following three sub-questions were posed to address Research Question 1:

- What is the nature of students' integrated knowledge of key concepts in quantitative genetics?



- Do students illustrate an understanding of the concept of *variance* at the start of a quantitative genetics module, by being able to link this concept with foundational concepts and graphical representations in quantitative genetics?
- To what extent does students' understanding of *variance* influence students' understanding of, and ability to apply, higher order topics such as *heritability*?



**Figure 4.1:** Illustration of which concepts could be considered as “critical” in a foundational quantitative genetics module.

## 4.2 METHODOLOGY EMPLOYED

Two types of concept maps were constructed during the research process namely, student-generated concept maps as well as researcher-generated concept maps. The student-generated concept maps were constructed by the students at the beginning (22 students), as well as the end (17 students) of the module, using specific concepts supplied by the researcher (details given in Section 3.2.2, page 57). The researcher-generated concept maps were constructed from the interview transcripts of interviews conducted with a sample of students both prior-to and post-teaching of the quantitative genetics module (Section 3.2.4, page 72). The protocol proposed by Nicoll (2001) was used in the analysis of the student-generated concept maps as well as the researcher-generated concept maps constructed from the interview transcripts (Section 3.2.2, page 59).

The student-generated concept maps, and those constructed by the researcher at the start of the module, were used to assess whether students were able to link the concept of variance to other important genetics and statistics concepts. The maps generated at the completion of the module provided data on whether the students were able to integrate their knowledge of variance with the concept of heritability and whether they were able to link heritability to a practical application.

An initial qualitative assessment, using the protocol described by Kinchin (2001) (Section 3.2.2, page 58), of the student-generated concept maps was conducted in order to initially ascertain whether students showed any evidence of fragmented knowledge structures which could imply that students lacked knowledge of certain key concepts.

## 4.3 RESULTS

### 4.3.1 Integration of student knowledge

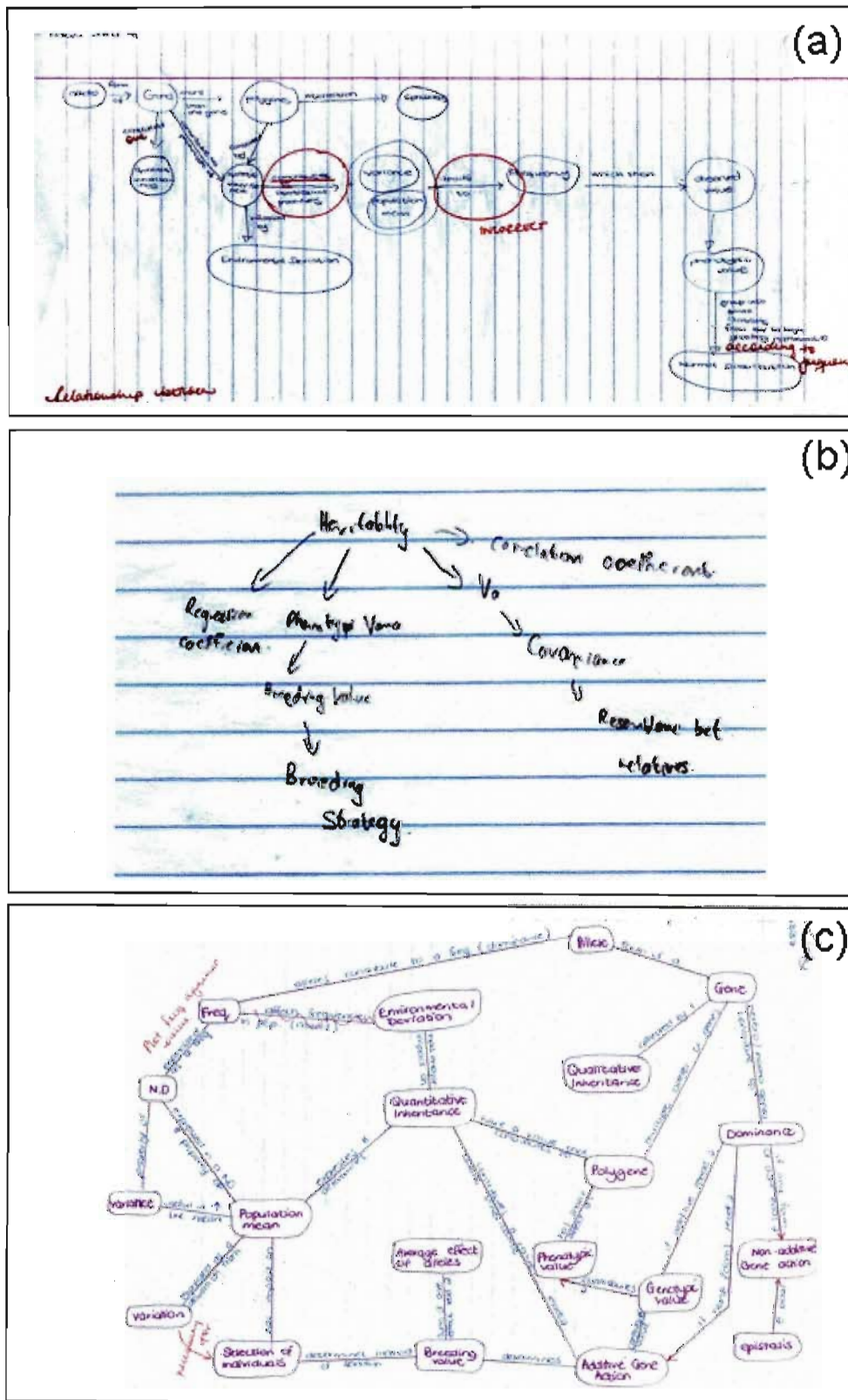
The first sub-question addressed was: What is the nature of students' integrated knowledge of key concepts in quantitative genetics? An assessment of the concept maps produced by each student, both at the start and at the completion of the module, revealed that students used three different formats to construct their concept maps; the *chain*, the *spoke* and the *net* type (Figure 4.2). An assessment of all the maps, 20 at the start and 17 at the completion of the module, revealed that

approximately 50% of the maps were of a *net* type and 50% *spoke* or *chain* types (Table 4.1). It should be noted that although all 20 students completed the module, only 17 were present on the day they were asked to complete the second concept map.

**Table 4.1: Types of concept maps produced by students.**

Time of map creation	Percentage of students		
	Spoke	Map Type Chain	Net
Maps at start of module	27	19	54
Maps at completion of module	29	24	47

The *net* type of concept map illustrated that students were able to effectively link concepts and that students had integrated their knowledge of the concepts included in their concept maps. In contrast, the *spoke* map formation showed only one hierarchical level and no understanding of interactions between concepts, while maps with a *chain* formation showed many hierarchical levels but a limited understanding of complex interactions between concepts. Kinchin (2001) postulated that maps of the *spoke* and *chain* types indicate that students are unable to effectively integrate their knowledge due to the absence of linkages between concepts. From the results presented in Table 4.1 it is evident that only 50% of the students were able to effectively link concepts and that the other 50% of students taking the module may not have recognised the relationships between concepts. As suggested by Heinze-Fry and Novak (1990), the observation that many important links were absent or missing in the student-generated concept maps could imply that these students were unable to integrate their knowledge of quantitative genetics. This implication was then further investigated with respect to the concepts of *variance* and *heritability*.



Comments written in red represent corrections made by the researcher.

Concept maps directly scanned from original documents. Indistinct pencil and colour markings have affected the reproductive quality.

**Figure 4.2: Examples of the different types of student-generated concept maps; (a) chain type, (b) spoke type and (c) net type.**



### 4.3.2 Students' understanding of variance

An analysis of both the student-generated concept maps produced by students at the start of the module and the interview transcripts was conducted to answer the question: Do students illustrate an understanding of the concept of *variance* at the start of the module, by being able to link this concept with foundational concepts and graphical representations in the context of quantitative genetics? This analysis indicated that students could be grouped into two broad categories, those who demonstrated some integrated understanding of variance, and those who were unable to link variance to other concepts important in quantitative genetics and thus showed no understanding of variance.

Students' level of understanding of variance was inferred from the manner in which they linked the following:

- The mean and the variance. An understanding of variance was assumed if the student demonstrated that they were aware that the variance specifically indicates how the values in a population deviate from the mean value.
- Genetics and statistics concepts. As quantitative genetics requires knowledge of the fundamental principles of both these subject areas, note was taken of whether students were able to link concepts such as individual phenotypic values with population parameters such as the mean and variance.
- The variance of a population and frequency distributions or histograms. Students' ability to apply their knowledge of variance was inferred if they could link variance to the shape of a normal distribution. This was considered as important as most quantitative traits show a normal distribution when the individual values are plotted against the frequency of their occurrence.

An assessment of the 20 student-generated concept maps constructed at the start of the module revealed that 53% of students did not make any connection between the concept of the mean of a population and the concept of variance (link classified as missing) and 7% of students made an incorrect connection (link classified as incorrect). The other 40% of students either correctly linked the concepts of the mean and the variance (7%) or showed some degree of understanding by linking the concepts without using meaningful linking words (link classified as emerging). In addition, 62% of the students did not see a connection between the genetics

concepts given for inclusion in the concept maps and the statistics concepts. What was interesting to note was that 68% of students seemed to be able to connect statistics with graphical representations such as histograms. However, none of these relationships were clearly defined. For example, students merely stated that the variance was a property of a normal distribution, but were not able to relate variance to the spread of the values from the mean. These results are presented in Table 4.2.

**Table 4.2: Analysis of student-generated concept maps constructed at the start of the module in terms of link classification.**

Relationships investigated	Percentage of students			
	Link classification			
	Missing	Incorrect	Emerging	Correct
Mean and variance	53	7	33	7
Genetics and statistics	62	0	38	0
Variance and histograms	16	16	68	0

The results presented in Table 4.2 suggest that, as approximately two-thirds of the class did not make meaningful connections to the concept of variance, they may not have fully understood this concept. This lack of a working knowledge of variance was seen by the researcher as problematic as many of these students were also not able to link statistical concepts to applied concepts in genetics or link descriptive statistics such as variance to graphs of a normal distribution. The researcher interpreted these outcomes as deficiencies in students' knowledge that could impact on students' subsequent understanding of concepts in quantitative genetics, such as heritability (which is calculated as the ratio of two variances), and the reasoning behind why quantitative traits usually show a normal distribution.

Of the twenty student-generated concept maps constructed at the start of the module, none of the concept maps were regarded as completely correct. Three were chosen as representative of the different categories of concept maps included in this chapter. These concept maps were selected according to the extent of integration of the student's knowledge and their inferred understanding of variance:

- Good integration of knowledge and some understanding of variance (Figure 4.3).

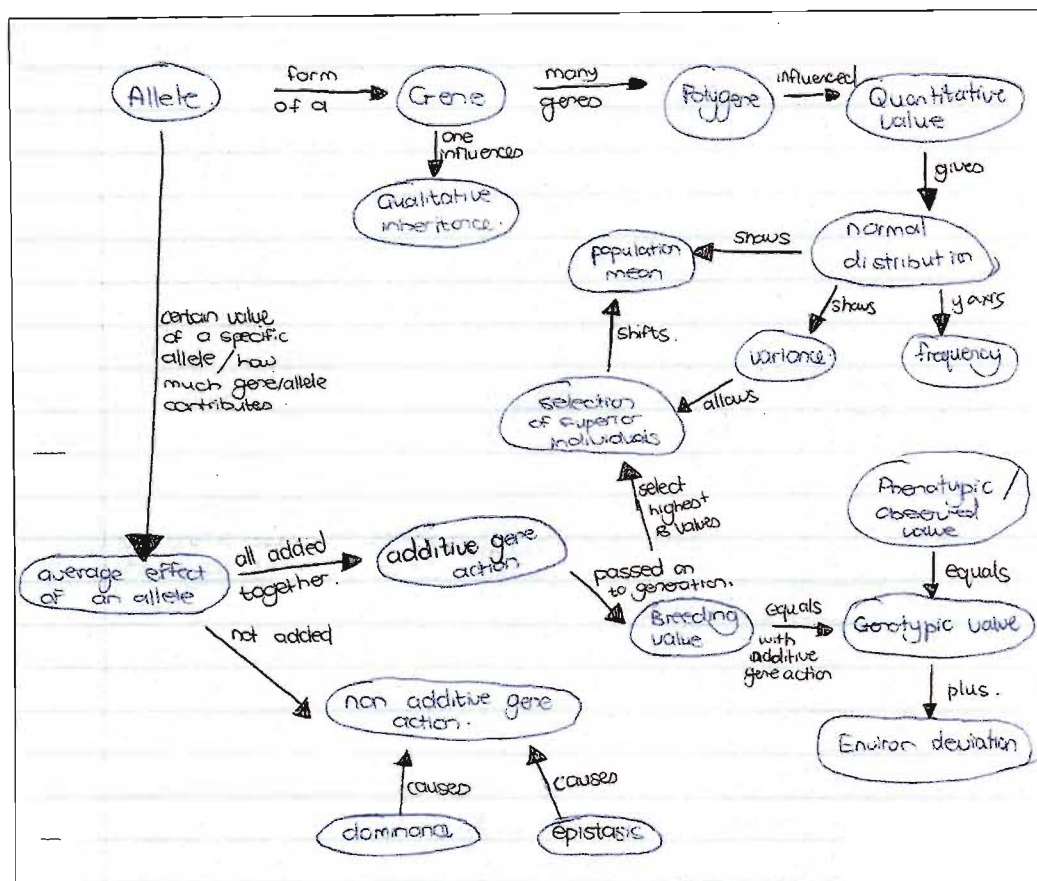


- An inability to link concepts in genetics and statistics, but some understanding of variance (Figure 4.4).
- Poor integration of knowledge and no understanding of variance (Figure 4.6).

Two of the five randomly selected students interviewed showed some understanding of variance, whilst the other three did not grasp the meaning of variance as they held alternative conceptions regarding this concept. Quotes from the interviews with these students and researcher-generated concept maps, generated from the interview data (Figure 4.5 and 4.7), are discussed below in order to add further support to the results obtained from the student-generated concept maps.

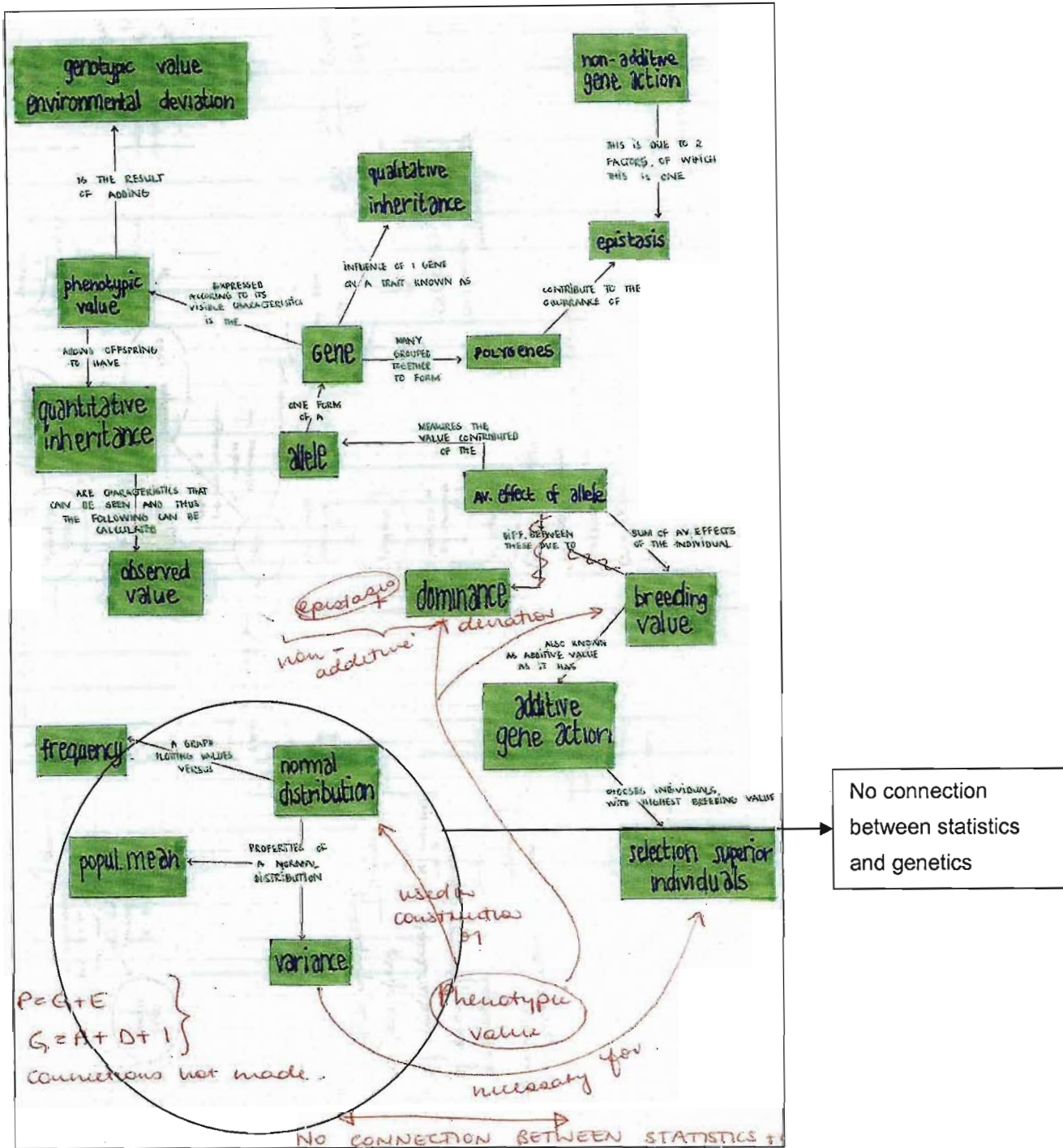
**(a) Concept maps from students with some understanding of variance**

The first of the selected student-generated concept maps is given in Figure 4.3. In this case, the student's integrated conceptual framework was evident from the scientifically correct relationships between concepts as well as the number of cross linkages between concepts. The student also showed some hierarchical organisation of her knowledge. In addition, she illustrated some understanding of variance and the relationships between statistical concepts and their application to genetics, which were classified as emerging. She was able to link variance with a normal distribution. However, this link was classified as emerging as the relationship was not clearly stated; she merely mentioned that a normal distribution "shows" variance. This student thus indicated that her knowledge of variance enabled her to apply her prior knowledge of statistics to the context of genetics. She also seemed to have some understanding of how the variation observed in a population for a particular trait may be summarised according to the frequency of each type of observation to produce a normal distribution.



**Figure 4.3: Student-generated concept map demonstrating integration of foundational knowledge of genetics and some understanding of variance.**

The second example is of a concept map produced by a student on entry to the quantitative genetics module that also inferred that the student had some understanding of variance (Figure 4.4). However, it was clear that this student's knowledge was more fragmented than the previous example as she was unable to make a connection between concepts learnt in two different modules completed the previous year; namely, biometry and genetics. The absence of this link was thus classified as missing. Nonetheless, the student could make some connection between various statistical concepts, such as the mean and variance, and a normal distribution, although the links were not clearly defined and therefore classified as emerging. The student merely stated that the mean and variance were "properties of a normal distribution". This student therefore appeared to have a limited understanding of variance and was thus apparently unable to apply her knowledge of descriptive statistics such as variance to the field of genetics.



The writing in red represents the corrections made by the researcher that were returned to the student.

**Figure 4.4:** Student-generated concept map highlighting the inability of the student to make any connection between statistical concepts and concepts related to quantitative genetics.

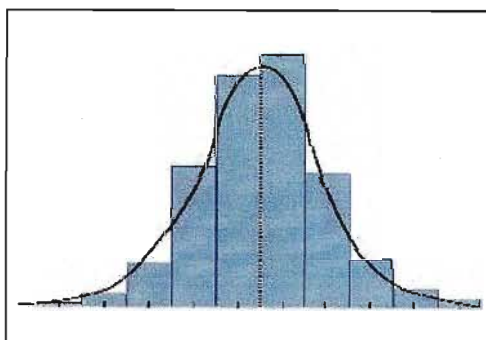
**(b) Interviews with students with some understanding of variance**

Information generated from the five interviews conducted were analysed to enable a more in depth description of student's understanding of the concept of variance. The interview transcripts of two of the students, designated students A and B (not the same students whose concept maps are shown), revealed some understanding of variance at the beginning of the module. The extent of their understanding of variance and how they related this statistic to graphs of a normal distribution is discussed below as their responses were considered typical of other students who also entered the module with some understanding of variance.

As can be seen from the following quote, student A was able to correctly interpret the terms *variation* and *variance*.

- I: What do you understand by the terms variation and variance?  
 S: Well I know that variation is how a population would differ with its phenotypes and genotypes and variance is basically how they differ from the mean. Like, how can I explain it..... like within a population you would get a certain amount of people with similar features and that would become the mean of the population and variance is how individuals would differ from that mean.

Student A was also able to use her knowledge of variance to *begin to* reason with the graph of a normal distribution given below.



- I: What do you think will go on each axis?  
 S: Height on the Y axis and then on the X axis it will be the amount of individuals. [incorrect assignment of the axes]  
 I: So what do you think each of the bars represents?  
 S: A height of a number of individuals.  
 I: How are you going to number the bottom axis?  
 S: [indecision]  
 I: Don't know? OK. You see that this tallest bar is somewhere near the middle. Do you think there is a reason for that?  
 S: That is the mean of the population so most people are that height. [correct interpretation]  
 I: OK so you think the mean is somewhere here in the middle. If I ask you to re-draw this graph with less variance – how would you do it?  
 S: I would change the values down here. [student vaguely points at X axis].  
 I: So these end points would change. Would the heights stay the same?

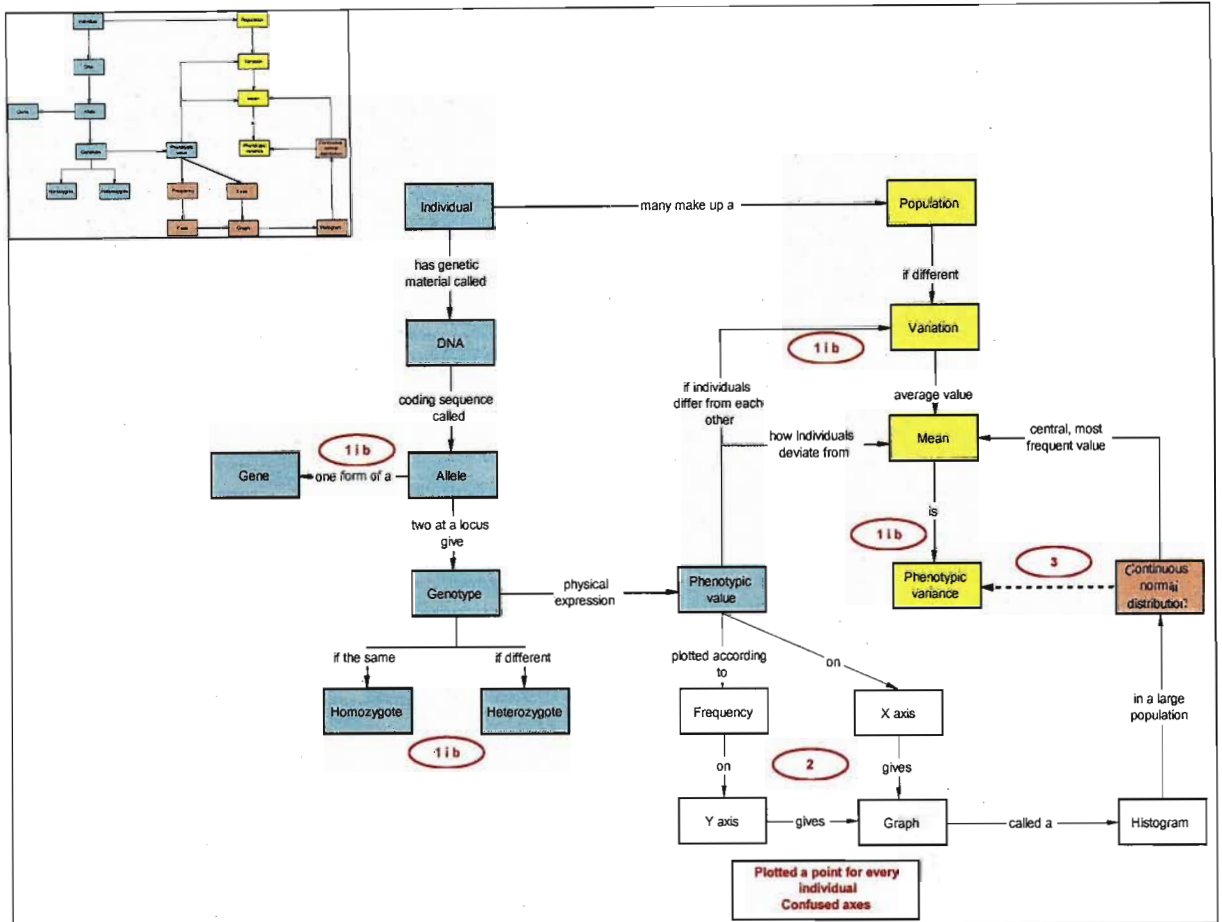


- S: The curve would be steeper – I think. [correct - the curve would be narrower and steeper]
- I: And you still think height is on the Y axis?
- S: Oh – less variance in the height. OK. So then X would be height and Y would be the number of individuals.
- I: Would that make more sense to you?
- S: I think so but I am a bit confused.

The interview transcript from student A thus indicated that she correctly linked the mean with the graph in question and knew that the curve would be steeper and narrower with less variance. However, this student incorrectly labelled the axes of the graph. These data support the findings from the student-generated concept maps that, notwithstanding the fact that students may have some idea of a definition of variance, they may still not be able to effectively apply this knowledge to concepts in genetics or to graphs such as a normal distribution.

A concept map of the interview with student A, which is also representative of the interview conducted with student B, was generated by the researcher (Figure 4.5). The concept map highlights that, although the students could give a correct definition of variance, they exhibited limited graphical understanding and this link was thus classified as incorrect. Their limited understanding of frequency distributions, as indicated by the preceding quotes from the interview transcripts, was demonstrated by their inability to group values into classes to form a histogram. Additionally, they also confused the X and Y-axes.

In order to create a visual representation of the status of the students' knowledge, concepts that the students did not understand were not coloured and an icon giving the "correct" map configuration (Figure 3.6) initially created by the researcher when developing the interview protocol was placed in the top left-hand corner. The presence of the non-coloured blocks at the bottom of Figure 4.5 indicated that the students were able to comprehend the more general concepts at the top of the hierarchy, such as values and variance, but that their understanding of topics became more difficult as an application of this foundational knowledge to graphs of a normal distribution was required.



Link classification: (1) correct, (2) incorrect, (3) missing, (i) defined, (ii) emerging, (a) example given, (b) a fundamental fact and (c) link explained by other links

Dotted lines: Incomplete understanding

Non-coloured blocks: Concepts not understood by the student(s)

Icon: "Correct" map configuration

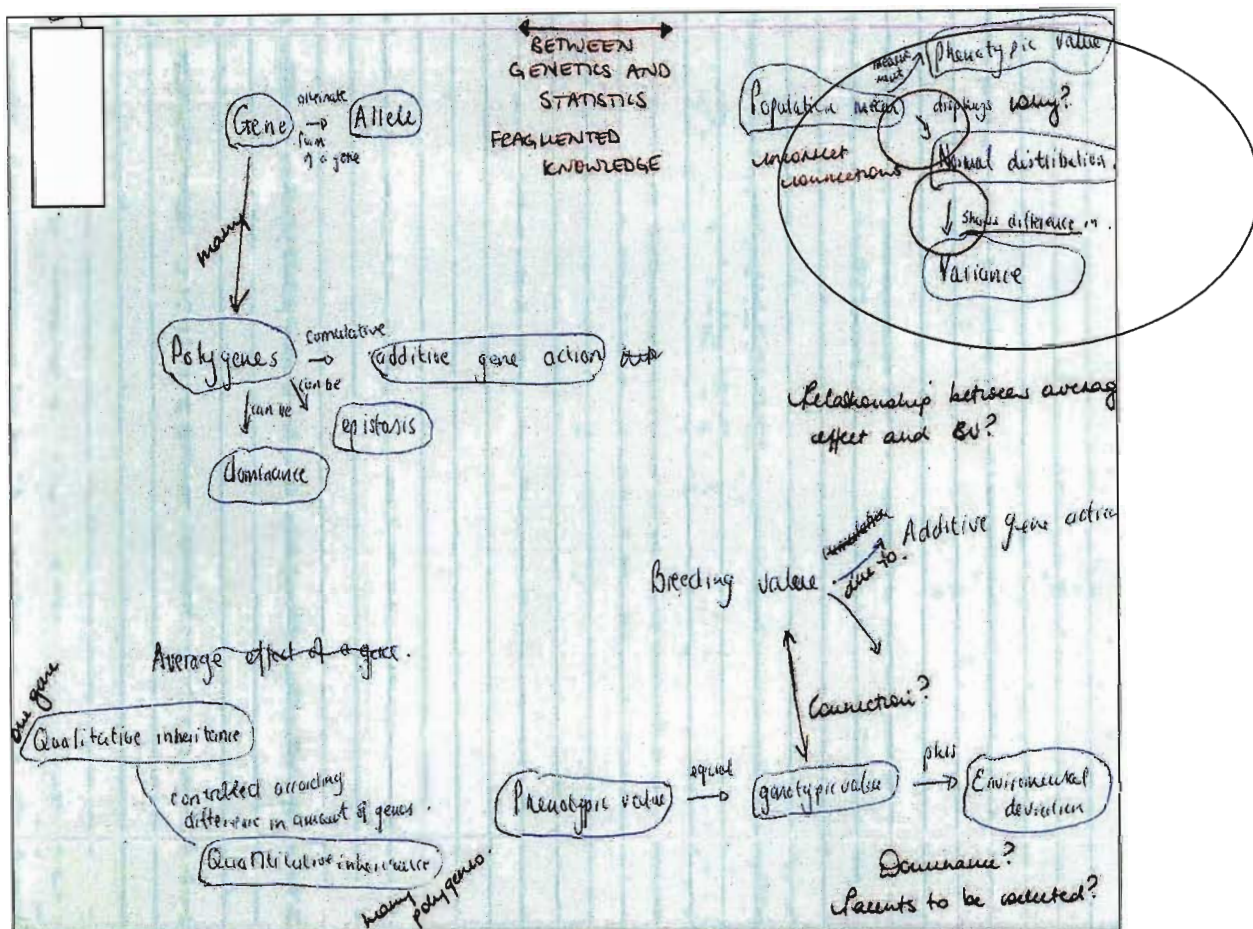
**Figure 4.5: Researcher-generated concept map depicting student A's conceptual framework at the start of the module, where the student had a foundational understanding of the descriptive statistic variance.**

Thus, in summary, the results obtained from students with some understanding of variance seemed to indicate that their knowledge of variance could have enabled them to link their prior knowledge of statistics to that of genetics as well as to link their knowledge of descriptive statistics, such as the mean and variance, to graphs of a normal distribution. However, it is interesting to note that most students only seemed to know a definition of variance, and perhaps how to calculate the value (their knowledge was classified as emerging), but were not always able to apply their knowledge.



**(c) Concept map from student with no understanding of variance**

An example of a concept map constructed by a student who typically showed all of the major shortcomings identified in the student-generated concept maps and who showed no understanding of variance is illustrated in Figure 4.6.



The writing in red represents the corrections made by the researcher that were returned to the student. The area of the concept map circled illustrates the fragmented nature of the student's knowledge; the statistical concepts are not linked to other ideas.

**Figure 4.6: Student-generated concept map highlighting a lack of understanding of key concepts and a highly fragmented cognitive structure.**

The shortcomings of the concept map presented in Figure 4.6 include a spoke map formation, disconnected or fragmented knowledge, poor integration of concepts and no hierarchical organisation of information. Furthermore, the concept map demonstrated that this student had a lack of understanding of variance, a limited understanding of the relationship between statistics and genetics as well as the

relationship between statistics such as variance and a normal distribution. Links between genetics and statistics and to variance were both classified as missing and the links to graphical representations were incorrect. This type of student-generated concept map suggested that a poor understanding of variance prevented students from understanding the importance of recognising the variation inherent in any population in the context of genetics.

**(d) Interviews with students with no understanding of variance**

The following data from three of the five students (designated C, D and E) interviewed, constitute evidence for alternative conceptions regarding the meaning of variance. The data further suggests that these alternative conceptions resulted in the students demonstrating difficulty in the interpretation of frequency distributions and an inability to link descriptive statistics with graphs of a normal distribution.

The following excerpt from an interview highlights one of the alternative conceptions held by these students with regard to the concept of variance. In this case, student C associates variance with change and not merely as a description of the current status of a population.

- I: So that's what you think of variation - something to do with differences or something to do with change. And variance?
- S: Quantify the amount of change. [student equates variation and variance with change and not difference]
- I: So is it a big change or a little change?
- S: Something like that.
- I: If I look at 10 individuals what's variance going to tell me about those 10 individuals?
- S: I don't know.
- I: You really don't know and this equation [equation provided] doesn't really help you?
- S: No.

Furthermore, a quote from the interview transcript of student D, demonstrates that the student may have been trying to remember a rote-learned definition of variance as he only knew that it has something to do with the words "mean" and "square".

- I: Do you think there is a relationship between the mean and the variance in a population?
- S: Well the mean is the square in a variance.
- I: The mean is the square in a variance?
- S: You square the mean to get the variance.
- I: Square the mean to get the variance?
- S: But the variance is a mean square ..... [laughter] I'm not sure.
- I: You think one is the square of the other?
- S: Yeah.

Student E, who did not attempt to group data in order to construct a frequency distribution when responding to the question below, illustrates the limited graphical understanding of students without a working knowledge of variance. This student tried to plot a different point on the graph for each observation.

Consider a group of people going to a Genetics conference in Durban. If all 100 of the delegates were weighed and a survey conducted on the influence of diet on levels of obesity at the start of the conference, could you draw a graph representing the weights of all the delegates?

- I: OK, so you'd have a point for every person?  
 S: Yes.  
 I: And it doesn't worry you that you might have 1 000 people – you are going to be very busy?  
 S: I can't think of another way.

In addition, the following quote illustrates how student E, who did not have a working knowledge of variance, was unable to reason with graphical representations of frequency distributions.

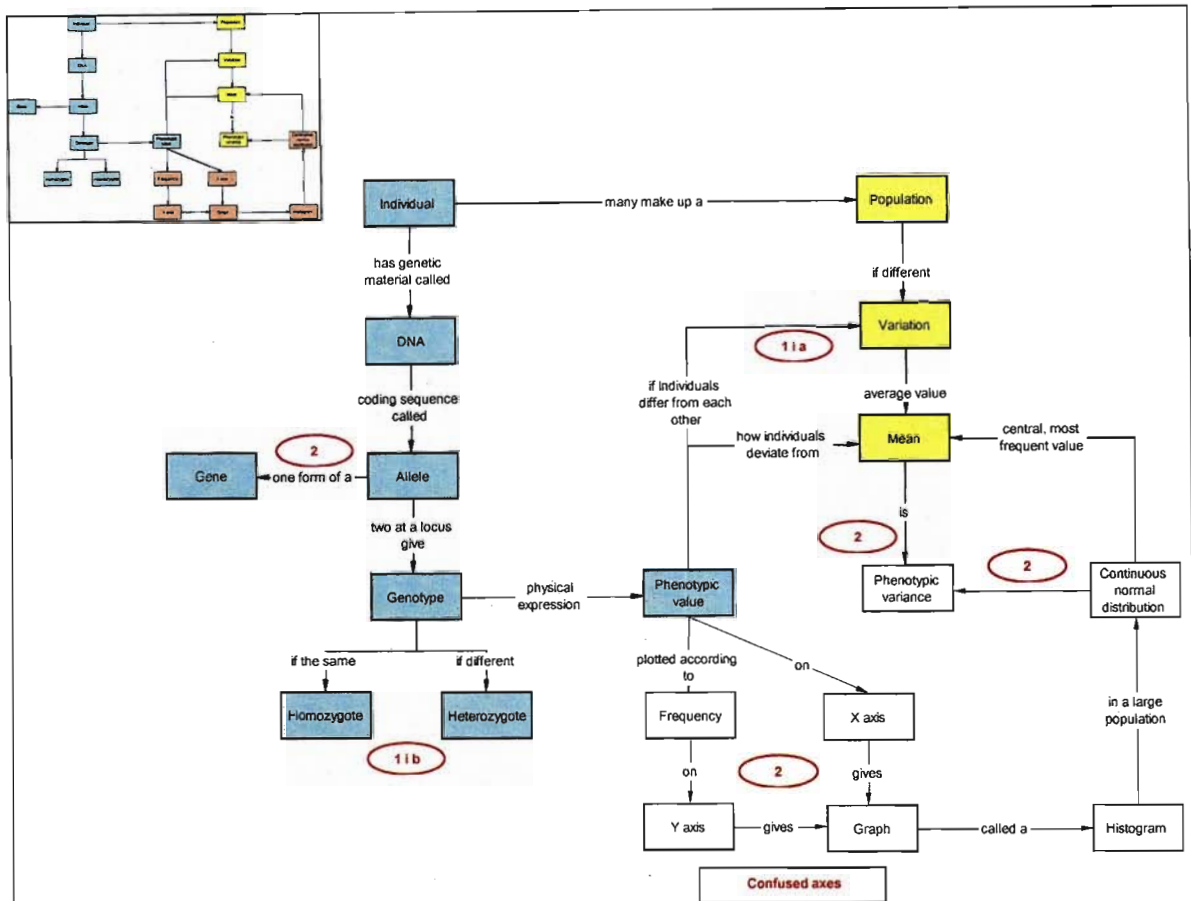
- I: Why do you think this tallest bar is somewhere here near the middle?  
 S: That is probably the mean taken from the two extremes.  
 I: The mean? OK. Why is it in the middle?  
 S: Because you added and divided it by 2 to get the mean. [incorrect understanding of how the mean is calculated]  
 I: So why should it be in the middle?  
 S: It has to be in the middle?  
 I: Has to be in the middle. OK if you have to redraw that graph with less variance how would you do it?  
 S: Well variance is square ..... something.  
 I: No just don't think about the formula now. How would you change the appearance of that graph? So if someone had to look at that one and another one that you drew next to it they would say oh this one has got less variance – how would you redraw it?  
 S: Well the curve would be much broader. [incorrect, the curve would be steeper and narrower]  
 I: The curve would be broader?  
 S: Be flatter.  
 I: Flatter? The top will come down?  
 S: The top will come down.  
 I: And the sides?  
 S: The sides will spread out.  
 I: Will spread and that will mean less variance? Why do you think that?  
 S: Well the mean will be much less.  
 I: So the mean will change. [incorrect, the mean does not necessarily change]  
 S: Variation from the mean will be less.

The opinion given by this student indicates that students without a sound understanding of histograms also had a limited understanding of variation and how it may be summarised. Such a lack of understanding is problematic in the context of

quantitative genetics as students need to understand why most quantitative traits are normally distributed and why genetic variation must be present before any changes can be made to the population. These results are supported by the findings of Meletiou and Lee (2002) on 33 statistics students at a university in the U.S.A. They concluded that students' understanding of histograms acted as a "stumbling stone" or as a "critical juncture" to students' understanding of the role of variation in statistics.

The researcher-generated concept maps from the interviews with students C, D and E were found to be highly similar. Thus only the researcher-generated concept map constructed from the interview with student E, who did not comprehend the concept of variance, is provided for discussion (Figure 4.7). This concept map highlights that the student gave an incorrect definition of variance (held an alternative conception) and therefore the link between the mean and variance is classified as incorrect. Furthermore, all the blocks below variance were not coloured, indicating that knowledge of variance is necessary before any of the links further down in the hierarchy could be made. The alternative conceptions, regarding the concept of variance, held by such students' thus seemed to act as a critical barrier to the application of their knowledge. This is evident from their difficulty with any application requiring knowledge of this statistic, such as the interpretation of graphical representations of a normal distribution, where the linkages between concepts were classified as incorrect.

These data thus led to the conclusion that as many as two-thirds of the students taking the module under consideration did not illustrate an understanding of the concept of *variance* at the start of a quantitative genetics module. This was evident as they were unable to link this concept with foundational genetics and statistics concepts and graphical representations in the context of quantitative genetics.



Link classification: (1) correct, (2) incorrect, (3) missing, (i) defined, (ii) emerging, (a) example given, (b) a fundamental fact and (c) link explained by other links

Dotted lines: Incomplete understanding

Non-coloured blocks: Concepts not understood by the student(s)

Icon: "Correct" map configuration

**Figure 4.7:** A researcher-generated concept map depicting the conceptual framework of student E at the start of the module, when the student had no understanding of the descriptive statistic variance.

### 4.3.3 Students' understanding of heritability

An analysis of both the student-generated concept maps and the concept maps constructed by the researcher from interview transcripts at the end of the quantitative genetics module were used to answer the third sub-question: To what extent does students' understanding of variance influence students' understanding of, and ability to apply, higher order topics such as heritability?



Students' understanding of variance and how it impacted on their knowledge of heritability was inferred from the manner in which they linked the following:

- Concepts related to individual values and population statistics. Particular note was taken of the manner in which students linked the concept of the breeding value of an individual and the concept of the additive variance of a trait within a population.
- The variance and the heritability of a trait in a population. This was considered important as the heritability of a particular trait in a population is calculated as the ratio of two variances.
- The heritability of a trait and the selection of an appropriate breeding strategy. Students' ability to apply their knowledge was inferred from whether they linked the concept of heritability to a practical application such as the determination of whether it would be preferable for a breeder to practice selection or crossbreeding.

The results obtained from the 17 student-generated concept maps produced at the end of the module, which were classified according to the above-mentioned three relationships, are presented in Table 4.3. The data indicate that a large number of students had a limited grasp of the concepts of variance and heritability. Many of the student-generated concept maps showed that, notwithstanding students' algorithmic knowledge regarding the calculation of heritability as the ratio of two variances, they still considered heritability as an individual measure.

**Table 4.3: Analysis of student-generated concept maps constructed at the completion of the module.**

Relationships investigated	Percentage of students Link classification		
	Missing	Incorrect	Emerging
Values and variances	29	24	47
Variance and heritability	29	36	35
Heritability and breeding strategy	71	6	23

Of the total number of maps analysed at the end of the module, 29% of students were still not able to link individual and population measures, such as breeding value and additive variance, while 24% of the students linked these concepts incorrectly. This result infers that these students did not have a sound understanding of variance.



Of particular importance is that a large group of students (65%) either did not link, or incorrectly linked, the concepts of variance and heritability. This implied that the understanding of variance could be a prerequisite to the understanding of a key concept in quantitative genetics, that of heritability. Furthermore, 77% of students did not, or incorrectly, applied the concept of heritability to the selection of an appropriate breeding strategy.

These results indicated that, even after receiving formal lectures on the foundational principles of quantitative genetics, a large proportion of the class did not have a sound understanding of the key concept of heritability. This may have prevented these students from understanding the manner in which such concepts are used in practical applications. Furthermore, it became evident that an understanding of variance should be reached at the start of the module as the foundational principles of quantitative genetics, such as the reasoning behind most quantitative traits being normally distributed and the understanding of heritability, all depend on an initial understanding of variance.

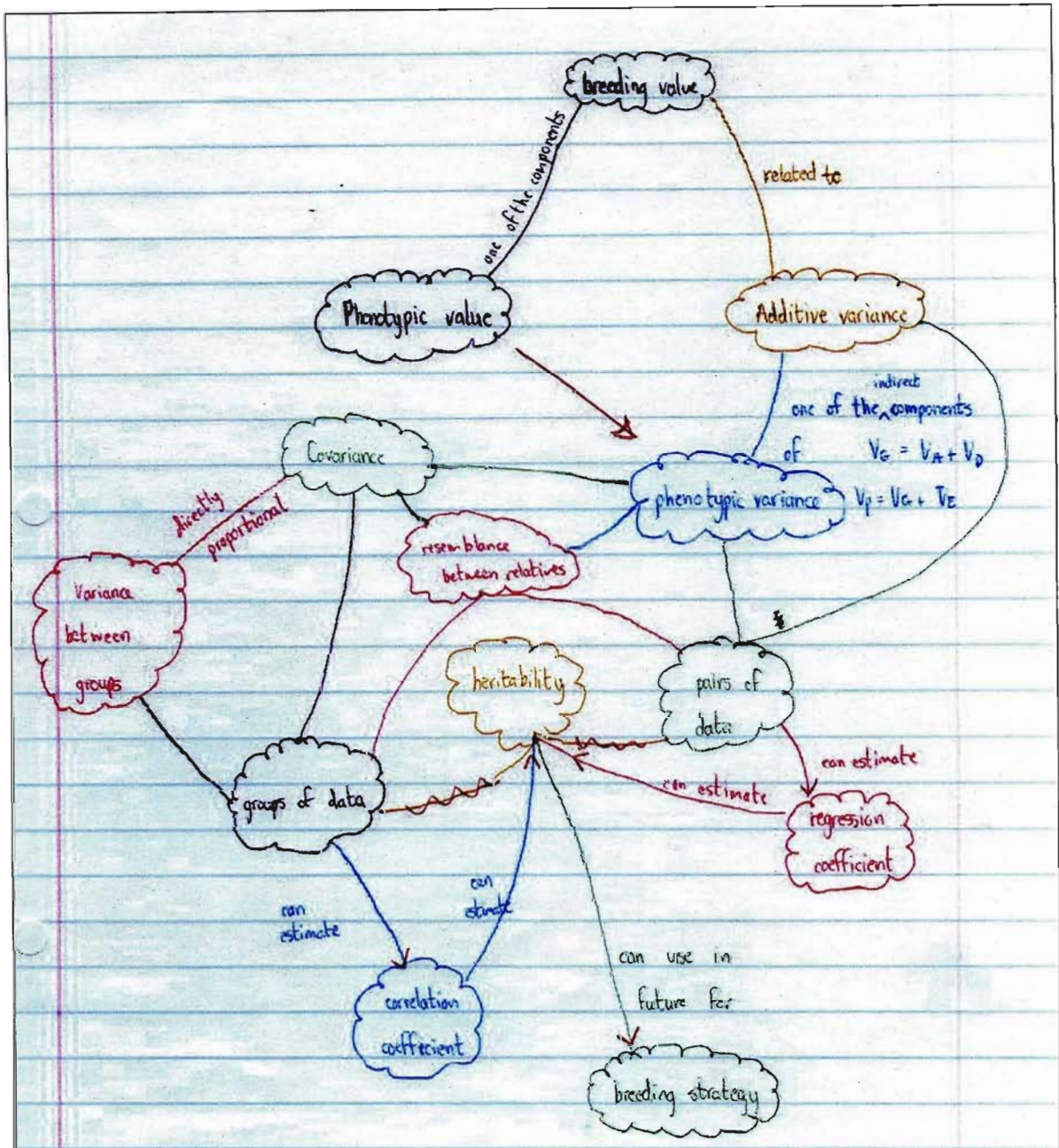
Three examples of student-generated concept maps are provided in this section as they represent the three primary types of maps that were produced by students at completion of the module. The concept maps provided are representative of students with:

- Some understanding of variance, heritability and the application of the heritability.
- Some understanding of variance and heritability but who did not exhibit the ability to apply their knowledge.
- No understanding of variance or heritability and who could not apply their knowledge to the determination of a breeding strategy.

In order to add support to the data obtained from the student-generated concept maps three students, who had performed poorly in a class test, were chosen to be interviewed. Quotes from the interviews with these students (designated G,H and I) and a researcher-generated concept map constructed from the interview data (Figure 4.10) are therefore discussed.

**(a) *Concept map from student with some understanding of heritability***

An example of a concept map produced by a student who showed some understanding of the concepts of variance and heritability, and an ability to apply her knowledge, is provided in Figure 4.8. This student seemed to understand that there was a link between breeding value and additive variance, and that the additive variance was one component of the phenotypic variance. She was also able to connect the regression coefficient and the concept of heritability, indicating that she had some knowledge of how the heritability of a trait is estimated. In addition, she linked the concept of heritability to a breeding strategy demonstrating that she understood that the heritability of a trait is used for the purpose of deciding on an appropriate breeding strategy for the trait in question. It is, however, important to note that this student's knowledge must still be classified as emerging as many of the labels used to link concepts were vague. For example, breeding value was simply seen as "related to" additive variance. In addition, certain links were omitted, for example, there was no clear link between the concepts of variance and heritability. This concept map, which is typical of those constructed by students with some understanding of heritability, suggested that students' knowledge of variance assisted them in the understanding of the concept of heritability and in the application of their knowledge in a practical manner.



The writing in red represents the corrections made by the researcher and returned to the student.

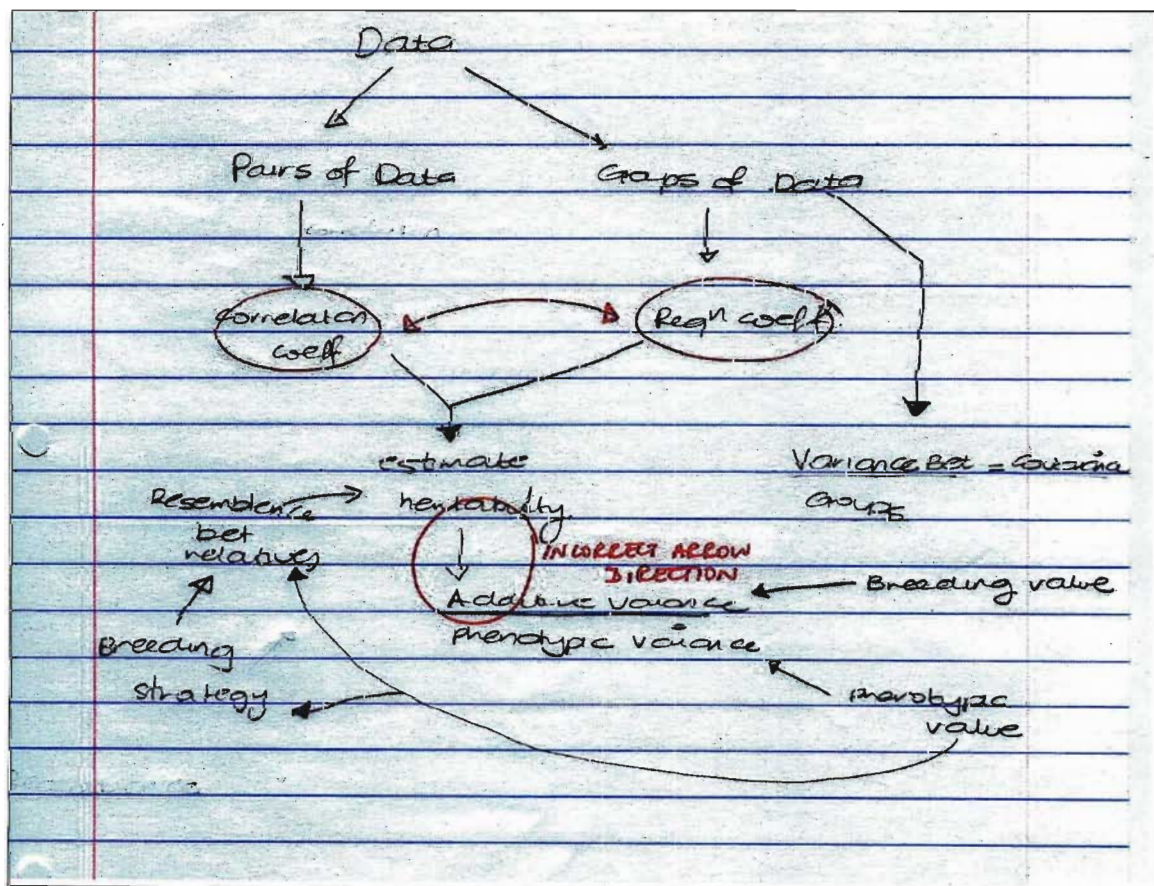
**Figure 4.8:** Student-generated concept map showing some understanding of the concepts of variance and heritability and the application of heritability.

**(b) Concept maps from students without a sound understanding of heritability**

An example of the second type of student-generated concept map was constructed by student H (Figure 4.9). In this concept map the student showed some



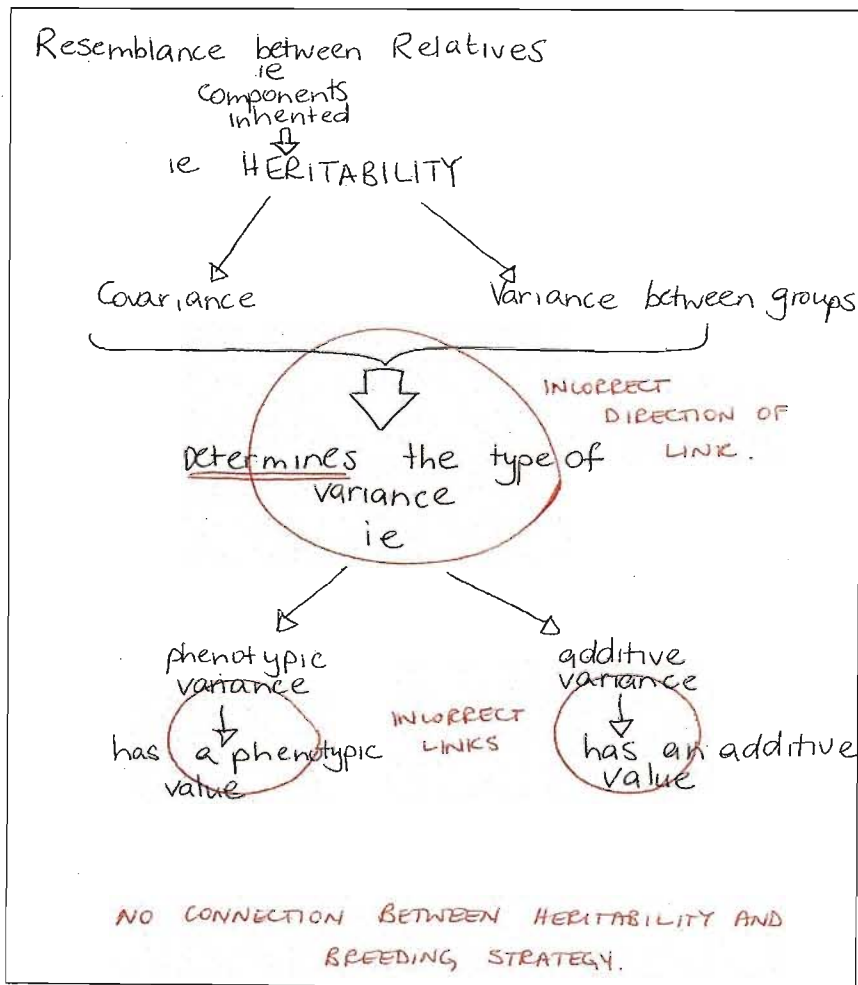
understanding of variance as she linked breeding value and additive variance, as well as phenotypic value and phenotypic variance. However, as these links were not labelled one cannot infer her level of understanding. In this map, the student used an arrow in the incorrect direction to connect the concept of heritability and the method whereby heritability is calculated. This implied that the student did not really understand the concept of heritability. Furthermore, there was no link between heritability and its application to the determination of a breeding strategy. The interpretation of this map thus implied that the student did not show a sound understanding of heritability as she was unable to apply her knowledge to the practical exercise of selecting an appropriate breeding strategy. It could therefore be concluded that this student's knowledge was not "useful" to her when considering the links under investigation.



The writing in red represents the corrections made by the researcher and returned to the student.

**Figure 4.9: Student-generated concept map showing the incorrect connection between variance and heritability.**

The final type of concept map to be discussed in this section is given in Figure 4.10. The student who constructed this concept map did not seem to understand the concepts of variance or heritability and was unable to apply her knowledge. Her lack of knowledge of variance is illustrated by the manner in which she stated that "additive variance had an additive value" implying that variance was an individual and not a population measure. She also incorrectly indicated that the heritability determines the type of variance in the population where the opposite is the case. Perhaps as a consequence of these deficiencies in her knowledge of the concepts of variance and heritability she was not able to include the concept of "breeding strategy" in her concept map, thereby demonstrating that she was unable to see any practical application of her knowledge.



The writing in red represents the corrections made by the researcher and returned to the student.

**Figure 4.10: A student-generated concept map showing no understanding of the concepts of variance and heritability or their application.**

The student-generated concept maps constructed at the completion of the module, like those constructed by students at the start of the module, seemed to indicate that an understanding of variance may be required for an understanding of the foundational principles of quantitative genetics. This is because students without a good grasp of the concept of variance were unable to make meaningful connections between values and variances and consequently between variance and heritability. Furthermore, it was evident that an understanding of the concept of heritability was required before students were able to demonstrate an ability to apply their knowledge to the selection of a breeding strategy.

**(c) Interviews with students without a sound understanding of heritability**

Three students designated G, H and I, were selected to be interviewed. The primary difficulty identified with *all three* of these students was a lack of understanding of heritability. In addition, these students demonstrated an incorrect or limited understanding of the concept of *additive variance*. It may be inferred that the alternative conceptions regarding the basic concept of variance seemed to impact on the students' understanding of additive variance and subsequently heritability, which is calculated as the ratio of two variances. A prevalent alternative conception noted concerning additive variance and heritability was the conception that these were individual, and not population, measures. The primary repercussion of this alternative conception seemed to be the incapacity of these students to relate heritability to the relationship between the phenotypic value and the breeding value of individuals in a population. Furthermore, students with this alternative conception seemed to be unable to meaningfully apply the concept of heritability to the determination of a breeding strategy.

The following quote illustrates the fact that student G did not understand the concept of variance and thought that the additive variance measured the differences between additive genes. In addition, she incorrectly associated the concepts of breeding value, additive variance and heritability and thought of them all as being individual measures.

- I: Tell me what you think what the additive variance is?  
S: The additive variance is the variance of the genotype which is due to the...[inaudible]?  
I: Okay, now try to give me a definition. If you were talking just about the variance of anything, what does variance measure?  
S: It's the differences between individuals.  
I: If we are looking at additive variance we're looking at differences in what?  
S: The additive genes.



- I: Or the breeding values?  
 S: Differences of breeding values. Okay.  
 I: You haven't thought of that?  
 S: No.  
 I: So you never got to that point, just thinking, I've got breeding values and they're not all the same.  
 S: No, I never thought of that.  
 I: You knew it had something to do with additive gene action.  
 S: I knew it had something to do with, yes, additive gene action. But where additive gene action and the breeding value were related, was fuzzy.  
 I: Do you think that additive variance is transferred from one generation to another?  
 S: Yes. [This illustrates that this student does not understand that variance is just a statistic and not something that can be inherited]  
 I: You do? Why?  
 S: Because when we work out the heritability you use that additive variance over the total variance and that's what's inherited. [Student gives a rote-learned definition]  
 I: That is what is inherited?  
 S: Yes.  
 I: You're sure?  
 S: No.  
 I: Do you think that these things go together, a high breeding value, a high additive variance, a high heritability? That if one is high, they must all be high?  
 S: Okay. I think that somehow I've associated the ideas of breeding value heritability, but not interchangeable but close to that.  
 I: Do you agree with me that maybe that you're associating the three?  
 S: Yes, I am defiantly associating the three.  
 I: Do you associate a whole lot of breeding values with an additive variance?  
 S: No, I think just one. Variance is...I'm fuzzy about variance.  
 I find it difficult to think of variance as a whole population and then each of them have breeding values and then all of them have heritability. Also the thing when variance is about a population and a breeding value is one individual. I have a problem with that... and then heritability is for a population not for an individual but you can work out the heritability for the individual.  
 I: What do you think is the main problem you had going into this test?  
 S: Something that you didn't understand properly.  
 S: The differences between the variance and the actual values and whether the heritability fits in with the variance or the value.  
 I: And you thought what?  
 S: I thought the heritability is an indication of the values. I associated heritability with an individual. So I need an actual breeding value and an actual phenotypic value, not a variance. I'm not sure how to work with variance.  
 I: So the values and the variances are getting confused?  
 S: Yes.

The premise that knowledge of variance and heritability is necessary for an integrated understanding of quantitative genetics is further substantiated by the following excerpts from the interview conducted with student H at the completion of the module. During the interview this student did not show a sound understanding of variance and thought that it related to differences between groups.

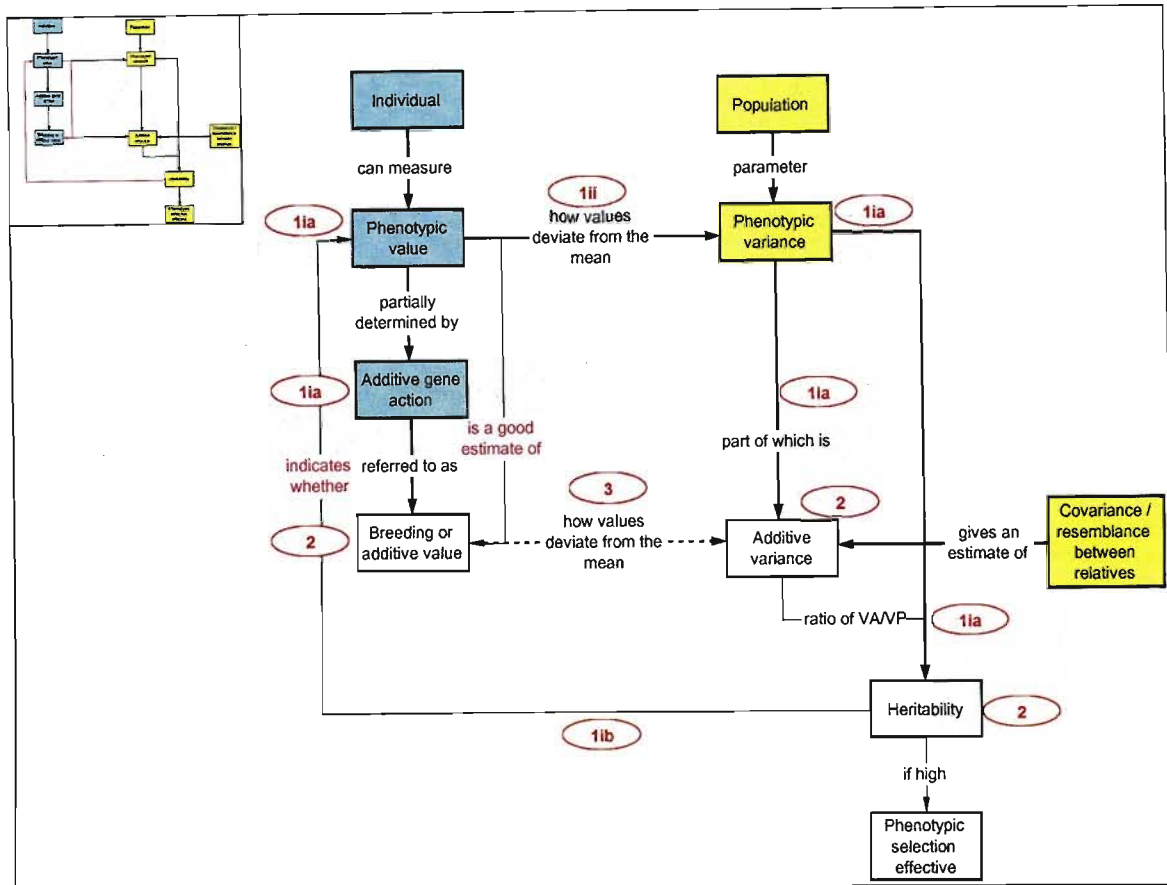
- I: What do you mean by variance?  
 S: The differences in...

- I: In what?  
S: Differences between groups.  
I: Between groups?  
S: Yes, in a population.

The above-mentioned alternative conception regarding variance seemed to then impact on the student H's subsequent understanding of the concepts of additive variance and heritability. This student confused individual and population measures and held the alternative conception that heritability is a value associated with an individual. This is illustrated by the following two quotes taken from the interview transcript.

- S: "Breeding value basically is the value that's passed on. An individual with a high breeding value doesn't necessarily mean that they have a high heritability."  
  
S: Well in my head it goes an individual with a high heritability can be selected for the next generation.  
I: Not an individual with a high breeding value?  
S: No, an individual with a high heritability.

A depiction of the conceptual framework of student G, which is also typical of the researcher-generated concept maps constructed from the interviews conducted with students H and I, is given in Figure 4.11. The researcher-generated concept map indicated that these students held alternative conceptions regarding breeding value, additive variance and heritability, with linkages to these concepts being classified as incorrect. These alternative conceptions then seemed to impact on the students' ability to relate the concept of heritability back to the implied relationship between the phenotypic and breeding values of individuals in the population. This link was therefore classified as incorrect. The non-coloured blocks below the concept of variance indicate that all concepts lower in the hierarchy were difficult for these students to understand. Furthermore, knowledge of these concepts seemed to impact on their understanding of the links between concepts higher in the hierarchy and thus the link between the phenotypic value and breeding value of individuals is classified as incorrect. These results thus implied that these students were unable to apply their knowledge of the concept of heritability.



Link classification: (1) correct, (2) incorrect, (3) missing, (i) defined, (ii) emerging, (a) example given, (b) a fundamental fact and (c) link explained by other links

Dotted lines: Incomplete understanding

Non-coloured blocks: Concepts not understood by the student(s)

Icon: "Correct" map configuration

**Figure 4.11: Researcher-generated concept map depicting student G's conceptual framework at the completion of the module.**

The results obtained from the interviews conducted with the three selected students confirmed the findings of the student-generated concept maps that a sound knowledge of variance and heritability is required before students are able to recognise the practical application of their knowledge. Thus students who held alternative conceptions, or who did not correctly link concepts, were unable to demonstrate an understanding of, or ability to, apply the fundamental principles of quantitative genetics. They thus showed poor integration of knowledge and alternative conceptual frameworks. The finding that knowledge of variance was a pre-requisite to the understanding of heritability and its application was substantiated by an overall analysis of the student-generated concept maps. These results are summarised in Table 4.4.

**Table 4.4: Analysis of student-generated concept maps indicating that knowledge of variance and heritability is required for the application of the foundational principles of quantitative genetics.**

Knowledge of variance	Knowledge of heritability	Ability to apply knowledge
Yes (8)	Yes (7)	Yes (5)
		No (2)
	No (1)	Yes (0)
		No (1)
No (9)	Yes (2)	Yes (1)
		No (1)
	No (7)	Yes (1)
		No (6)

The results indicated that 82% of the concept maps constructed by students conformed to the following pattern:

- The students understood variance, heritability and the application of these concepts (Illustrated in green in Table 4.4).
- The students understood the concept of variance but not the concept of heritability or its application.
- The students did not understand the concepts of variance or heritability and were not able to apply their knowledge (Illustrated in blue in Table 4.4).

Five of the 17 students who constructed concept maps showed some knowledge of variance and heritability and were able to illustrate some ability to apply their knowledge (example given in Figure 4.8), whereas 6 students did not seem to understand either of the concepts or apply them to the determination of a breeding strategy (example given in Figure 4.10). Two students showed some knowledge of variance and heritability but could not apply their knowledge and one student exhibited some knowledge of variance but not heritability and could not practically apply his knowledge (example given in Figure 4.9). Only 3 of the 17 students (18%) did not fit the pattern described above.

The results thus indicated that approximately one third of the students (35%) who could not correctly link values and variances, and therefore did not demonstrate a sound understanding of variance, were also unable to correctly link variance and heritability, as well as heritability and its application. Furthermore, just over half (53%) of the students who had a problem with the link between variance and heritability,



and who therefore did not illustrate that they understood the concept of heritability, could also not link heritability with a practical application. These results showed the “knock on effect” of deficiencies in the understanding of these key concepts.

It may be concluded that this investigation revealed that an integrated knowledge of the concepts of *variance* and *heritability* as population measures was necessary before students could apply their knowledge and effectively solve problems in this field of genetics. This result is supported by the findings of Konold *et al.* (1997) who concluded after investigating four university students' problem-solving performance in the context of statistics that students' inability to make the transition from thinking about individuals to thinking about groups and populations may act as a “critical barrier” to a sound understanding of the relationships between concepts and thus students' ability to solve problems.

#### 4.4 DISCUSSION OF RESEARCH FINDINGS

Numerous researchers have proposed terms to describe concepts which students must understand before they are able to build on their knowledge and thus learn in a meaningful manner. These include the terms “critical conceptions” and “protoconcepts”, described by Fisher and Moody (2000: 74) as concepts which “interfere with [the] learning of numerous higher level topics”. The terms “critical concepts” and “propositions” have also been used by Wallace and Mintzes (1990) in the description of concepts and propositions which are central to the understanding of a subject area. Konold *et al.* (1997) referred to “critical barriers” when investigating conceptions held by statistics students which could interfere with students' problem-solving ability. Similarly, two papers written on a study conducted during an introductory statistics course referred to critical junctures as being “stumbling stones” to future understanding (Meletiou and Lee 2002; Meletiou-Mavrotheris 2002). Elaborating on this idea and considering *when* students may require knowledge of certain concepts, Trowbridge and Wandersee (1994) described “critical junctures” as “conceptual watersheds” that divide students into two groups, those who have the necessary prior knowledge of foundational concepts and those that do not. They further proposed that it is important to identify critical junctures in a science module because unified understanding of the module, after the critical juncture, may not be possible for the students lacking the required foundational knowledge (Trowbridge and Wandersee 1994).



In this investigation it has been shown that many students are unable to integrate their knowledge of key concepts in quantitative genetics such as variance and heritability. Furthermore the results infer that students required knowledge of variance and heritability before they were able to fully understand the foundational principles of quantitative genetics. These concepts could thus be termed *critical concepts*.

The results of this investigation also indicated that concept mapping is an effective tool for the analysis of the integration of students' knowledge in science modules. The integration of students' knowledge and the possible presence of *critical concepts* may be inferred by an analysis of the hierarchical organisation of concept maps as well as the number, clarity and correctness of the linkages between concepts.

As this study was the first of its kind in the field of quantitative genetics, the results can only be compared to those obtained from other disciplines which are based on statistical principles. Accordingly, Schau and Matter (1997) studied the use of concept map techniques in applied statistics courses and concluded that connected understanding is of critical importance in statistics education. In addition, they pointed out that statistics is only useful in the application of knowledge and that students cannot apply statistical concepts without the relevant structural knowledge. The present study confirms these findings as an understanding of quantitative genetics is dependent upon a thorough understanding of foundational statistical concepts such as variance and heritability. Where students did not illustrate connected understanding of foundational concepts, they were unable to understand new concepts in a meaningful manner and to apply their knowledge in practical situations.

In this investigation the initial week of the module could represent a *critical period* (Pearsall *et al.* (1997) or *critical juncture* (Trowbridge and Wandersee 1994) at which students must clarify their knowledge of variance before they will be able to learn higher order concepts in the context of genetics. In a study on 68 science majors and 93 non-science majors which investigated successive changes in the knowledge structures of first year university students in the U.S.A. using student-generated concept maps, Pearsall *et al.* (1997) found that the majority of knowledge restructuring occurred during the first few weeks of the module, during which time teachers should employ strategies to assist students in organising their knowledge constructively so that subsequent learning may take place. In this investigation an additional *critical juncture* was identified; introduction of the concept of heritability. At the introduction of this concept students must first establish a sound understanding of

this concept before they will be able to apply their knowledge to the solution of practical problems.

From an epistemological point of view, Liu (2004) stated that if a student's belief regarding a concept is intelligible, then there should be type-of relationships between concepts. If a student's understanding is plausible then there should be cross links between different branches of the concept map and finally, if the link is fruitful an application of knowledge should be evident. The student-generated concept maps and interviews with students, in this study showed that the concepts of variance and heritability may have been intelligible or even plausible to the students in that they knew a definition of the concept and were able to calculate the statistics, but they were unable to link the concepts to one another and thus seemed unable to apply their knowledge to solve practical problems. It was interesting to note that the concept maps constructed, in the current investigation, at the completion of the quantitative genetics module did not illustrate any significant improvement in the perceptions of students of the concept of variance. This observation indicated that the formal transmission method of lecturing followed at this university does not effectively address the fragmented nature of students' cognitive frameworks or address specific alternative conceptions harboured by many students. Consequently, students were unable to effectively learn higher order concepts, such as those of additive variance and heritability in the context of quantitative genetics. The therapeutic phase of this investigation thus aimed to address this problem.

#### 4.5 CONCLUDING REMARKS

The results presented and discussed in Chapter 4 indicate that *variance* and *heritability* are both concepts which are central to a student's ability to construct sound knowledge and understanding of the foundational principles of quantitative genetics. Consequently, the results suggest that variance and heritability may be *critical concepts*. Further longitudinal studies of students' conceptions over time would need to confirm this conclusion. The results presented in this chapter did, however, indicate the need to investigate students' difficulties with the concepts of variance and heritability and the need to gather empirical evidence of alternative conceptions which may be held by students. This was the focus of the component of the research presented in Chapter 5.

## CHAPTER 5

# STUDENT DIFFICULTIES WITH QUANTITATIVE GENETICS

**Research Question 2:**

Which concepts in quantitative genetics do students find difficult?

**Research Question 3:**

What is the nature of the difficulties experienced by students taking a module in quantitative genetics?

**Research Question 4:**

What are the possible source(s) of students' difficulties with quantitative genetics?

### 5.1 INTRODUCTION

Previous research (Cooper 1998; Podlich and Cooper 1998), as well as the many years of teaching experience of the researcher, have indicated that quantitative genetics is a subject which many students find difficult. During this investigation an attempt was made to assess the level of integration of students' knowledge of quantitative genetics and their ability to link key concepts. As detailed in Chapter 4, the investigation revealed two key concepts namely, *variance* and *heritability*, which students seemed to find difficult to link to other concepts and which seemed necessary for their understanding of higher order concepts. These were termed *critical concepts*. The investigation then proceeded, in an iterative manner, with the second component of the research aiming to acquire empirical evidence of the nature of the difficulties experienced by, and specific alternative conceptions held by students with regard to concepts in quantitative genetics.

The identification of student difficulties, including alternative conceptions, was undertaken using the theory of constructivism as the underlying theoretical framework (Chapter 2). The key principle of constructivism states that knowledge is not passively transferred from the lecturer to the student. Rather, students construct

their own meanings of concepts, using what they already know (Bahar *et al.* 1999b). However, many students hold a passive view of learning in that they view the learning of science as an accumulation of facts and mathematics as memorization of formulas (Treagust *et al.* 1996a). This attitude of students towards learning may lead to knowledge being assimilated in a fragmented manner thus preventing the meaningful acquisition of new information, leading to difficulty in the understanding of a subject and encouraging the development of alternative conceptions (Eylon and Linn 1988). Knowledge of students' prior knowledge, on entry to a module is thus necessary before any insight into students' ways of thinking and understanding of a particular field of science may be obtained. For this reason students knowledge of concepts on entry to a module (*prior knowledge concepts*) were initially assessed. Thereafter, their understanding of concepts taught during the module (*quantitative genetics concepts*) was investigated and the manner in which their prior knowledge impacted on their subsequent learning of concepts in quantitative genetics noted.

As discussed in Chapter 1, there is a dearth of previous research on the existence of student difficulties and alternative conceptions in the context of quantitative genetics. This component of the investigation therefore aimed to:

- (a) Identify any difficulties experienced by students, including alternative conceptions.
- (b) Estimate the incidence of all difficulties and alternative conceptions.
- (c) Rank the concepts probed in order of their relative difficulty.
- (d) Describe the *nature* of the difficulties experienced by students.
- (e) Model the source(s) of the identified difficulties.

## 5.2 METHODOLOGY EMPLOYED

To investigate student difficulties with quantitative genetics three different methods of data collection were used namely multiple-choice diagnostic tests, interviews with selected students and a word association study. The details thereof are provided in sections 3.2.3, 3.2.4 and 3.3.2, respectively. The analysis of data was undertaken in three stages:

- (1) The identification of students' difficulties and alternative conceptions.



(2) Description of the *nature* of students' difficulties and alternative conceptions. (3) The formulation of a model of the source(s) of the identified student difficulties and alternative conceptions.

The first stage of the data analysis process addressed Research Question 2 and involved an assessment of students' answers to the multiple-choice diagnostic tests. The aim was two-fold: firstly, to identify and estimate the incidence of difficulties experienced by certain students for each item on the multiple-choice diagnostic tests. This process was repeated for the student data collected from the three years during which the tests were administered. Secondly, to use the Rasch model to rank the items on the multiple-choice diagnostic tests in order of their relative difficulty. This process was conducted on data from the 2004 student group who completed the final versions of the multiple-choice diagnostic tests.

Students were asked to complete a multiple-choice diagnostic test at the commencement of the module to gather data on student's pre-instructional conceptions (prior-knowledge diagnostic test). In addition, a further multiple-choice diagnostic test was completed by the students at the end of the module, to obtain information on alternative conceptions that may have developed during the teaching process (post-teaching diagnostic test). Each item of the multiple-choice diagnostic tests probed students' understanding of certain concepts, particularly those of *variance* and *heritability*, the critical concepts previously identified.

During the second stage of data analysis the results obtained from data, collected both prior-to and post-teaching of the modules under consideration, were synthesized to provide an overall understanding of the *nature* of the difficulties experienced by students taking introductory modules in quantitative genetics, thereby addressing Research Question 3. This analysis entailed a more in-depth qualitative assessment of the reasons given for the students' choice of answer given on the multiple-choice diagnostic tests, an analysis of interview transcripts and the results of a word association study. This analysis revealed further insight into the reasoning processes undertaken by students and validated and supported the categorisation of student difficulties from the multiple-choice diagnostic tests.



The final stage of the data analysis process aimed to answer Research Question 4 and involved the formulation of a model of the possible source(s) of students' difficulties and alternative conceptions. This required an inductive analysis of answers given by students on the diagnostic tests, along with the more in depth probing of students' cognitive structures during student interviews and the word association study.

### 5.3 RESULTS AND DISCUSSION

An analysis of the answers given by students on the multiple-choice diagnostic tests, as well as the reasons students gave for their answer choice, interviews with certain students and the word association study aimed to address Research Questions 2, 3 and 4.

#### 5.3.1 Identification of student difficulties

Applying the theory of constructivism, the researcher deemed it necessary to test students' knowledge before starting a module in quantitative genetics. This was to ascertain the status of their knowledge of concepts, termed *prior knowledge concepts*, which the students had learned in both genetics and statistics modules undertaken by the students in the previous semester. As *variance* had been identified by the researcher as a *critical concept*, particular attention was paid to the construction of items that probed students' understanding of the terms *variation* and *variance*. Furthermore, students' ability to apply their knowledge of *variation* and *variance* in the construction and interpretation of histograms was investigated. At the completion of the module, students' knowledge was assessed to ascertain what they had learned during the module; their knowledge of *quantitative genetics concepts*. In this assessment attention was paid to students' understanding of *heritability* as it was also previously identified as a *critical concept*. Students' ability to apply their knowledge of *quantitative genetics concepts*, including heritability, to frequency distributions was also included in the study.

Students' difficulties and alternative conceptions for each concept probed by both the prior-knowledge and the post-teaching diagnostic tests were identified and the incidence of each difficulty or alternative conception calculated. Thereafter, the

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relative difficulty of both the *prior knowledge concepts* and *quantitative genetics concepts* was determined using the Rasch model.

**(a) Student difficulties with prior knowledge concepts**

*Description and incidence of difficulties*

Many students were found to experience a number of difficulties in understanding and applying the concepts probed by the prior-knowledge diagnostic test. Students' understanding of the concepts of variation and variance, as well as their ability to apply these concepts, was probed by the prior-knowledge diagnostic test. Students' ability to apply these concepts was primarily determined by their ability to construct and interpret histograms.

A description of the difficulties and alternative conceptions found from the multiple-choice diagnostic tests used in this investigation and the incidences thereof are given in Table 5.1. The questions and their corresponding answers are given in Appendix 4 on page 299. For clarity and purposes of comparison the incidences are cited as percentages. The number of students in each module may be found in Table 3.2 on page 77.

The results show that up to 78% of students exhibited difficulty in understanding and distinguishing between the concepts of variation and variance (items 1, 3 and 4). As a consequence of this difficulty, and the observation that as many as three quarters of any student group had a limited understanding of variance, the students were unable to apply the concept of variance in problem-solving exercises (for example, item 4). Furthermore, approximately one-third of each student group showed difficulty in constructing (items 6 and 7) or interpreting histograms (item 2).

**Table 5.1: Description and incidence of difficulties and alternative conceptions held by students on entry to a quantitative genetics module during 2002, 2003 and 2004**

(- indicates that the question was not asked of that student group)

Concept probed	Item	Difficulty or alternative conception	Incidence (%)		
			2002 n = 40	2003 n = 22	2004 n = 32
Understanding of variation and variance	1	Variation and variance are dynamic concepts associated with change in a population and not differences.	-	8	12.5
		Confusion between variation and variance.	75	49	68
Application of graphical understanding	2	Association of frequency with variation and not value.	49	23	41
		Association of the presence of a "pattern" with the absence of variation.	26	15	25
Application of variation to an inbred population	3	Confusion between variation and variance.	-	12.5	22
		An inbred population has no variation as there are no heterozygotes.	30	30	16
		Variation and variance are dynamic concepts associated with change in a population and not differences.	10	10	12.5
Application of variance	4	Confusion between variation and variance.	-	74	78
		Association of variation with heterozygosity.	4	16	12.5
		Association of variation with frequencies or ratios.	-	4	31
		Association of variance with range.	-	4	6
Status of population when variance = 0	5	There will be no variance in population when the mean is zero or one.	33	14	19
		Variance is associated with change or equilibrium.	16	4.5	12.5
Construction of frequency distributions with discrete values	6	Line graph drawn.	-	12.9	41
		Insufficient understanding of the functions of the X and Y axes – confusion between histograms and scatterplots.	-	22.6	37.5
Construction of frequency distributions with continuous values	7	Discontinuous distribution.	-	-	19
		No grouping of data, one point plotted per individual.	-	-	16
		Insufficient understanding of the functions of the X and Y axes – confusion between histograms and scatterplots.	-	27 - 35	25

The prior-knowledge multiple-choice diagnostic test indicated the following four primary difficulties or alternative conceptions:

- Students showed limited understanding of the concepts of variation and variance by confusing these two terms. In particular, certain students thought of *both* variation and variance as a measure of the number of different

genotypes in a population (revealed by items one, three and four). In addition, some students were under the impression that *both* variation and variance were associated with a change or process and not the current status of a population (items one, three, four and five).

- Students confused the variation in a population with the heterozygosity of an individual. This was evident as students were under the impression that variation and variance were only evident in a population which contains heterozygous individuals (questions one, three and four) and not an inbred population (item 3).
- Students inappropriately associated the values of zero and one with the absence of variation and equilibrium (item 5).
- Students had difficulty in the construction and interpretation of histograms (items two, six and seven).

#### *Relative difficulty of prior knowledge concepts*

A Rasch analysis (discussed in Section 3.2.3) of the answers given to the prior-knowledge multiple choice diagnostic test administered during 2004 was conducted to ascertain the relative level of difficulty of the various probes used and therefore the concepts under investigation. This was deemed necessary as the incidence of each difficulty and alternative conception varied between the student groups under investigation. This was probably due to the limited number of students registered for each module and thus the small sample size. It was therefore not possible, using only the frequency of each difficulty or alternative conception, to determine which concepts were most difficult for students to understand.

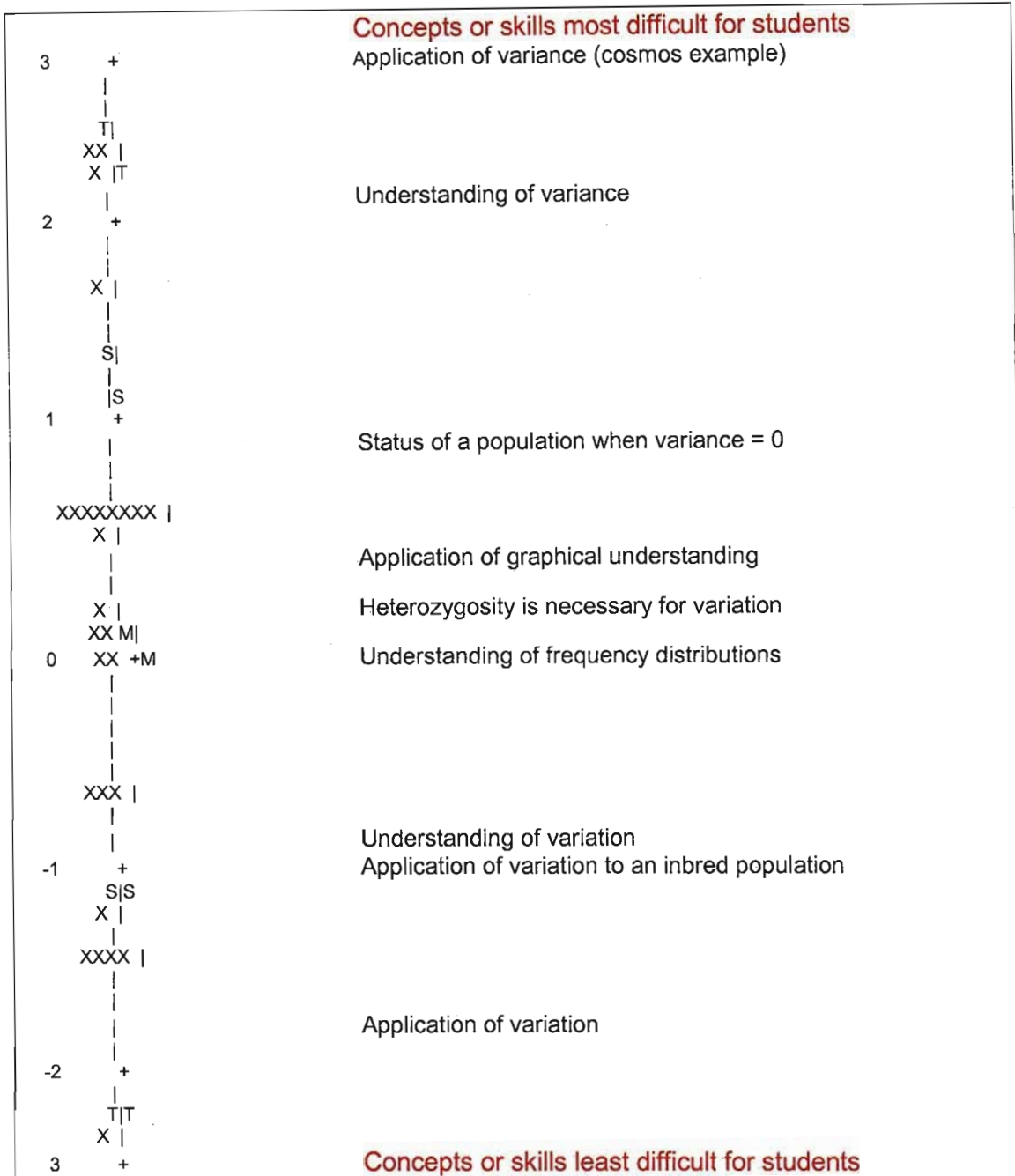
The application of the Rasch model enabled the generation of an “item map” by the *Winsteps software* (2003) using the answers given by students to items on the prior-knowledge diagnostic test (Figure 5.1). The item map provides an immediate interpretation of the relative difficulties of the concept or skill that was probed by each item. Concepts or skills described at the top of the map are those that students found most difficult, with those at the bottom being those probed by items that most students could answer correctly. Therefore, students should have been able to answer questions relating to concepts or skills probed by items presented lower

down on the map, but have had trouble answering items above their position on the map.

The Rasch analysis supported and extended the results presented in Table 5.1 in that students, on entry to a quantitative genetics module, exhibited the greatest degree of difficulty with regard to the understanding and application of the concept of *variance*, followed by the construction and interpretation of *histograms*. The item map (Figure 5.1) clearly indicates that the concept of variance was extremely difficult for most students in the class to understand, with only one student being able to correctly answer the item requiring an application of the concept of variance in a problem-solving exercise. Only four students had a 50% chance of correctly answering the item probing students understanding of the composition of a population in the absence of any variance. Thirteen of the twenty-seven students exhibited a limited ability to interpret histograms, whilst a slightly larger number were able to correctly construct frequency distributions. The majority of students were, however, able to answer items requiring an intuitive understanding of the concept of variation.

In support of the results obtained in this investigation, DelMas and Liu (2005) point out that very little is currently known of students understanding of “measures of variation” such as the standard deviation or variance. They further also suggest that these concepts may be very difficult for students and postulate that a reason for this difficulty may be that students must first have (1) a visual or graphical understanding of the concept of a variable and the associated frequency of its possible values, (2) knowledge of the mean and possess an image of it acting as a “self adjusting fulcrum” and (3) a conception of how values deviate from the mean. In order to coordinate all of the above requirements the students must also be able to relate statistics to graphical representations. The findings of this investigation support this claim as the concept of variance was found to be extremely difficult for many students. As many as 75% of students participating in this study did not recognise that variance related to the manner in which values deviate from the mean, nor did they seem able to relate this descriptive statistic to frequency distributions.





M indicates the average difficulty for the items.  
 S and T indicate one and two standard deviations respectively.  
 The X's indicate the number of students that had a 50% chance of correctly answering an item addressing a particular concept or skill.

**Figure 5.1: Item map depicting the relative difficulty of concepts and skills probed by each item on the prior-knowledge multiple-choice diagnostic test.**

**(b) Student difficulties with quantitative genetics concepts***Description and incidence of difficulties*

Students were found to experience a number of difficulties with *quantitative genetics concepts* (Table 5.2). Students' understanding of a number of quantitative genetics concepts was probed. The concepts and skills probed included whether students understood and could apply their knowledge of the concepts of breeding value, additive variance and heritability. The post-teaching diagnostic test probed students' ability to apply their knowledge of heritability to histograms and to the understanding of why most quantitative traits are normally distributed. Table 5.2 describes and indicates the incidence of difficulties experienced by, and alternative conceptions held by, students at the completion of a quantitative genetics module. As much as 68% of any one student group showed that they did not understand the concept of heritability as they did not realise how heritability values might be improved (item 4) or the meaning of the extreme values of zero and one (items 5 and 6). Furthermore students' responses to items 2 and 3 revealed that more than half the class did not understand the concepts of breeding value, additive variance and heritability. Between 22 and 27% of students still confused the X and Y axes of histograms and up to one-third of students could not relate the concept of heritability to frequency distributions (item 7).

The final version of the post-teaching diagnostic test used to gather these data, and the relevant propositional statements, are provided in Appendix 5 on page 304. The student groups, who answered the post-teaching multiple-choice diagnostic test, including the number of students in each group, are shown in Table 3.2. It should be noted that certain values in the table are missing. The reason for this is that during the research process, it became increasingly evident that students often thought of population measures such as variance and heritability, as belonging to individuals and not populations. Consequently, during 2004 item 3 was again included in the test. Furthermore, items 5 and 6 were added to the diagnostic test in order to ascertain whether the students would be able to correctly interpret heritability values of zero and one. This was deemed necessary as students seemed to inappropriately associate these values when thinking of the absence of variation or variance in the prior-knowledge diagnostic test. In addition, students' inability to link descriptive statistics such as heritability to graphical representations was identified as a particular area of concern and an item (item 7) addressing this difficulty was suitably amended to probe for this difficulty.

**Table 5.2: Incidence of difficulties and alternative conceptions held by students on completion of quantitative genetics modules during 2003 and 2004.**

(- indicates that the item was not asked of that student group)

2003(a): Genetics 332 student group 2003(b): Genetics 350 student group

Concept probed	Item	Alternative conception (inferred from students' answer choice)	Incidence (%)		
			2003 (a) n=22	2003 (b) n=29	2004 n=32
Reason for quantitative traits being normally distributed	1	Quantitative traits are normally distributed because:			
		• The genes have an additive or cumulative effect.	50	18	45
		• The population is undergoing random mating.	21	9	26
Association of breeding value and heritability	2	• Genes exert a positive or negative effect on the trait, leading to positive or negative deviations from the mean.	23	21	38
		A high heritability does not necessarily mean an individual will have a high breeding value because:			
		• There will be a range of breeding values in the population, most of which will be high.	36	16	23
What is inherited?	3	• Breeding values are a function of gene frequency.	36	0	19
		• The trait may be highly heritable, but undesirable, causing breeding values to be low.	21	38	6
		Non-additive gene action is passed from parents to offspring.	7	-	13
Improvement of heritability	4	Additive variance is passed from parents to offspring.	29	-	16
		Heritability may be improved by increasing the breeding values in the population.	14	54	68
Understanding of a heritability of zero	5	A heritability of zero means that:			
		• There is no genetic influence on the trait.	-	22	50
Understanding of a heritability of one	6	• No genes are transferred between generations.	-	9.4	12.5
		A heritability of one means that:			
		• All individuals are genetically identical.	-	-	6
Understanding of graphical representations of heritability	7	• All of an individuals breeding value is transferred to the next generation.	-	34	32
		Confusion of axis on a histogram; give breeding value on the Y-axis.	25	27	22
		Inability to relate descriptive statistics to graphical representations.	-	25	31

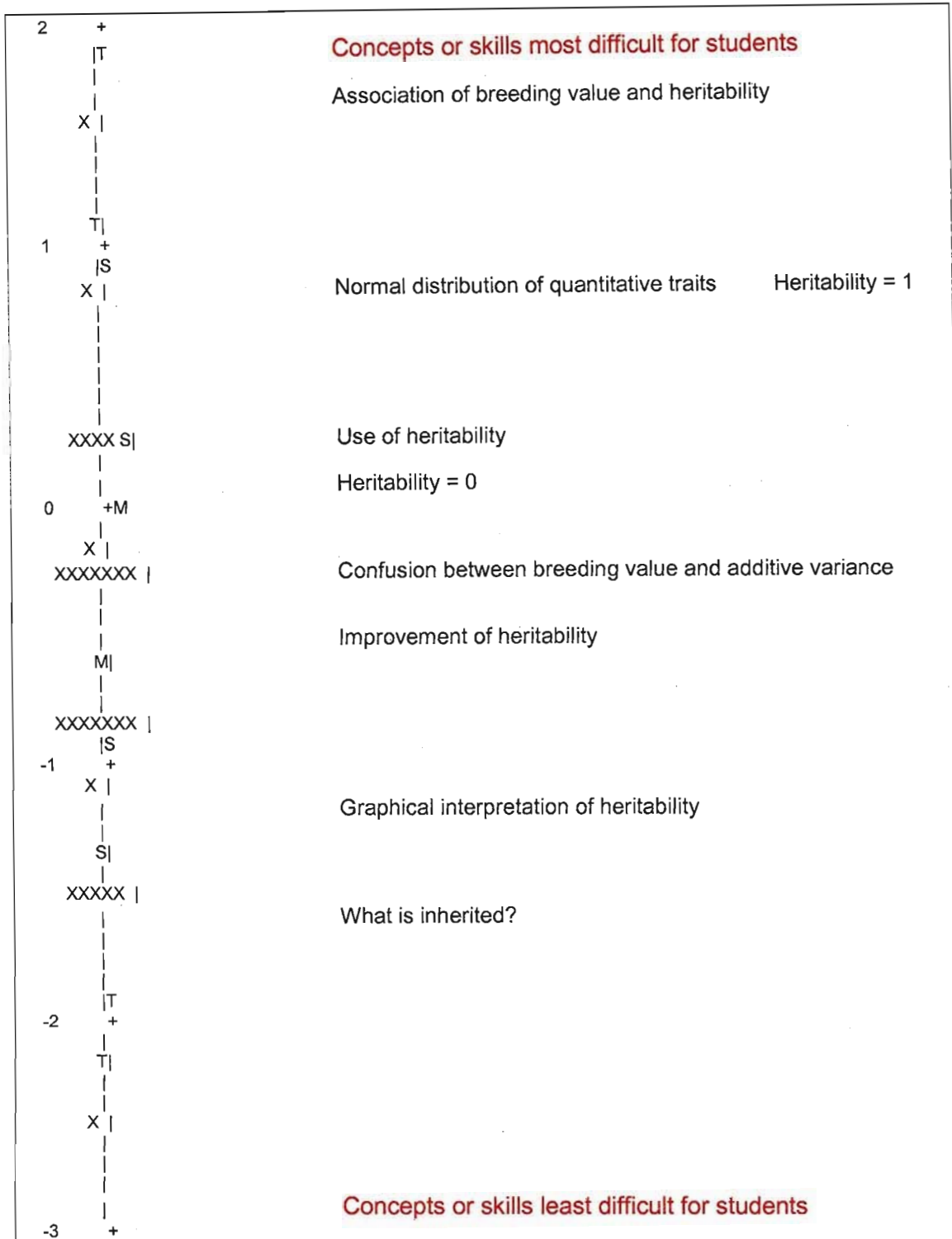
The results indicated three primary difficulties:

- Students' could not effectively differentiate between individual values and variance estimates relating to populations (revealed by items 2, 3, 4, 5 and 6). In particular many students inappropriately thought of breeding values, additive variance and heritability as *all* being individual measures.
- Students' inappropriately associated the words inheritance and heritability. Such students thus thought of heritability as having a function or being associated with change (items 3, 5 and 6).
- Many students were unable to correctly link descriptive statistics and frequency distributions thereby exhibiting an inability to apply their knowledge to graphical representations (items 1 and 7).

#### *Relative difficulty of quantitative genetics concepts*

In order to expand on the results obtained from the multiple-choice diagnostic tests on the incidence of each difficulty which had been identified (results presented in Table 5.2) and to obtain clarification on which concepts and skills students found most difficult at the completion of the module, a Rasch analysis was conducted on the results from 32 quantitative genetics students who answered the multiple-choice diagnostic test in 2004. The item map produced from the *Winsteps software* (2003), using the scale defined by the Rasch model, is given in Figure 5.2. The item map indicates that at least half of the students had difficulty understanding the statistics of additive variance and heritability. The most difficult concept for students to understand was that heritability is *not* an individual measure and that a high heritability does *not* mean that all the individuals will have high breeding values. It was thus evident that students' ability to apply their algorithmic knowledge of heritability was extremely limited. In addition, an understanding of the heritability values zero and one, as well as the graphical interpretation of heritability, were also problematic for most students. In contrast, basic concepts such as an understanding of "what is inherited" were within the grasp of most students.

The results of the Rasch analysis thus extend the results presented in Table 5.2 and those presented in Chapter 4 where heritability was found to be a *critical concept*. It may now be concluded that not only is heritability a concept that is critical to the learning and understanding of higher order concepts in quantitative genetics, but it is also a concept that many students find difficult to understand and to apply.



M indicates the average difficulty for the items.  
 S and T indicate one and two standard deviations respectively.  
 The X's indicate the number of students that had a 50% chance of correctly answering an item addressing a particular conception or skill.

**Figure 5.2:** Item map depicting the relative difficulty of concepts and skills probed by each item on the post-teaching diagnostic test.



It may be concluded that the two concepts that were identified as being *critical* concepts in this investigation (variance and heritability), were also found to be those which the students found most difficult. In addition, the students were found to hold numerous alternative conceptions regarding both *prior knowledge concepts* and *quantitative genetics concepts*, particularly the concepts of variance and heritability. The results presented in this section thus extend the previous findings detailed in Chapter 4.

### 5.3.2 Description of the *nature* of students difficulties with quantitative genetics

The difficulties and alternative conceptions noted in section 5.3.1 were elaborated on, and validated by a qualitative analysis of data taken from the reasons given by students for their answer choices on the multiple-choice diagnostic tests, interview transcripts and a word association study. An overall synthesis of the results (presented in Table 5.3) from data collected both at the start and the completion of modules on quantitative genetics highlighted two primary difficulties:

(a) Inappropriate association of terms or topics:

The *complex terminology used in genetics* has led to as many as 78% of students illustrating confusion between terms such as *variation* and *variance* as well as *heritability* and *inheritance*. In addition, almost two-thirds of students demonstrated confusion between individual and population measures such as breeding value and heritability. Furthermore, up to half of any student group inappropriately associated the values of zero and one with the absence or presence of certain phenomena.

(b) Difficulty in the construction and interpretation of histograms:

Approximately one-third of the students who participated in this investigation demonstrated some difficulty in the construction and/or interpretation of histograms. This difficulty primarily involved students confusing the functions of the X and Y axes across different graphical representations.

**Table 5.3: Classification of the nature of student difficulties and alternative conceptions.**

(P-K: Prior-knowledge diagnostic test P-T: Post-teaching diagnostic test)

Category of difficulty	Description of sub-categories of difficulties and specific alternative conceptions	Probe which revealed difficulty or alternative conception
Inappropriate association of terms or topics	Confusion between variation and variance:	
	• Association of variation and variance with difference.	Items 1,2,4 P-K and interviews
	• Association of variation and variance with change.	Items 1,3,4,5 P-K and interviews
	Confusion between individual and population measures:	
	• Association of variation in a population with heterozygosity of an individual.	Items 1,3,4, P-K, word association study and interviews
	• Association of the absence of variation with inbred populations.	Item 5 P-K
	• Association of breeding values, additive variance and heritability with individuals.	Items 2,3,4,5,6, P-T and interviews
	Confusion between the numerical values of zero and one with the absence or presence of phenomena:	
	• Association of the value of zero with the absence of variation or variance.	Item 5 P-K and word association study
	• Association of the value of zero with the genetic influence on a trait.	Item 5 P-T
• Association of the value of one with the absence of variation and equilibrium.	Item 6 P-T and word association study	
	Confusion between heritability and inheritance.	Items 3,5,6, P-T
Difficulty in the construction and interpretation of histograms	Confusion between assignment of the X and Y axes of histograms.	Items 2,6,7 P-K, item 7 P-T and interviews
	Confusion between histograms and scatterplots.	Items 2, 6,7 P-K and interviews
	Inability to relate descriptive statistics to histograms.	Items 1,7 P-T and interviews

A number of subcategories of difficulty were also noted. For example, students thought of *both* variation and variance as being associated with difference or change. With regards to students' confusion between individual and population measures, approximately one-third of students associated the heterozygosity of an individual with the presence of variation. Conversely, these students related the absence of variation with completely homozygous inbred populations. Up to 68% of students also thought of breeding value, additive variance and heritability as *all* being

individual measures. Between 19 and 33% of students inappropriately associated the absence of variation with a value of zero or one. Furthermore, between 4.5 and 16% of students also associated the value of one with equilibrium. When students' understanding of heritability was probed, it was found that between 6 and 50% of students incorrectly related the values of zero and one with the degree of genetic influence on a trait. Of the third of students who seemed to have difficulty in the construction and interpretation of histograms, some were confused as to which axis should account for the values in a population and which axis the frequency of each set of values, whilst others confused histograms and scatterplots. As a consequence, many students could not relate the descriptive statistics of variance and heritability to graphical representations of frequency distributions.

**(a) Difficulty 1: Inappropriate association of terms or topics**

*Confusion between variation and variance*

The observation that numerous students were not able to distinguish between variation and variance was illustrated by their responses to items 1, 2, 3, 4, and 5 of the prior-knowledge multiple-choice diagnostic test. In their responses, when giving reasons for their answer choices on the multiple-choice diagnostic test, most students recognised that variation was a measure of the number of different forms of something, for example, "Something that can vary", "something that can have a range of values", "different types of alleles or traits" or "the number of different types". However, in the case of variance, students viewed variance as the "rate of change", "the degree of variation", "the difference between means", "difference between samples" or "the range of the difference". This indicated that although many students recognised that variance was measuring the difference of "something", they did not indicate that they understood that this difference was the sum of the squared differences of values from the mean. Students generally commented that the population with the greater number of genotypes had the greater variation **and** the greater variance. For example, they did not recognize that a population with only red and white flowers would have a greater variance, as the sum of the squared deviations from the mean (pink) would be greater than a population with three genotypes; red, pink and white. The following quotes taken from interview transcripts with students designated 1, 2, 3, 4 and 5 confirm the findings from the multiple-choice diagnostic test that some students confused the terms variation and variance.

Student 1 indicated that he thought that the terms variation and variance were synonyms.

- I: OK so if this one has got the greatest variation, which one do you think has got the greatest variance – the same or different?
- S: The same.
- I: So for you there's no difference really between the term variation and the term variance?
- S: No.
- I: In your head they are the same thing?
- S: Sort of.

Student 2 thought that variation and variance were measured in the same manner.

- I: OK. And then do you think that the statistic variance is different to that? What do you think of variation and variance – are they the same thing or do you think that variance is measuring something else?
- S: The same.
- I: The same. If you were to measure the amount of variation in the number of cobs on a mealie, the way that you would measure the variation would be the same as the way that you measure the variance?
- S: I'd say it's the same.

Similarly, student 3 also thought of variation and variance as identical measures.

- I: And then if I wanted to work out the variance. Would you work it out a different way or would you work it out the same way as the variation? Does it mean anything different to you – the terms variance and variation?
- S: It is more or less the same.
- I: So if you were going to calculate how much variation you have got or how much variance you have got?
- S: Yep to get variance - it's the same.
- I: So why do you think that these statisticians in their wisdom look at this statistic called variance?
- S: I think they were just trying to get a different thing from the general view.
- I: So they are just being difficult?
- S: Yes some are [laughter].

Notwithstanding that student 4 knew that variance had something to do with mean values, she was still unsure of the precise relationship between the two concepts.

- I: Now, if you had to calculate what's the variance here how would you do it? Do you think there's variance here [indicating a depiction of a population]. You told me there is variation do you think there is also variance?
- S: Yes there is.
- I: How would you measure the variance?
- S: I would compare the mean of the two.
- I: OK. Then how do you think the term variance relates to variation? Do you think there is a difference between those two terms?
- S: I think there is a difference but it's not such a difference but they are related.
- I: The statisticians thought up this term. What do you think their reason for it was?
- S: Why do we always work with the variance of something?
- S: Because you can calculate the measure but I think it is a measure of the variation.
- I: It is a measure of the variation but do you have any idea of what kind of measure? Is it measuring something particular?
- S: Something to do with the genes.

Finally, student 5 incorrectly associated the terms variation and variance with a process or change, rather than the differences between individuals at one particular time. The following excerpt from the interview transcript indicates that she incorrectly associated variation with a change over time.

- I: OK first of all can you tell me what you understand by the term variation?  
S: I think that it just means that a character or a trait or changes over time – it doesn't stay the same. Whatever you are looking at it changes. It changes over time.

Furthermore, this student also incorrectly associated variance with both change and difference.

- I: Why do you think the statisticians thought up this statistic variance – what were they trying to describe do you think?  
S: Because you have got to try and explain kind of how big the change in the difference is.

The results of this investigation suggest that students only had some intuitive feel of the meaning of the concept of variation. However, many students did not seem to understand the concept of variance and simply realised that the terms variation and variance are related, with the variance perhaps being some measure of variation. Hammerman and Rubin (2004) and Makar and Confrey (2005) postulated that the traditional formalist method of teaching statistics and students' apparent reliance on the memorisation of formulae and algorithms may be a cause of students' lack of understanding of many statistical concepts. As the modules studied in this investigation were taught by means of formal lectures and students seemed to attempt to memorise many formulae and algorithms, this may have led to the lack of students' understanding of variance and the apparent confusion between terms which has been described.

#### *Confusion between individual and population measures*

Some students seemed to associate the terms variation and variance with the heterozygosity of an individual and consequently inferred that an inbred population, consisting only of homozygous individuals, would have no variation. Some students thus suggested on their answer sheets that "an inbred population has no variance" and "variation is only evident in heterozygous individuals". The following three excerpts from interviews with students, designated 6, 7 and 8, illustrate these students associated heterozygosity with variation and that they may be thinking of variation on an individual and not a population level.

Student 6 indicated that he associated variation with heterozygosity as heterozygous individuals have two different alleles. This student did not seem to realise that he

should be thinking of an entire population and that in a population made up of different types of homozygous individuals there will also be different alleles present.

- I: When you think of variation do you think of heterozygous or do you just look at the number of different things?
- S: I look at heterozygotes. [Student indicates that he associates variation and heterozygosity.]
- I: What do the heterozygotes tell you? Why do you think that they are showing you that you have got variation?
- S: Because they have got two different alleles. [Student indicates that he may be thinking of an individual and not a population.]
- I: Because the alleles are not the same, whereas the homozygous have got two alleles that are the same?
- S: Yes.

The quote taken from the interview with student 7 also indicates that the student associated variation in a population with the presence of heterozygotes. Student 7 was therefore similarly thinking on an individual level and not a population level, where it is the total number of different alleles in a population which determines the variation.

- I: Which one of these, if this is the parental generation here and the offspring generation which just has the heterozygotes - which one do you think has the greatest amount of variation? The offspring or the parents? Look at the whole generation. [The student is shown a parental population consisting of only homozygotes and an offspring generation consisting entirely of heterozygotes.]
- S: The offspring.
- I: Why?
- S: Because of heterozygote - they have the most variation. [Student indicates that she associates variation and heterozygosity. The student also indicates that she may be thinking of an individual and not a population.]

Student 8 confirms the inference made from the interviews with students 6 and 7 that some students are thinking of individuals and not the entire population as she thinks that a deterministic ratio of 1:2:1 should result from the crossing procedure discussed. This ratio would however only occur when two heterozygous individuals were crossed. In a population the ratio would depend on the frequencies of the alleles present. (It should be noted that only part of the interview has been included in the thesis and that it was, in fact, made clear to the student that the interviewer was referring to a population consisting of 40 red flowers and a population of 40 white flowers.)

- I: If I have got 40 red flowers and I have got 40 white flowers and I let cross-pollination occur, what do you think I am going to get in the next generation?
- S: It would depend if you because if you cross 40 and 40 there will be somewhere where the .... white gene is dominant. There you will have more of the white but broadly speaking you will have a mixture of red and pink and white. [Student indicates that she thinks that an additional colour, pink, will appear in the next generation.]
- I: So what - you will have three different kinds red pink and white?
- S: Yes.
- I: OK but you are not sure how many of each one you will have?



- S: Yes because that will depend if the crossing is - you should get 1:2:1. [Student indicates that she may be thinking of the cross between two individuals and not crossing between many individuals in a population, the result of which would be dependent on the allele frequencies in the population.]

The results of the word association study, details of which are given in Section 3.3, corroborate the above. In this study, students associated heterozygosity with "variation", "the production of variation", "increased variation", a "sign of variation", a "requirement for the production of variety", "two different alleles (A and a)", "dominant and recessive alleles at one locus" and the "combination of different alleles".

It was therefore evident from: (1) the responses given by students on the multiple-choice diagnostic test, (2) the students interviewed and (3) the word association study that students seemed to be equating heterozygosity (the presence of two alleles at a locus of an individual) with variation. When considering a single individual a heterozygote does have greater allelic variation than a homozygote. However, when a population is considered, there are many individuals and variation is measured by the number and frequency of alleles in the population. An inbred population will contain all types of homozygotes and so will contain all the alleles that will be present in an outbred population which contains heterozygous individuals. The allele frequencies in inbred and random mating populations are the same, only the genotypic proportions differ. Students are thus required to understand that an inbred population will be expected to have less variation on a genotypic level, the same variation on an allelic level and a greater variance in genotypic values than a random mating population.

The rigid teaching of the 3:1 ratio when considering monohybrid crosses has been blamed for the deterministic and not probabilistic mindset of many students (Mertens 1992), the result of which is that students do not comprehend the role of chance in the process of inheritance (Hackling and Treagust 1984). The inappropriate association of heterozygosity with variation, in this investigation, may have been due to the rigid teaching of crosses in introductory genetics modules. In such modules, parental crosses are used to produce a heterozygous  $F_1$  which is then crossed to produce an  $F_2$  which has all of the possible genotypes. Each individual in this heterozygous  $F_1$  generation is seen to have two different alleles and it is the mating of these individuals that gives rise to many different genotypes in the next generation. Heterozygosity may thus become associated in the minds of students with variation on an individual level (they have two different alleles), and when considering future generations students may recall that it is heterozygotes which when crossed produce many different genotypes, thereby creating variation.

Alternative conceptions which may have been a result of students' initial confusion between individual and population measures at the start of the module were also evident from an analysis of the results from the post-teaching multiple-choice diagnostic tests. Table 5.4 gives student responses (items 2,3,4,5 and 6 on the post-teaching diagnostic test) which indicate two alternative conceptions that may have developed during the teaching of a quantitative genetics module namely; that breeding value, additive variance and heritability are all individual measures and that additive variance is an individual commodity that may be transferred between generations. Note that the reasons given by students for their answer choices are not verbatim statements, but are typical answers given by students.

**Table 5.4: Student responses which indicate confusion between individual values and the statistics of variance and heritability.**

Alternative conception	Reasons given by students for their answer choice
Breeding value, additive variance and heritability are all associated and are individual measures.	<ul style="list-style-type: none"> <li>• Breeding value is equal to the additive variance.</li> <li>• Breeding value is half the effect of additive variance.</li> <li>• The higher the breeding value, the more likely that trait will be inherited i.e. has a high heritability.</li> <li>• If additive variance is high, then heritability is high, which indicates to the breeder that the progeny would also have high heritabilities and breeding values.</li> <li>• Breeding value, additive variance and heritability are all related in that if breeding value increases then additive variance will increase because they are all related – therefore this relationship is important to the breeder.</li> <li>• Heritability is the ratio of breeding value to phenotypic value.</li> <li>• Cows with high breeding values and high heritability will produce cows with equally good milking ability.</li> <li>• Parents with high breeding values will also have high heritabilities.</li> </ul>
Additive variance may be transferred between generations.	<ul style="list-style-type: none"> <li>• Additive variance is what can be transferred from parents to offspring.</li> <li>• Variance is passed onto the next generation.</li> <li>• Additive variance measures the value that will be passed to the progeny.</li> </ul>

The mathematical definitions of the concepts of breeding value and additive variance may be the source of some of the confusion between individual values and the variance associated with populations. Initially, students learn that breeding values are estimated as deviations from the population mean. Breeding values are estimated in such a way so as to enable comparisons between individuals in different populations i.e., to answer the question; “is an individual better or worse than the population average?” Subsequently, students are introduced to the concept of additive variance;

which is calculated as the sum of the squared deviations of breeding values from the mean. In contrast to breeding values, variance answers the question: “does a population contain individuals much better or worse than the mean, or do the values of individuals in the population all lie close to the mean?” As a result of these mathematical definitions, along with the fact that both breeding values and additive variance are related in some way to additive gene action, students may begin to associate the concepts of breeding value and additive variance. Furthermore, as heritability is the ratio of the additive and phenotypic variances, it is then also assumed to be associated with breeding values and additive variance.

An additional factor for the confusion between individual and population measures may be that some students do not relate the additive variance to the variance of all breeding values in the population. In contrast, they think of additive variance as a description of the variance in the values of a single individual’s progeny. Consequently, they also think that every individual will have their own heritability value. This alternative conception highlights the propensity of students to think on an individual, rather than a population level.

Once students think of heritability as an individual measure associated with breeding values, the idea that heritability indicates the proportion of genes transferred becomes plausible. Thus some students think that an individual with a high heritability will have a high breeding value and many good genes will be transferred to the following generation. Consequently, they deduce that a heritability of zero will mean that no genes are transferred or there is no genetic influence on the trait. Similarly, a heritability of one indicates that the entire breeding value is passed from one generation to the next. The following excerpt from an interview with a student demonstrates that the student has undergone a degree of conceptual change after originally thinking that a heritability of zero would mean that there was no genetic influence on the trait.

- I: So you know the right things now? You didn’t before? Can you try and tell me what you thought before?
- S: What I thought before that?
- I: Were you differentiating between values and variances?
- S: No. Before I did think if  $H^2$  equals 0 then the genes have no effects, but that’s actually a silly thing to think because obviously the genes have effects because they’re determined (inaudible) of an individual, but it can from where  $H^2$  equals 1 and that’s at the variance is due to the gene action, before you think well the whole variance is due to the gene action so the environment has no effect.

In addition, students did not think of partitioning of the total variance in a population ( $V_P = V_A + V_{GCV} + V_E$ ); rather they consider the individual values ( $P = A + GCV + E$ ) and thus incorrectly thought of heritability as the ratio of A and P. To these students a heritability of zero indicated that the genes have no effect on the trait, rather than the correct interpretation that individuals would be genetically identical. Similarly, in a population with a heritability estimate of one, it was inappropriately assumed that the environment does not influence the trait, rather than a constant environmental influence as demonstrated by the following quote.

- I: OK. And if I look at the amount of variance now, the environmental variance is equal to the genotypic variance, would that affect the phenotypic variance if they are equal?
- S: No.
- I: So the phenotypic variance would be equal to what then?
- S: To the genotypic variance.  
Just to the genotypic variance. [incorrect, it would be equal to twice the genotypic variance.]

The propensity of students to think on an individual and not on a population level has been observed by other researchers working within the field of statistics education. For example, Hancock *et al.* (1992: 354) noted whilst conducting an investigation on 5<sup>th</sup> – 8<sup>th</sup> grade scholars working with a computer-based data analysis tool, at a public school near Boston in the U.S.A. that “students often focused on individual cases and sometimes had difficulty looking beyond the particulars of a single case to a generalised picture of the group.” Despite the teaching teams efforts during the year to develop group-orientated vocabulary such as “clump”, “cluster”, and “range”, many students held onto more individual ways of describing data. The researchers claim that this inability of students to construct values relating to groups may act as a barrier to their ability to solve problems. Furthermore, Konold *et al.* (1997) whilst interviewing four students who had completed a statistics course, found that these students had not been able to make the transition from thinking about individuals to thinking about populations. Similarly, in another investigation, Ben-Zvi (2004) studied students working on “prediction type” graphical exercises and observed that the students wanted to reason with individual points or the majority of values and not the entire shape of the distribution.

The results of this investigation support the findings cited above as many students were unable to show a meaningful understanding of population measures such as *variance* (phenotypic and additive) and *heritability*. It is interesting to note that these two concepts were also classified as *critical concepts* in Chapter 4. Thus, notwithstanding that these concepts are crucial to the learning of higher order

concepts, they were extremely difficult for students to understand and consequently some students developed alternative conceptions of the meaning of these population measures.

*Confusion between the numerical values of zero and one and the absence and presence of certain phenomena*

Some students associated the heritability value of zero with the absence of variation. The reason for this could be because they related the idea of *zero* with *nothing* or the *absence of anything*. This deduction is confirmed by the results of the word association study where students associated the value *zero* with a “state of *no* variation”, “*no* heterozygotes”, “*no* environmental effects”, “*no* evolutionary forces”, “*no* linkage”, “*no* change” and “*no* difference”. Similarly, some students answering the post-teaching multiple-choice diagnostic test associated a heritability value of *zero* with *no* genetic influence on a trait and *no* genes being transferred between generations.

Students' inappropriate association of the absence of variation with *no change* is particularly interesting as students also associated an absence of variation with a state of *equilibrium* and a value of *one*. This could be as a result of students holding the alternative conception that variation and variance are related to a change of some sort. By a process of deductive thinking they would then think of an absence of variation as being associated with the absence of change or equilibrium. The association of the *absence of variation* and *equilibrium* with the value of *one* may have been a result of students having practiced a system of rote-learning of algorithms and definitions in a previously completed module on population genetics as they related these ideas to the unity associated with the sum allele frequencies in a population ( $p + q = 1$ ) and Hardy-Weinberg equilibrium ( $p^2 + 2pq + q^2 = 1$ ).

The association of the *absence of variation* with *no difference* could have led to the conception that all the individuals are of *one* type and thus the connection with the value of *one*. This association of the absence of variation with the value of *one* is supported by the observation that some students answering the post-teaching multiple-choice diagnostic test thought that a heritability value of *one* meant that all individuals in the population would be genetically identical.

*Confusion between heritability and inheritance*

The association some students have with the words heritability and inheritance is highlighted in Table 5.5. Some students thought of heritability as having a predictive function and that heritability indicated the proportion of the genes passed from parents to offspring. These students therefore thought that if heritability is equal to zero then no genes are transferred from parents to offspring and conversely if the heritability is equal to one then all of an individual's breeding value is transferred to the next generation.

Certain students also seemed to assume that heritability has a function associated with inheritance. Thus, students thought that if the heritability of a trait was high then the breeding values would be high and therefore the progeny will also have high breeding values. This is indicated by one student's comment when discussing the statistic of heritability, "good inheritance means good breeding values". Such students then also suggested that if the heritability of a trait was zero there would be no genetic influence on the trait (no inheritance) and conversely if the heritability of a trait was one then the individuals must all be genetically identical or would have all inherited the same genes (full inheritance). The alternative conceptions identified in this investigation (presented in Table 5.5) could be due to students confusing the terms heritability and inheritance and erroneously thinking of heritability as giving an indication of the ability to inherit a particular trait.

Bahar *et al.* (1999a) commented that students may confuse certain terms and topics in genetics. In a study on 207 1<sup>st</sup> year biology students these researchers observed that many students found genetics to have a very complex vocabulary and that students confused terms such as allele and gene. Furthermore, many students confused look-alike and sound-alike terms such as homologue, homologous, homozygous and homozygote. This type of confusion could well extend to the confusion between terms that has been noted in this investigation, particularly between the terms *variation* and *variance* and, *heritability* and *inheritance*. In this regard, Wandersee (1985) and Pearson and Hughes (1988) suggested that students easily become confused as terms used in biology often have many synonyms and numerous words are homonyms and that educators should only emphasize the most important terms and topics necessary for an understanding of the subject matter.



**Table 5.5: Student responses which indicate the view that heritability has a function or is associated with change.**

Alternative conception	Reasons given by students for their answer choice
Heritability indicates the proportion of the genes passed from parents to offspring.	<ul style="list-style-type: none"> <li>• Heritability is the amount which can tell us how much of the good genes are passed onto the next generation.</li> <li>• Additive variance shows the proportion of genes that are heritable.</li> <li>• If heritability is 0.8 then 80% of alleles are heritable. Therefore additive variance is high and hence breeding value is good.</li> <li>• If the heritability is zero the genes will not be inherited by the next generation.</li> <li>• If heritability is one it means that 100% of the breeding value will be transferred to the following generation because as heritability increases breeding value increases.</li> </ul>
Heritability has a function. Association of heritability and Inheritability (ability to inherit).	<ul style="list-style-type: none"> <li>• Heritability is responsible, in part, for the determination of the breeding values of the following generation.</li> <li>• Heritability determines the resemblance between relatives.</li> <li>• If the heritability is equal to zero then there is no genetic influence on the trait.</li> <li>• If the heritability is equal to one all the individuals have the same genes and are genetically identical.</li> <li>• Heritability will affect the next generation and can only bring about change there. One is able to predict breeding values of the next generation with heritability.</li> </ul>

**(b) Difficulty 2: Difficulty in the construction and interpretation of histograms**

Students were found to have problems with both the construction and interpretation of histograms. The primary difficulty experienced by students seemed to be that they were confused by the functions of the X and Y axes of histograms. This was evident in that: (a) students often confused histograms and scatterplots by not grouping values according to their frequency and plotting a point for each individual. (b) certain students realised that frequency should be on one of the axes but when constructing or interpreting graphs of a normal distribution they thought of value, and not frequency, as being on the Y axis and (c) some students were unable to relate descriptive statistics such as variance and heritability to frequency distributions.

*Construction of histograms*

A number of problems were observed when students were asked to construct frequency distributions in response to the question displayed in Figure 5.3. A selection of graphical responses produced by students is presented in Figure 5.4.

Forty chickens were weighed and the following weights obtained.									
5.14	12.23	13.35	13.96	22.07	24.69	17.54	15.43	10.07	11.09
14.26	6.15	19.74	14.15	14.14	10.14	15.07	13.6	26.98	19.48
14.91	13.88	9.98	20.15	25.15	8.76	14.97	13.13	16.19	21.00
10.56	15.95	16.79	11.81	18.99	15.58	16.10	20.57	15.99	11.04
Draw a suitable graph to summarise this information. (Label the axes).									

**Figure 5.3:** Question given to students which generated the graphical representations shown in Figure 5.4.

The graphs designated (a) and (b) are both graphs which may be considered correct. Frequency is plotted on the Y axis and weight on the X axis. In graph (a) the student has drawn a normal distribution, whilst in graph (b) the student has grouped the values into classes to plot a histogram. If the students had included values, this graph would have approximated a normal distribution. Graph (c) shows how a student has confused the X and Y axes by attempting to create a linear relationship. This may indicate that she confused histograms and scatterplots as she tried to find a causal relationship between two variables. Graphs (d) and (e) are both examples of students who have made no attempt to group the values into classes and have tried to plot a point for every individual.

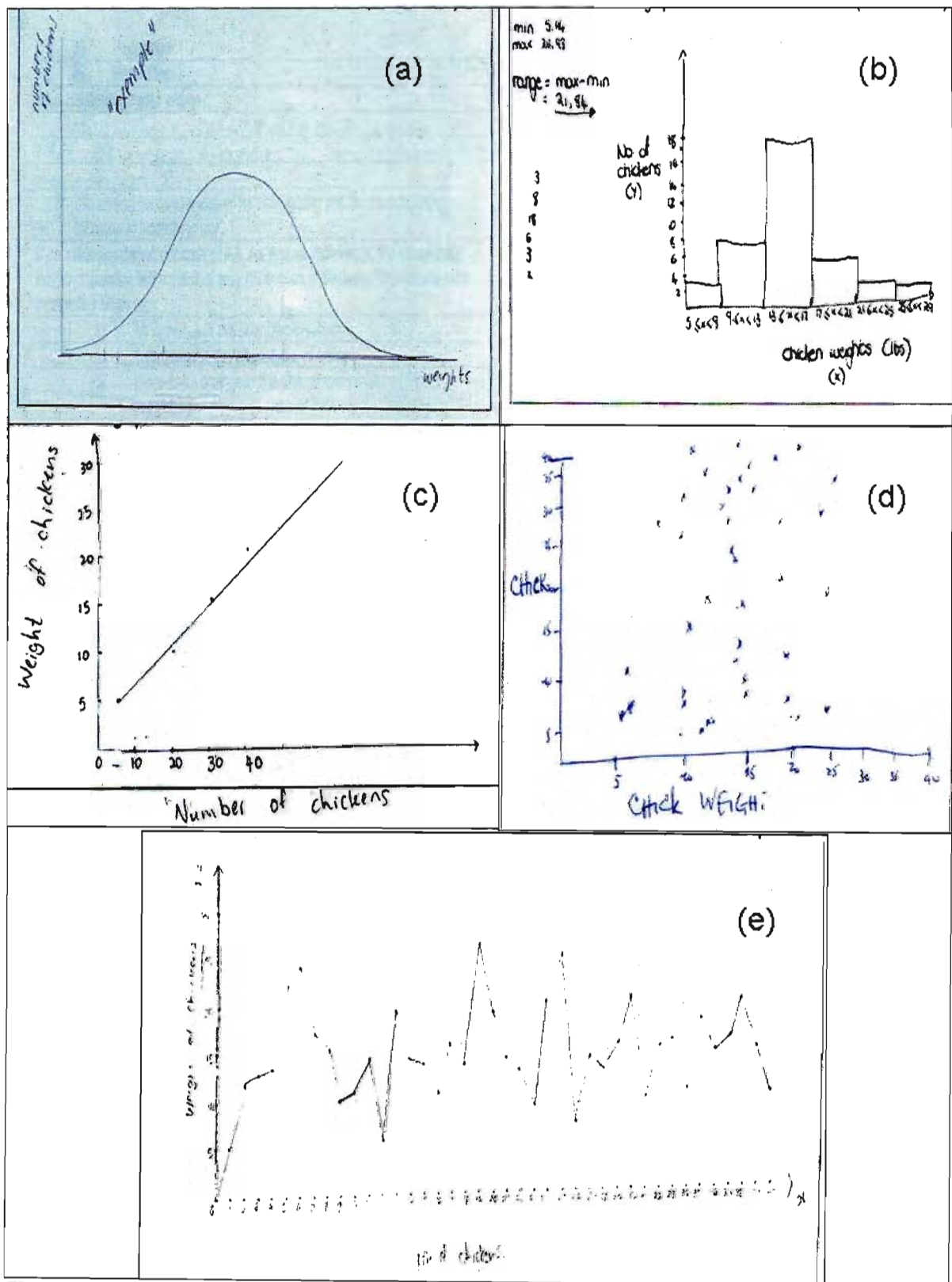


Figure 5.4: Graphs generated by students in response to a question asking for a plot of chicken weight against frequency (number of chickens).

Students' difficulty in constructing histograms was also highlighted by a different student group's response to a question on the length of elephant tusks, which is displayed in Figure 5.5. Students' graphical responses are provided in Figure 5.6.

**Consider measurements taken on the length of elephant tusks in the entire population of African elephants.**  
**Draw a graph to represent the data.**  
**How could this graph be of use to a breeder who was trying to improve tusk length?**

**Figure 5.5: Question given to students which generated the graphical representations shown in Figure 5.4.**

Graph (a) is an example of a student-generated graph that is correct. Tusk length is plotted on the X axis and frequency on the Y axis. Furthermore, a normal distribution is drawn and correctly interpreted. Graph (b) highlights the propensity of some students to confuse the X and Y axes. The student expected a normal distribution but does not seem to understand why a normal distribution should result. The student has placed the mean in the correct place and correctly indicated which individuals would be selected to increase tusk length, but has not realized that the graph does not support her answer as frequency is plotted on the X axis. Graph (c) once again, shows confusion between the X and Y axes. In addition, this student drew a discrete distribution. Graph (d) is an example of a student confusing histograms and scatterplots. This student has plotted tusk length against age, assuming that two variables must be plotted, an independent variable (age) and a dependent variable (tusk length).

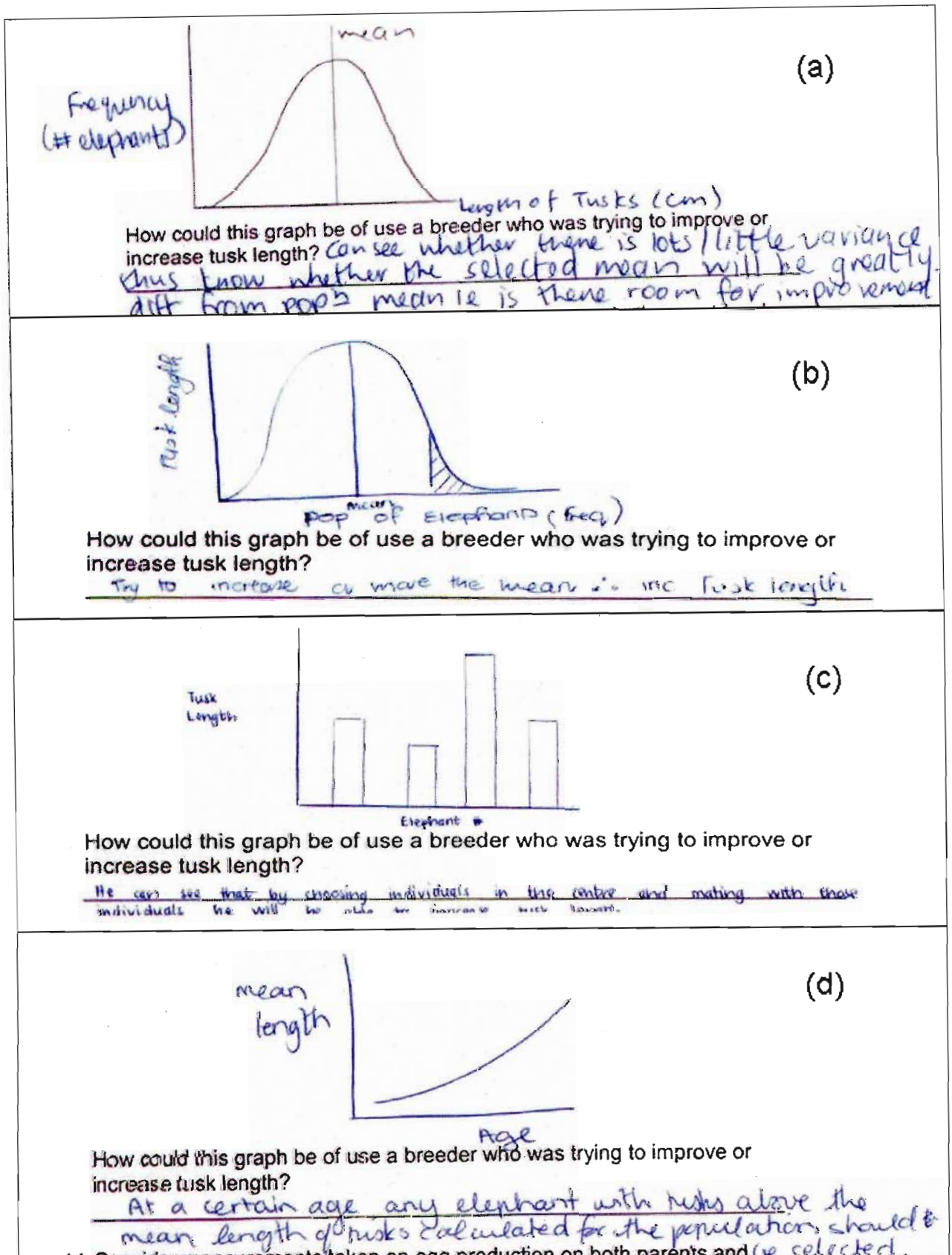


Figure 5.6: Graphs generated by students in response to a question asking for a plot of tusk length against frequency (number of elephants).



Meletiou and Lee (2002) suggest that the transformation of raw data into a different form is challenging for students and that they need help to recognize the respective functions of the X and Y axes. This view has also been expressed by Hancock *et al.* (1992) after conducting a study on school children. The researchers noted that the children often preferred to use Venn diagrams as opposed to axis plots. This result was seen to indicate that the fact that an axis consists of a range of different values makes it harder for students to understand, rather than the simpler use of a circle Venn diagram which only reveals data points on either side of a certain value. These results may be extrapolated to the more applied use of axes in histograms where students have to group data values and plot a variable against the frequency of its occurrence.

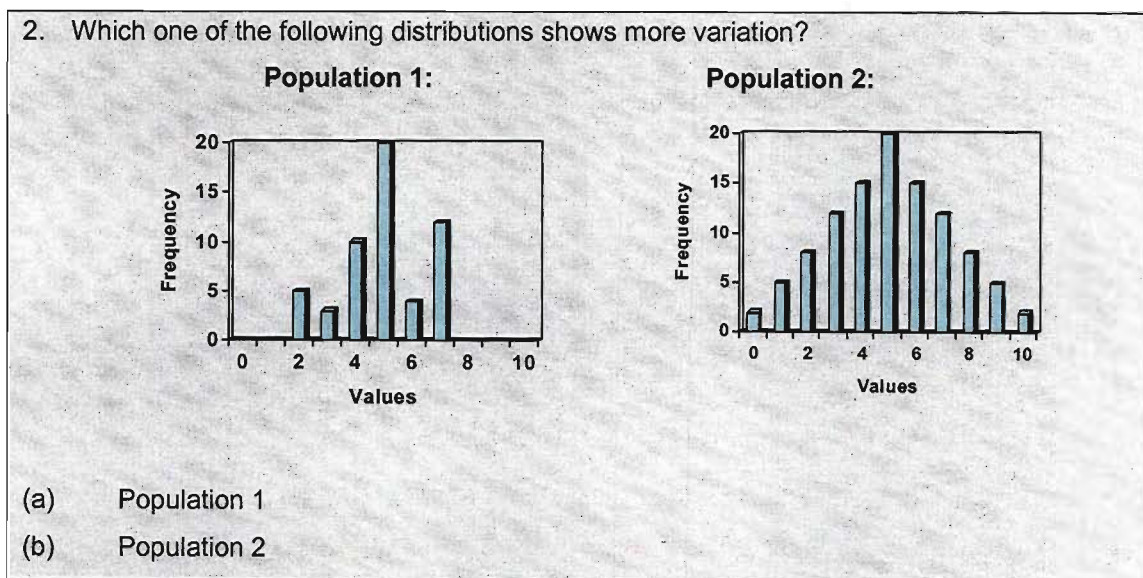
#### *Interpretation of histograms*

Some students were able to correctly construct a frequency distribution but were unable to interpret the graph. The following quote indicates how a student was able to correctly draw a graph depicting a normal distribution, but that the student did not realise that the highest point of the distribution represented the highest frequency of values. In this case the student thought that the “top of the distribution” must indicate the highest yield i.e., this student still showed confusion between what was plotted on each axis when she had to interpret the graph.

- I: What do you think the graph would look like?  
S: Sort of like a normal distribution.  
I: OK so draw that for me and label your axes.  
(A pause whilst the student draws it)  
And then what is this at the bottom?  
S: Yield.  
I: That would be your yield okay. So what is that graph telling you? It's correct but tell me what it is telling you.  
S: It is telling you that the yield from all the trees in the population are normally distributed so there would be very little difference. There will be a difference but when the mean is calculated you get the highest yield distributed at the mean.  
I: The highest yield is at the mean?  
S: Most individuals that are producing the best.  
I: Are you sure?  
Why did you say it was going to be normally distributed – did you just take a guess?  
S: No I realised that that would be the case in the population.  
I: And you are correct but now I'm wanting you to explain to me what this graph means. Its one thing to say it is normally distributed but its better if you understand why it's normally distributed.  
S: I supposed because individuals... at this point have the best performance in the yield.  
I: So around the mean they have the best performance?  
S: Yes.



Students' inability to distinguish between the functions of the X and Y axes when interpreting graphs was also highlighted by their answers to item 2 of the prior-knowledge multiple-choice diagnostic test (Figure 5.7). Many students did not relate variance to the spread of values in a population, but rather looked for a "pattern" or for the greatest difference between the bars of the graph, not realising that one must look for variation in a value and not a frequency. Many students that answered this item argued that Distribution 1 had more variation because "the frequencies are very different and showed no pattern". Even among the students who chose Distribution 2, some showed misunderstandings. Many of these students chose Distribution 2 because "it has a nice pattern" or "that the frequency increases with the values until it reaches a maximum and then drops". This indicated strongly that the students did not necessarily realise that variation means the spread or range of values; they only saw variation as large differences between bars on the graph.

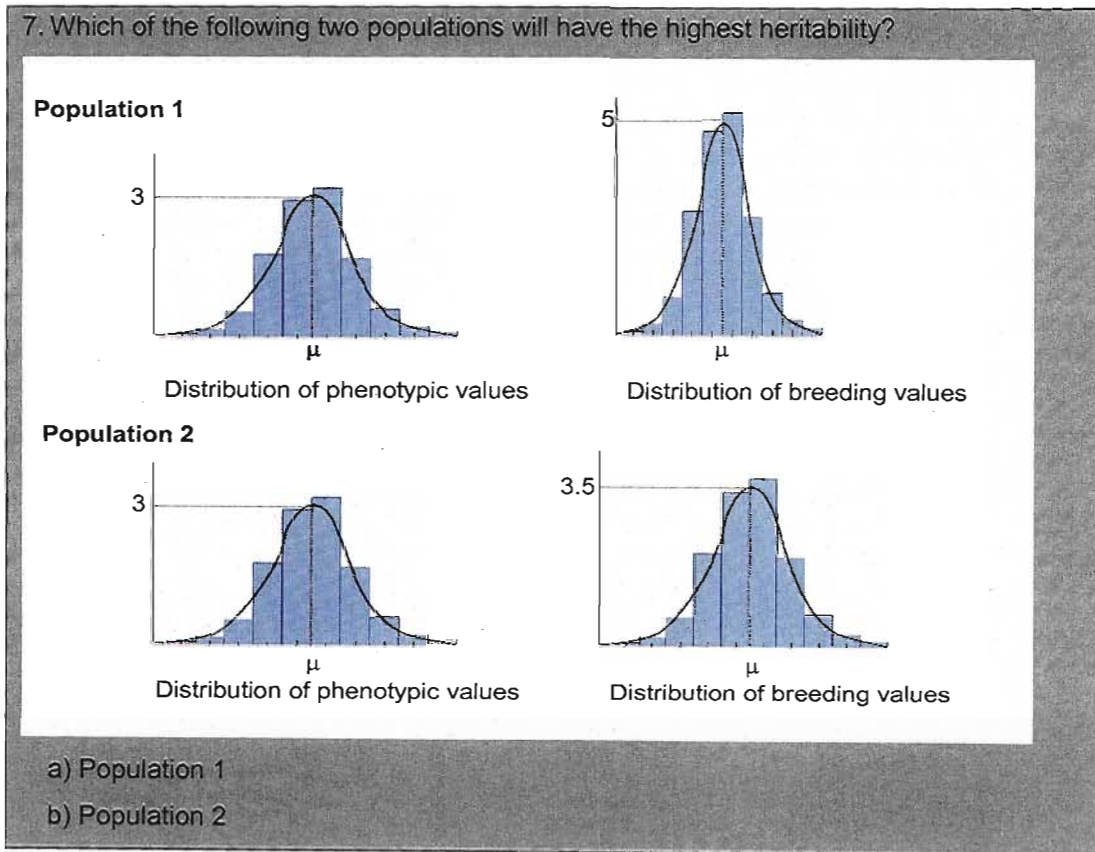


**Figure 5.7:** Item 2 of the prior-knowledge diagnostic test.

The results obtained from students answers to item 2 are supported by the results from a study conducted by Meletiou and Lee (2002) and further elaborated in another paper by the authors (Lee and Meletiou-Mavrotheris 2003). This study took place in an introductory course in statistics at Central Michigan University in the USA and involved 33 students. The findings from this study indicated that when comparing two histograms, students who did not receive instruction which focused on their understanding of histograms and where the concept of variation was not emphasized, could not decide which histogram had more variation. Furthermore, several students also confused histograms with scatterplots. In contrast, students

receiving instruction aimed at improving their understanding of histograms and variation were more able to understand concepts such as the mean and had a good grasp of the idea of a standard deviation. Similarly, Ben-Zvi (2004) when conducting an in depth qualitative study on two seventh grade students' methods of comparing graphical distributions, noted that the students often confused the X and Y axes.

Students' difficulty in the interpretation of frequency distribution was further confirmed when they were tested at the completion of the module with item 7 of the post-teaching multiple-choice diagnostic test (Figure 5.8). A number of students answering this item seemed unable to reason with the graph in a meaningful manner and thus were not able to link the statistic of heritability to the graphical representations.



**Figure 5.8:** Item 7 of the post-teaching diagnostic test.

Students' responses to this item included that they were unsure of what was plotted on the X axis and confused individual values with population measures. Three inappropriate conceptions were observed:

- Some students were of the opinion that breeding value was plotted on the Y and not the X axis. Students with this type of conception typically answered:

"Population 1 has a higher average breeding value [reading Y-axis]. This means that it will have a higher additive variance and hence a higher heritability".

- Some students were of the opinion that additive variance was plotted on the Y axis, instead of looking at the spread of values from the mean on the X axis. These students typically answered: "The additive variance must be higher than the phenotypic variance [reading variance as the height of the graph on the Y-axis] since heritability is directly proportional to the additive variance.
- Some students confused individual values with statistics and did not consider the variance of all the values from the population mean when considering a heritability estimate. These students seemed to think the equations  $h^2 = V_A / V_p$  and  $h^2 = A / P$  were equivalent. Such students gave answers such as: "In population 2 the average breeding value is 3.5 and the average phenotypic value is 3 [reading the frequency of the mean value]. Since  $A = h^2P$ , the closer heritability is to one, the more A equals P therefore A and P are more similar in population 2.

The difficulty that some students have with the graphical interpretation of statistics such as variance and heritability has recently been addressed by other researchers working in the field of statistics education. This research has been directed towards improving students' ability to link descriptive statistics, such as the mean and standard deviation, with graphical representations. This has been deemed necessary as in order for students to understand the concept of variation they must possess an understanding of graphical distributions (Makar and Confrey 2005). It is thought that an understanding of distributions will allow students to think on a population level and to visualise data as a unit with its own properties and not as individual values. As Bakker (2004: 65) states "the concept of distribution is a structure with which students can conceive aggregate features of data sets". Similarly, Makar and Confrey (2005: 31) claim that "intuition about variation may be fostered through a lens of seeing variation". Consequently, one aim of the remediation phase of this investigation focused on assisting students in the construction and interpretation of graphical representations such as histograms (discussed in detail in Chapters 6 and 7).

It should be noted that the student answers given to item 1 of the post-teaching multiple-choice diagnostic test also indicated that they had difficulty in the interpretation of histograms, specifically normal distributions seen for quantitative

traits. Item 1 addressed the reason quantitative traits are normally distributed and typical student answers are provided in Table 5.6.

**Table 5.6: Student responses which indicate a poor interpretation of why quantitative traits are normally distributed.**

Alternative conception	Reasons given by students for their answer choice
Lack of understanding as to why quantitative traits are normally distributed. (item 1)	<ul style="list-style-type: none"> <li>• Many genes from different loci contribute to the character of a trait. The addition of the effects of all these genes produces a normal distribution.</li> <li>• Genes do not have discrete values. They add together forming a continuous line.</li> <li>• Quantitative traits are controlled by many genes. Each gene contributes a relatively small effect which can be positive or negative.</li> </ul>

It must be clarified that these answers are not totally incorrect. Students hold conceptions which are based on facts which they have learnt during the module. For example, when discussing the simplest model of quantitative inheritance, certain assumptions of additive gene action and an equal effect of each gene on the trait of interest are made. These assumptions are then used by the students when trying to address the question. However, these students are not able to fully account for the reasoning behind the normal distribution of values seen in most quantitative traits.

In an attempt to address students' understanding of frequency distributions and to assist students in the understanding of why quantitative traits are normally distributed, Lawson (1996) suggested that a learning cycle consisting of three steps: explanation, term introduction and concept application could assist genetics students in recognising the importance of variation in genetics and why quantitative traits are normally distributed. The teaching method proposed by Lawson makes use of assorted shells for which the students have to list the differences in a particular trait and thereafter calculate the frequency of each variant and plot a frequency distribution. If the sample is large enough a normal distribution will result and the implications thereof may be discussed. He also advocates the use of a pair of dice each of which represents a male and female gamete. He suggests that students throw the dice 100 times and add together the two resulting values. This exercise will emphasize the random nature of inheritance and when the summed values are plotted according to their frequency a normal distribution will result.

The incomplete understanding shown by certain students of why quantitative traits are normally distributed, along with many students confusion between the X and Y

axes of a histogram, seemed to impair their ability to reason with and interpret graphs of frequency distributions. As a result, these students could not distinguish between graphs illustrating more or less *variance* or differences in *heritability* between two populations. Consequently, students with these difficulties will almost certainly be unable to apply the statistics of variance or heritability to any practical situation. These results once again confirm students' difficulty with both the understanding and interpretation of the *critical concepts* of variance and heritability.

### 5.3.3 Model of the source(s) of student difficulties with quantitative genetics

As the ultimate aim of the research was to design teaching strategies that could remediate or prevent the development of student difficulties and alternative conceptions, the possible source of the difficulties and alternative conceptions noted in this investigation needed to be ascertained. Accordingly, the modelling framework proposed by Justi and Gilbert (2002) was then used to model the possible source(s) of student difficulties with quantitative genetics (methodology described in Section 3.3).

The researcher performed the following steps in the formation of a model of the source(s) of students' difficulties with quantitative genetics.

Firstly, she studied the results of the difficulties and alternative conceptions regarding students' understanding of *prior knowledge concepts* (presented in section 5.3.1(a)). This analysis revealed that students:

- (a) Inappropriately associated the terms variation and variance.
- (b) Confused the variation in a population with the heterozygosity of an individual.
- (c) Inappropriately associated the values of zero and one with the absence of variation and equilibrium.
- (d) Had difficulty in the construction and interpretation of histograms, specifically depictions of normal distributions.

Secondly, she hypothesized that the primary source of the above-mentioned difficulties was the sequence in which concepts are introduced to students; the genetics curriculum. She proposed that the curriculum may have led to the confusion between, and inappropriate association of, terms and topics that were discussed in section 5.3.2.

Thirdly, the researcher constructed an *initial mental model* of the source of these difficulties.



Fourthly, the *initial mental model* was expressed in the form of a flow diagram, termed the *initial model* (Figure 5.9 on page 152), which illustrated the manner in which students may have inappropriately associated certain terms and topics with the absence and presence of variation.

Fifthly, the *initial model* was tested and validated by comparing the results with those obtained from the answers given by students to the prior-knowledge diagnostic test, student interviews and a word association study.

Finally, the *initial model* was extrapolated to account for students understanding of *quantitative genetics concepts*, thereby producing the *final model*.

### **(a) Construction of the initial model**

#### *Description of the genetics curriculum*

When considering the students' conceptions of *prior knowledge concepts* it was proposed that a possible source of student difficulties and alternative conceptions may be the sequence in which concepts are introduced to students; the genetics curriculum.

All genetics students begin by studying the inheritance of traits determined by single genes termed qualitative inheritance. One of the first concepts taught to genetics students is that of a "genotype". Students learn that at any one position in the genome (locus), there are different forms of genes; alleles. Furthermore, they learn that the combination of these alleles at any locus determines the genotype of the individual. The prefixes of *homo* meaning one, and *hetero* meaning more than one, are introduced when discussing the two possible genotypic types: (1) homozygotes with only one type of allele and (2) heterozygotes with different allelic types. Subsequently, students learn that certain alleles may be dominant over others so that at a locus with complete dominance, one may not be able to differentiate between homozygous and heterozygous individuals. In order to discriminate between the different genotypes and to ascertain the degree of dominance, students learn that certain crosses are undertaken by researchers or breeders. The initial cross involves the crossing of different homozygous parents to produce heterozygous offspring in the first filial generation, the  $F_1$ . The heterozygotes are then crossed with one another to give all possible genotypes in the second filial generation, the  $F_2$ . The phenotypic ratio of the  $F_2$  is then used to infer the degree of dominance at the locus under consideration.



It should be noted that this curriculum applies to the teaching of qualitative genetics and crosses between particular individuals. Once students have to transfer the above-mentioned ideas to the consideration of quantitative inheritance and entire populations of individuals they may inappropriately associate certain terms and topics.

*Impact of the genetics curriculum on students' understanding of prior knowledge concepts*

The sequence in which concepts are introduced to students may encourage students to inappropriately associate certain terms or topics with the absence and presence of variation. For example certain students associated heterozygosity with different allelic forms and the ability to produce a range of genotypes in the  $F_2$ . These perceptions may have been the source of the alternative conception that in order for a population to show variation, heterozygous individuals must be present. These students were therefore confusing the heterozygosity of an *individual* with levels of heterozygosity in a *population*. Furthermore, these perceptions could account for the belief by some students that variation was a dynamic concept causing change in a population.

To exacerbate the above-mentioned confusion between individual and population measures, students are later taught that when considering entire populations the concept of equilibrium describes the state of a population where no change in the genotypic proportions occurs between generations. The researcher hypothesized that students who associated variation or variance with change may then have associated equilibrium with populations without variation. In addition, the word equal, when thought of in terms of an equation, implies that terms are equivalent on either side of an equation. This could have been visualized graphically by students as a pattern and ultimately connected in their minds with a normal distribution.

The researcher used the thinking presented above to construct a model of how the inappropriate association of certain terms and topics by students may have led to the development of some of the difficulties and alternative conceptions detailed in this chapter.

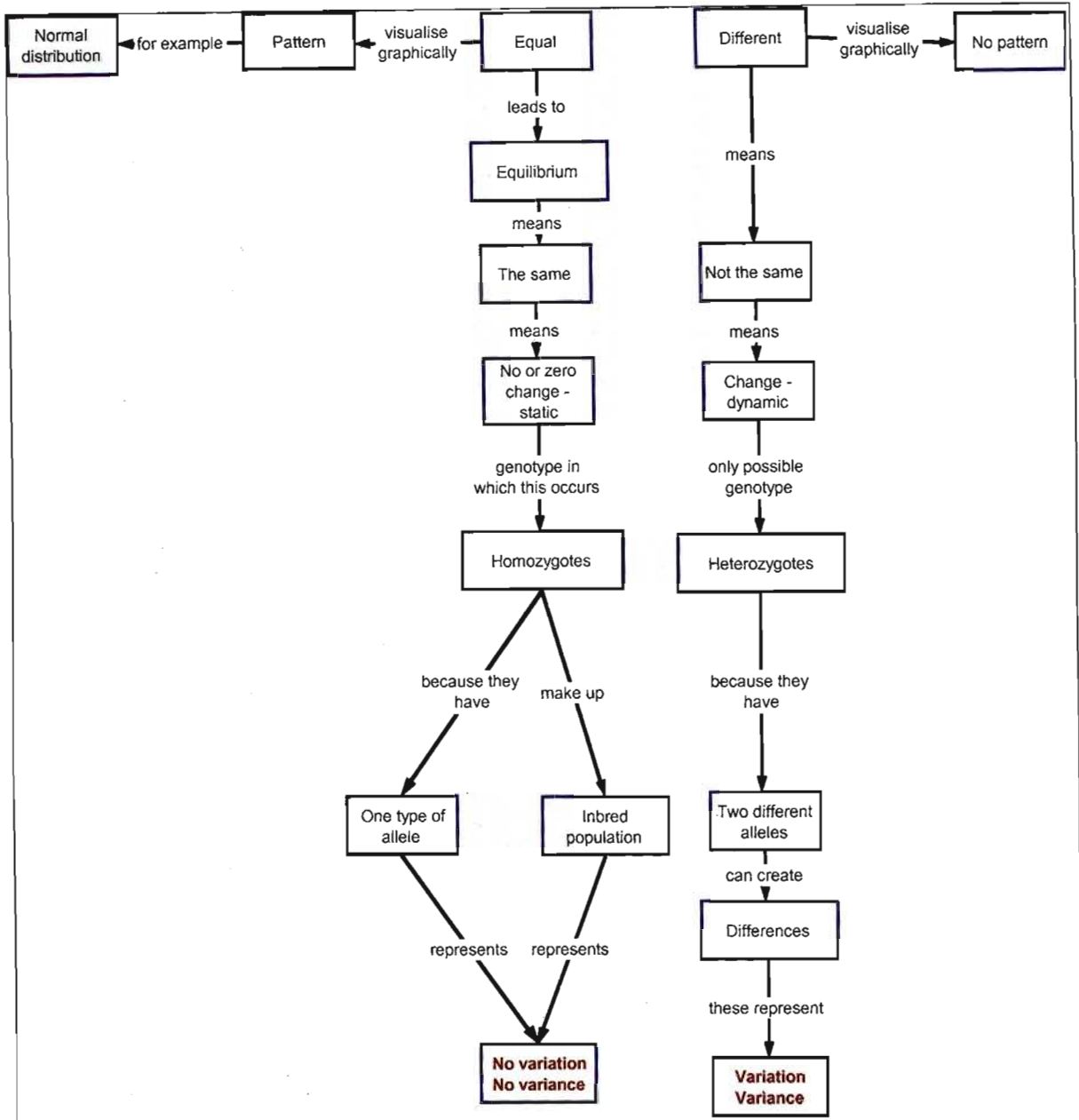
*Initial model of students inappropriate association of terms and topics*

The inappropriate association of terms or topics with the absence or presence of variation is expressed visually in the form of a flow diagram in Figure 5.9. This

diagram shows how students may take the genetic concept of *homozygosity* and inappropriately associate it with the *absence of variation* or variance in a population. Students think of homozygotes as having only *one* type of allele and *one* genotype. Students may then associate homozygotes with the absence of variation and inbred populations. In addition, as they may be thinking of homozygotes mating with homozygotes of the same type, they will think of the offspring generation being identical to the parental generation i.e., a state of *no change* or *equilibrium*. The idea of equilibrium could then be associated with *equal values* on either side of the mean and the smooth pattern observed in a *normal distribution*.

Conversely, students make inappropriate associations between the genetic concept of *heterozygosity* and the *presence of variation* in a population. This is because the students are thinking on an individual and not a population level. They then think of heterozygotes as having *two different* alleles (showing variation). Furthermore, they think of the mating of one heterozygote with another as producing a range of different genotypes in the next generation i.e., of causing some *change* in the offspring generation. The idea of difference may also then be inappropriately associated with the presence of variation in a distribution where students look at differences in the heights of bars in a histogram (no pattern) and not the spread of values from the mean (evident in students' answers to item 2 of the prior-knowledge diagnostic test, discussed in section 5.3.2).

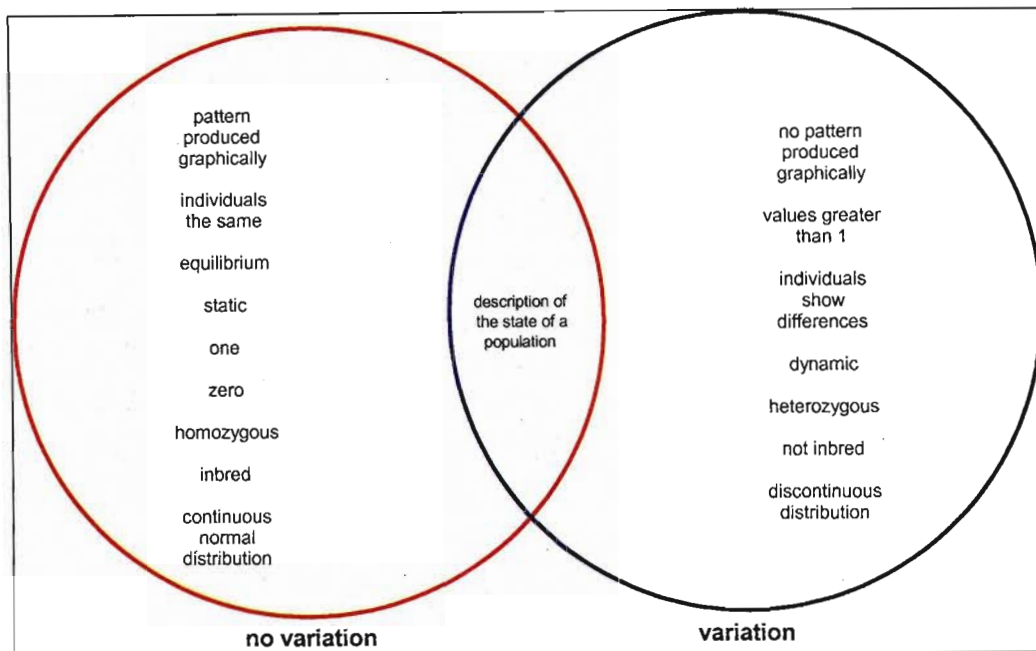
It is evident from the proposed *initial model* that students' conceptions of variation and variance have been grouped together. This is because the results (described in Sections 5.3.1 and 5.3.2) suggested that numerous students think of these two terms as synonyms.



**Figure 5.9: Initial model to illustrate the inappropriate association of certain terms with the absence or presence of variation or variance.**

*Validation of the initial model*

Evidence of the inappropriate association of terms and topics was provided by the results from the prior-knowledge multiple choice diagnostic test, student interviews and the word association study, the results of which are presented in Section 5.3.1(a) and elaborated on in Section 5.3.2. Figure 5.10 depicts a summary of the terms or topics that students generally associated with the absence or presence of variation and variance.



**Figure 5.10: The inappropriate association of groups of concepts with the absence or presence of variation or variance.**

The findings from all the research instruments confirmed the thinking behind the *initial model* that the teaching process could account for the following inappropriate associations between terms and topics:

- The association of heterozygosity and variation and thus the conception that inbred populations cannot have variation;
- The association of change with variation in a population;
- The association of the absence of variation with values of zero or one;
- The association of the absence of variation with some form of equilibrium;
- The association of the presence of variation with a pattern such as a normal distribution when represented graphically.

**(b) Construction of the final model**

It is widely accepted that students' prior knowledge directly impacts on the further learning of applied concepts (Duit et al. 1996). Therefore, the *initial model* which had been constructed to account for the possible source of students' difficulties and alternative conceptions regarding *prior knowledge concepts* was extended to relate these preconceptions to their understanding of *quantitative genetics concepts*, thereby constructing the *final model*.

*Impact of the initial model on students' understanding of quantitative genetics concepts*

The inappropriate association of terms and topics with the *prior knowledge concepts* of variation and variance was hypothesized to influence students' understanding of *quantitative genetics concepts*. For example, the inappropriate association of the concepts of variation and variance with change could have led to certain assumptions by students. Students may have thought that as heritability is calculated as the ratio of two variances, it must have a predictive function; it must predict the breeding values of individuals of the *next* generation. Furthermore, the conception that variance relates to change may cause the alternative conception that the additive variance is transferred from parents to offspring.

Students are taught early on in a quantitative genetics module that quantitative traits are determined by many genes and as a result most individuals will possess some level of heterozygosity. Students who associated variation and variance with the heterozygosity of an individual may have deduced that heterozygous individuals will produce many gametes and thus numerous different genotypes in the offspring. Furthermore, students may have thought that it is the differences in the offspring of *one* individual that gives rise to the additive variance, which in turn indicates whether the offspring resemble their parents. Subsequently, students could have deduced that if the offspring are very similar to their parents then the trait is "fully inherited". This train of deductive thinking may have led to some students confusing the concepts of breeding value, additive variance and heritability. In addition, the alternative conception that heritability is an individual measure may have arisen; partly due to the confusion between the terms inheritance and heritability.

The inability of certain students to link descriptive statistics and graphical representations may have been due to the association of the absence of variation or variance with the pattern of a normal distribution. These students would consequently have been unable to understand why it is that quantitative traits are normally distributed.

Some students related an absence of variation with the number zero or nothing. These students then incorrectly assumed that as heritability is estimated as the ratio of two variances, a heritability of zero indicated that the genes would have no effect on the trait, or that no genes were passed on or there was no genetic influence on the trait in question. Similarly, the association of homozygosity with one type of allele and the value of one implied to some students that a heritability of one indicated that



all of the breeding value was transferred to the next generation or all of the genes were transferred or that all of the individuals (parents and offspring) were identical. Students with these conceptions thus seemed to be thinking on an individual and not a population level.

The above-mentioned factors were taken into consideration and the *initial model* expanded to account for the student difficulties and alternative conceptions with *quantitative genetics concepts* previously noted to be held by students in this investigation.

#### *Construction of the final model*

A *final model* of the possible source of student difficulties and alternative conceptions identified in this study, an elaboration of Figure 5.9, is detailed in Figure 5.11. This diagram proposes that the preconceptions held by students, their knowledge of *prior knowledge concepts* impacts on their subsequent understanding of *quantitative genetics concepts*. The *initial model* is shown in green and the difficulties and alternative conceptions students hold with regard to *quantitative genetics concepts* in red.

The findings of this phase of the investigation therefore highlight the fact that knowledge of students' prior knowledge on entry to a module is necessary before one can fully appreciate why students experience difficulty with the concepts presented in applied modules such as quantitative genetics. Furthermore, it is evident that the sequence in which concepts are introduced to students may be the source of certain difficulties and alternative conceptions in the field of quantitative genetics.

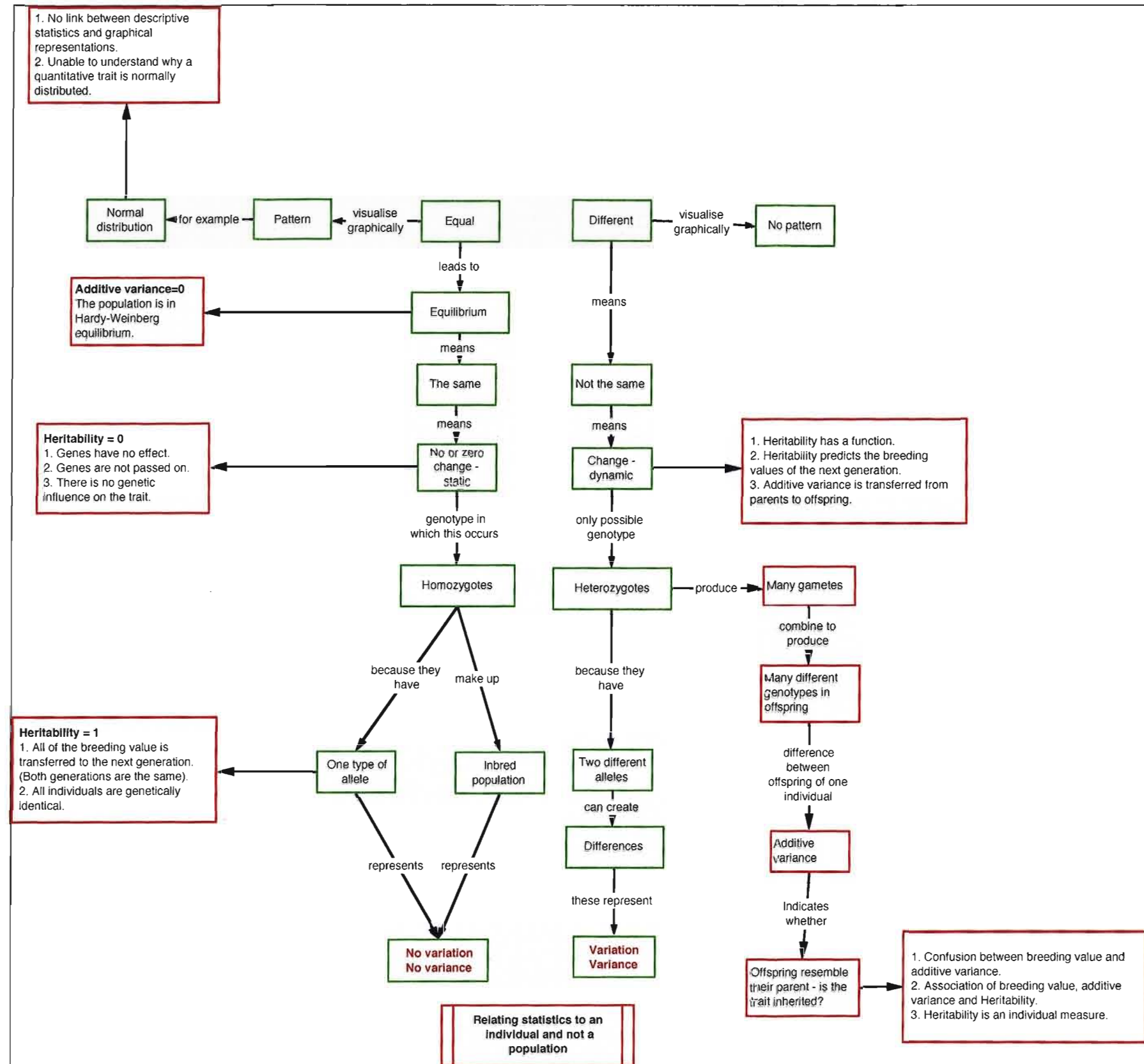


Figure 5.11: Extension of the *initial model* to create the *final model* of the potential source of students' difficulties and alternative conceptions with regard to *quantitative genetics concepts*.

#### **5.4 CONCLUDING REMARKS**

Knowledge of students' conceptual frameworks and the possible existence of *critical concepts* (Chapter 4), the identification of students' difficulties and alternative conceptions (Chapter 5), as well as the model of the possible source of student difficulties with quantitative genetics (Chapter 5), were all used to inform the final stage of the research project; the development of teaching and learning strategies which could prevent or remediate difficulties experienced by students and thereby promote meaningful learning in this discipline (Chapters 6, 7 and 8).

## CHAPTER 6

# REMEDIATION PHASE: DESIGN AND DEVELOPMENT OF THE INTERVENTION

**Research question 5:**

What is an appropriate intervention strategy for use in a quantitative genetics module?

### 6.1 INTRODUCTION

As this research project was of the action research type (Section 2.3, page 42), one of its aims was the improvement of practice. Thus, the remediation phase of the research aimed to develop and evaluate teaching and learning strategies that could be employed in an introductory module of quantitative genetics to address the difficulties and alternative conceptions shown to be held by students during the diagnostic phase of this investigation. The results of the diagnostic phase of this investigation thus informed the design of the intervention.

The diagnostic phase of the research indicated that students showed difficulty integrating their knowledge and that two concepts, namely, variance and heritability, were *critical* to the learning of *quantitative genetics concepts*. The results also indicated that not only were the *critical concepts* of variance and heritability extremely difficult for a large proportion of students to understand but also that many of the students evaluated held alternative conceptions regarding both the *prior knowledge concepts* and *quantitative genetics concepts* investigated during this study. Summaries of the difficulties and alternative conceptions revealed in this investigation are given in Tables 5.1 (page 118) and 5.2 (page 123) and the nature of the difficulties and alternative conceptions is described in Table 5.3 (page 127).

As students were shown to confuse: (a) the concepts of variation and variance, (b) individual and population measures, (c) the values of zero and one with the absence or presence of certain phenomena, (d) the terms inheritance and heritability, (e) the assignment of the X and Y axes of histograms and (f) histograms and scatterplots,

particular attention was directed towards improving students understanding of these ideas during the design and implementation of the intervention.

The design of the intervention was informed not only by the results of the diagnostic phase, but also the theories of constructivism, conceptual change and metacognition, literature on remediation strategies and tools used by other researchers in the broad field of science education.

## 6.2 THEORETICAL FRAMEWORK UNDERPINNING THE INTERVENTION

Venville and Treagust (1998) stated that research, such as that described in the diagnostic phase of this investigation, which has focused on students' conceptions at a particular point in time and the study of students' difficulties and alternative conceptions in science, has not traditionally considered *the manner in which* students' current views interact with new and possibly incompatible ideas. The currently held knowledge of students may or may not be seen as compatible with the present view of the scientific community, but it nevertheless is the student's foundation for any future learning (Hewson and Lemberger 2000) and is gradually replaced in the cognitive frameworks of students whilst learning by a process known as *conceptual change* (Merenluoto and Lehtinen 2004). As the therapeutic phase of this investigation aimed to assess the effectiveness of an intervention and the manner in which students ideas changed over time, the theories of constructivism and meaningful learning, conceptual change and metacognition are relevant to this component of the research. These theories provided both a basis for the design of the intervention and were used as a framework for interpreting the data.

### 6.2.1 Constructivism and meaningful learning

The principles of constructivism and meaningful learning are described in Section 2.1, page 25.

### 6.2.2 Conceptual change

Learning is a result of an interaction between what students are being taught and what they already know (Posner *et al.* 1982) and according to constructivist principles is a process of conceptual change (Hewson 1996) where knowledge acquisition is acknowledged as being a process of actively generating and testing alternative



propositions (Tyson *et al.* 1997). Learning is therefore a rational activity where someone begins to comprehend and accept new ideas on the basis of available evidence (Posner *et al.* 1982). However, it should be noted that whereas learning may be viewed by some science educators as an additive process where existing knowledge is expanded (Vosniadou and Verschaffel 2004), conceptual change may involve a process by which a person's conceptual framework changes from one set of conceptions to another, incompatible with the first (Posner *et al.* 1982).

It is commonly accepted that there are two types of conceptual change.

- (1) There may be weak knowledge restructuring or *evolution* known as *conceptual capture*, *assimilation* (Tyson *et al.* 1997; Duit and Treagust 2003) or *subsumption* (Novak 1977; Martin *et al.* 2000).
- (2) Secondly, there may be *accommodation* (Posner *et al.* 1982) or *superordination* (Martin *et al.* 2000) where *conceptual exchange* involving radical changes to the conceptual framework occurs which is *revolutionary* in nature (Tyson *et al.* 1997; Duit and Treagust 2003).

Research indicates that much of the conceptual change that has been documented in science students is of the *evolutionary* kind (Treagust *et al.* 1996b; Pearsall *et al.* 1997; Martin *et al.* 2000; Taber 2001) and when radical restructuring of knowledge occurs, it usually takes place at the beginning of a module (Pearsall *et al.* 1997; Martin *et al.* 2000).

Tyson *et al.* (1997) have proposed a multidimensional framework for the interpretation of conceptual change. This framework takes previous research into account and views conceptual change from three perspectives, epistemological, ontological and social or affective.

The *epistemological* perspective is concerned with the manner in which a student views his or her own knowledge. This perspective, first proposed by Posner *et al.* in 1982, views conceptual change as a radical process of accommodation. These researchers suggested that four conditions must be met, in a linear fashion, before conceptual change can occur. Firstly, students must become dissatisfied with their existing conceptions. Secondly, the new concept must appear "intelligible" or be understood by the student. Thirdly, the conception must be "plausible" or believable. Finally, the student must find the conception "fruitful" in that it assists in the solution of novel problems or problems which the student was previously unable to solve. Furthermore, an individual's conceptual ecology will influence the process of conceptual change. An individual's conceptual ecology includes anomalies,



analogies and metaphors, epistemological commitments, metaphysical beliefs and competing conceptions (Posner *et al.* 1982; Taber 2001). The extent to which a person's conception meets the above-mentioned criteria of intelligibility, plausibility and fruitfulness, within their conceptual ecology, determines the conception's status (Hewson 1996; Hewson and Lemberger 2000; Duit and Treagust 2003). The more conditions being met, the higher the status of the new conception and the more likely that it becomes the preferred conception held by the individual by a process of conceptual capture (Hewson 1996; Duit and Treagust 2003). A successful student would then be one with a low status for alternative conceptions and a high status for scientifically correct conceptions (Tyson *et al.* 1997).

It should be noted that individual scientists and students may hold valid alternative ideas for any one conception in their cognitive structure and that the application of a particular version of a scientific concept will depend on the context in which they are working (Tyson *et al.* 1997; Taber 2001; Duit and Treagust 2003; Vosniadou and Verschaffel 2004). Once a certain alternative becomes seen by the individual as having greater explanatory worth (i.e. a higher status) it will become the preferred theory with which the individual will operate (Treagust *et al.* 1996b; Taber 2001). However, many students maintain conflicting beliefs and make distinctions between knowledge gained in different arenas, for example, biological and mathematical knowledge, which may be related but is compartmentalised by students (Edmonson and Novak 1993). Long term conceptual change will only occur once the student recognises the commonalities between the different contexts and the manner in which the scientific conception applies across these contexts (Gunstone and Mitchell 1998).

In the case of students who hold alternative conceptions of certain scientific ideas, a radical process of conceptual change must occur whereby the alternative view is replaced by a scientifically accepted conception. In order for radical changes or accommodation to occur two features of one's conceptual ecology are important; anomalies and fundamental assumptions about science and knowledge. Anomalies provide a cognitive conflict which may lead to accommodation of a new conception (Posner *et al.* 1982). Therefore, lectures and demonstrations which create cognitive conflict in students by destabilising students' confidence in their existing unscientific conceptions and the substituting them with scientifically accepted ones, may lead to conceptual change (Posner *et al.* 1982; Kang *et al.* 2005). However, in a study conducted by Merenloto and Lehtinen (2004) on the radical change required from the use of discrete natural numbers to rational numbers, cognitive conflict was shown to not always support conceptual change. Furthermore, Kang *et al.* (2005) found in a

study of 159 Korean high school students understanding of the concept of density, that a certain level of reasoning ability, a meaningful orientation towards learning and a tolerance for failure were necessary in order for students to achieve conceptual change through a process of cognitive conflict.

According to the constructivist paradigm, reality may be seen in terms of students' beliefs regarding three ontological categories; what something is made of, what you can do to it and what it can make happen (Mariani and Ogborn 1991). Accordingly, the *ontological* dimension of conceptual change arose from the argument that conceptual change must result from changes in student's beliefs regarding the ontological categories to which conceptions belong (Chi *et al.* 1994). It is proposed that students' alternative conceptions may be associated with a tendency to associate conceptions with the incorrect ontological category, for example, matter versus process, cause versus effect, discrete versus continuous and real versus imaginary (Mariani and Ogborn 1991). The ontological status of the initial and the scientifically accepted conceptions held by individuals will determine the ease of learning and conceptual change. If the two conceptions held by students belong to different ontological categories then conceptual change will subsequently be difficult (Chi *et al.* 1994).

As students' epistemological commitment and ontological beliefs must exist within *social and affective* contexts, Pintrich *et al.* (1993) argued that student's motivational beliefs and their role in a classroom learning community will influence the process of conceptual change. In this regard, science instruction which aims to develop students' interest in the subject area will most certainly also develop their pre-instructional conceptions towards the scientifically accepted views (Duit and Treagust 2003). For example, if new information is regarded as worthless by the student, there would be no motivation on the part of the student to change his or her existing knowledge (Kang *et al.* 2005).

In a multidimensional framework, the epistemological perspective thus examines the manner in which a student perceives his or her own knowledge about the issue under study. The ontological view considers the way in which a student perceives the nature of the conception being studied. Finally, the social or affective perspective examines the social and affective conditions necessary for conceptual change to occur (Tyson *et al.* 1997). Venville and Treagust (1998) used this unifying framework to establish students' ontological perspectives of the gene, and then to examine this conception from both an epistemological and a social or affective perspective. The results indicated that students elaborated on their conception of the gene as a

passive particle rather than that of an active, productive, sequence of instructions. During the learning process the status of more scientifically acceptable models of genes was raised at the expense of the prior conception of the gene as a passive particle, by a process of conceptual capture or assimilation. This process was enhanced by an interest on the behalf of the students and the approach of the teacher. Research of this nature indicates the applicability of a multidimensional framework of conceptual change to the current investigation into the learning of the foundational concepts of quantitative genetics.

In this investigation the epistemological and ontological views of students were inferred from an analysis of a series of concepts maps which students had constructed throughout the module. The nature of the links between concepts that were created by students was used to infer the epistemological and ontological beliefs of students (full details of how the concept maps were analysed are provided in Section 8.2.1, page 212). The affective views of the students were ascertained from the answers given by students to Likert-style attitudinal questionnaires (described in Section 8.2.2, page 215).

### **6.2.3 Metacognition**

Metacognition refers to knowledge, awareness and control of ones own learning (Georghiades 2004a; Liu 2004). In order for conceptual change to occur students must recognise their conceptions, decide whether to reconstruct the status of their conceptions by a process of evaluation and then reconstruct and review their knowledge; all metacognitive activities (Gunstone and Mitchell 1998; Hewson and Lemberger 2000). Metacognitive reflection is then the critical examination of the learning process by a student, where important points of the procedure followed are noted, mistakes are acknowledged, relationships identified and a connection between understanding and the learning outcome is traced (Georghiades 2004a). Research suggests that science students who learn in such a meaningful manner are more cognizant of their own learning and are therefore more successful than students who learn in a rote fashion (Edmonson and Novak 1993; Martin et al. 2000).

The role of the student is thus to take responsibility for their own learning, recognise different views and be prepared to change their own conceptions (Baird and White 1996). To assist the student, the role of the teacher is to have respect for and knowledge of students' ideas and to use a range of teaching strategies and support materials that will assist students in the learning process (Posner et al. 1982;

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Hewson and Lemberger 2000). The classroom climate should also support the open expression of ideas and motivate students to learn (Hewson 1996).

#### **6.2.4 Application of the theoretical framework to this investigation**

In this investigation a comprehensive model of the manner in which students' conceptions change over time was thought to include the following: Firstly, students' cognitive development on the *content level*. Secondly, students' views on the *epistemological nature* of their knowledge. Thirdly, students' views on the *ontological status* of their knowledge. Fourthly, students' *willingness and motivation to learn* (Duit and Treagust 2003).

In order to assess all of the four factors which indicate changes in students' conceptions over time various methods of data collection were utilised. The content knowledge of students was probed using multiple-choice diagnostic questionnaires, whilst the epistemological and ontological views of the students were deduced from the concept maps which they constructed throughout the module. The attitudes of students towards the subject and the manner in which it was taught were quantified using a Likert-style questionnaire as well as interviews with students.

The educational principles of constructivism, meaningful learning, conceptual change and metacognition that provided a framework for the design and analysis of the intervention, their implications for classroom practice and the strategies used in this investigation are presented in Table 6.1

**Table 6.1: Educational principles underpinning the intervention.**

Educational principle	Implications for classroom practice	Strategies used to apply the principles in this study
<p><b>Constructivism:</b> According to Driver and Bell (1986) a person with a constructivist view of learning believes that:</p> <ul style="list-style-type: none"> <li>(i) What students' learn is idiosyncratic and dependent on their prior knowledge and learning experience.</li> <li>(ii) Learning is a continuous and active process.</li> </ul> <p><b>Meaningful learning:</b> According to Ausubel (1968) meaningful learning occurs when new ideas, which have some significance for the student, are incorporated into a student's conceptual framework in a systematic, intentional fashion. In addition, the students must have sufficient prior knowledge upon which to anchor new ideas.</p> <p><b>Conceptual change:</b> Conceptual change occurs during the learning of new concepts. It may be evolutionary (the knowledge base is expanded) or revolutionary (old ideas are replaced by new ones) in nature (Tyson <i>et al.</i> 1997).</p> <p><b>Metacognition:</b> According to Edmonson and Novak (1993) and Martin <i>et al.</i> (2000), research suggest that science students who learn in a meaningful manner are more cognizant of their own learning and therefore more successful than students who learn in a rote fashion.</p>	<p>For constructive, meaningful learning and conceptual change to occur:</p> <ul style="list-style-type: none"> <li>(i) New ideas must be explicitly connected to students' prior knowledge;</li> <li>(ii) Learning experiences should encourage students to actively re-evaluate their current beliefs and to alter their ideas if necessary;</li> <li>(iii) Learning experiences should clearly indicate the practical application of new ideas.</li> <li>(iv) Students must take responsibility for their own learning experience and be prepared to change their conceptions.</li> <li>(v) The teacher and the classroom climate should assist the student to be aware of the status of their own knowledge and to encourage thoughtful reflection.</li> </ul>	<ul style="list-style-type: none"> <li>(i) Computer-based tutorials were designed so that they specifically addressed any alternative conceptions and difficulties that had been documented during the diagnostic phase of this investigation. The first tutorial addressed possible inadequacies in students' prior knowledge. Subsequent tutorials ensured that new ideas were clearly and correctly related to previously learned concepts.</li> <li>(ii) Students constructed their own knowledge through interaction with their peers and tutors.</li> <li>(iii) The computer-based tutorials were designed to ensure that students were encouraged to make and test predictions.</li> <li>(iv) The computer programmes used examples familiar to the students such as egg weight and coat colour.</li> <li>(v) As concept maps are regarded as metacognitive tools which promote meaningful learning and the process of mapping as employing many metacognitive skills, the students were required to construct concept maps depicting the relationships between key concepts of quantitative genetics throughout the module. They were thus actively engaged in their own learning and were encouraged to reflect on their knowledge.</li> </ul>

### 6.3 REVIEW OF RELEVANT THEORY-DRIVEN INTERVENTION STRATEGIES

A number of different strategies have been designed to encourage understanding and conceptual change in science classrooms. These include the use of graphic organizers such as concept maps (Trowbridge and Wandersee 1998), computer assisted learning (Mills 2002), analogies (Dagher 1998; Martin 2003), co-operative learning environments (Jones and Eichinger 1998; Jones and Roach 1998), historical



vignettes (Wandersee and Roach 1998), concept substitution (Grayson 1996) and the idea of science as argument (Kuhn 1993; Zeidler 1997; Zohar and Nemet 2002).

Despite carefully organised lectures and reading assignments, research has shown that many students are not able to firmly grasp the foundational principles of genetics and are thus unable to apply them to the field of quantitative genetics (Brand *et al.* 1991). It was thus deemed necessary in this investigation to provide some form of theory-driven intervention in an introductory module of quantitative genetics. Due to the abstract nature of concepts in quantitative genetics and the perceived need to promote the metacognitive activities of students, computer-assisted learning and the use of concept mapping were chosen as teaching strategies for this investigation.

### **6.3.1 Computer-assisted learning**

#### **(a) *Rationale behind the use of computer-based tutorials for teaching of quantitative genetics concepts***

A constructivist view of teaching, challenges teachers to create classroom environments where the students are encouraged to think, explore and construct their own understanding of concepts (Steinhorst and Keeler 1995). Computer-assisted learning may allow students the opportunity to learn by constructing their own ideas and knowledge from a computer simulation experience, thereby developing their own understanding of statistically-based concepts. Furthermore, research indicates that students who are actively involved in their own learning will usually become more independent problem solvers and learners (Mills 2002).

Various computer simulation models have been developed by other researchers for the teaching of quantitative genetics. One of the first programmes was developed by St. Martin and Skavaril (1984) to simulate methods of plant selection which are too lengthy to perform during the teaching time allocated to a module. The researchers found when students utilised the simulation exercises in a plant breeding module; their interest in plant breeding was stimulated. Another such model developed for teaching purposes at Edinburgh University also simulates the response of quantitative traits to selection (Partner *et al.* 1993). Two further studies using the Gregor software for quantitative traits, which provides a visual display of a group of individual's chromosomes as well as displaying phenotypic data in the form of a histogram, demonstrated that students responded in a positive manner and were motivated to use this genetic simulation tool (Michaels 1993; Tinker and Mather

1993). However, none of these studies explicitly determined whether the simulation brought about any degree of conceptual understanding. Another software programme, QU-GENE was developed to provide a simulation platform for the analysis of quantitative genetic models of alternative breeding strategies (Podlich and Cooper 1998). In a study conducted on twenty-two students taking an introductory plant breeding course in Australia, Cooper (1998) concluded that the simulation tool operated by reinforcing and integrating concepts that had been introduced in lectures, but that the simulation on its own was insufficient in establishing an understanding of quantitative genetics. Furthermore, Cooper proposed that it is only in students who devote sufficient time and who actively seek to develop a deep understanding of the subject matter that the simulation was truly effective.

Due to the lack of empirical evidence on the effectiveness of computer-assisted learning in the field of quantitative genetics, this investigation aimed not only to develop computer-based tutorials which would assist students to reinforce and integrate concepts learned in lectures, but also to gather empirical data on the effectiveness of the intervention.

**(b) *Benefits and limitations of computer-assisted learning***

A review of the literature on computer-assisted learning in statistics and genetics was conducted before the development of the tutorials so as to ascertain recognised advantages and disadvantages of this form of teaching and learning, as well as to gather information on suggested requirements for any computer-based learning programme.

Numerous advantages of computer-assisted learning have been identified and are summarised in Table 6.2. (Rossman 1997) has identified three main uses of technology in the teaching of statistics-based modules: Firstly; the use of real datasets on which to perform calculations so that graphical displays are immediately provided by the computer; secondly, the use of simulations to illustrate the behaviour of sample statistics under random sampling and thirdly; exploring statistics by making and testing predictions and then revising these predictions in an iterative manner. However, other researchers have found that computer-assisted learning is also beneficial in that it provides a multi-media learning environment which allows for the visualisation of certain concepts. Furthermore, students' attitudes towards statistics and genetics have been seen to improve when using computer-based learning tools. Some students have also overcome their mathematical anxiety, perhaps as a result

of the computer performing many of the complex calculations for the student, thereby allowing the student time to concentrate on their conceptual understanding.

In the design of the intervention used in this investigation care was taken to exploit the advantages of computer-assisted learning. As students in the diagnostic phase had shown that they had great difficulty in (1) the understanding of statistics such as variance and heritability and (2) the construction and interpretation of frequency distributions, the computer-based tutorials aimed to create visual graphical displays of the relevant statistics and to allow students the time and opportunity to make and test predictions on different randomly generated populations.

The disadvantages of this form of learning experience are detailed in Table 6.3 and include the fact that technology must be supplemented with a level of tutoring, the learning experience may not cater for all ability levels, the cognitive load of the tasks may be too high for some students, teachers may be unskilled in this form of instruction, the tutorials will be time-consuming and the hardware or software may be inadequate. Furthermore it must be noted that at present, there is still insufficient knowledge of the educational effect of educational technology and further research is required to determine how and where computers should be used to have the maximum impact on student learning (Schuyten and Dekeyser 1997).

The researcher tried wherever possible to minimise the disadvantages of computer-assisted learning documented in the literature. In this regard, the computer-based tutorials were designed so as to cater for the cognitive abilities of the weaker students in the class, the tutors and teacher of the module were well trained in the use of the software and sufficient tutors were available during the tutorial to assist students where necessary. In addition, the researcher ensured that the hardware and software used were modern and, in her opinion, of a sufficiently high standard.

Table 6.2: Advantages of computer-assisted learning.

Advantage	Relevant literature
Use of realistic data sets	Research indicates that the active involvement of students in the learning process and the use of statistics in relevant applications, such as genetics, may facilitate learning (Gnanadesikan <i>et al.</i> 1997). It is beneficial for students to use statistics generated from realistic data sets and to apply them to appropriate situations (Steinhorst and Keeler 1995). Computers may serve as powerful computational tools and also help to reinforce concepts by providing realistic settings in which genetics students may apply statistical concepts and techniques (Slack and Stewart 1989; Mills 2002). In this manner, computer simulations may help render abstract ideas more concrete (Gnanadesikan <i>et al.</i> 1997; Huppert <i>et al.</i> 2002).
Ability to make and test predictions	It has been documented that computer simulations, in the disciplines of both statistics and genetics, allow students to formulate predictions, analyse the subsequent data and interpret the results by synthesizing the results with their existing knowledge (Slack and Stewart 1989; Johnson and Stewart 1990; Slack and Stewart 1990; Simmons and Lunetta 1993; Eichinger <i>et al.</i> 2000; Akpan 2001; Huppert <i>et al.</i> 2002; Soderberg and Price 2003; Bakker 2004). This personal journey of discovery and exploration allows the unique and personal construction of knowledge (Rieber <i>et al.</i> 2004). Furthermore, computer simulations allow students to reason from effects to causes (Slack and Stewart 1989; Johnson and Stewart 1990; Slack and Stewart 1990; Simmons and Lunetta 1993). In this way, computer assisted learning may aid in the correction of any alternative conceptions the students may hold and facilitate conceptual change (Hawkins 1997; DelMas and Liu 2005). Moreover, students become aware of the nature of science, rather than the memorisation of facts (Johnson and Stewart 1990). Furthermore, computer simulations may help students learn about quantitative genetics by posing "what if" questions about a population of interbreeding individuals (Soderberg and Price 2003). Students may be able to alter the characteristics of the initial population, the relative fitness and frequency of alleles, the number of alleles affecting the trait and perhaps the heritability of the trait to investigate computer-generated changes in the population. These type of simulations may help students shift their thinking about genetics from an individual or familial level to a population level; which is what is required for problem solving in quantitative genetics (Soderberg and Price 2003).
Multi-media learning	Well-designed computer-based activities provide opportunities for multi-media learning (Bodemer <i>et al.</i> 2004); learning from both pictures (graphics) and words (written or spoken). As people have two processing systems, a verbal and a visual system which complement one another (Mayer 2001), effective learning results when information is received both visually and verbally, as proposed by Paivio's dual coding theory and Mayer's theory of multi-media learning (Ploetzner and Lowe 2004; Rieber <i>et al.</i> 2004). This is because as information is coded in two different formats, the chance is doubled that the learners will assimilate the information (Rieber <i>et al.</i> 2004). In addition, the explicitness of diagrammatic representations can facilitate comprehension of the subject matter by alleviating the need for students to mentally manipulate text-based information (Lowe 2004). Although the visual and verbal channels are not equivalent, words and pictures are useful for presenting different kinds of material. Understanding then occurs when students build meaningful connections between these visual and verbal representations (Mayer 2001; Bodemer <i>et al.</i> 2004).
Visualisation of characteristics of graphical representations	Many software programmes allow students to easily visualise the characteristics of graphical distributions and to dynamically manipulate data displays (Hammerman and Rubin 2004). Visualisation, through the use of graphical representations, has been shown to aid in the understanding of statistical concepts, such as variation (Makar and Confrey 2005) and other complex principles in quantitative genetics (Cooper 1998). A reason for this may be that by placing graphs alongside values or parameters on the computer screen, students can better visualise and thus reconcile descriptive statistics or equations and graphical representations (Good and Berger 1998; Mills 2002; Stern <i>et al.</i> 2003). This has been confirmed by a study conducted by Rieber <i>et al.</i> (2004) where it was empirically demonstrated that graphical simulations are more beneficial when they are supplemented with written explanations.



	<p>Roth (2002) found that many students do not fully understand graphs and as a result misinterpret them. In a 1989 study by Stuessy and Rowland on the "Advantages of Micro-based Labs: Electronic Data Acquisition, Computerised Graphing or both?", it was observed that students who used the micro-based labs to acquire and display temperature data in the form of graphs showed a vast improvement in their graphing skills when tested, over students who did not. Furthermore, students who have knowledge of the fundamental elements of different graphical representations are more able to apply these representations in various contexts, thereby enabling cross-content transfer across interdisciplinary boundaries (Stern <i>et al.</i> 2003), such as between statistics and quantitative genetics. Computer simulations may thus be used to teach quantitative genetics and to help in the improvement of graphing skills and the interpretation of graphical knowledge (Soderberg and Price 2003). For example, there are many interactive simulation programs for concepts such as the Central Limit Theorem on the World Wide Web (West and Ogden 1998; Mills 2002). These simulation experiments may be used to relate the Central Limit Theorem to the occurrence of a normal distribution, when considering a quantitative trait in one population. The students may discover that the more genes involved (and environmental effects), if each have a small, additive effect, the closer the distribution approaches that of a continuously distributed normal type. They will be able to see that the majority of the individuals will have values near the mean value of the population, as many gene combinations may produce the same value and that very few gene combinations produce extreme values, so that extreme values occur at a low frequency. Students should then have a better understanding of histograms and the reason why quantitative traits are normally distributed.</p>
Improvement in student attitudes	<p>Computer assisted learning has also been shown to improve the attitude of students towards the study of genetics and other statistically-based subjects and helps students to think like scientists (Mills 2002; Tsui and Treagust 2002; Soderberg and Price 2003). The traditional form of lecturing as a passive learning experience is usually unproductive, especially for unmotivated students (Steinhorst and Keeler 1995). Educational technology has addressed this problem by creating a far greater variety of teaching and learning strategies (Hawkins 1997). One such strategy is the use of software which acts as a tutoring programme which identifies a student's difficulties and provides corrective instruction tailored to the unique errors of each individual student (Browning and Lehman 1988). Cognitive psychologists regard this type of individual feedback as necessary for assisting students in restructuring their knowledge and supporting their metacognitive processes (Rieber <i>et al.</i> 2004).</p>
Students can work at their own pace	<p>Computer-assisted learning strategies give students the ability to control the pace at which they work (Gifford and Enyedy 1999; Akpan 2001; Huppert <i>et al.</i> 2002) and to co-ordinate and link foundational concepts (DelMas and Liu 2005). This is important to students who require additional time to formulate their own understanding of concepts (Gifford and Enyedy 1999). Students have the time to reflect on, question and evaluate the statistical concepts behind the results which they obtain from calculations (Forman and Pufall 1988).</p>
Students may overcome mathematical anxiety	<p>As quantitative genetics is taught in terms of mathematical and statistical models, many principles are defined in terms of equations. This use of mathematical frameworks to depict biological phenomena is often seen as a barrier to students' learning (Longden 1982; Browning and Lehman 1988). The use of computer simulations in quantitative genetics may thus be effective in overcoming the mathematical anxieties of students and provide a mechanism to stimulate greater student interest (Cooper 1998).</p>
Computer performs complex calculations	<p>A further problem encountered by many students undertaking courses in statistics and genetics is the drudgery associated with long, repetitive and complex calculations (Forman and Pufall 1988; Hawkins 1997). The speed, dynamic nature, range of software, increased storage capacity and processing power of computers allow students to timeously and effortlessly explore all facets of a statistical process (Forman and Pufall 1988), graphical representations (Stern <i>et al.</i> 2003) and the results of genetic crosses (Slack and Stewart 1989; Johnson and Stewart 1990). A learning experience which makes use of computers may thus ensure that students are not swamped by the mechanics of procedural methods so that they are more eager and more likely to learn in a meaningful manner (Steinhorst and Keeler 1995; Mintzes and Wandersee 1998; Gardener and Hudson 1999).</p>



**Table 6.3: Disadvantages of computer-assisted learning.**

Disadvantage	Relevant literature
Technology on its own is insufficient	Simply introducing students to technology is not a recipe for success (Behrens 1997). For example, it is necessary not only to introduce students to concepts like the Central Limit Theorem but to illustrate the purpose of the theorem. If the software cannot show the students more than just an abstract representation of the concept, then the software is a failure (Meletiou 2000). Most students can master the mechanisms of data analysis, but when statistical packages are used to apply techniques, abstract statistical concepts may still not be understood and misconceptions may be compounded (Mills 2002). In addition, the use of technology can lead to the assumption by the student that because the computer has done something, it must be correct (Nicholson 1997). Claims cannot simply be made that dynamic and interactive software allows students to explore and experiment with statistical concepts, evidence of how, why and when insight occurs must be obtained (Hawkins 1997). For example, it has been demonstrated that while computer simulations allow students the opportunity to develop their understanding of genetics, they do not of themselves promote problem-solving performance in genetics (Slack and Stewart 1989; Slack and Stewart 1990).
Students vary in their aptitude and computer skills	Students in any class will vary in their general learning ability, computer skills and prior knowledge. It is thus very difficult to design a learning experience that begins at the correct level for all students (DelMas 1997; Hawkins 1997; Huppert <i>et al.</i> 2002). The variety and complexity of information presented may also distract students, particularly if they have low levels of diagrammatic literacy, causing them to get lost in irrelevant details (Stern <i>et al.</i> 2003). Furthermore, in order to take full advantage of a computer-based activity, students need to be carefully guided to ensure that they are exploring a concept in a meaningful manner (Behrens 1997; Huppert <i>et al.</i> 2002).
The cognitive load of the computer-based task may be too high for some students	The cognitive load theory proposed by Mayer (2001) claims that both the visual and verbal channels have limited processing capacity. If the demands of the content and the task exceed the capacity of the individual to manage the information as well as the relationships between the pictorial and verbal information, then little or no learning will occur (Mayer 2001; Bodemer <i>et al.</i> 2004; Ploetzner and Lowe 2004; Rieber <i>et al.</i> 2004). As a consequence, students may fail to integrate different sources of information into coherent mental representations which results in fragmented knowledge structures (Bodemer <i>et al.</i> 2004). In this regard, it should be noted that dynamic visualisations and animations place even greater information on students than do static representations (Lowe 2004; Ploetzner and Lowe 2004) and few studies have shown an advantage of animated over static displays (Hegarty 2004).
Teachers may be unskilled	Using any new teaching tool requires a change in the content and pedagogy of instruction. Unfortunately, many teachers are not prepared for these changes (Hammerman and Rubin 2004). The teachers must be prepared to guide the activities (Rieber <i>et al.</i> 2004), be familiar with the software and be able to select relevant software for use in the classroom (Tsui and Treagust 2002). Teachers must thus be trained in the use of the relevant hardware and software.
Computer tutorials are lengthy	Computer-based tutorials are time consuming and thus fewer topics can be covered than when using conventional teaching methods (Mintzes and Wandersee 1998). As a result of such time constraints, teachers have to decide whether to cover a few topics in depth using computer simulations, or many topics in a broader context using traditional methods.
The hardware or software may be inadequate	Technology-based teaching may achieve less than optimal results either because the hardware, the software, or both, may be inadequate. This inadequacy of the hardware may be a result of insufficient computers being available for student use. The software, on the other hand, may be inadequate with respect to pedagogic strategies used, the tutorial design, the database available and poor graphics. For example, a weakness that has been identified with students who have taken applied statistical courses is that they cannot form connections between the important concepts in the discipline. This is problematic as the learning of a statistical concept, without understanding its connections to other statistical constructs cannot lead to proper understanding (Lachance and Confrey 1996). As many computer simulation software packages address concepts singularly, this problem is often not addressed. Furthermore, it should be noted that not all learning institutions may be able to afford the costs of the new hardware and software required for the successful implementation of a computer assisted learning program (Novak 2003).

**(c) Requirements of an effective computer-assisted learning programme**

Computer assisted learning programmes and the associated graphics, are assumed to facilitate comprehension, learning, memory and deduction capabilities of students. However, research indicates that this will only take place if the computer programmes are carefully designed and are appropriate for the group of students taking the course (Morrison *et al.* 2002). Table 6.4 indicates how the requirements for an effective computer-assisted learning programme were incorporated in this investigation.

**Table 6.4: Manner in which the requirements for a computer-based learning experience were incorporated in this investigation.**

<b>Requirement</b>	<b>Application to this investigation</b>
The programme must start at the level of each student and not the teacher, thus accommodating the student's conceptual development, common alternative conceptions and prior knowledge (DelMas 1997; Chandler 2004; DelMas and Liu 2005).	In order to cater for weaker students, highly descriptive computer programmes were utilised such as Tinkerplots, Genup and Excel. Furthermore, a brief written and verbal summary of the topic under consideration was provided at the start of each tutorial to remind students of the correct interpretation of the principles of the topic being studied. In addition, the language used in the tutorial guides was clear and simple.
The programme should promote learning as an active process and provide guidance and additional explanations that allow for discovery learning (DelMas 1997; Rieber <i>et al.</i> 2004).	The tutorials promoted learning as an active, constructive process by allowing students the opportunity to interact with their peers and tutors during the tutorial.
When using statistical software, educators should provide an example, real or imagined, that the students can relate to, as well as supplementary problems so that students may look at the problem systematically by manipulating one variable at a time. Furthermore, students should always make a prediction prior to each run of a simulation so as to address any intuitive beliefs they may have and to bring about conceptual change (Soderberg and Price 2003; Bodemer <i>et al.</i> 2004; DelMas and Liu 2005).	The tutorial guides encouraged the students to make and test predictions and to reflect on what they had learned.
The computer program should utilise familiar models and representations to help the students decipher relevant knowledge by integrating old and new information (DelMas 1997).	The computer-based tutorials used examples familiar to the students such as egg size, cat colour and weight.
Computer simulations should place emphasis on aspects of a simulated problem that may be disregarded or overlooked in normal learning conditions (DelMas 1997).	The tutorial guides contained questions that the students were required to answer which targeted previously identified alternative conceptions and difficulties that students had with a particular topic.
Students must be carefully guided through the activity so that any misconceptions harboured by the students may be remediated (Behrens 1997).	A comprehensive written tutorial guide was provided and tutors were available to assist students where necessary.
The program should aid students in bridging interdisciplinary boundaries and encourage thoughtful reflection (Mintzes and Wandersee 1998; Rieber <i>et al.</i> 2004).	The tutorials focused on relating specific statistics to graphical representations and their use in the field of quantitative genetics.

The order of the use of the simulation relative to the lectures was also seen as an important factor. However, research on this aspect of computer-assisted learning in genetics is contradictory. Brand *et al.* (1991) found that it was beneficial to follow the simulation with lectures on the topic, whereas Cooper (1998) found that it was better if the simulation built on what had been covered in lectures. When used as pre-instructional activities simulations seem to serve to motivate students, to reveal alternative conceptions, to provide an organizing structure for receiving novel material and serve as concrete examples of abstract concepts. In contrast, post-instructional use of simulations seem to be beneficial in that they facilitate the integration and application of newly acquired knowledge and they may also reveal alternative conceptions (Brand *et al.* 1991). In this investigation, the students completed the first tutorial before the topics were covered in class. As the first tutorial covered concepts which should have been taught in previous modules, it was assumed that the students would already have some knowledge of these topics. The other two tutorials were introduced after the students had been taught the topics in class. The tutorials therefore served to reinforce the concepts learned and to assist the students in the integration of their knowledge.

### 6.3.2 Concept mapping as a learning tool

#### (a) *Rationale behind the use of concept mapping to encourage meaningful learning of quantitative genetics concepts*

Due to the rapid changes in science and the enormous amount of information that is becoming available, skills needed for meaningful learning are becoming more important for students as they must be encouraged to become life-long learners, in order to keep up to date with this information explosion (Pinto and Zeitz, 1997). As a result, the emphasis in education has changed from teaching students to be “knowers” to being “learners” and knowing how to learn more about related topics on their own (Trowbridge and Wandersee 1994). Concept mapping has been shown to be effective in encouraging meaningful learning by promoting the connection of new concepts and propositions into existing, relevant frameworks (Heinze-Fry and Novak 1990; Okebukola 1990; Roth and Roychoudhury 1992; Novak 1996, 2003) thereby changing students from being rote learners to individuals able to obtain a meaningful understanding of biology (Fisher *et al.* 2000). It is for these reasons that the task of concept mapping was included as a metacognitive tool in this investigation.



**(b) Benefits of concept mapping**

The literature abounds with research studies which have indicated the effectiveness of concept mapping as a tool for promoting meaningful learning. The reasons given for the success of this technique are primarily that it requires students to explicitly think of the relationships between concepts and to organise their knowledge into a manageable form so that information can be easily accessed when necessary. Furthermore, students may work together when constructing their concept maps and during the process of map construction various ideas will be discussed. In this way the information to be learned may be assimilated in both a verbal and visual fashion, something which according to the dual-coding theory (Mayer and Sims 1994) may be of great benefit to the student. All of the factors discussed in Table 6.5 point towards the fact that concept mapping is a tool which may be used by students to promote conceptual change as they will be encouraged to learn in a meaningful manner and in the process of map construction will reflect on the status of their own knowledge.

**Table 6.5: Advantages of concept mapping as a learning tool.**

Advantage	Inferences made by researchers
Concept mapping aids in the organisation of knowledge	In modern times, with the explosion of knowledge, cartography (map-making) provides a means of succinctly presenting large amounts of information so that it is interesting and comprehensible to the learner. It enables the learner to identify important concepts, patterns and trends from information sources (Novak 1996; Trowbridge and Wandersee 1998; Wandersee 2000), creating a coherent graphic representation of a group of concepts and a manageable piece of information that is easily assimilated (Fisher <i>et al.</i> 2000). It is a technique or tool, which helps the student to transform data and information to knowledge and wisdom (Fisher <i>et al.</i> 2000) and also improves their problem-solving abilities as a result of better knowledge organisation (Okebukola 1992).
The process of concept mapping provides a link between the working and long-term memory	Most textbooks and lecturers do not explicitly explain the relationships between concepts; a requirement for the meaningful understanding of science (Novak 2003). In contrast, concept maps require students to make connections between concepts (Fisher 2000). During this process of thinking about the nature of the link between concepts, concepts are brought into the working memory, are joined by a related concept and are broadcast to every subconscious molecule of the mind. In this way concept mapping provides a link between the working-memory and long-term memory (Fisher 2000; Fisher <i>et al.</i> 2000) through the organisation of knowledge (Schau and Mattern 1997). Furthermore, mapping exercises make the learner think in many directions and to switch back and forth between different levels of abstractions (Okebukola 1990). Concept mapping thus replaces uni-directional thinking with thinking in many interconnected directions (Pinto and Ziets 1997).
Concept mapping acts as a metacognitive tool	Concept mapping involves more work from the student than conventional learning (Fisher 2000), actively engages students in the learning process (Trowbridge and Wandersee 1998; Fisher <i>et al.</i> 2000) and encourages students to reflect on the status of their knowledge (Beyerbach and Smith 1990; Rice <i>et al.</i> 1998). As a result concept maps may be regarded as metacognitive tools which promote meaningful learning (Trowbridge and Wandersee 1998) and the process of mapping as employing many metacognitive skills (Fisher 2000; Van Zele 2004).

Advantage	Conclusions made by researchers
Concept mapping allows for information to be assimilated verbally and visually	According to the dual-coding theory, meaningful learning will take place when the learner builds internal representations of both verbal and visual information, as well as referential connections between these two types of information (Mayer and Sims 1994). As a concept map presents a visual image as well as verbal information, concept mapping has been described as one of the most potent techniques at a teacher's disposal for presenting information (Okebukola 1990). Concept mapping enables students to access knowledge structures, to accurately retrieve information and to transfer knowledge to novel situations (Van Zele 2004). As we thrive on visually stimulating environments in the 21 <sup>st</sup> century, graphic organisers such as concept maps are likely to increase in their appeal, credibility and utility for today's science teachers and students (Trowbridge and Wandersee 1998). However, it must be recognised that generating concept maps requires a high level of cognitive demand, both spatial-visual and verbal. This may be problematic for lower-achieving students and for students whose first language is not used in the assessment task (Schau and Mattern 1997).
The construction of concept maps may be a social process	Students may also construct maps in pairs or groups and through the process of social interaction and extended discussions about the meaning of concepts, including the relationships between them, develop sound understanding of a subject area (Okebukola 1992; Novak 1996; Trowbridge and Wandersee 1998; Fisher 2000; Freeman and Jessup 2004; Van Zele 2004). The process of concept mapping provides a structure whereby students can engage in learning the language patterns of a particular science context by hearing, speaking and being corrected by their peers (Roth and Roychoudhury 1992; Roth and Roychoudhury 1993).
Concept mapping improves student attitudes	In a meta-analysis of 19 studies, Horton <i>et al.</i> (1993) found that concept mapping not only had positive effects on student achievement but also their attitudes. It seems that the positive effects on students' understanding of science and attitudes towards science curricula further lead to a reduction in the anxiety levels of students (Novak 1990; Fisher 2000; Wandersee 2000). Therefore, students' self esteem may be enhanced as a result of the sense of accomplishment which comes from the realisation that they can identify important concepts and construct their own meanings thereof (Trowbridge and Wandersee 1998). Students should not be discouraged by the frustration they may initially feel as they begin concept mapping (Heinze-Fry and Novak 1990), as it takes time before students become comfortable with the technique and start improving their performance (Wandersee 2000).

As indicated in Table 6.5, the process and products of concept mapping are generally thought to assist students in the organisation and integration of knowledge in a systematic, coherent and meaningful manner. However, Kinchin (2001) warns that empirical evidence of these claims is lacking in the biological sciences. This is also evident in the discipline of statistics (Schau and Mattern 1997) and the field of quantitative genetics, which is based on statistical principles.

Schau and Mattern (1997) comment that research has shown that post-secondary students who have completed an introductory module in statistics often lack knowledge of the relationships between foundational statistical concepts, something



that is a prerequisite for the application of statistical principles. Furthermore, Novak (2003) states that the ability to apply concepts learned in one context to novel problems requires a high level of meaningful understanding. In order to ascertain whether it was possible for students to achieve a higher level of meaningful understanding in the discipline of statistics, Shau and Mattern (1997) made use of concept maps of the incomplete, fill-in type. These researchers found that when graduate level statistics students were asked to complete fill-in concept maps, that their marks increased significantly throughout the module. Following this study, Broers (2001) proposed that any topic in elementary statistics could be parcelled into constituent propositions that students are likely to use. He claimed that this reduction of course material into a list of propositions (charting) would reduce the complexity of the task students were faced with and could encourage students to think of the relationships between the various propositions. In this regard, he suggested that students could be presented with problems and subsequently asked to identify the concepts, propositions and mathematical relationships pertaining to a particular problem. Through this process students could be encouraged to form a logical argument and to address the relationships between concepts (Broers 2002). A recent study by Broers and Imbos (2005) implemented this method of charting and the use of a problem to stimulate students to think of the relationships between propositions, knowledge of which they would require to successfully solve the problem. The results of this study suggest that this may be a suitable way to encourage students to reflect on the connections between statistical concepts and to promote meaningful learning in this discipline.

With regard to the discipline of genetics, there is a lot of evidence to show that students perform poorly in this discipline (Johnstone and Mahmoud 1980; Bahar *et al.* 1999a). This is particularly evident in the levels of attainment of students studying topics such as evolution which is based on the principles of population and quantitative genetics and is seen as being conceptually challenging with increasingly sophisticated concepts being developed and related to one another, as courses progress (Trowbridge and Wandersee 1994). As students seem to find genetics so difficult, Okebukola (1990) suggested that if meaningful learning were promoted in the teaching of genetics then improved performance of students could be promoted (Okebukola 1990). This claim has been substantiated by research conducted by Okebukola (1990) and Esiobu and Soyibo, (1995), in respective studies on 138 university students and 808 high school children studying biology modules in Lagos, Nigeria. These studies were both able to show that groups of students that used the concept mapping techniques performed significantly better than a control group of

students that was only exposed to lectures, in tests of meaningful learning of genetics concepts.

The research studies presented in this chapter indicate that learning should involve a change in the form of one's knowledge so that new concepts can be assimilated to pre-existing knowledge. Furthermore, it is evident that concept mapping may allow students to realise that concepts in subjects such as quantitative genetics do not exist in isolation and that the process of map construction may assist students in relating their pre-existing statistical and genetic knowledge to new ideas learned in applied fields of genetics. It is for these reasons that concept mapping tasks were included in the intervention used in this investigation.

In order to improve students' understanding of the *prior knowledge concepts* and *quantitative genetics concepts* under investigation a series of computer-based tutorials were designed. These tutorials specifically aimed to assist students with the understanding of the *critical concepts* of *variance* and *heritability*. In addition, the computer interface and various graphical software packages such as *Tinkerplots™*, *Genup* and *Microsoft Excel*, were used to assist students in the visualisation of the *critical concepts* and to help students link statistical concepts with frequency distributions. This was necessary as students had displayed difficulty with the construction and interpretation of histograms during the diagnostic phase of the investigation. Furthermore, students were required to construct a series of concept maps at different times during the teaching of the module. The active construction of concept maps by students was considered a metacognitive activity and as such it was hoped that the map construction process would encourage students to think of the relationships between key concepts in the subject area. The student-generated concept maps were also used by the researcher to infer the nature of the conceptual change which occurred in the minds of the students during the learning process.

## 6.4 DESCRIPTION OF THE INTERVENTION

The intervention consisted of two components: (1) The students completed a series of computer-based tutorials which were developed to assist students in the understanding of concepts that they had shown difficulty with during the diagnostic phase of the investigation. Particular attention was paid to improving students' understanding of the *critical concepts* of variance and heritability as well as their ability to construct and interpret histograms. (2) The students were required to construct concept maps at different stages throughout the teaching of the quantitative

genetics module. The students were supplied with the concepts to be included in their maps and were encouraged to think about the relationships between key concepts.

#### 6.4.1 Computer-based tutorials

The students completed three computer-based tutorials. The stage in the module when each tutorial was completed is provided in Table 6.6.

*Tutorial 1.* This tutorial took students 3 hours to complete, consisted of three tasks:

- a) How can data be summarised? This task made use of the *Tinkerplots*<sup>TM</sup> (2004) software.
- b) What are descriptive statistics and why do geneticists need them?
- c) How do populations vary? Tasks “b” and “c” made use of *Microsoft Excel* spreadsheets constructed by the researcher.

*Tutorial 2.* This tutorial was completed in an hour and considered the question: “Why are quantitative traits normally distributed?” This task made use of a component of a programme named, *Genup*, which is freely available on the world-wide-web.

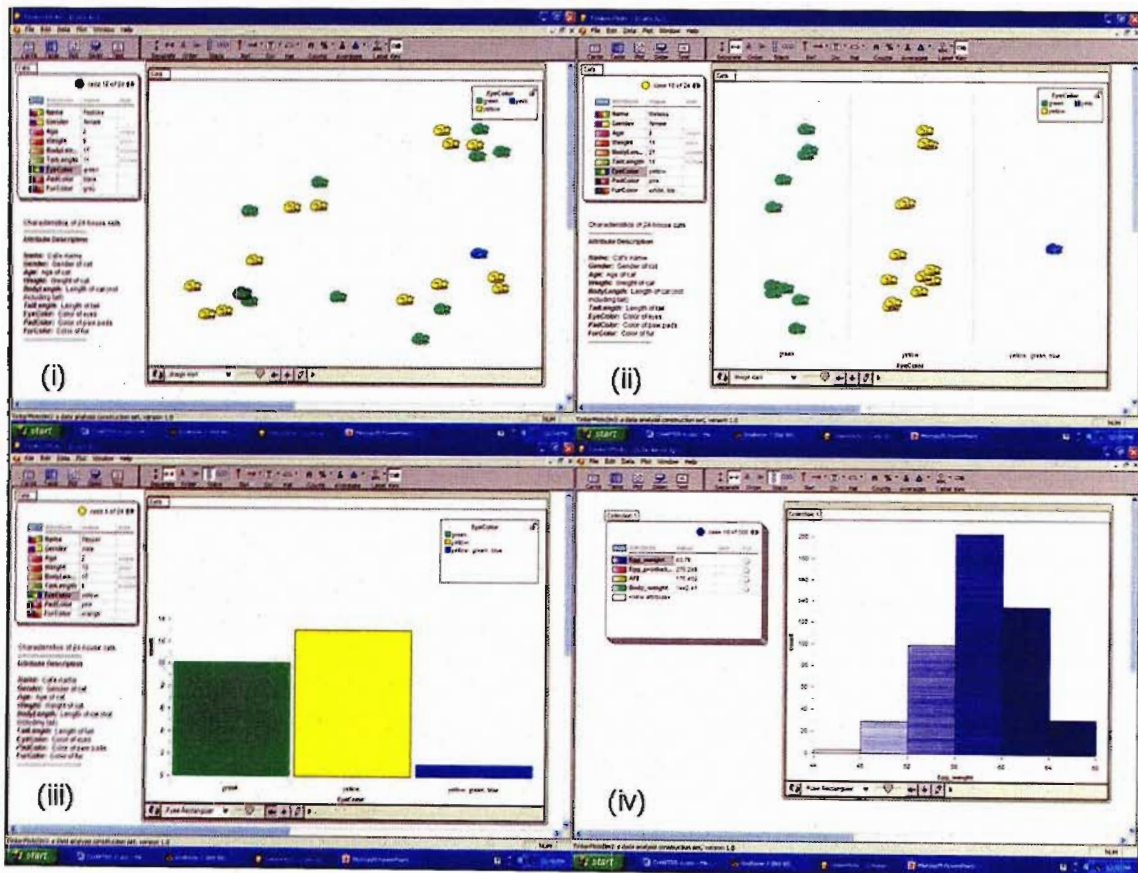
*Tutorial 3.* The third tutorial was a three hour task where the students used a Microsoft Excel worksheet, which was altered by the researcher from a suggested model proposed by Donovan and Weldon (2002) to investigate the concept of heritability, with particular reference to the fact that it is a population measure and its relationship to individual phenotypic values and breeding values.

The students were supplied with a *tutorial guide* for each tutorial. The *tutorial guides* started with a brief explanation of the concepts and ideas which would be covered during the tutorial. The *tutorial guides* then contained step-by-step instructions on various activities that needed to be completed, followed by questions addressing what the students had learned from the tutorial. These questions specifically addressed alternative conceptions and difficulties which had been identified during the diagnostic phase of the investigation. The three *tutorial guides* are provided in Appendix 9 on page 335.

**(a) Description of Tutorial 1**

The *Tinkerplots*<sup>TM</sup> (2004) software was used for *Tutorial 1* task (a). This software package was selected for use as it creates multiple “bins” along one axis and visually shows how this reduces the variation present in a dataset. Once the data has been separated into “bins” the software then enables the students to “fuse” all the individual points together so that a frequency distribution results. The students then clearly see how grouping data may be used to summarise variable datasets. Students also see that when the dataset increases in size and a variable which varies in a continuous manner (a quantitative trait) is plotted a normal distribution results. This task was considered necessary as students had shown difficulty with the construction and interpretation of frequency distributions during the diagnostic phase of the investigation.

Figure 6.1 illustrates the computer interface that the students sequentially worked with when using the *Tinkerplots*<sup>TM</sup> (2004) software. Block (i) shows the data randomly presented, block (ii) shows the same data grouped into “bins”, block (iii) shows a discontinuous frequency distribution resulting from a dataset and block (iv) illustrates the result obtained for a large dataset when considering a quantitative trait.



**Figure 6.1: Computer interface that students worked with when using Tinkerplots™ (2004).**

The spreadsheet package *Microsoft Excel* was used for tasks 1(b), 1(c) and *Tutorial 3*. As suggested by Ben-Zvi (2004), spreadsheet formats are considered suitable for the exploration of data as they are flexible and dynamic and allow students to easily experiment with and alter displays of data. In addition, certain input values may be altered and the change to a graphical display instantly seen. Finally, spreadsheets are commonly used by people from all walks of life and are a fundamental component of computer literacy. Therefore, mastering the use of spreadsheets is not only a life skill but also helps students to feel as if what they are doing is connected to the real world.

Tasks 1(b) and 1(c) made use of spreadsheets which contained data on the weight of eggs produced by 500 randomly generated “chickens”. Students used the first spreadsheet to learn how to produce a frequency table and plot a frequency distribution. Furthermore, they used the programme to calculate the mean, variance and standard deviation for the dataset and were encouraged by certain questions in the *tutorial guide* to relate these statistics to a histogram. They were also asked to use only a sample of the population and to observe the resultant changes to the graphical representation. As the values in the spreadsheet had been randomly generated the students could push the F9 key at any time to obtain a new set of random numbers and thus a “new population”. Figure 6.2 illustrates part of the dataset used in the first spreadsheet and the type of graphical representation produced. It is evident from the output shown in Figure 6.2 that as the values for a continuously varying trait (quantitative trait), egg weight, were considered in a large population (500 individuals), the shape of the distribution approximates that of a normal distribution.



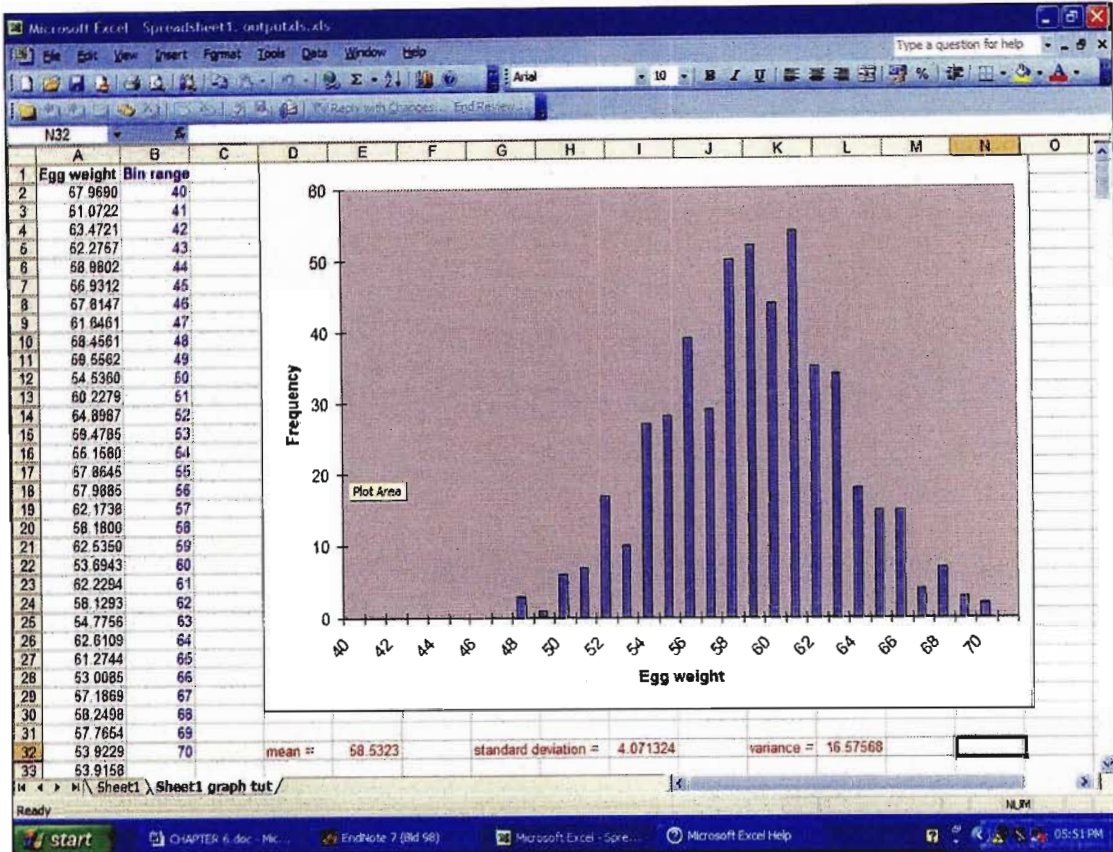


Figure 6.2: Illustration of the dataset and output created for *Tutorial 1* task (b).

A second spreadsheet containing data on four different populations, with differing standard deviations, was used to assist students to make comparisons between populations. Students were asked to produce frequency distributions for all four populations and to make decisions on which had the most variation and would thus respond better than the others to the process of selection. Figure 6.3 contains a sample of the type of frequency distributions produced for the four different populations of chickens. This task was used to assist students in relating the statistic of variance or the standard deviation to graphical displays such as histograms, a difficulty shown by students during the diagnostic phase of the investigation. Students were able to see that the smaller the standard deviation or variance, the narrower the distribution (for example Population 1) and the larger the standard deviation or variance the more spread out (further from the mean) the values plotted on the distribution became (for example Population 2).

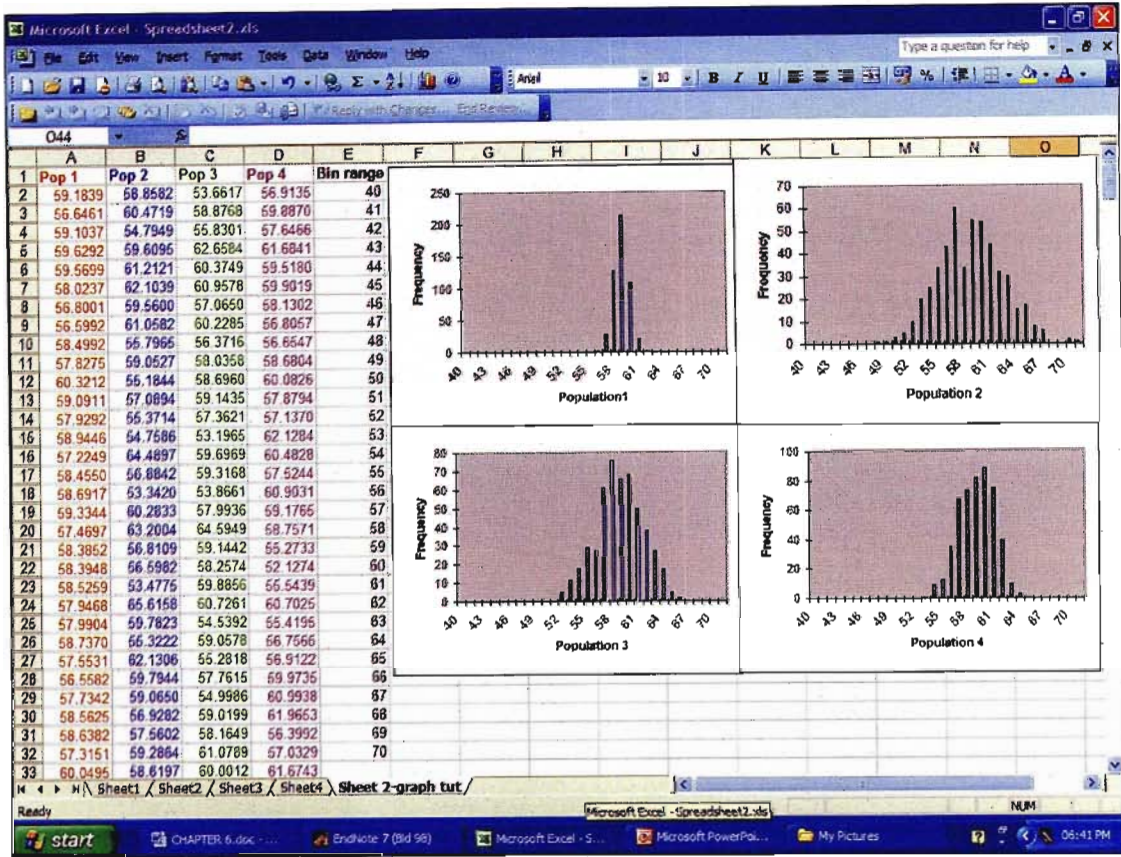


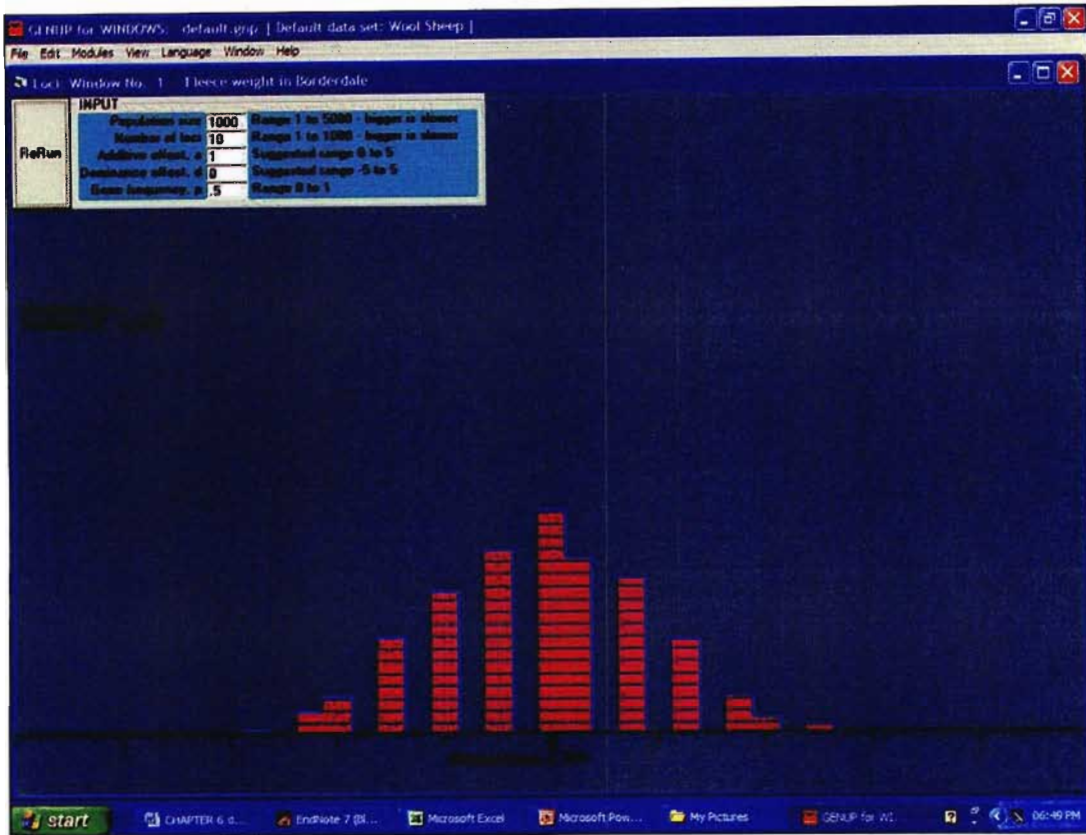
Figure 6.3: A sample of the dataset used for Tutorial 1, task (c) and an indication of the histograms created for the populations with different variances.

(b) Description of Tutorial 2

Tutorial 2 made use of a component of the *Genup* software which allowed students to alter the number of loci affecting a particular trait as well as the population size. Students were then able to see the effects of these two variables. Students were able to see that as the number of loci affecting a trait is increased the distribution takes on the shape of a normal distribution. In addition, it should become evident to the students that as the population size is increased, a continuous normal distribution, as opposed to a discrete distribution, is produced. Figure 6.4 is an illustration of the interface that the students worked with when considering a large population and a trait influenced by alleles at 10 loci. Due to the large number of loci and the population size, the distribution approximates a normal distribution. It is clear that the largest frequency of individuals occurs at the mean value and that there are few individuals with the extreme values measured for the trait under consideration. This exercise aimed to address students understanding of why quantitative traits are



normally distributed, an idea that students had difficulty with during the diagnostic phase of the investigation.



**Figure 6.4:** The Genup interface for a large population and a trait affected by many alleles at many loci.

### (c) Description of Tutorial 3

Tutorial 3 considered the *critical concept of heritability* and made use of a *Microsoft Excel* spreadsheet. The spreadsheet had certain model inputs and model outputs. The students were encouraged to change the model inputs and observe the manner in which the model outputs changed. The tutorial guide asked students to change the model inputs of the environmental variance of the population and of the allele frequencies of the population. The model outputs included the different components of the phenotypic variance and an estimate of the heritability of the population. The following graphical representations were automatically created: (1) a scatterplot of the midparent versus mean offspring value, (2) a column graph of the breeding values, environmental deviations and phenotypic values for 20 individuals and (3) a histogram of the frequency of the different phenotypes in the parental and offspring populations. *Tutorial 3* thus addressed students' understanding of heritability and the manner in which this statistic relates to various graphical representations. Figure 6.5

illustrates the model input variables and output variables of the spreadsheet used for *Tutorial 3*.

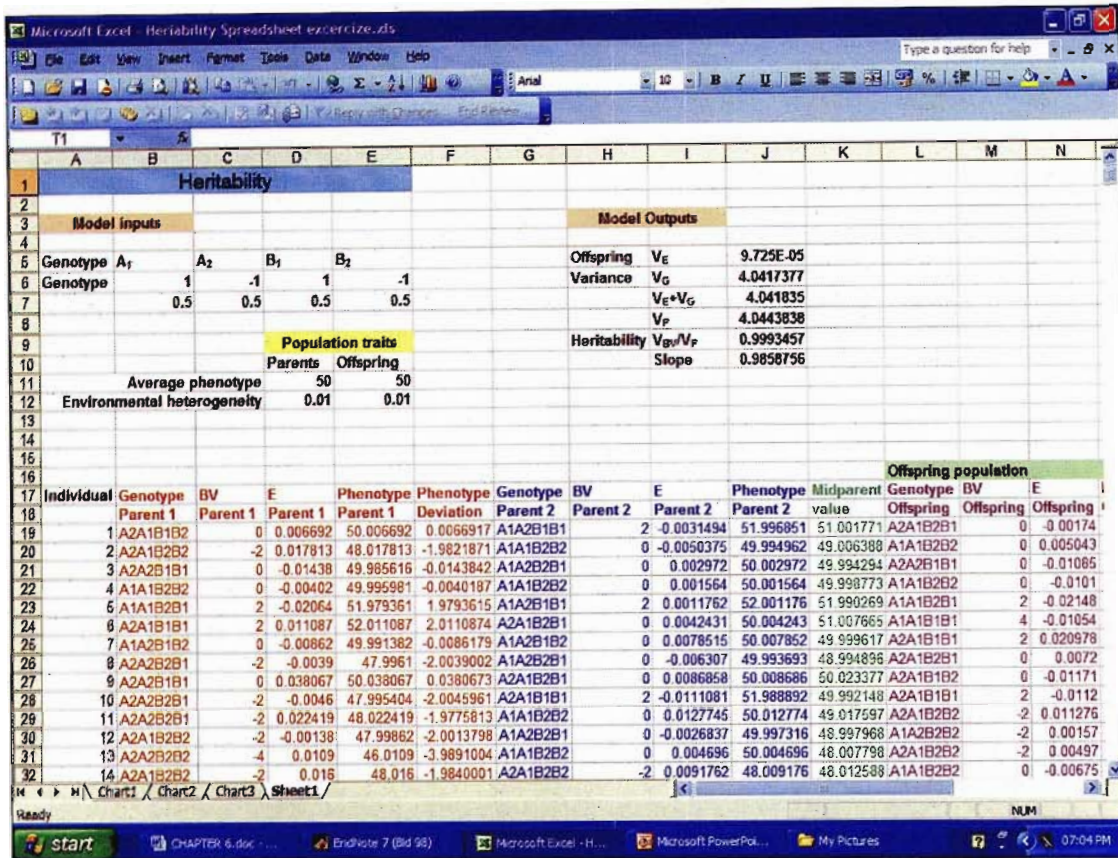


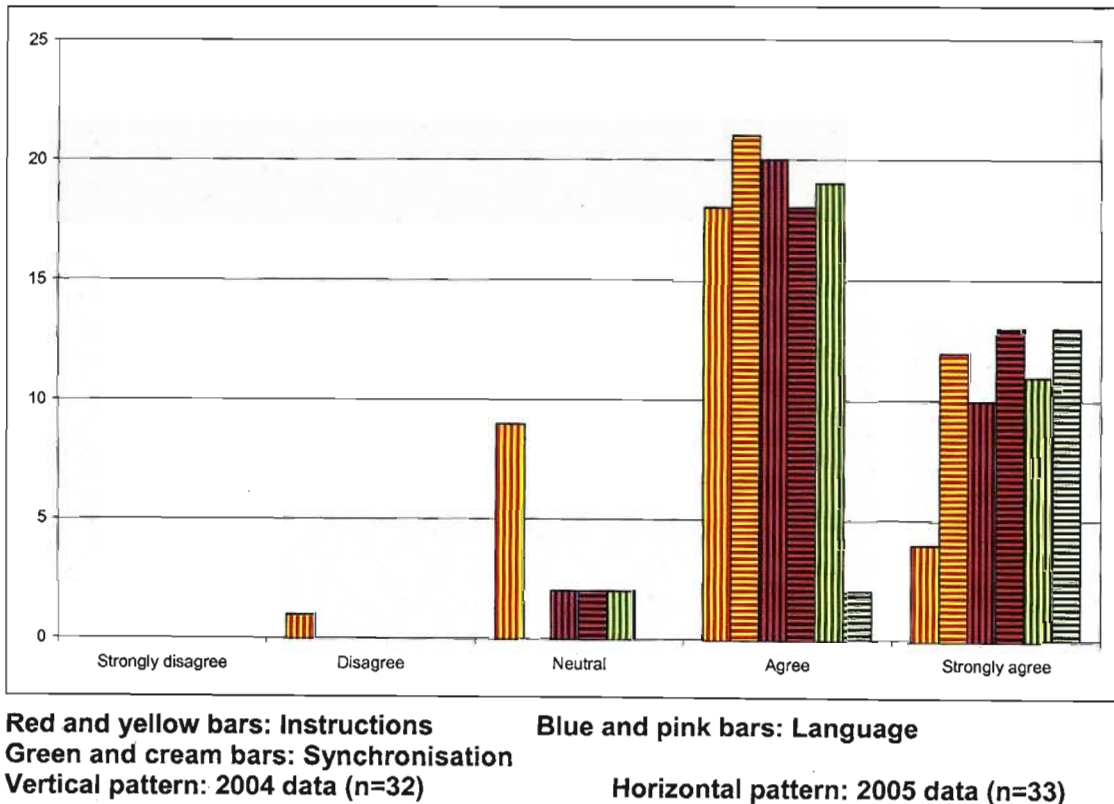
Figure 6.5: Computer interface showing the model inputs and outputs for *Tutorial 3*.

(d) *Piloting of the computer-based tutorials*

All of the computer-based tutorials were piloted during the second semester of 2004 with the students taking *Genetics 350*. The pilot study revealed, firstly, that for *Tutorial 3* it would be beneficial for the software to automatically generate the graphical representations as this was very time-consuming and tedious for the students. The generation of graphs by the students was not deemed necessary at this stage, as the students had learned this skill in the previous tasks. It was thus decided to focus, rather, on the conceptual understanding of heritability. Secondly, it became evident in the pilot study that a number of additional tutors were required to ensure that all students had easy access to assistance when required. The assistance would be in the form of aid in the use of the software as well as explanations of the concepts addressed by the tasks. It should be noted that the additional number of tutors could have contributed to students' understanding of the

topics under consideration but that this effect was not directly evaluated in this investigation. Thirdly, a questionnaire (provided in Appendix 8, page 331) which asked whether the students agreed that the instructions on the *tutorial guides* were clear, that the language used in the *tutorial guides* was understandable and that the lectures and computer-based tutorials were well synchronised was given to the students to answer.

The results presented in Figure 6.6 indicated that the majority of students felt that the instructions given in the *tutorial guides* were clear, that the language used was understandable, and that the tutorials and lectures were well synchronised. The same questions were asked of the 2005 student group after they had completed the tutorials and very similar, slightly more positive, responses were given by students.



**Figure 6.6:** Distribution of students' responses (%) to questions regarding the clarity of the instructions and language used in the tutorial guides and the degree of synchronisation between lectures and tutorials.



### 6.4.2 Concept mapping exercises

As part of the intervention strategy the students were required to construct a series of concept maps during the teaching of the quantitative genetics module. The stage in the module when the students were required to construct each concept map is given in Table 6.6.

#### (a) *Description of concept mapping exercises*

Students were trained, at the start of the module, in the technique of concept mapping and the relevant terminology. Furthermore, students were trained in the use of the *Inspiration software* (1997) by means of a detailed tutorial which the students worked through with the assistance of tutors. The primary benefit of using the *Inspiration software* (1997) was that it enabled students to easily modify, rearrange and print their work. The *Inspiration* tutorial is provided for the reader in Appendix 7 on page 314.

Students were required to construct a total of five concept maps and were provided with a list of concepts to be included in their concept maps. The first four maps each represented different sections of the course content and map 5 contained all the key concepts covered in the module and as such was a summary of the course content. The concept mapping exercises which students were asked to complete are provided in Appendix 7 on page 314.

The students were encouraged to work in pairs if they so desired in order to allow for the exchange of ideas and to create the opportunity for discussion and revision of students' perceptions on the relationships between certain concepts. This was encouraged as Roth and Roychoudhury (1993) found when working with high school physics students who constructed concept maps in groups, that the students engaged in lengthy conversations about the subject area and thus began to correctly use the terminology associated with the topic. Once the students had completed their concept maps they were handed in to the lecturer who provided feedback to the students regarding any missing or incorrect linkages made by the students.

Once the students had received individual feedback on their concept maps the lecturer spent some time during lectures showing the students a map which she had created. Although it is recognised that all concept maps created by individuals will differ, the literature suggests that experts, such as teachers and lecturers usually possess larger amounts of knowledge, all of which is better organized into integrated

structures. Novices, in contrast, possess less knowledge and it is not coherently organized (Ruiz-Primo 2000). Therefore, it is thought that good concept maps that have been constructed by an expert may be effective learning aids (Pinto and Ziets 1997; Schau and Mattern 1997). However, it should be noted that maps that have been constructed by experts should be used with care as students will tend to memorize the map, which will not lead to meaningful learning on their behalf (Pinto and Ziets 1997). Research evidence clearly shows that the most meaningful learning is acquired when learners create several networks themselves (Ruiz-Primo *et al.* 2001), with maps created by experts being used only as a reference for students who are having difficulty with the construction of their own maps (Fisher, 1990). This was then the process followed in this investigation.

### **(b) Piloting of the technique of concept mapping**

During 2002 students taking *Genetics 332* were asked to construct concept maps which were used to ascertain whether they were able to integrate their knowledge of quantitative genetics. These students constructed their maps using a pen-and-paper technique. During this time the researcher noted that many students became frustrated with the time it took to make changes to their maps. If large changes were required the entire map would have to be re-drawn. It was for this reason that the *Inspiration software* (1997) was then introduced. This software makes it very easy to move concepts to different places in the map, thereby allowing the information to be organised into a coherent form. In addition, linkages between concepts may be effortlessly altered and different symbols and colours used to add interest to the map and to highlight key concepts.

During 2004, the *Genetics 350* class was asked to construct some concepts maps using the *Inspiration software*. This process indicated that the software was very easy for students to master, and fun to use. These students gave input to the researcher which was used in the construction of the tutorial guide which was developed by the researcher for the *Inspiration software* (1997) (Appendix 7).

## **6.5 DESIGN OF THE INTERVENTION**

The sequence in which new concepts were introduced to students and the tasks required of the students is presented in Table 6.6. The concept mapping exercises are presented in Appendix 7 (page 314) and the computer *tutorial guides* in Appendix 9 (page 335). Thirty seven students were part of the therapeutic phase of the

investigation. All students were taking the *Genetics* 332 module which covered all introductory the components of quantitative genetics (*quantitative genetics* concepts) as discussed in Sections 2.2. As detailed in Section 3.1 all students taking *Genetics* 332 were asked to sign a document agreeing to participate in the investigation. All students consented to participate in the therapeutic phase of the study.

**Table 6.6: Implementation of the intervention and assessment tasks.**

Week	Course content covered	Tasks performed by students	Assessment tasks
1	Introduction to the inheritance of quantitative traits	Computer tutorial 1 Introduction to Inspiration software tutorial and concept mapping exercise 1	Prior-knowledge multiple-choice diagnostic test, student interviews and first attitudinal questionnaire.
2		Computer tutorial 2	
3	The composition of the phenotypic values of individuals	Concept mapping exercise 2	
4		Pen-and-paper tutorial exercise	
5	The composition of the phenotypic variance of a population	Concept mapping exercise 3	
6		Pen-and-paper tutorial exercise	
7	The calculation of the additive variance from the degree of resemblance between relatives	Pen-and-paper tutorial exercise	
8		Computer tutorial 3	
9	The calculation and meaning of heritability	Concept mapping exercise 4	
10		Pen-and-paper tutorial exercise	
11	Revision	Concept mapping exercise 5	Post- teaching multiple-choice diagnostic test, student interviews and second attitudinal questionnaire.
12	Module examination		

## 6.6 CONCLUDING REMARKS

Chapter 6 has outlined the rationale behind the choice of the teaching and learning tools used in the intervention as well as the development and implementation of the intervention. Chapter 7 will present the methodology and results which indicate the effectiveness of the intervention (Research Question 6). Chapter 8 will present the methodology and results of the nature of the conceptual change which occurred (Research Question 7).

## CHAPTER 7

### ASSESSMENT OF THE INTERVENTION

**Research question 6:** To what extent did the intervention assist students in the understanding of quantitative genetics?

#### 7.1 INTRODUCTION

Edmonson and Novak (1993) comment that many students have a positivist view of the study of science. This means that such students believe that knowledge can be obtained through observation alone and that prior knowledge is not important. Due to this epistemological view, these students will often practice a system of rote-learning or memorisation when assimilating new information. As previously detailed in this thesis, information which is learnt in a rote fashion will lead to the accumulation of isolated propositions, poor knowledge retention and the inability to retrieve ideas during the process of problem-solving (Ausubel 1968). Therefore, numerous teaching strategies and tools to promote the meaningful acquisition of knowledge have been proposed and investigated by science educators (Mintzes and Wandersee 1998). As discussed in Chapter 6, two teaching tools were used in the remediation phase of this investigation to address the student difficulties and alternative conceptions identified by this research project (results are detailed in Chapters 4 and 5). These were: (1) computer-based tutorials and (2) concept mapping.

The intervention was designed so as to address students' understanding of *prior-knowledge concepts* and *quantitative genetics concepts* which had been found to be difficult for students to understand during the diagnostic phase of the investigation. With regard to students' understanding of *prior-knowledge concepts*, particular attention was paid during the implementation of the intervention, to the *critical concept* of *variance* and students' ability to construct and interpret histograms. This was necessary as during the diagnostic phase of the investigation it became clear that it could not be assumed that students started a quantitative genetics module with a good grasp of these ideas. Thus, part of the intervention specifically addressed students' understanding of these *prior-knowledge concepts*. The intervention also addressed students' understanding of *quantitative genetics concepts* with particular

attention being paid to students understanding of the *critical concept* of heritability and students ability to interpret histograms.

The assessment of the intervention was conducted in two phases: (1) statistical analyses were conducted to evaluate the overall effectiveness of the intervention and (2) students' understanding of specific *prior-knowledge concepts* and *quantitative genetics concepts* was assessed.

## 7.2 METHODOLOGY EMPLOYED

### 7.2.1 Employment of research instruments

The effectiveness of the intervention was determined using the multiple-choice diagnostic tests and interview protocols used to assess students' understanding of *prior knowledge concepts* and *quantitative genetics concepts* during the diagnostic phase of the investigation. Descriptions of the multiple-choice diagnostic tests and interview protocols are provided in Sections 3.2.3 and 3.2.4.

The intervention was implemented during the first semester of 2005 and the final versions of the prior knowledge and post teaching diagnostic tests were given to students at the start and completion of the module respectively, to assess the status of students' knowledge. In addition, four students who performed badly on the prior-knowledge diagnostic test were interviewed at the start of the module. A further eight students were interviewed at the completion of the module. In order to get a representative cross-section of students taking the module, the students who were interviewed were selected as follows: two of the students chosen had performed consistently badly throughout the semester, two had performed consistently well, two had improved greatly during the semester and two were part of the group interviewed at the start of the module. The semi-structured interview protocols provided in Appendix 6 were used in this part of the investigation. All the interviews were audio-taped and transcribed. The stage at which each assessment was administered is indicated in Table 6.6.

### 7.2.2 Experimental design and data analysis

The analysis of the data was undertaken in three steps. (1) A determination of whether the 2004 student group (control group who did not participate in the intervention) and the 2005 student group (test group who participated in the intervention) were comparable. (2) The overall effectiveness of the intervention was



assessed by conducting various statistical tests on the data generated by students' answers to all the items on the multiple-choice diagnostic tests. (3) In order to ascertain whether students' understanding of specific concepts had improved, students' answers given for each item of the multiple-choice tests were considered separately. These results were validated using data gathered from the interviews conducted with students.

In order to determine whether the intervention had been successful in improving students' overall understanding of quantitative genetics, certain statistical tests were carried out only using data from the 2004 and 2005 student groups who had completed exactly the same versions of the prior-knowledge and post-teaching diagnostic tests. The 2004 student group acted as the "control" group as these students had only participated in formal lectures and pen-and-paper tutorials and were not exposed to the intervention. In contrast, the 2005 student group participated in the intervention in that they attended not only the formal lectures, but also the computer-based tutorials, and each student constructed a series of concept maps during the teaching of the module.

To ensure that accurate comparisons would be made between the two student groups, the data from the multiple-choice diagnostic tests was all transformed onto the same interval scale. In order to do this, the prior-knowledge data and post-teaching data from both the 2004 and 2005 student groups was initially combined and the Rasch model (details of the model are provided in Section 3.2.3) used to provide logit values for each person.

To ascertain whether it was possible to assume that the 2004 and 2005 student groups were comparable certain tests were carried out on data collected at the start of the quantitative genetics modules in question.

- a) A two-tailed t-test was used to test for differences between the means of the two student groups given the prior-knowledge diagnostic test with the null hypothesis that there would be no significant difference between the two student groups as they had received the same form of teaching until this point.
- b) The Rasch model was used to construct an item map for the 2005 student group. This item map was compared to that obtained from the 2004 student group to ensure that the relative level of item difficulty was the same for both student groups.

To assess the overall effectiveness of the intervention a range of statistical tests were performed using the GENSTAT statistical package (GENSTAT 2004). It should be noted that all statistical tests were conducted using the scaled Rasch logit values. In addition, as not all students completed both the prior-knowledge and post-teaching diagnostic tests in each year, such unpaired data was excluded for all statistical analyses.

- a) To compare students' overall understanding of *quantitative genetics concepts* at the completion of a quantitative genetics module, a one-tailed t-test was used to test for differences between the means of the two groups given the post-teaching diagnostic test with the null hypothesis that the 2005 student group, who had participated in the intervention, should out-perform the 2004 student group.
- b) To evaluate any improvement in the performance of the 2005 student group after participation in the intervention, the differences in the scores obtained by students for the prior-knowledge and post-teaching diagnostic tests were calculated and compared. Firstly, a one-tailed t-test was performed with the null hypothesis that the 2005 student group would show a greater improvement in performance than the 2004 student group due to participation in the intervention. Secondly, in an attempt to improve the precision of the statistical tests, an analysis of covariance was performed.
- c) To assess the relationship between the prior-knowledge scores of students and the improvement in their knowledge after the teaching of various components of the module, a regression analysis was performed using the differences between the prior-knowledge and post-teaching scores of each student.

In order to ascertain whether the intervention had been successful in improving students' understanding of specific *prior-knowledge concepts* and *quantitative genetics concepts*, the following analyses were conducted.

- a) To assess the improvement in students' understanding of particular *prior-knowledge concepts* after participation in the intervention, a comparison was made between the number of students who had been able to correctly answer items probing students' understanding of *prior knowledge concepts* such as variation, variance and the interpretation of frequency distributions at the start of the module and after the implementation of the intervention during 2005. This was possible as certain items had been included in both the prior-knowledge and post-teaching diagnostic multiple-choice tests administered

during 2005. The findings from the multiple-choice diagnostic tests were validated using data from the student interviews.

- b) To assess whether the intervention improved students' understanding of certain *quantitative genetics concepts*, the relative level of item difficulty for the two student groups was determined using item maps that were generated by the *Winsteps software* (2003). The item map generated for the 2005 student group was compared with the item map from the 2004 "control" group in order to assess whether certain concepts had become easier for students to understand after they had participated in the intervention. Furthermore, a comparison between the average number of students who correctly answered items in the post-teaching diagnostic test during 2002, 2003 and 2004 (student groups who had been taught using the traditional lecture method) and the 2005 student group who had participated in the intervention was carried out. The findings from the analyses conducted on data from the multiple-choice tests were supported by data from interviews with students.

## 7.3 RESULTS AND DISCUSSION

### 7.3.1 Assessment of equality of the two student groups

To ensure that it was possible to assess the effectiveness of the intervention by comparing the 2004 and 2005 student groups, a t-test was conducted to determine whether there was a significant difference between the means of the two student groups. Thereafter, the Rasch model was used to create item maps for the two student groups to ascertain whether both student groups concurred on the relative level of difficulty of each of the concepts probed.

#### **(a) Comparison of students' overall understanding of prior-knowledge concepts at the start of a quantitative genetics module**

A t-test comparing the answers given by students to the multiple-choice diagnostic tests given to the 2004 and 2005 classes at the commencement of the module indicated that there was no significant difference between the two students groups. The probability, given by the GENSTAT programme used, was 0.813. This non-significant result was expected as both student groups had received the same level of teaching until this point. Thus there was no reason, other than random sampling; to expect that the two student groups would differ i.e. the 2004 student group could

act as a “control” group for comparison against the 2005 student group. The summary statistics provided by the GENSTAT programme are given in Table 7.1.

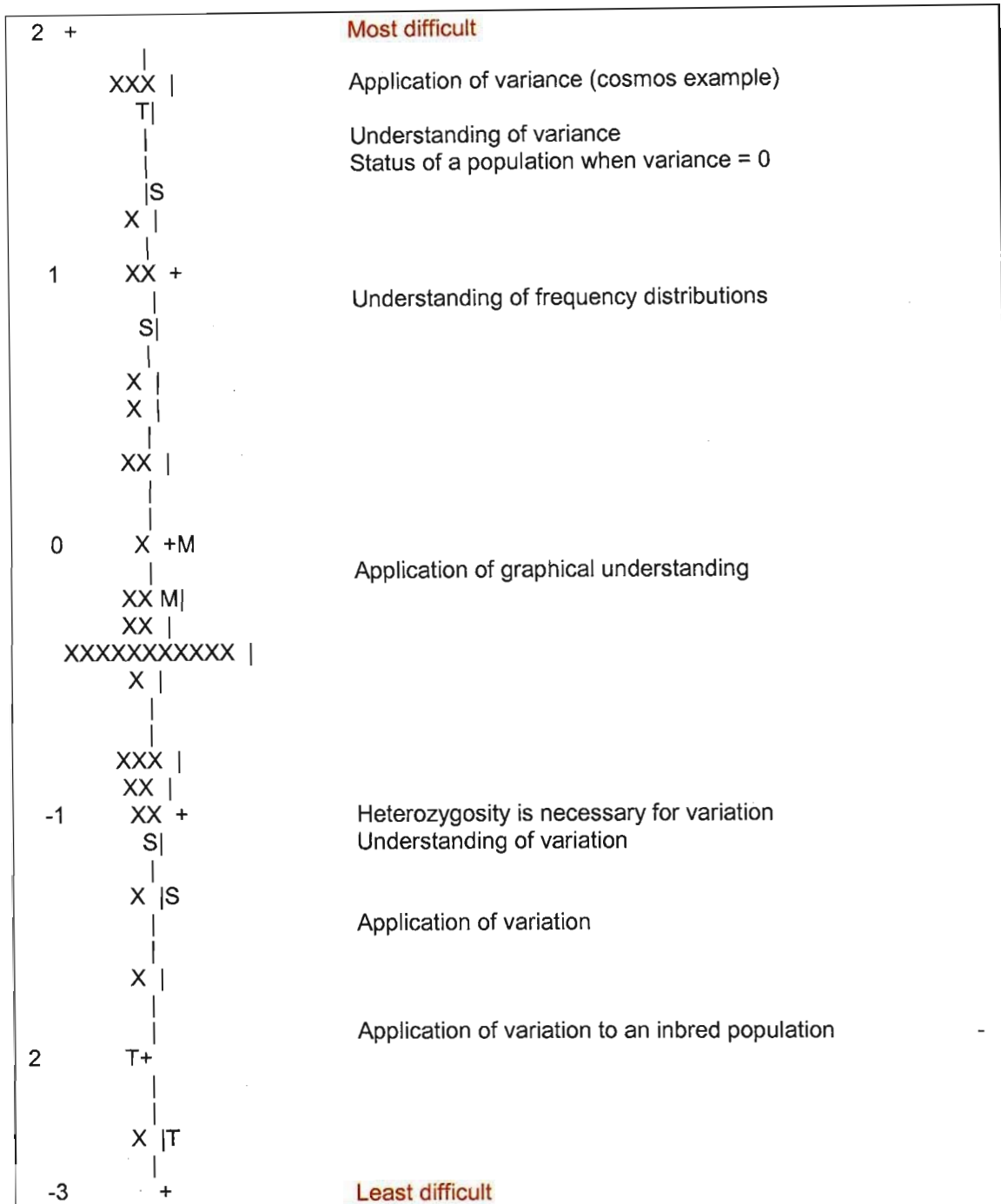
**Table 7.1: Results of the t-test on the prior-knowledge scores of the two student groups (degrees of freedom = 51).**

Sample	Sample size	Mean	Variance
2004 student group	23	-0.04522	0.9011
2005 student group	30	-0.1020	0.6152
<b>Test statistic: t = 0.24</b>		<b>Probability = 0.813 (NS)</b>	

**(b) Comparison of the relative level of difficulty of prior-knowledge concepts**

An item map was generated for the answers given by students for each concept probed by the prior-knowledge diagnostic test administered to the 2005 student group (Figure 7.1). A comparison between the item maps generated for the prior knowledge diagnostic test given to the 2004 (Figure 5.1, page 121) and 2005 class showed that in both years students found the concept of variance and its application most difficult, the understanding of graphical representations was of intermediate difficulty and the concept of variation and its application was the least difficult for students to understand.

This result confirms the results obtained from the t-test that there was no significant difference between the two student groups on entry to the *Genetics 332* module, when considering the difference between the group means, or the students' perceived degree of difficulty of the concepts and skills under investigation. It was thus concluded that it would be possible to make comparisons between the two student groups to evaluate the effectiveness of the intervention.



**Figure 7.1:** Item map depicting the relative difficulty of concepts and skills probed by each item of the prior knowledge diagnostic test administered in 2005.



### 7.3.2 Assessment of the overall effectiveness of the intervention

The overall effectiveness of the intervention was assessed by making comparisons between the 2004 (control group) and 2005 (test group who participated in the intervention) student groups.

**(a) Comparison of students' overall understanding of quantitative genetics concepts at the completion of a quantitative genetics module**

When considering students' overall understanding of *quantitative genetics concepts*, using the results obtained from the post-teaching diagnostic test, the 2005 student group demonstrated a higher level of understanding than the 2004 group as a one-tailed t-test of the difference between the two means yielded a probability value of 0.007. This highly significant result indicates that the intervention was effective in improving students overall understanding of *quantitative genetics concepts*. The summary statistics are provided in Table 7.2.

**Table 7.2: Results of the t-test on the post-teaching scores of the two student groups (degrees of freedom = 51).**

Sample	Sample size	Mean	Variance
2004 student group	23	-0.5296	0.8486
2005 student group	30	0.08700	0.6994
<b>Test statistic: t = 2.55</b>		<b>Probability = 0.007 **</b>	

**(b) Comparison of the improvement in the performance of the 2004 and 2005 student groups**

A significant result (probability of 0.014) was obtained from the t-test which was performed on the *differences* between the prior-knowledge and post-teaching scores of each student. This indicated that the improvement made by the student group who participated in the intervention was greater than the improvement made by the student group who only had access to lectures and "pen-and-paper" tutorials, a result consistent with those presented in Tables 7.1 and 7.2. The summary statistics generated by GENSTAT are given in Table 7.3.

**Table 7.3: Results of the t-test on the *difference* between the prior-knowledge and post-teaching scores of each student for the two student groups (degrees of freedom = 51).**

Sample	Sample size	Mean	Variance
2004 student group	23	-0.4843	1.0207
2005 student group	30	0.1890	1.0106
<b>Test statistic: t = 2.27</b>		<b>Probability = 0.014**</b>	

When the differences between the prior-knowledge and post-teaching scores of the students was considered, the prior-knowledge scores were used as a covariate to the post-teaching scores (ANCOVA) so as to account for some of the unexplained variation in the post-teaching scores and a 56% improvement in the precision of the analysis was noted. This was made possible as the statistical procedure accounted for some of the variation that existed between the prior-knowledge scores of the two student groups thereby reducing the error variance. This resulted in a greater level of significance than the t-test with a probability of 0.011 (Table 7.4).

**Table 7.4: Analysis of covariance for the differences between the prior-knowledge scores and post-teaching scores of the individual students.**

Source of variation	d.f.	S.S.	M.S.	F	Efficiency	Probability
Group	1	5.1634	5.1634	7.01	1.00	0.011 **
Covariate	1	21.8280	21.8280	29.66		
Residual	50	36.8029	0.7361		1.56	
Total	52	64.5336				

The results of both the t-test and ANCOVA indicate that the intervention had been effective in improving students' performance and understanding of the principles of quantitative genetics.

**(c) *Assessment of the relationship between the prior-knowledge scores of students and the improvement in their knowledge after the teaching of various components of the module***

The results of the regression analysis which are presented in Table 7.5 indicate that the regression relationship between the two student groups is constant (probability of 0.644).

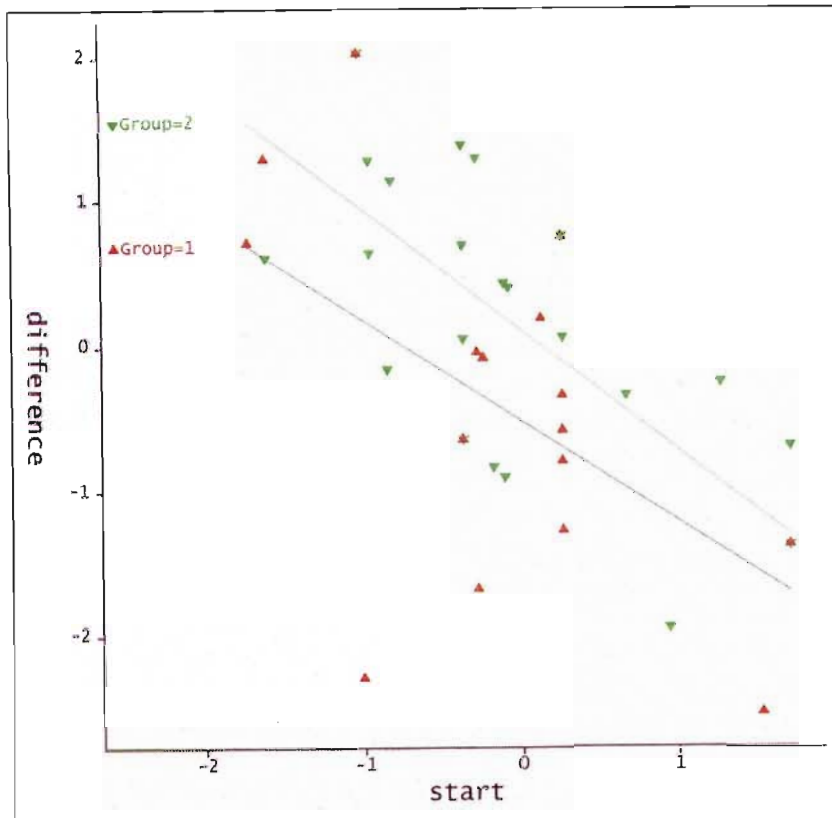
**Table 7.5: Results of regression analysis indicating that the regression relationship between the two student groups is constant.**

	Estimate	Standard error	t (49)	t (probability)
Constant	-0.516	0.181	-2.86	0.006
Prior-knowledge scores	-0.699	0.194	-3.60	<0.001
2005 student group	0.620	0.241	2.58	0.013
Prior-knowledge. 2005 student group	-0.131	0.282	-0.47	<b>0.644 (NS)</b>

The results of the regression analysis presented in Table 7.6 illustrate the highly significant negative relationship between the improvement in performance (difference between prior-knowledge and post-teaching scores) and the prior-knowledge scores of students (probability = <0.001). This indicates that the poorer students at the start of the module benefited the most from both the traditional form of teaching as well as the intervention. This is shown graphically in Figure 7.2 where group 1 represents the 2004 student group and group 2 the 2005 student group who participated in the intervention. The results presented in Table 7.6 also confirm the results of the t-test (Table 7.3), namely that the improvement in the scores observed for the 2005 student group who had participated in the intervention was greater than for the 2004 group (probability = 0.011).

**Table 7.6: Results of the regression analysis.**

	Estimate	Standard error	t (50)	t (probability)
Constant	-0.519	0.179	-2.90	0.006
Prior-knowledge scores	-0.761	0.140	-5.45	<0.001
2005 student group	0.630	0.238	2.65	<b>0.011</b>



Start: prior-knowledge scores

Difference: Difference between the prior-knowledge and post-teaching scores

Group 1: 2004 student group

Group 2: 2005 student group

**Figure 7.2: The observed values and fitted relationships for the difference between the prior-knowledge and post-teaching scores of each individual.**

Notwithstanding that it was noted that variation existed in both the prior-knowledge and post-teaching scores of students and that not all students responded to the intervention in the same manner, it should be noted that all the statistics discussed in this chapter indicate general trends in the data.

As the intervention used in this investigation consisted of both computer-based tutorials and the metacognitive activity of the construction of concept maps, the results of this study have been compared with other studies in statistics and biology education where these “remediation tools” have been used. However, it is important to note that this study was unique in that the intervention consisted of both the above-mentioned components and that it was not possible to ascribe any portion of the success of the intervention to either of these “remediation tools”.

With regard to the improvement in the students' understanding of subject matter after an intervention, Schau and Mattern (1997) and Esiobu and Soyibo (1995) in studies where certain statistics and biology students respectively were required to construct concept or vee maps, found that the students who had been involved in the mapping exercises outperformed those who had not. Similarly, Hienze-Fry and Novak (1990) performed a study with 20 volunteer students who created concept maps on nutrition and gas exchange. This study revealed that the students who constructed concept maps performed better than the control group. These students also appeared to integrate their knowledge better and retained their knowledge for longer, indicating that they had made a move towards a meaningful approach to learning. Okebukola (1990) claimed that this improvement in the organisation of students' knowledge seemed to indicate that the problem-solving ability of students was also enhanced. These research results and those of the investigation discussed in this thesis indicate that concept mapping can improve the academic performance of students by assisting students in effectively structuring their knowledge thereby enabling them to access relevant information during the process of problem-solving.

When considering computer-based instruction in the discipline of genetics, there are numerous studies in the literature which have used software programmes such as *Genetics Construction Kit* to assess the manner in which students approach problem-solving and how this may inform model-based forms of instruction. Some of these studies include those conducted by Browning and Lehman (1988), Slack and Stewart (1989), Slack and Stewart (1990), Johnson (1990), Stewart *et al.* (1992), Hafner and Stewart (1995), Johnson and Stewart (2002) and Thomson and Stewart (2003). Some of these studies found that an emphasis on model building and problem-solving using computer software can assist students in attaining a deeper understanding of transmission genetics and "science in the making". However, these studies did not specifically look at whether a software package explicitly addressed students' conceptual understanding, as was the case in this investigation. Nevertheless Simmons and Lunetta (1993: 171) after using a software programme called *CATLAB* in the teaching of a genetics module stated that "learning environments which incorporate computer-based instructional activities can stimulate the formation and development of science concepts and problem-solving skills and abilities in learners". This statement indicates that the computer-based teaching strategy not only enhanced students' procedural knowledge but also their conceptual knowledge indicating that other research confirms the results of this investigation; i.e. computer-assisted learning can improve students' conceptual understanding.



If one considers studies conducted in the field of quantitative genetics, some software packages have been developed for research and teaching purposes (St. Martin and Skavaril 1984; Michaels 1993; Partner *et al.* 1993; Tinker and Mather 1993; Podlich and Cooper 1998), but their effectiveness in improving the conceptual understanding of students has not been explored. Reports on these software packages merely comment on the positive feedback the educators received from students. In addition, Michaels (1993) remarked that the incorporation of new software tools into coursework is advantageous to students in that it exposes them to communication and research tools that may be important to them in their careers. The results of this investigation thus add to the statements made by these researchers by obtaining empirical evidence of the effectiveness of computer-assisted learning in the field of quantitative genetics.

One study that specifically evaluated whether a computer simulation tool, *QU-GENE*, could enhance students' understanding of concepts in population and quantitative genetics was conducted by Cooper (1998). This study was conducted at the University of Queensland and compared the performance of two groups of students taking the same module. The one group was exposed to conventional lectures and the other group to the simulation practicals. Cooper concluded that the simulation was one variable that could have helped some students in attaining a deep understanding of quantitative genetics and that as all students are unique in their approach to learning there would always be some students who would not extend themselves sufficiently and would thus never perform well in this field. Attitudinal data from this study indicated however, that most students felt that the computer simulation had helped them to understand the subject matter. The results of this investigation add to those of the study conducted by Cooper (1998) by confirming that computer-based learning tools can enhance the conceptual understanding of students in the field of quantitative genetics. However, in this investigation students were also encouraged to learn through the metacognitive activity of concept mapping which may have further enhanced their ability to effectively learn *quantitative genetics concepts*.

Previous research thus seems to be in agreement with the findings of this investigation as both studies on whether concept mapping or computer-based learning were able to improve students' understanding in biology, and specifically the field of genetics, indicated the effectiveness of these two teaching and learning tools. It is therefore not surprising that when they were used concurrently with one another a positive trend in students' understanding of quantitative genetics was observed.

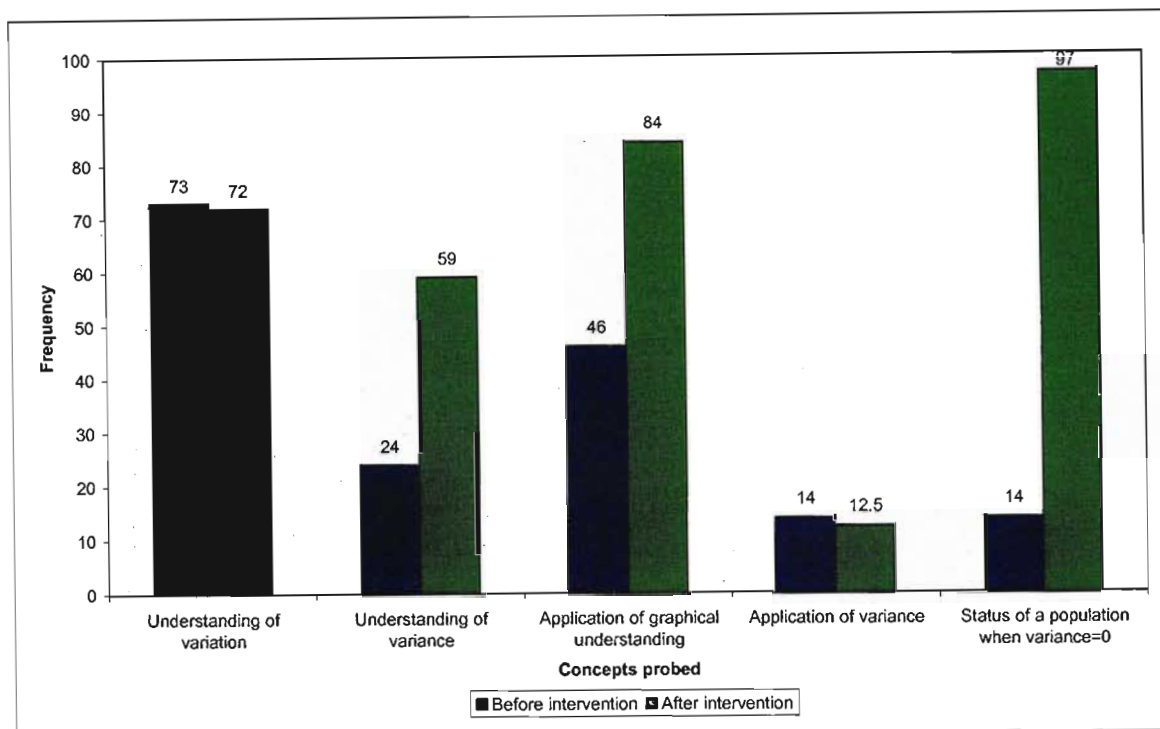
### 7.3.3 Assessment of the effectiveness of the intervention on students understanding of specific concepts

Once it had been ascertained that the intervention had succeeded in improving the overall level of students' understanding of quantitative genetics, students understanding of: (a) *prior knowledge concepts* and (b) *quantitative genetics concepts* was analysed.

#### (a) **Determination of whether the intervention enhanced the level of students' understanding of prior knowledge concepts**

A comparison was made between students understanding of *prior knowledge concepts* at the start of the module and after the intervention had been implemented in 2005. The aim of this comparison was to ascertain what *prior knowledge concepts* had become easier for students to understand after participation in the intervention. This was possible as certain items were included in both the prior-knowledge and post-teaching diagnostic multiple-choice tests administered during 2005. Figure 7.3 is a frequency distribution that indicates the percentage of students who correctly answered the items which were repeated in the prior-knowledge and post-teaching diagnostic tests administered to the 2005 student group that participated in the intervention.

The comparison depicted in Figure 7.3 revealed that there had been a large improvement in the number of students who correctly answered the items relating to an understanding of variance, what a population without variance would look like and the interpretation of frequency distributions. This indicates that the intervention successfully addressed many students' difficulty in understanding variance and their ability to interpret graphs such as histograms. There was no improvement in students' understanding of variation. This was not considered to be a problem as most students had answered this item correctly on both occasions. The only item which the majority of students' were not able to answer required students' to apply their knowledge of variance (cosmos example). These results indicate that although many students were able, after the intervention, to describe the concept of variance they were still unable to apply their knowledge of this concept. In other words, on an epistemological level, the concept of variance may be considered *intelligible* and even *plausible* but not *fruitful* to these students as they were unable to apply their knowledge to the solution of the problem in question.



**Figure 7.3: Frequency distribution showing the percentage of students who correctly answered questions repeated in the prior-knowledge and post-teaching diagnostic tests given in 2005.**

The results from the multiple-choice diagnostic tests, that most students had a better understanding of variance, and that they could successfully interpret histograms was confirmed by interviews conducted at the completion of the module.

Of the four students who were interviewed after the first computer-based tutorial and who had performed poorly in the first multiple-choice diagnostic test, all could correctly define the concepts of variation and variance and could successfully distinguish between the terms. One student's correct understanding of variance as being a measure of how values deviate from the mean is borne out by the following quote:

S: "The variance is measuring the – like how are the individuals – how is the population being spread out."

I: "Compared to what?"

S" Compared to the mean."

In addition, the students interviewed expressed the opinion that they felt their understanding of variation and variance had improved because the computer-based tutorials had helped them visualise the concepts. An example of how a student thought he was more able to visualise and apply the concept of variance in a genetics context is illustrated by the following quote.

- S: "I understand variance much better now."  
 I: "What made you understand it?"  
 S: "I think it was that first tutorial on the computer.....it made me start seeing all these statistics from a genetic point of view rather than just as numbers."

Another student expressed the opinion that she understood the concept of variance better because the computer tutorials helped her relate the concepts to graphs of frequency distributions.

- S: "It made a huge difference working on the computer. Cause then you put it into practice and then you can.....well I like seeing what I am learning, then I understand it better."  
 I: "Okay, when you say seeing it, seeing it how?"  
 S: "Like when you do it and your graphs change – you can like visualise it more than if you just had to do questions. So now I know what happens on a graph when the variance changes. Before, if I was just given figures I wouldn't have known much."  
 I: "So you think that the computer tutorials helped?"  
 S: "Yes definitely. Well I think I am sort of starting to understand, compared to that first survey thing we did."

Three of the four students interviewed actually illustrated that they could relate the statistic of variance to a depiction of a frequency distribution. The following quote shows how a student could correctly interpret histograms and thus knew how the shape of a normal distribution would alter with a change in variance.

- I: "If I asked you to draw a normal distribution with less variance, would the shape of the graph change?"  
 S: "It would be narrower."  
 I: "And the height? Would that change?"  
 S: "Not necessarily. It could change, but it doesn't have to."

However, it is important to note that some students still had some difficulty with certain tasks. For example, one of the students interviewed still confused the X and Y axes and wanted to plot a point for every individual. This student could also not relate the statistic variance to a frequency distribution and thought that a graph with less variance would be "flatter and wider".

- I: "So what do you think each of the bars represents?"  
 S: "The weight of each person."  
 I: "So you would have one bar for each person?"  
 S: "Yes."  
 I: "Then how about if there were ten thousand people – you would have ten thousand bars. Are you happy with that?"  
 S: "Yes"  
 I: "If I asked you to draw that graph (indicating a normal distribution) with less variance, what would it look like?"  
 S: "It would be flatter and wider."

The reason why many of the students interviewed still showed some confusion regarding the X and Y axes seemed to stem from a limited understanding of the concept of frequency. This is illustrated by the following quote from a student interview.

- I: "Why do you want to look at the Y axis all the time?"  
 S: "I don't know – because I don't like that whole frequency thing."

- I: "The idea of frequency?"  
S: "Yes."  
I: "So it's the idea of frequency that is difficult for you to get your head around?"  
S: "Yes, cause I don't exactly know what it is. I know things like height and weight, you know I can see it – but frequency, I don't know exactly what a frequency is. Is it just a number of people?"

This finding is of importance as it indicates the need to pay particular attention to the concept of frequency in the development of any future tutorials. It also reinforces the need for students to spend time using the Tinkerplots™ (2004) software where they actively have to look at summarising data by grouping certain "individuals" together. Perhaps in future when teaching concepts related to quantitative genetics, the word "frequency" must be used more often and its meaning made explicit.

It has recently been recognised that students studying statistics need to understand the concept of variation as it is central to statistical reasoning and thinking (Ben-Zvi and Garfield 2004). In this regard, Meletiou-Mavrotheris and Lee (2002) noted an improvement in students' understanding of histograms, the mean and the standard deviation in a study comparing two groups of students, those taking a statistics module where variation was emphasized and those where the concept of variation was not given any priority. However, as in the investigation described in this thesis, some students in the module emphasizing variation still could not tell which of two distributions had the most variation and some still confused histograms and scatterplots. These results indicate the high level of difficulty associated with understanding frequency distributions.

Many studies which have tested the use of different teaching strategies and tools aimed at improving students' understanding of variation and its relationship to graphical representations have recently been conducted, some of which have utilised computer software. This was deemed necessary as Mills (2002) concluded after reviewing the literature on computer simulation methods to teach statistics, that although many people advocate the use of this method to improve the conceptual understanding of students, there was a lack of empirical research to substantiate these claims. The investigation described in this thesis provided some empirical evidence to support the fact that computer-assisted learning does enhance students' understanding of variation and variance and how these ideas are related to histograms.

The improvement in students' understanding of variance and its relationship to a frequency distribution noted in this investigation was also observed by DelMas and Liu (2005) when they used a computer-based environment to promote students'



understanding of the standard deviation and its relationship to the mean. The researchers interviewed twelve students and noted that after using the software they all seemed to start relating the shape of histograms to the size of the standard deviation. All the students seemed to understand that a small standard deviation was produced when most of the values clustered around the mean and a large standard deviation was associated with values placed further from the mean in both directions. Bakker (2004) also used software tools to assist students reasoning about the “shape of data” and concluded that the instructional activities used had promoted conceptual growth of ideas such as centre (average, majority), spread (range) and the shapes of distributions and aided students in their understanding of statistical terminology.

The effectiveness of the *Tinkerplots<sup>TM</sup>* software (2004) used in this investigation was also illustrated by Hammerman and Rubin (2004) when observing the manner in which middle and high school teachers used the software to deal with variability when analysing data. The teachers successfully used the software to group data and even sometimes noted the variation in data at the expense of the mean or centre which may have been due to the visual nature of the distributions produced. Of particular interest to this investigation was that the teachers used the pie graphs produced by the software to compare relative proportions of observations in two different populations. This feature of the programme could be incorporated into an intervention used in a quantitative genetics module in the future to encourage the proportional reasoning required for an understanding of the concept of heritability. In addition, Hammerman and Rubin (2004) point out that the software allows one to plot the covariance between two sets of data. This feature of the software could be used in future tutorials to allow students to visualise the covariation exhibited by the phenotypic values of parents and offspring in a population.

The results of this investigation as well as those reported from other studies thus indicate that computer-assisted learning may be an effective way of promoting students’ understanding of variation and variance. However, it must be noted that researchers such as Ben-Zvi (2004) comment that students need guidance from a teacher when working with software so that they focus on key information. A possible reason postulated by researchers such as Bodemer *et al.* (2004), Lowe (2004) and Rieber *et al.* (2004) is that especially when working with animations, the information processing requirements may be too high for students to extract the relevant information. In this regard, Chandler (2004) suggests that it could be beneficial to present text and graphics together. In this investigation, this was not done. However, the students were provided with a detailed *tutorial guide* as well as access to tutors during the time they were working on the computer.

**(b) *Determination of whether the intervention enhanced the level of students' understanding of quantitative genetics concepts***

A comparison between the item map for the 2005 student group (Figure 7.4) and the item map for the 2004 group (Figure 5.2, page 125) provided evidence that there had been a change in the rank order of item difficulty after the teaching of the module. The most notable change is that in 2004 students found the item requiring knowledge of the association of breeding value and heritability most difficult, followed by the item asking why quantitative traits are normally distributed, with only 7% of the students having a 50% chance of being able to answer these questions. In contrast, 54% of the 2005 student group had a 50% probability of correctly associating the concepts of breeding value and heritability and 95% of the students a 50% chance of being able to explain why quantitative traits are usually normally distributed. Students in both groups found the interpretation of a heritability value of one more difficult than a heritability value of zero. These results imply that the intervention had been effective in improving students' understanding of graphical representations, particularly histograms, as well as assisting students in being able to distinguish between individual measures such as breeding values and population measures such as heritability.

These results are particularly noteworthy as the intervention had aimed to address the difficulties identified during the diagnostic phase of the investigation (detailed in Chapters 4 and 5). These included: (a) students' understanding of the *critical concept* of heritability; (b) students' inability to differentiate between individual and population measures such as breeding value and heritability and (c) students' difficulty with the interpretation of histograms. The results of the Rasch analysis indicate that all of these areas of difficulty seemed to become easier for most students after they had participated in the intervention.

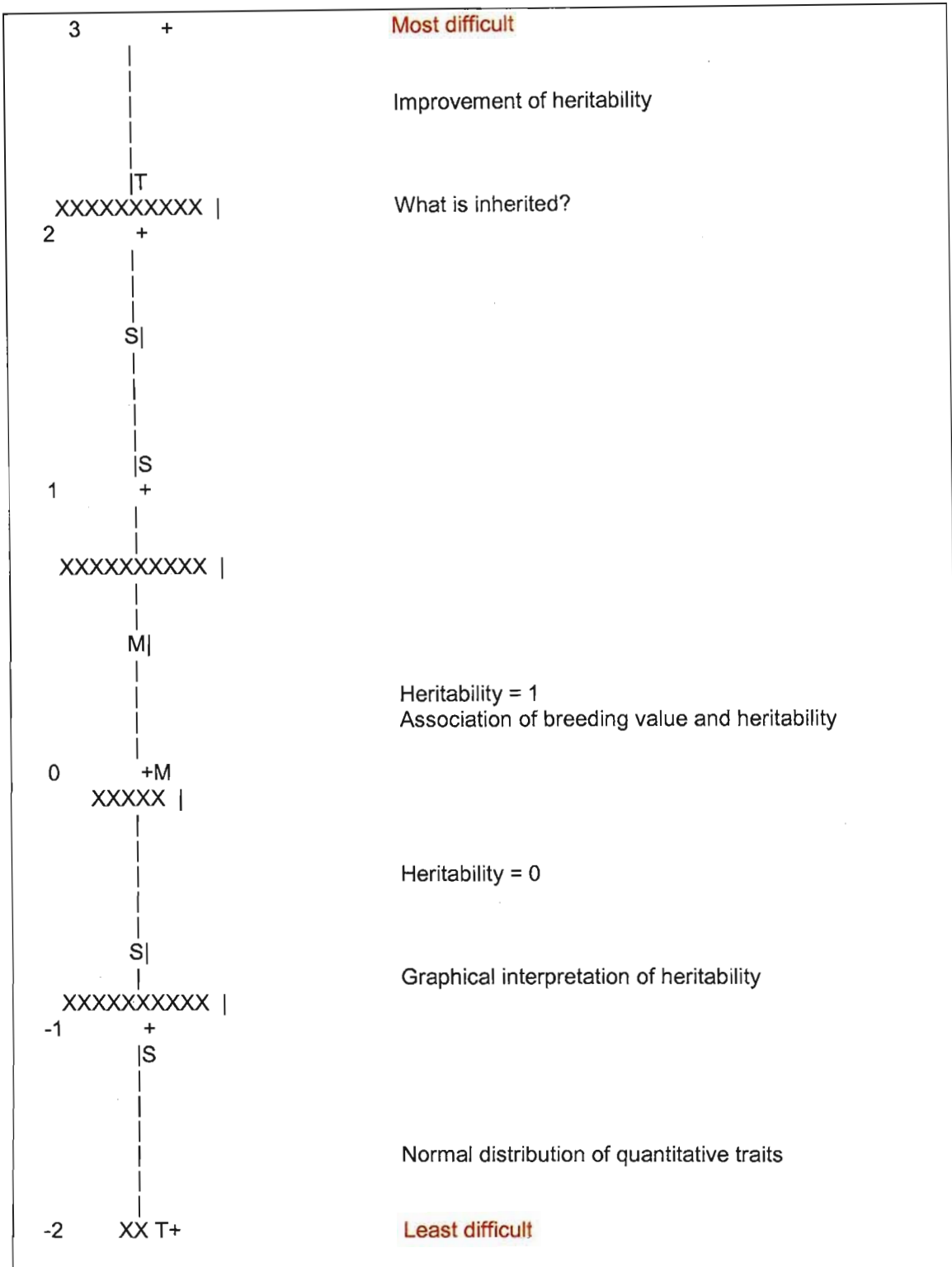
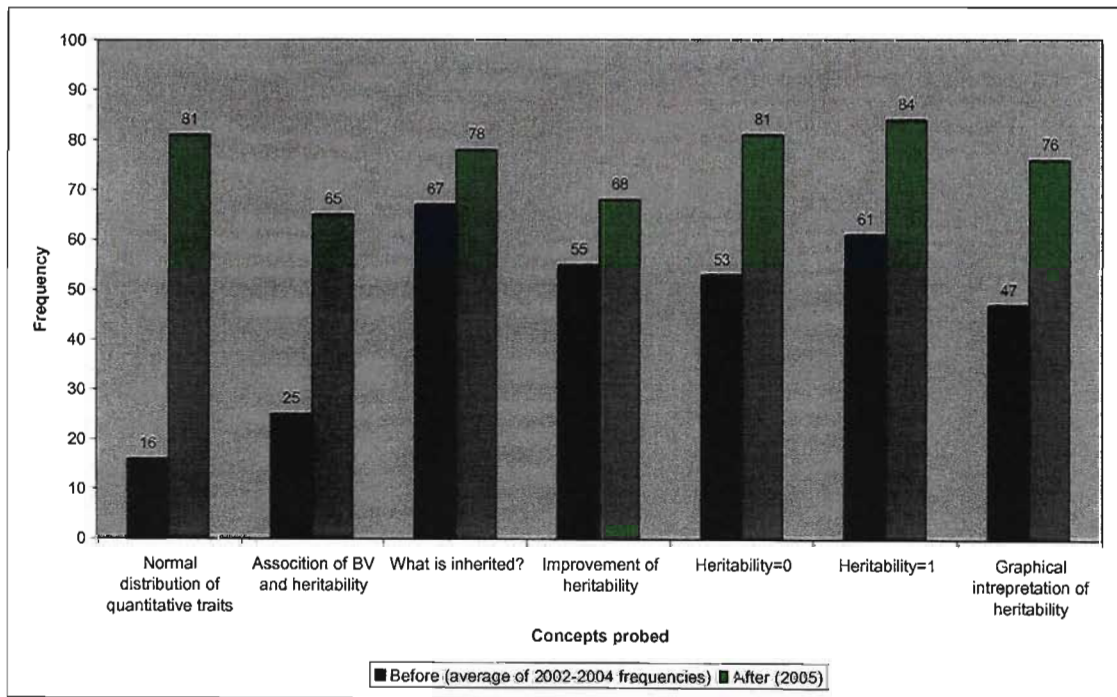


Figure 7.4: Item map depicting the relative difficulty of concepts and skills probed by each item of the post-teaching diagnostic test.

In order to validate the above finding, an analysis of students' understanding of all the *quantitative genetics concepts* under investigation was conducted. The percentage of students from the 2002, 2003 and 2004 student groups who could correctly answer items, on the post-teaching diagnostic test, probing their knowledge of certain concepts was compared to the 2005 student group that had participated in the intervention. An improvement in the performance of students was noted for all the *quantitative genetics concepts* under investigation (Figure 7.5). This result indicates that the intervention had been effective in improving many students' understanding of the concepts, such as heritability, that the intervention had aimed to improve. Figure 7.5 is a frequency distribution indicating the percentage of students who were correctly able to answer the items given in the post-teaching diagnostic tests.



**Figure 7.5:** Frequency distribution of the percentage of students able to correctly answer items on the post-teaching diagnostic tests that were administered before (2002-2004), and after (2005), the implementation of the intervention.

As an improvement in the understanding of key concepts in quantitative genetics was noted in the students who participated in the intervention, 8 students were interviewed at the completion of the module to gather in-depth data on the nature of their understanding. Of the 8 students interviewed, six of the students could correctly define the concepts of breeding value, additive variance and heritability as well as the relationships between these concepts. Furthermore, these students showed sound

graphical understanding and could describe what a heritability value of zero or one would indicate.

As in this investigation, Soderberg and Price (2003) concluded that a software programme had helped students to shift their thinking from an individual to a population level. However, notwithstanding that students' ability to think on a population level generally improved in the investigation described in this thesis, one of the two students, who had consistently performed badly throughout the module, still found thinking on a population level difficult. He commented: "In the back of my mind, I don't really see the population part."

The other student who consistently performed badly throughout the module indicated that the fact that each section of the module built on the previous sections was problematic in that she had not kept up with the work and had become "lost." She said: "It's like one thing leads onto the next.....I think I got left behind. I guess I just gave up!"

It is interesting to note that three of the students interviewed still showed some confusion between the terms *breeding value* (the value associated with the alleles carried by an individual and inherited by its progeny) and *heritability* (the proportion of the phenotypic variance that may be accounted for by differences in the breeding values of individuals) as both concepts have something to do with what is inherited. This is highlighted by the following quote.

- I: "Do you think you sometimes still confuse breeding value and heritability?"  
S: "Sometimes – because I think heritability and breeding value are both things that you think of being passed on."

This result is important as one of the primary difficulties identified during the diagnostic phase was that students confused certain terms and topics. Although an effort was made to distinguish between terms and to make their meaning explicit during the teaching of the module, some students still showed this difficulty.

Furthermore, four of the students were confused about the meaning of the idea of *additive gene action*. This result suggests that in future tutorials more emphasis must be placed on ensuring that students realise that as the words suggest, *additive gene action* simply describes a mechanism whereby the alleles at different loci act in an additive fashion. A student who showed a sound understanding of the concept described it as follows:

- I: "What do you understand by the term additive gene action?"  
S: "Well the additive gene action is which genes are passed on from the parents to the offspring. That is additive gene action, its like the mechanism where it is passed on. I don't know how to explain it."  
I: "Okay, so it is a mechanism but what gets passed on?"



- S: "Alleles."  
 I: "Is there a relationship between additive gene action and the breeding value of an individual?"  
 S: "I think so because each allele has an additive effect – so it has a value, and then those can be.....so you can almost measure how much is passed onto the offspring and that its breeding value sort of – what it passes onto its offspring."

In contrast, one student who did not understand the concept of additive gene action and thought of the word average (perhaps because she was thinking of the average effect of an allele) but not the mechanism involved, responded as follows:

- I: "What do you think we mean by additive gene action?"  
 S: "Its all – it's the average again but of the genes, the genes which.....oh I don't know. It's the average of all the genes which well have an effect.....no.....I don't know."

Another student also seemed to be thinking of the average effects of alleles and how they are added together to obtain a phenotypic value. However, this student still did not think of the term *additive gene action* as relating to a type or form of gene action.

- S: "It's like a whole lot of alleles making up the trait. So depending on how many that you would have – and there would be like dominance – then the combination of all that gives the phenotype."  
 I: "So does additive gene action belong to an individual or is it something else?"  
 S: "I think it belongs to an individual."  
 I: "The words additive gene action – do they tell you anything?"  
 S: "They do but I am confused."  
 I: "Do you think of it as a process?"  
 S: "No, well each allele has a value. When those come together and you add up all of those then you will get a specific value that is the phenotypic value."

It may thus be concluded that most students responded favourably to the intervention in that their understanding of population measures such as heritability and the manner in which descriptive statistics relate to histograms was far better than the students groups who had not participated in the intervention. However, a small number of students still confused certain terms and battled to think on a population level.

#### 7.4 CONCLUDING REMARKS

The results obtained strongly suggest that the intervention was, in most cases, effective in improving students' overall understanding of quantitative genetics and their understanding of *prior knowledge concepts* such as *variance* and *quantitative genetics concepts* such as *heritability*. Furthermore, the intervention seemed to effectively address students' understanding of the relationship between population parameters and graphical representations. The concepts of *frequency* and *additive gene action*, however, remained difficult for some students and are concepts that should be addressed when improvements are made to the intervention in the future.

## CHAPTER 8

# DETERMINATION OF THE NATURE OF CONCEPTUAL CHANGE WHICH OCCURRED DURING THE MODULE

**Research Question 6:** What was the nature of the conceptual change which occurred during the module?

### 8.1 INTRODUCTION

The results and discussion presented in Chapter 7 strongly indicate that the intervention was effective in improving students overall understanding of quantitative genetics as well as their understanding of specific concepts. However, as the students had all constructed a series of five concept maps throughout the module, the researcher was able to use these student-generated concept maps to assess the *nature* of the conceptual change which had occurred during the teaching of the *Genetics 332* module in 2005. The student-generated concept maps were thus used for two independent purposes; (a) as a metacognitive tool as part of the intervention; and (b) as a research assessment tool to assess the nature of the conceptual change that occurred. The latter is described in this chapter.

### 8.2 METHODOLOGY EMPLOYED

Conceptual change over time was measured using two research instruments: (1) concept maps and (2) attitudinal questionnaires.

#### 8.2.1 Concept maps

##### **(a) Description of concept mapping as a research instrument**

A description of concept maps and the reason why concept maps may be used as an evaluation tool is discussed in Chapter 3, Section 3.2.2. A description of the concept mapping exercises is provided in Chapter 6, Section 6.3 and the stage in the module

when each concept map was constructed is given in Table 6.6. In each concept mapping exercise students were provided with a list of concepts to be included. The researcher used this list of concepts to create a series of five concept maps which could be used to create a list of linkage relationships that would be used to evaluate each student-generated concept map.

**(b) Analysis of concept map data**

An overall analysis of the student-generated concept maps was initially conducted to determine whether the maps could be grouped into broad categories. These categories were whether the series of maps constructed by a student were: (1) consistently of a high standard illustrating a good grasp of the concepts included in the maps, (2) consistently of a poor standard illustrating a lack of understanding and (3) inconsistent in that the first in the series of maps showed poor understanding of concepts but the maps constructed later in the module illustrated that the students had undergone some conceptual change and subsequently showed an understanding of the subject matter.

The student-generated concept maps were then used to assess any changes which had occurred in the conceptions of students from an epistemological and ontological perspective. The nature of conceptual change that occurred throughout the teaching of the module was initially viewed from an epistemological perspective and all the linkages on the student-generated concept maps were examined using the protocol of Nicoll (2001). This protocol is described in Chapter 3, Section 3.2.2. The reader will note that the first level of analysis considers the accuracy of the link and links are coded as *correct* (coded as "1"), *incorrect* (coded as "2") or *missing* (coded as "3"). The second level of analysis evaluates how confident students were with their knowledge and codes their knowledge as *defined* (coded as "i") or *emerging* (coded as "ii"). The final level of analysis looked at the complexity of the students' conceptual frameworks where the links were coded as: *an example* (coded as "a"), *a fundamental fact* (coded as "b") or *a link explained by other links* (coded as "c").

In the first step of the analysis, from an epistemological perspective, the researcher took all the linkages analysed on the student-generated concept maps and assessed whether any changes which occurred had been *revolutionary* or *evolutionary* in nature. When the form of the change was *revolutionary* in nature, in that the conception of the students changed from *incorrect* (coded as "2") to *correct* (coded as "1"), this was considered *conceptual exchange*. When the change was *evolutionary* in nature and the students recognised that a certain relationship

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between concepts did in fact occur and they included the relationship on subsequent maps (the coding of the link changed from *missing* or “3” to *correct* or “1”) this was considered as conceptual *capture*. Finally, if the knowledge of the students became more clearly defined over time (the coding of the link changed from *emerging* or “ii” to *defined* or “i”) then this type of change was termed conceptual *development*.

In the second step of the analysis from an epistemological perspective, the researcher examined students’ knowledge of the *critical concepts* of *variance* and *heritability*. The linkage relationships relevant to these concepts were analysed and coded as *intelligible*, *plausible* or *fruitful*. In order to do this the protocol of Liu (2004) was utilised.

Liu (2004) in a study on grade 12 chemistry students who constructed concept maps using the *Inspiration* computer package, considered conceptual change from an epistemological perspective. Liu hypothesized that if:

- A student’s belief was intelligible then there should be *type-of* relations indicating the student’s knowledge was in the form of *fundamental facts* (coded by Nicoll’s classification scheme as “b”).
- A student’s belief was *plausible* then there should be *cross-links* between parts of the concept map (coded by Nicoll’s classification scheme as “c”).
- A student’s belief is *fruitful* then examples should be given (coded by Nicoll’s classification scheme as “a”).

The researcher thus continued with the classification scheme proposed by Nicoll (2001) but students’ epistemological views of the concepts of *variance* and *heritability* were inferred using the reasoning proposed by Liu (2004).

Changes in the ontological beliefs of students were also classified according to a scheme proposed by Liu (2004). In this scheme different ontological beliefs are believed to be demonstrated by different types of relations in concept maps. For example, if a student’s belief changed from *passive* to *active* the links should change from the *type-of* form (e.g. a definition or equation for the concepts of *variance* and *heritability*) to a *leads-to* (*cross-links* evident) form, for example *cross-links* between concepts such as *heritability* and the selection of a breeding strategy.

In addition, conceptual change was viewed from an affective perspective. In order to conduct this analysis, students were asked a series of questions using attitudinal questionnaires and some students were interviewed.

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## 8.2.2 Attitudinal questionnaires

### (a) *Description of attitudinal questionnaires*

In order to gauge the students' attitudes towards certain factors, students were asked to answer Likert-style questionnaires. A Likert-style questionnaire makes use of rating scales, such as *strongly disagree*, *disagree*, *neutral*, *agree* and *strongly agree* (Cohen *et al.* 2000). The respondents are asked to choose one option in response to a particular statement or question. As Cohen *et al.* (2000) state this type of questionnaire is useful in research as it allows for flexible responses from the students which may then be quantified in the form of frequencies.

However, Cohen *et al.* (2000) caution that the researcher cannot tell if the respondents are being truthful and many respondents will give a "neutral" answer so as not to take a stand on any issue. In this regard, McMillan and Schumacher (1993) believe that the "neutral" choice should be included as it may be the way that a respondent feels and that if a respondent is forced to make a choice then the individual may choose not to answer the question at all. The "neutral" choice was thus included in the questionnaires used in this investigation.

As suggested by Cohen *et al.* (2000), questionnaires which make use of rating scales only elicit fixed responses from students. They therefore recommend that some open-ended questions be included in the questionnaire so as to allow students to expand on their opinions. Thus open-ended questions were also included in the post-teaching questionnaire. The questionnaires used in this investigation are provided in Appendix 8 on page 331.

### (b) *Implementation of attitudinal questionnaires*

In order to gauge how students' attitudes towards certain issues may have changed during the teaching of the module they were asked to complete attitudinal questionnaires at the start of the module and at the completion of the module.

### (c) *Data analysis of attitudinal questionnaires*

The students' responses were analysed by calculating a frequency for each type of response given on the rating scale. Where applicable a comparison was made between answers given by students before and after the intervention. The open-ended responses were analysed and any responses of interest noted for inclusion in



the results. These data gave an indication of any attitudinal changes which may have occurred during the teaching of the module.

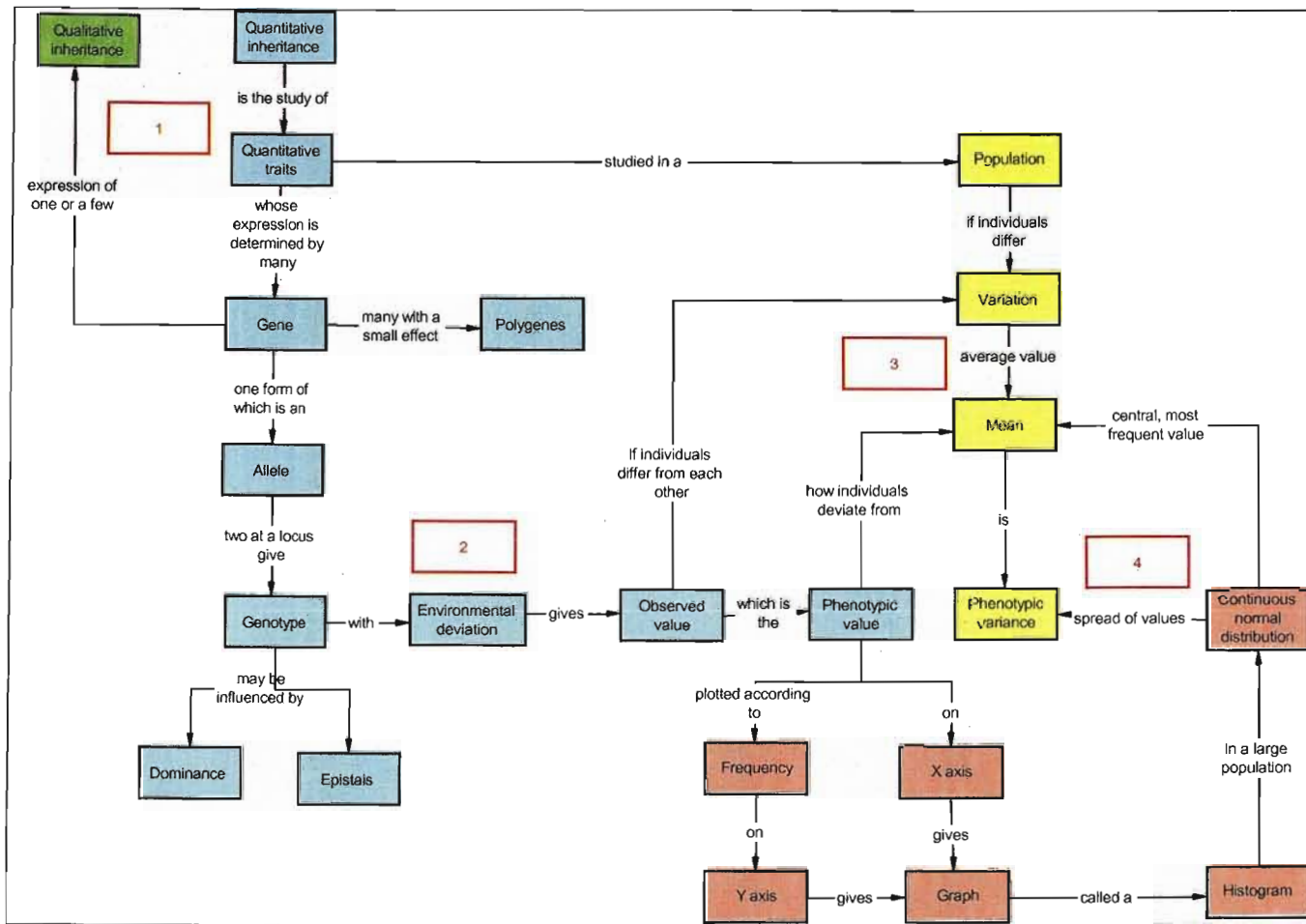
The nature of the conceptual change which occurred in the minds of the students who completed the *Genetics 332* module during 2005 was thus examined from three perspectives:

- (a) From an *epistemological* perspective i.e. whether the conceptual change which occurred was of a *revolutionary* or *evolutionary* nature. In addition students' conceptions of the *critical concepts* of variance and heritability were described as *intelligible*, or *plausible* or *fruitful*.
- (b) From an *ontological* perspective i.e. whether the ontological status of a student's conceptions changed from, for example, *passive* to *active*.
- (c) From an *affective perspective* i.e. whether the students' attitude towards the subject of quantitative genetics had altered during the teaching of the module. It should be noted that this student group had participated in the intervention and so these results also indicated the success of the intervention from an affective standpoint.

## 8.3 RESULTS

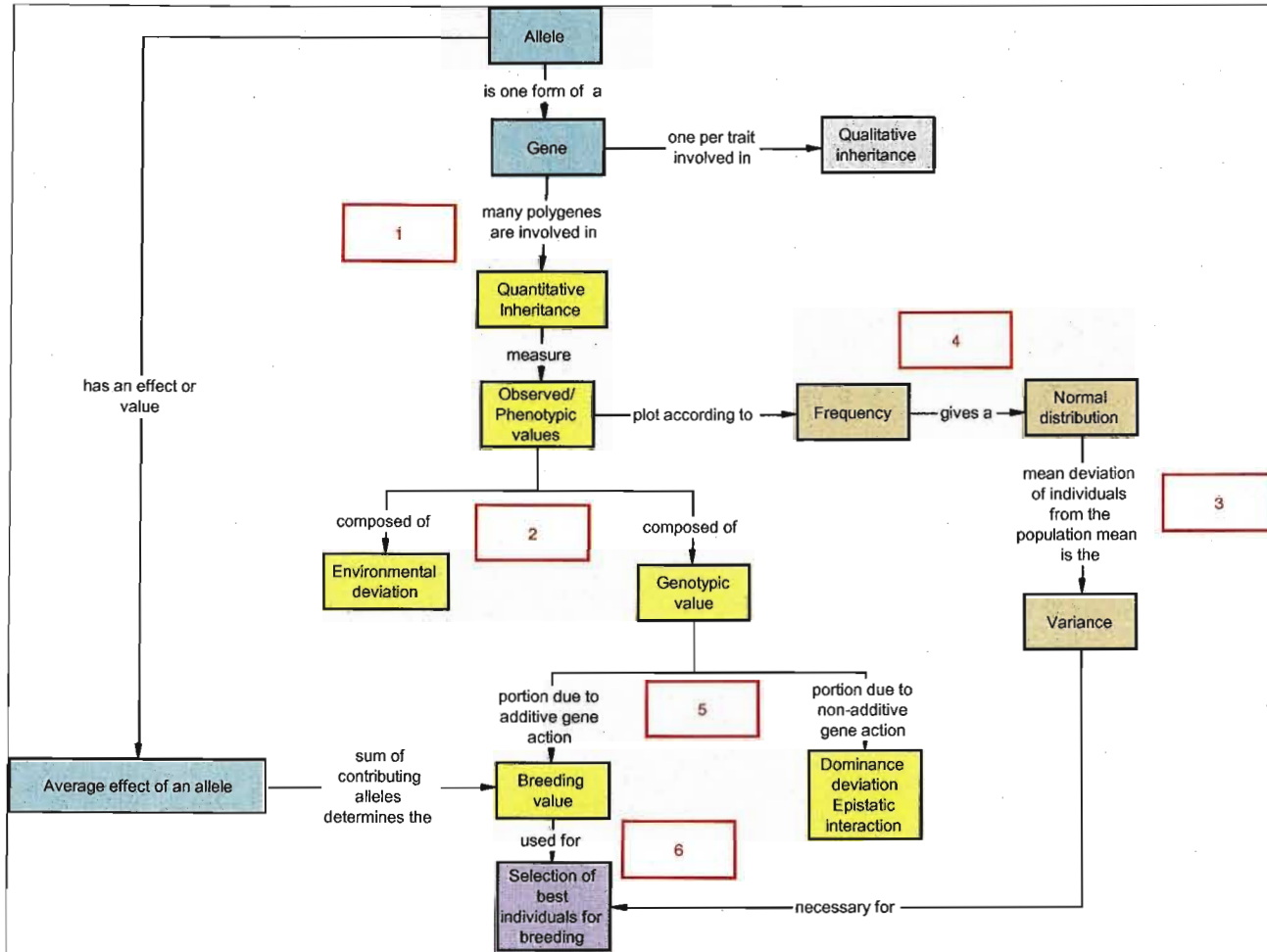
### 8.3.1 Assessment criteria

The lecturer-generated concept maps are shown in Figures 8.1- 8.5. Twelve linkage relationships were identified by the researcher as being important and were thus used as part of the assessment criteria (depicted by the numbers in red on Figures 8.1 – 8.5). Each of these links was assessed in each of the concept maps and where relationships were included in successive maps, any changes in students' conceptions were noted.



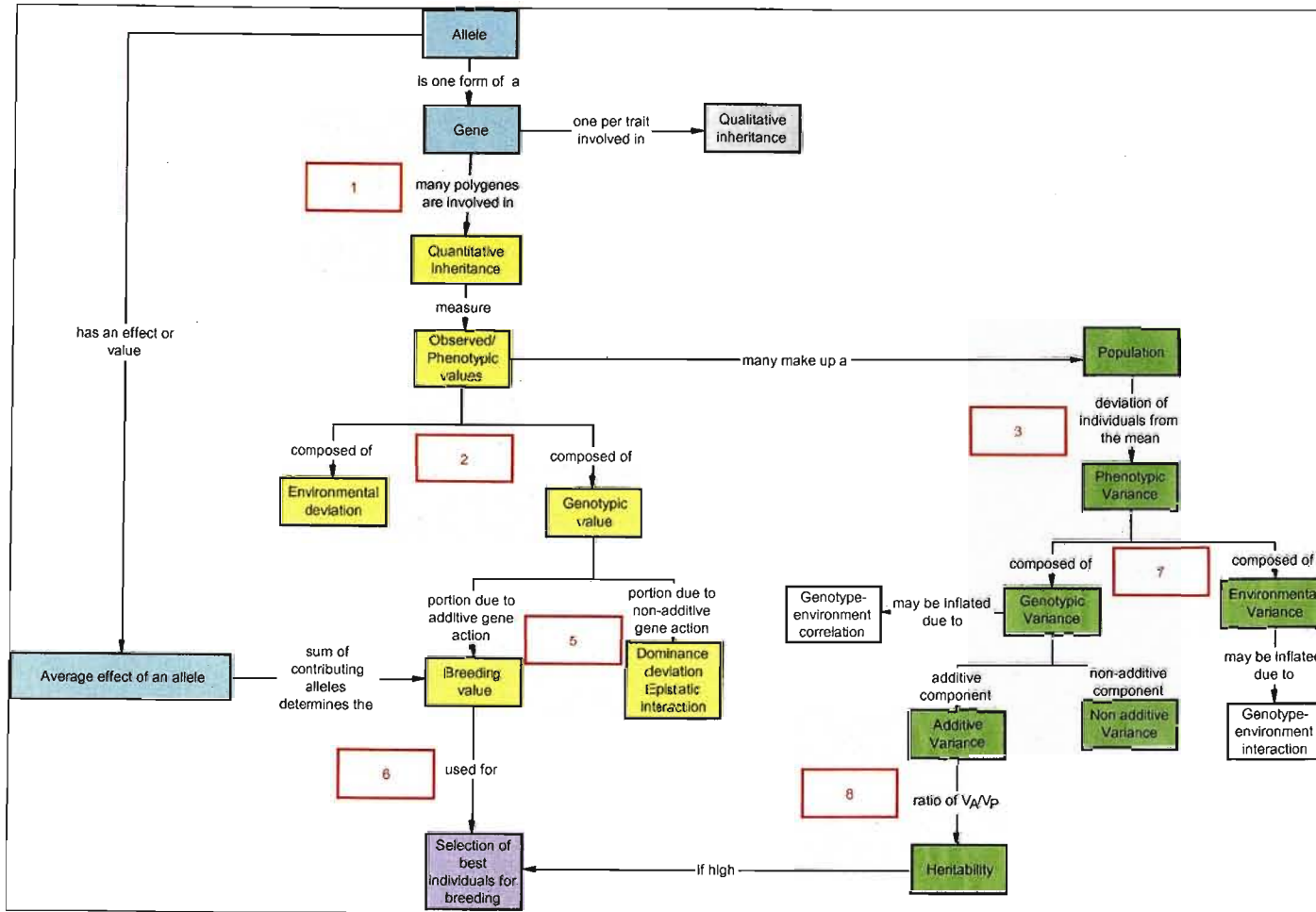
Numbers depicted in red illustrate the linkage relationships investigated

Figure 8.1: Lecturer-generated concept map 1.



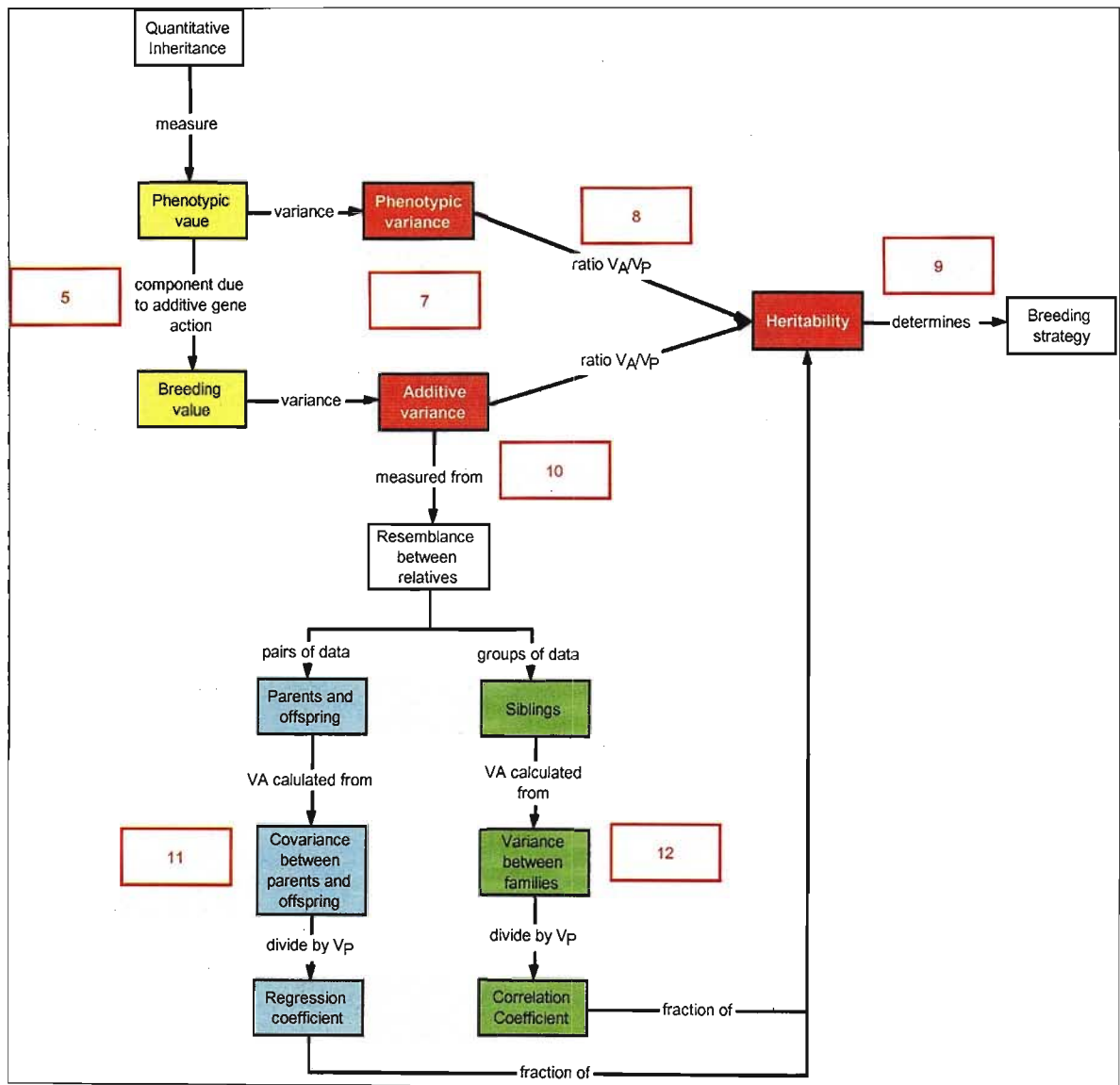
Numbers depicted in red illustrate the linkage relationships investigated

**Figure 8.2: Lecturer-generated concept map 2.**



Numbers depicted in red illustrate the linkage relationships investigated

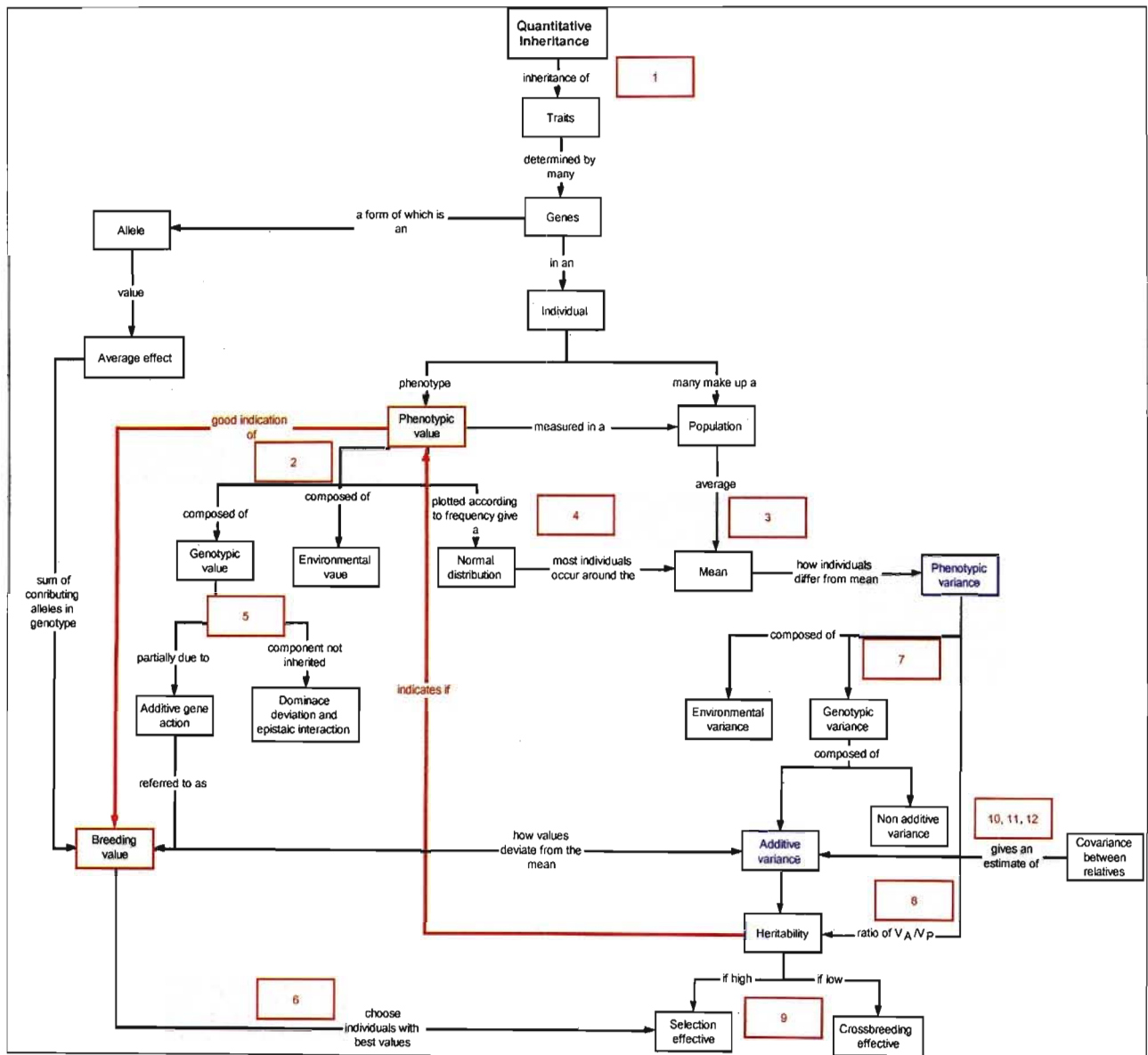
**Figure 8.3: Lecturer-generated concept map 3.**



Numbers depicted in red illustrate the linkage relationships investigated

Figure 8.4: Lecturer-generated concept map 4.





Numbers depicted in red illustrate the linkage relationships investigated

Figure 8.5: Lecturer-generated concept map 5.

Student-generated concept maps were scored on whether the students illustrated an understanding of the following twelve links or relationships.

1. The difference between quantitative inheritance and qualitative inheritance.
2. The relationship between the phenotypic value of an individual and their corresponding genotypic value and environmental deviation value.
3. The relationship between phenotypic values and descriptive statistics.
4. The relationship between descriptive statistics and graphical representations, particularly histograms.
5. The relationship between the genotypic value of an individual and their corresponding breeding value, dominance deviation and epistatic interaction value.
6. The relationship between the breeding values of individuals and the selection of a breeding strategy.
7. The relationship between the phenotypic variance ( $V_P$ ) and the additive variance ( $V_A$ ), dominance variance ( $V_D$ ) and variance due to epistatic interaction ( $V_I$ ).
8. The relationship between the heritability of a trait and the additive variance and phenotypic variance ( $h^2 = V_A/V_P$ ).
9. The relationship between heritability and the selection of a breeding strategy.
10. The relationship between the additive variance and the resemblance between relatives.
11. The relationship between regression and heritability.
12. The relationship between a correlation coefficient and heritability.

Table 8.1 indicates which links were analysed in each of the five maps created by the students. It should be noted that map 5 was the concept map that students were expected to construct at the completion of the module and as such included all 12 relationships investigated.

**Table 8.1: Indication of the links analysed in each concept map.**

Map	Links examined
1	1-4
2	1-6
3	1-3, 5-8
4	5, 7-12
5	1-12

### 8.3.2 Categorisation of student-generated concept maps

An overview of the student-generated concept maps allowed them to be categorised as (1) consistently showing a good understanding of the subject matter, (2) consistently showing a poor understanding of the subject matter or (3) inconsistent in that the maps showed that the students' understanding of the subject matter had improved over time.

It should be noted that 33 students completed the Genetics 332 module in 2005 and thus participated in the intervention. However, the students were allowed to work on the construction of their concept maps in pairs if they wished. As a result the researcher analysed 20 different sets of concept maps ( $n=20$ ) as some students chose to work alone and some in pairs. Twenty percent of the sets of concept maps analysed could be classified as consistently of a high standard with a further twenty percent of the students not showing a good grasp of the subject matter in any of the maps they constructed. The remaining sixty percent of the sets of student-generated concept maps showed that their understanding of concepts had improved during the teaching of the module. Examples of two sets of student-generated concepts maps are provided in Appendix 10 (page 355). The first set of maps is representative of a set of concept maps which were consistently good, the second set of maps are representative of a set of maps which were consistently unsound. A set of student-generated concept maps, constructed by one student using the *Inspiration software* and where a great deal of conceptual change was evident are included in this chapter as Figures 8.6 – 8.10.

The student who constructed the concept maps given in Figures 8.6 – 8.10 chose to use colour to highlight the relationships that he saw to be evident between certain concepts. The reader will also note that the student organised his knowledge more effectively throughout the module and that he consistently expanded on and corrected his knowledge. Thus the final concept map (Figure 8.10) illustrates that the student made meaningful connections between all the primary concepts covered in the teaching of the module. The development of this student's knowledge is illustrated by the following examples.

- The student's understanding of the difference between qualitative and quantitative inheritance is more clearly defined in Figure 8.7 than Figure 8.6.
- The student more correctly partitions the phenotypic value into genetic and environmental components in Figure 8.8 than Figure 8.7.

- The student correctly indicates the manner in which the heritability of a trait relates to the selection of a breeding strategy in Figure 8.10, whereas in Figure 8.9 this relationship is incorrectly depicted.

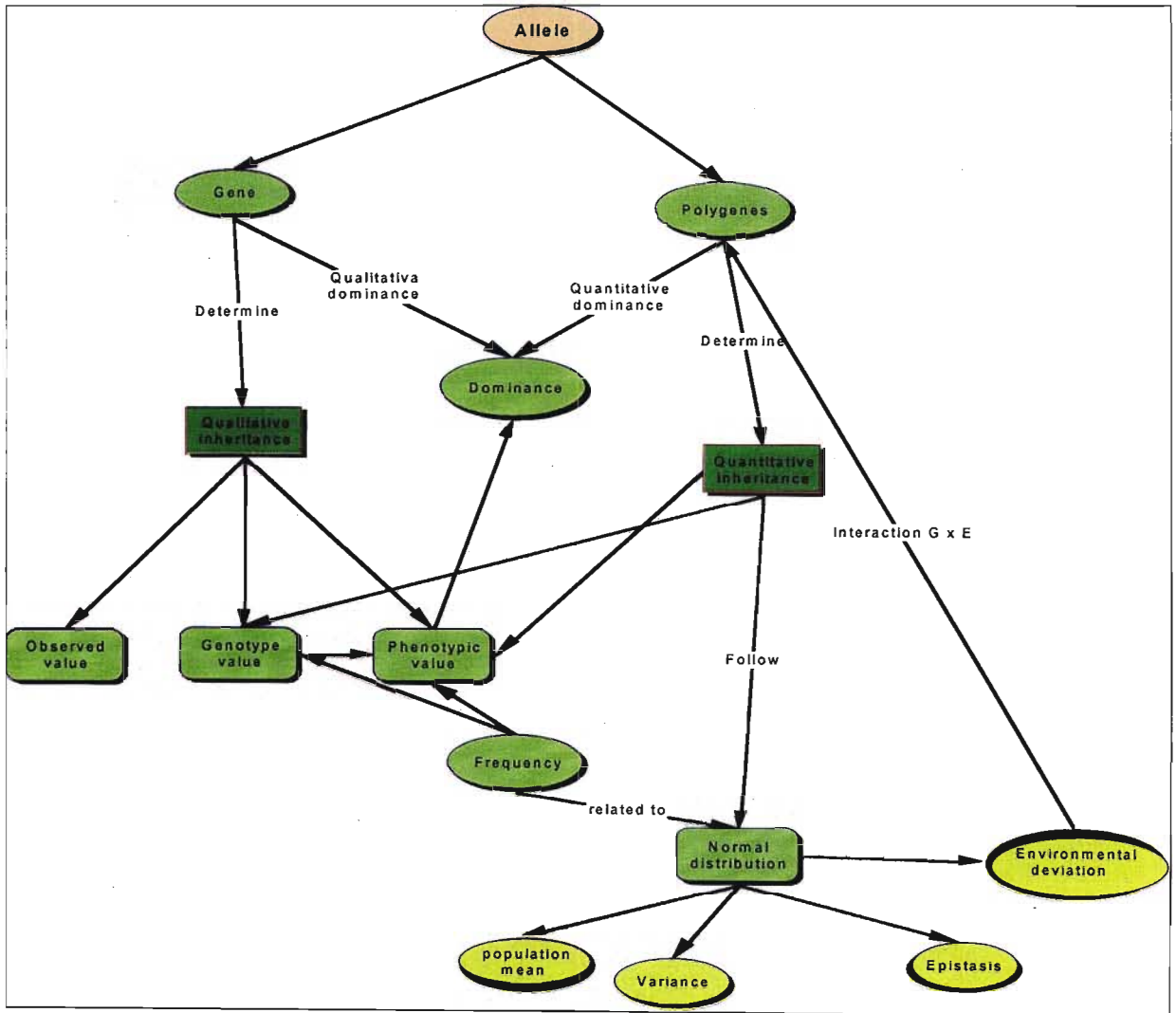


Figure 8.6: Student-generated concept map 1.

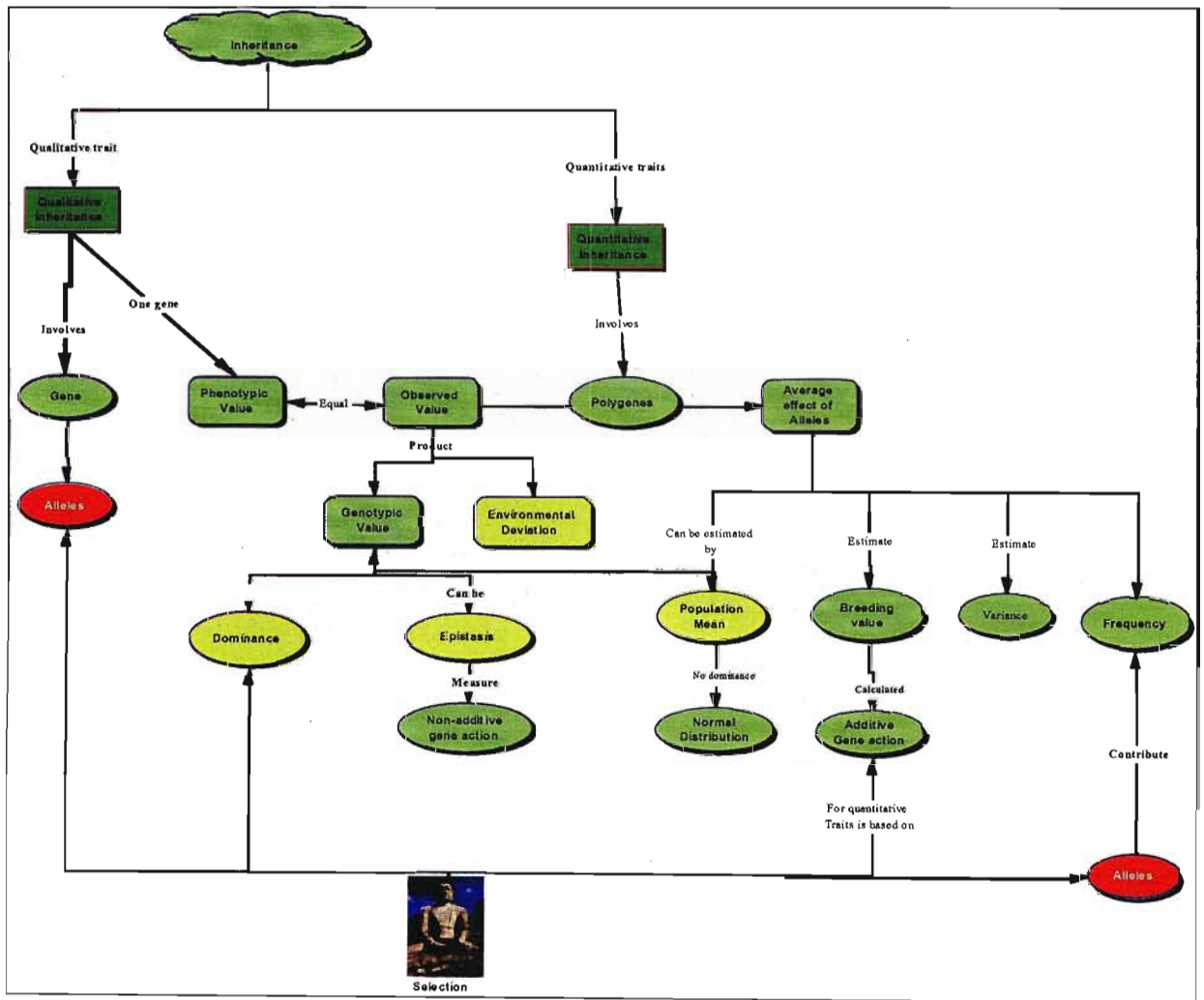


Figure 8.7: Student-generated concept map 2.



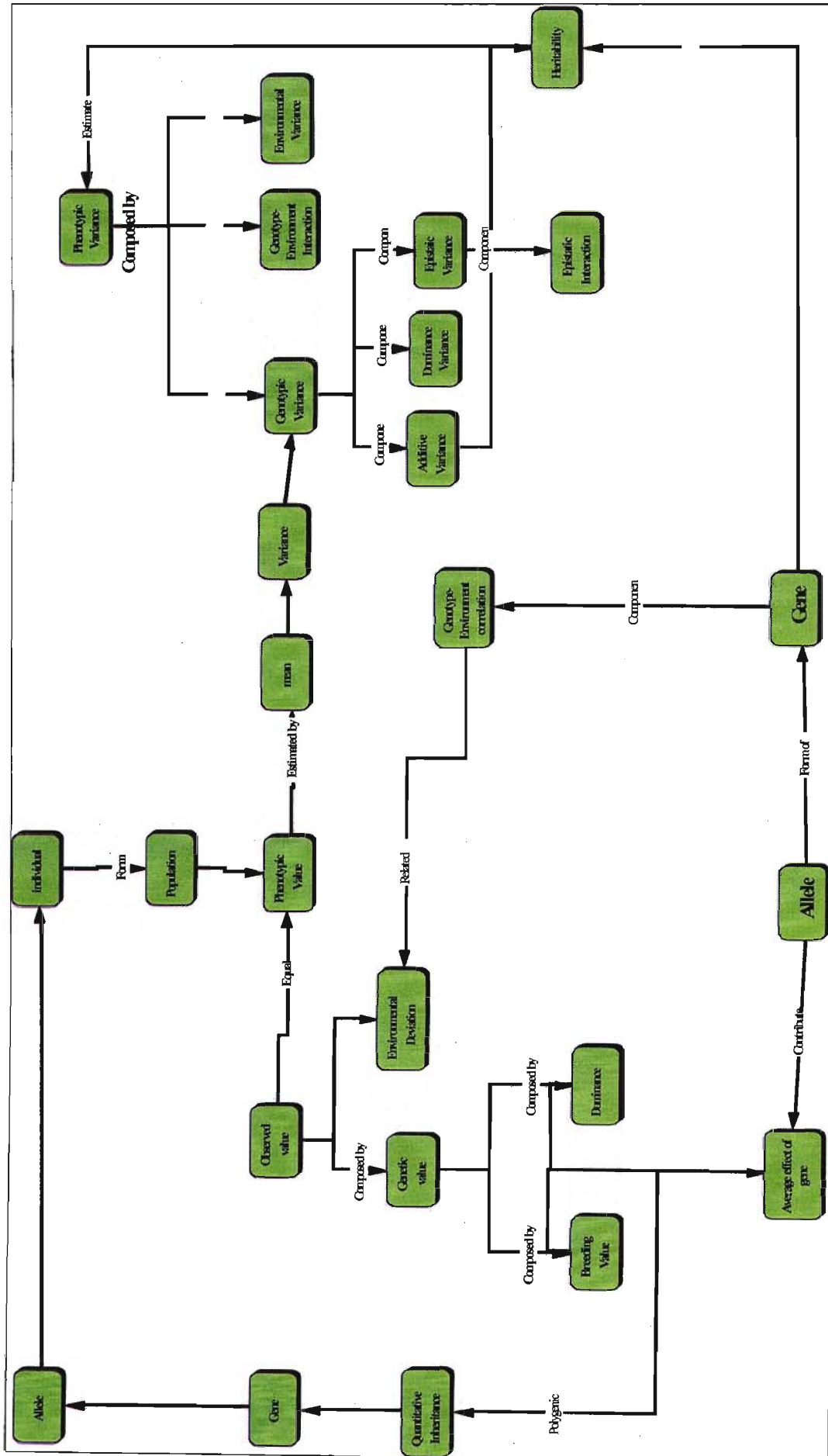


Figure 8.8: Student-generated concept map 3.

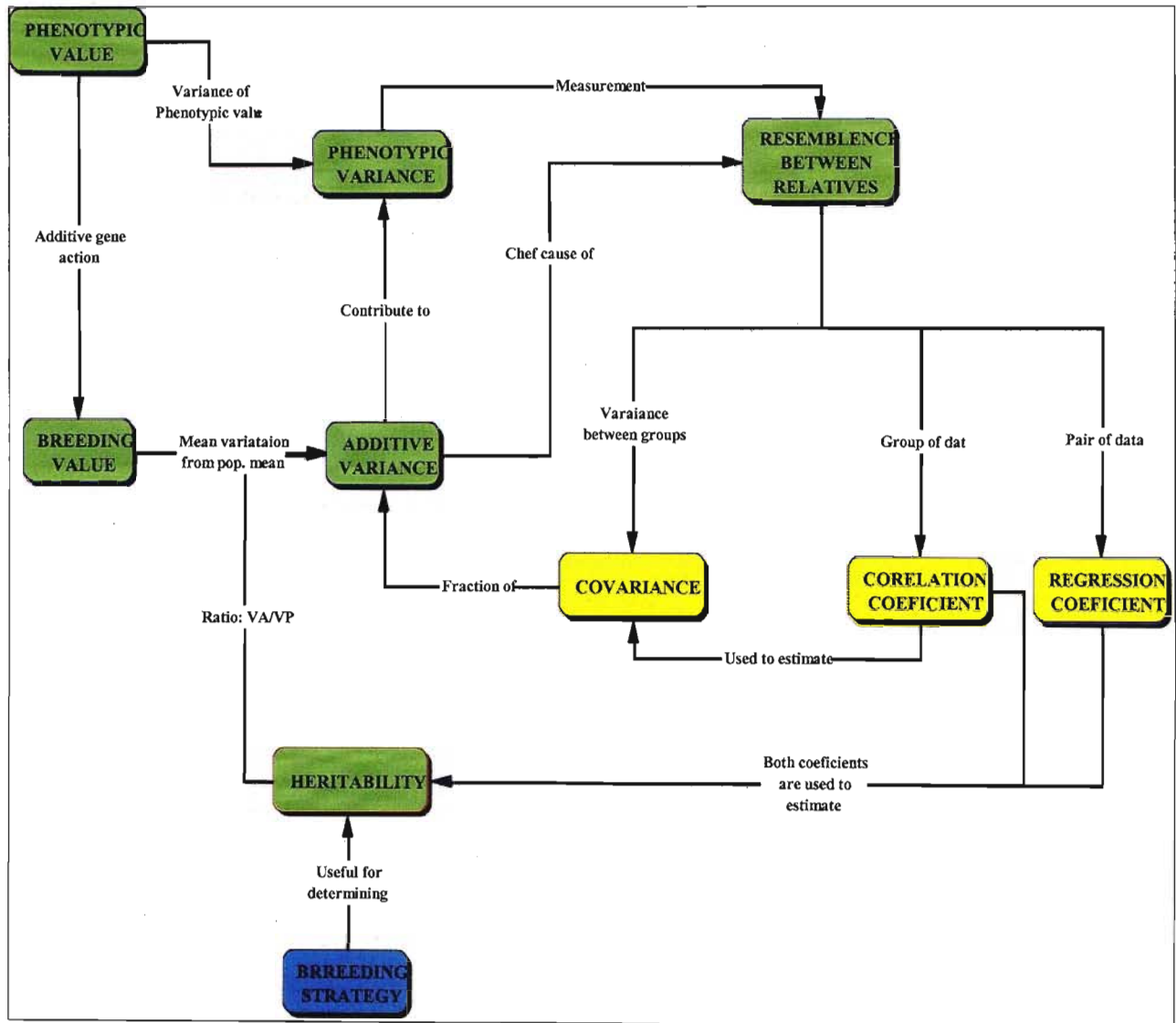


Figure 8.9: Student-generated concept map 4.

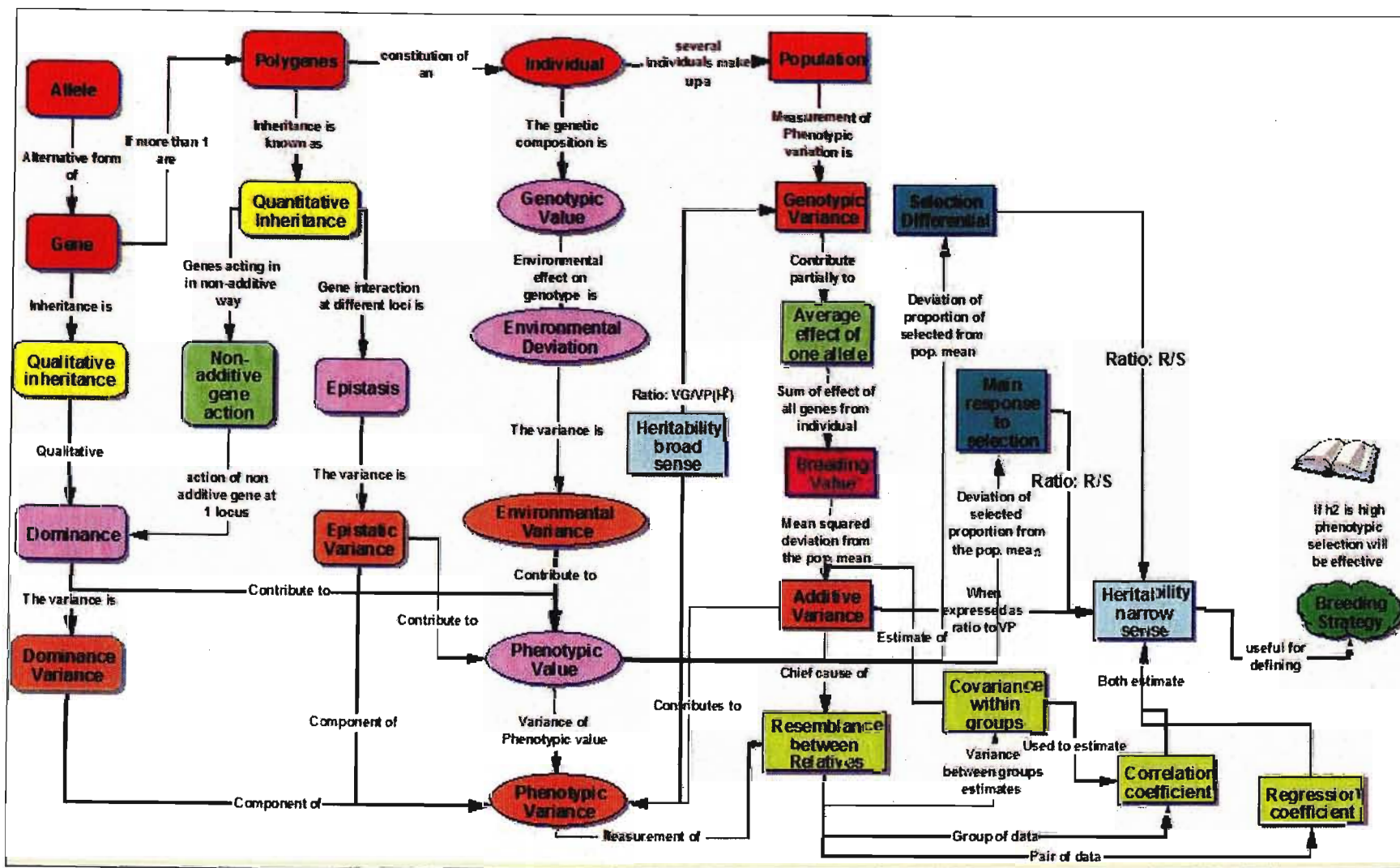


Figure 8.10: Student-generated concept map 5.

### 8.3.3 Nature of conceptual change

Conceptual change was viewed from the following three perspectives:

(a) epistemological, (b) ontological and (c) affective.

#### (a) *Epistemological perspective*

Tyson *et al.* (1997) refer to two types of conceptual change, *revolutionary* and *evolutionary*, both of which were observed in this investigation. Firstly, there were changes of a *revolutionary* nature, where it became evident in later concept maps constructed by certain students that a previously held alternative conception had changed to a conception which could be classified as correct. This type of change will be referred to in this thesis as *conceptual exchange*. Secondly, changes which were *evolutionary* in nature and which showed an increase in the amount and the depth of knowledge were also observed. Where a previously missing link was made in subsequent concept maps constructed by a student, the change will be referred to as *conceptual capture*. Alternatively, where a link became more clearly defined over time the change will be referred to as *conceptual development*.

#### *Conceptual capture or development*

*Conceptual development* and *conceptual capture* accounted for 82% of the changes in link classification found in the twenty sets of concept maps which were analysed. Table 8.2 contains the classification of the links for all the twenty sets of concept maps constructed by students during the module where some sort of *conceptual capture or development* occurred.

A synthesis of the results in Table 8.2 suggests that *conceptual development*, where a conception became more clearly defined, accounted for 43% of the developmental changes which were found in the student-generated concept maps. In this case the classification of the links changed from correct, emerging and a fact given (1iib) to correct, defined and a fact given (1ib). *Conceptual capture* occurred throughout the module and accounted for 57% of the assimilation of knowledge during the semester. In this case, the classification of the links changed from missing (3) to correct (1).

**Table 8.2: Classification of links where *evolutionary* change (conceptual development or conceptual capture) occurred in each of the 20 sets of concept maps over time.**

Set of 5 maps	Link 1	Link 2	Link 3	Link 4	Link 5	Link 6	Link 7	Link 8	Link 9	Link 10	Link 11	Link 12
1		1iib-1ib		1iib-1ib					1iib-1iic	1ib-1ic		
2	1iib-1ib	3-1ib	3-1ib						1iic-1ia			
3					3-1ib	3-1iib	3-1ib				1iib-1ib	1iib-1ib
4				1iib-1ib								1iib-1ib
5		3-1ib			3-1ib							
6	1iib-1ib	1iib-1ib	1iib-1ib				3-1ib	3-1ib	1iic-1ib			
7		3-1iib	1iib-1iic						1iic-1ia			
8	3-1iib		3-1iib								1iib-1ib	1iib-1ib
9			3-1iib									
10			3-1iib		3-1iib							
11								3-1ib	3-1ib			
12		3-1ib		1iib-1ib					3-1iib			
13								3-1ib				
14				3-1iib								
15												
16		3-1ib			3-1ib							
17												
18			3-1ib									
19	1iib-1ib		3-1ib							3-1ib	1iib-1ib	1iib-1ib
20					3-1ib				3-1iib			

An example of *conceptual development* can be seen in Figure 8.11 which is taken from the first two maps constructed a by student. In map 1 qualitative and quantitative inheritance are both seen as being “involved with genes”. However, in map 2 the relationships are more clearly defined and qualitative inheritance is related to single genes and quantitative inheritance to many genes.

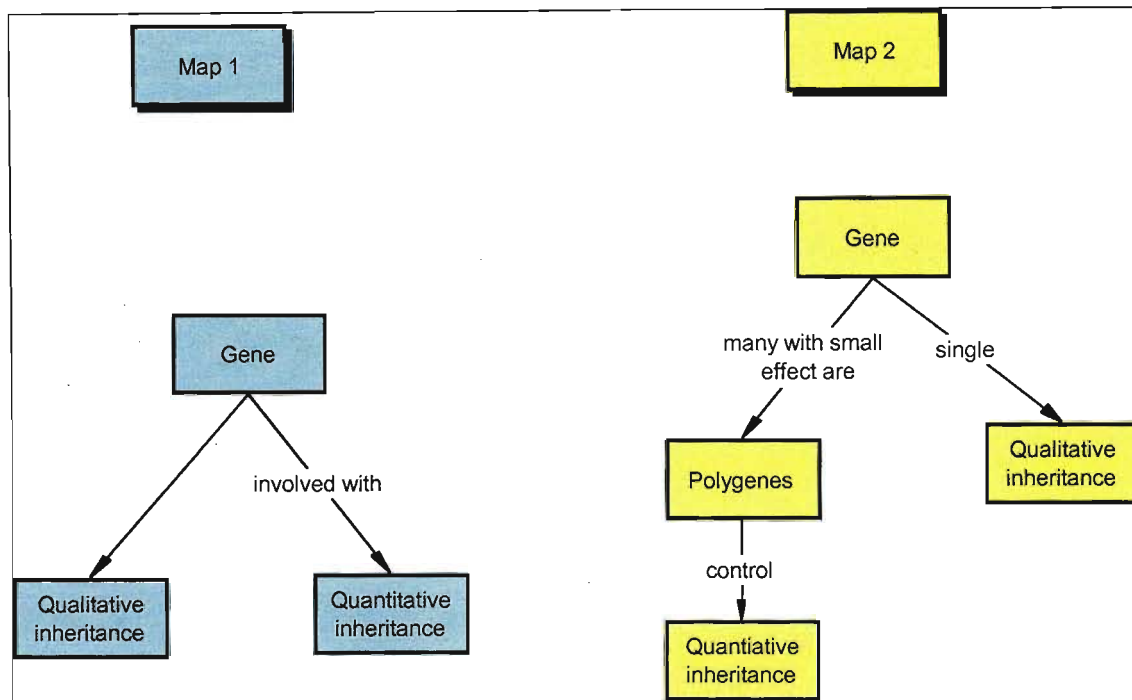


Figure 8.11: Illustration of conceptual development.

An example of *conceptual capture* may be seen in Figure 8.12. The student who constructed this set of concept maps did not, in map 2, relate the phenotypic value of individuals to descriptive statistics in any way. However, in map 3 the same student related the phenotypic value to both the mean and variance of a population.

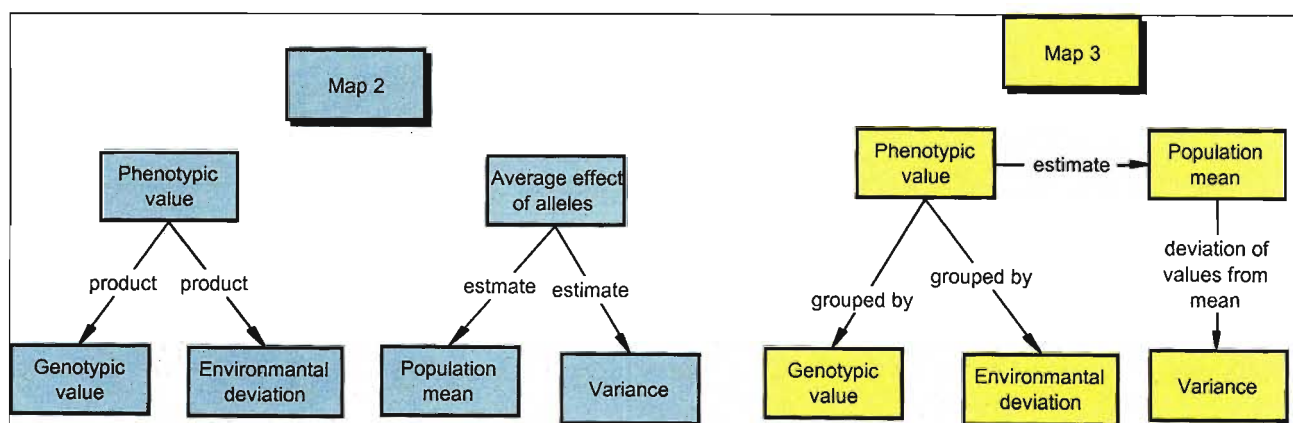


Figure 8.12: Illustration of conceptual capture.

The number of students that showed either *conceptual development* or *conceptual capture* for each of the relationships studied is summarised in Table 8.3. From the



results in Table 8.3 it is evident that *conceptual development* or the refinement of knowledge primarily occurred for linkage relationships 1-4 which represent concepts which are learnt near the start of the module and links 11 and 12 which are taught towards the end of the module. This may be because at the beginning of the module the students may have reflected on their knowledge and formed relationships between their prior knowledge and newly introduced ideas. The change which occurred at the end of the module may have been due to students wanting to consolidate their knowledge before the examination process.

**Table 8.3: Summary of number of students that illustrated *conceptual capture* or *conceptual development* for each linkage (relationship) studied. (n=20)**

Type of change	Link											
	1	2	3	4	5	6	7	8	9	10	11	12
Conceptual development	3	2	2	4	0	0	0	0	3	1	3	4
Conceptual capture	1	6	6	1	5	1	2	3	3	1	0	0

### *Conceptual exchange*

*Conceptual exchange* accounted for 18% of the changes detected in the student-generated concept maps. An example of *conceptual exchange* may be seen in Figure 8.13. In this set of maps the student initially incorrectly states that the breeding strategy determines the heritability (map 4) whereas in a map constructed later in the module (map 5) the student correctly states that it is the heritability that determines the breeding strategy. In addition, the student later included a comment on what may be inferred from high and low heritability values. (This example of conceptual exchange is also documented in Table 8.4 under map set 10 and link 9).

Table 8.4 shows the eleven types of difficulty which students exhibited when the links were classified as incorrect. These primarily included an initial confusion between qualitative and quantitative inheritance and confusion between individual and population parameters. It is interesting to note that only approximately 50% of incorrect relationships were corrected in later concept maps constructed by the same student. This finding confirms those discussed in Chapter 7 that notwithstanding the success of the intervention, some students still held alternative conceptions at the completion of the module.

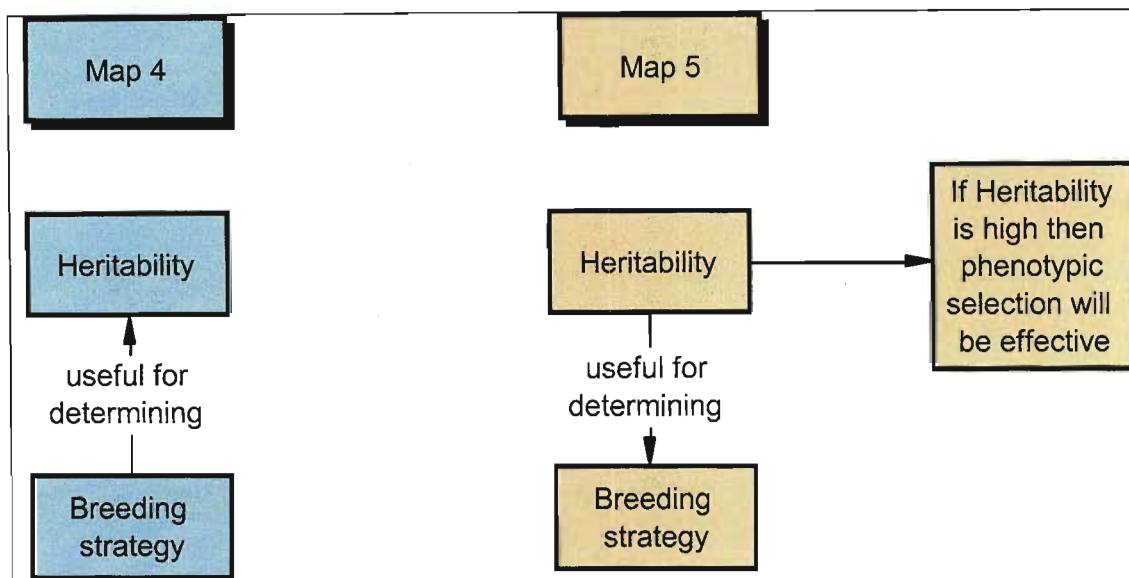


Figure 8.13: Illustration of conceptual exchange.

Table 8.4: Classification of incorrect linkages made by students. (n=20)

Map set	Link 1	Link 2	Link 5	Link 7	Link 8	Link 9
1						
2						
3		Initial confusion between quantitative and qualitative inheritance				Incorrect application of resemblance between relatives
4						
5						
6						
7				Initial confusion between values and variances		
8			Association of genotypic value with frequency. Changed to $G = A+D+I$		Initial confusion between values and variances	
9						
10	Initial confusion between quantitative and qualitative inheritance	Confusion between values and variances				Incorrect arrow direction which was corrected
11		Confusion between values and variances			Initial confusion between values and variances	
12 - 20					Initial confusion between $h^2$ and BV	
<b>Total</b>	<b>1</b>	<b>3</b>	<b>1</b>	<b>1</b>	<b>3</b>	<b>2</b>

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Numerous studies have examined changes in students' knowledge over time and have reported, as in this investigation, that most of the changes which have been observed have been of the *evolutionary* type. For example, in a study which employed an analogical teaching approach to bring about conceptual change, Treagust *et al.* (1996b) found that most conceptual change did not include an *exchange* of one conception for another, but rather that students began to more frequently use a conception which made sense to them. This situation was also found in an in depth case study conducted by Taber (2001) where a college level chemistry student began to more frequently use a particular conception of chemical bonding over time as it had greater explanatory power than other conceptions held by the student. Similarly, Pearsall *et al.* (1997) and Martin *et al.* (2000) both examined college level biology students' understanding of certain topics over time and found that up to 75% of the knowledge restructuring which took place was incremental in nature and where radical restructuring of knowledge occurred it primarily took place during the first few weeks of the course.

Hewson and Lemberger (2000) comment that as most of the conceptual change which is observed in classrooms is evolutionary in nature, educators must realise that not all prior knowledge held by students is problematic. In fact, as one's prior knowledge is the foundation for any future learning, it is the student's epistemological view of a conception (its status) that will determine whether the student expands on their existing conception or whether it is replaced by another conception; a situation they found in a study on high school students' conceptions of the concept of a gene. In a further study on students' perceptions of a gene, conducted by Venville and Treagust (1998), the researchers also found that the conceptual changes which occurred were mostly due to a process of raising the status and thus use of certain conceptions. The changes observed were therefore of the weaker form where previous conceptions were not replaced, but merely elaborated.

#### *Students' perceptions of variance and heritability*

As both *variance* and *heritability* had previously been identified as concepts which students found difficult to grasp (details given in Chapters 4 and 5), the manner in which students' epistemological understanding of these concepts changed over the semester was investigated in more detail. Links 3 and 4 were examined with respect to students' understanding of the concept of variance and links 8 and 9 with respect to their understanding of heritability. The results of this analysis are presented in Table 8.5.

**Table 8.5: Number and percentage of students who demonstrated conceptual change of an epistemological nature with regard to the concepts of variance (links 3 and 4) and heritability (links 8 and 9). (n=20)**

Classification of conceptual change	Variance	Heritability	Epistemological status at completion of module
No change (1ib)	13 (65%)	3 (15%)	Intelligible
1ib – 1ic	7 (35%)	8 (40%)	Plausible
1ic – 1ia	0	5 (25%)	Fruitful
2 – 1ib	0	2 (10%)	Intelligible
2 – 1ic	0	1 (5%)	Plausible
2 – 1ia	0	1 (5%)	Fruitful

At the completion of the module, the concept of variance seemed to be intelligible for 65% of students (Table 8.5) as they were able to give accurate definitions of the concept and relate descriptive statistics and histograms. 35% of students seemed to find the concept plausible in that they not only linked the concept of variance to histograms but also to other concepts such as heritability.

With regards to the concept of heritability (Table 8.5), 25% of students found the concept intelligible in that they knew a definition and equation for the concept. 45% found the concept plausible in that they could relate heritability to a practical outcome – the selection of a breeding strategy and for 30% of students the concept appeared fruitful as a high or low heritability value was linked to specific breeding strategies. When these results are compared to those presented in Chapter 4, where heritability was identified as a *critical concept* as 71% of students could not link heritability to a breeding strategy, 65% of the students who participated in the intervention were able to make this link. The intervention thus seems to have effectively addressed the previously identified problem of heritability being a concept which created a barrier to the learning of higher order concepts in quantitative genetics for most of the students.

That key conceptions became fruitful for some students was also found in a study on whether students' understanding of human and molecular genetics could be enhanced through the use of multiple external representations and the *Biologica* software. In this study, Tsui and Treagust (2002) found that the higher achievers reached the level where some conceptions were intelligible, plausible and fruitful to the students.

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From an epistemological perspective, it may be concluded that most of the conceptual change which occurred was *evolutionary* in nature and thus involved a process of *conceptual development* or *conceptual capture*. Furthermore, the results suggest that students' knowledge of the concepts of *variance* and *heritability* improved over the course of the module.

**(b) Ontological perspective**

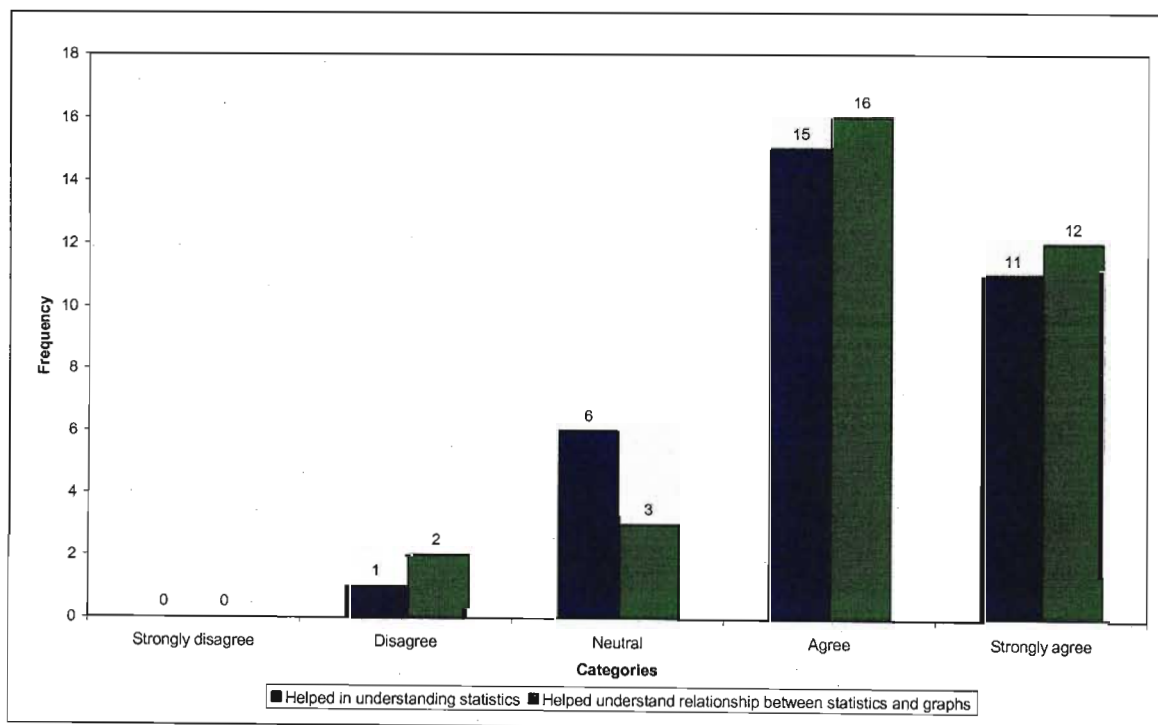
Students' knowledge of the *critical concepts* of *variance* and *heritability* were analysed from an ontological perspective. With regard to the ontological status of the concept of variance; 65% of students' knowledge seemed to remain more algorithmic in nature in that they merely knew the equation or formula. It was thus classified as *passive*. For the 35% of students who identified linkages with concepts such as heritability and the selection of a breeding strategy, the ontological status was classified as *active* as these students saw the concept as being useful in many applications. With regard to the concept of heritability, 75% of students saw some connection between heritability and a practical outcome, indicating that the concept could be described as *active* for these students. This result suggests that the concept of variance may also have been *active* for up to 75% of students. It was not possible to verify this result as fifteen of the twenty of the students left out links 3 and 4 in map 5. As 75% of students found the concept of heritability *plausible* or *fruitful*, they must have had a good grasp of the concept of variance, the concept identified as representing one *critical concept* in the module. Thus the primary ontological change which seemed to occur with respect to students' understanding of these concepts is that their status changed from *passive* (rote learning of equations and definitions) to *active* (students had knowledge of the possible application of the concepts).

A similar conclusion was reached by Venville and Treagust (1998) in a study on students' conceptions of the concept of a gene. In this case, Grade 10 students' conceptions changed over a 10 week period from thinking of a gene as a *passive* particle passed from parents to offspring to considering a gene as an *active* particle that controls the expression of characteristics. In the study conducted by Tsui and Treagust (2002), mentioned previously, it was found that most students' perceptions remained in the ontological category of matter, with the conceptions of a few students changing from the ontological category of matter to process.

**(c) Affective perspective**

The attitudinal questionnaires given to the students at the commencement and completion of the module indicated that in general students felt more positive about their understanding of certain descriptive statistics and their relationship to graphical representations as well as their understanding of quantitative genetics at the completion of the module. The majority of students also had a more positive attitude towards the subject of quantitative genetics at the completion of the module. These results are encouraging as Pintrich *et al.* (1993) point out that it is not sufficient to view conceptual change from purely ontological and epistemological perspectives as certain motivational constructs such as students' goals, values and beliefs will all influence their desire to alter any of their currently held conceptions. Kang *et al.* (2005) also commented after conducting a study with 159 seventh grade students in Korea that in order for conceptual change to occur students had to recognise the relevance and importance of new information.

With regard to the computer-based tutorials, it is clear from Figure 8.14 that most of the 33 students, who completed the attitudinal questionnaire at the completion of the module, agreed that the computer-based tutorials had assisted them to better understand fundamental statistics and the relationship between descriptive statistics and graphical representations.



**Figure 8.14: The frequency of student responses to questions on their feelings about their understanding of statistics and graphical representations. (n=33)**



Further benefits of the computer-based tutorials were described by students in the free-response open-ended questions in the attitudinal questionnaires. These included the fact that the graphics assisted students to visualise the concepts, the tutorials made the concepts seem easy, the tutorials enabled students to appreciate the practical aspects of quantitative genetics and that the tutorials were fun and gave them sufficient time to master difficult concepts. The quotes given in Table 8.6 highlight the fact that the tutorials helped the students visualise the concepts, made the concepts seem easier and more relevant, and that the tutorials were enjoyable.

**Table 8.6: Quotes indicating students positive feelings about the computer-based tutorials.**

Benefit of computer-based tutorials	Student quotes
Helped to visualise concepts	<ul style="list-style-type: none"> <li>• “Nice to be able to see changes i.e. when altering <math>V_E</math> what happened to the distribution.”</li> <li>• “They were helpful in that you got a <i>better picture</i> in your head about the concepts.”</li> <li>• “The computer-based tuts were very helpful. Helped to see <i>things</i> in more graphical terms and understand the stats behind it as well.”</li> <li>• “I have particularly enjoyed the variation and heritability tutorials. They gave me a <i>pictorial description</i> of terms like heritability, high versus low heritability, normal distribution and quantitative traits.”</li> <li>• “They are very helpful because you <i>observe</i> what changes take place in terms of statistical measures.”</li> <li>• “I enjoyed the computer-based tuts and I thought they did help in that you could see <i>the relationship</i> between things e.g. if you increased the environmental effect and heritability decreased – what happened to the breeding values and phenotypic value etc.”</li> <li>• “I personally found the computer tutorials beneficial as they supplemented the lectures and introduced the concepts in a different way. It was helpful to <i>visualise</i> the practical uses of the concepts.”</li> </ul>
Made the concepts seem easy and applicable to real life	<ul style="list-style-type: none"> <li>• “Did enjoy them because it made understanding the genetics <i>much easier and more enjoyable</i>.”</li> <li>• “They made it <i>easier to link concepts</i> like heritability, additive variance and environmental variance. It also made it easier to link these concepts to a population.”</li> <li>• Helped in the understanding of concepts by showing practical application of concepts</li> <li>• “These tutorials helped by placing quantitative genetics into perspective. They gave an overall, <i>practical understanding</i> in terms of why quantitative genetics is used and of importance.”</li> <li>• “I did enjoy the computer tutorials because they show exactly what we have learned in the class, I got a chance to see <i>it practically</i> and then begin to understand the topic.”</li> <li>• “I really enjoyed the heritability tut – especially seeing how changing different values affected the graphs. This tut really helped me a lot.”</li> <li>• “They were well organised and <i>gave more meaning</i> to what was covered in lectures.”</li> </ul>
Exciting and fun	<p>“Computer tuts were exciting and fun. They helped me in a way that when I did not understand a thing I could take a long time redoing it until I knew what was going on.”</p>

These results were confirmed by the following comments made by the students who were interviewed. One student commented that the one tutorial had helped him understand the concept of heritability because changes in the statistic could be viewed in a graphical format.

- I: "You have improved enormously over the semester. Did you just not learn for the first test or what?"  
S: "The first test came at a bad time and I understood the heritability section a lot more, especially after doing that computer tutorial."  
I: "In what way did the tutorial help you?"  
S: "I liked the graphs. Being able to change things and seeing how it affected the graphs. That helped a lot and I could think of that during the class test."

Another student agreed that the tutorial which had focused on heritability had helped her understand the concept.

- I: "Do you think the computer tutorials were better than the pen-and paper ones we did?"  
S: "Definitely. Like that heritability one. That was the cherry on the top – after all the lectures, it really helped me to understand."

Two further students commented on the fact that the tutorials made the work seem more relevant to everyday life. The one said:

"Yes, I think they made a huge difference. I think part of the reason I did so well in the second test was the computer tutorial we did on heritability. Because you can take that and it makes you think of what is happening, because you have to write those answers down. Also you can relate it almost to real life situations because you've got a population in front of you and you can see how they change and how if you change one thing, like the heritability will change and if you change the allele frequencies what will happen."

The other student commented:

"Yes, 'cause I got a chance to see what you were talking about in class. Like when you were saying if the heritability is high then the phenotypic values are a good indication of the breeding values. I would take it as that – that what you were telling me. But when we are doing those tutorials I just got the chance to see it and it proved that you were correct."

The only negative feedback given was that two students found the tutorials easy and less constructive than regular, pen-and-paper tutorials. One student said:

"I enjoyed them but found them quite easy. They did make some of the concepts much clearer, but I find I learn more from the regular tutorials (pen and paper)."

Other studies have similarly reported that students enjoy computer-based exercises. For example, Eichinger *et al.* (2000) found during a two year study biology students' perceptions of computer laboratories, that students generally liked the visual images created by the software and that they were happy to use computers as they recognised the need to be computer literate when working in the field of science. Tsui and Treagust (2002) also noted the software used in their investigation seemed to

not only improve the genetics reasoning ability of students but also their levels of motivation. In the area of statistics education Schuyten and Dekeyser (1997) recorded that the software used in their study seemed to have a positive impact on students' understanding of statistics and that 30% of the students reported that the software had improved their attitude towards the subject.

With regard to the concept mapping exercises, students responded to a free-response question in the attitudinal questionnaire that they had enjoyed using the *Inspiration software* (1997), that concept mapping had played a positive role in that they were forced to reflect on their knowledge. Furthermore, the concept mapping exercises had helped them identify key concepts and to better understand the subject matter. Thus the concept mapping exercises which addressed students' understanding of quantitative genetics successfully encouraged the students to practice what Georghiades (2004a) describes as *situated metacognition*. This is encouraging as although the long term retention of knowledge was not examined in this investigation, a recent study of primary school childrens' conceptions of electricity revealed that children who made use of metacognitive activities, including concept mapping, retained the knowledge taught over a long period of time (Georghiades 2004b). In another study conducted by Liu (2004) where grade 12 chemistry students made use of the *Inspiration software*, many students thought that concept mapping had been beneficial to their learning experience and that it had aided them in seeing how concepts were related. In fact, Novak (2003) comments that the use of computer software for creating concept maps is the way of the future. A sample of quotes which echo these sentiments and which were given by students in the investigation described in this thesis is given in Table 8.7.

**Table 8.7: Quotes indicating students' positive feelings about the concept mapping exercises.**

Benefits of concept mapping exercises	Student quotes
Benefits of Inspiration	<ul style="list-style-type: none"> <li>• "Inspiration was easier and preferable to drawing on paper."</li> <li>• "I did enjoy using Inspiration software as you could add colour, change things around, add pictures."</li> <li>• "I enjoyed using Inspiration software. The technology was very easy to utilise."</li> <li>• "The software was very easy to understand. It is much preferred instead of drawing a map on paper. The software has many interesting features."</li> <li>• "Inspiration is a very valuable and user friendly programme. I enjoyed using it."</li> <li>• "The software was <b>good</b>. It allowed you to correct mistakes without redrawing the whole map. It made pretty maps!"</li> </ul>
Concept mapping acted as a metacognitive tool	<ul style="list-style-type: none"> <li>• "It made me read my notes more often than I would have. It <i>made me make links and draw comparisons</i> between important concepts."</li> <li>• "Concept mapping did help me understand the concepts as it <i>made me think</i> about and understand the relationships between concepts."</li> <li>• "Although it was tough to construct the concept maps but <i>I was forced to think</i> of the way I could link the concepts."</li> <li>• "Concept maps did make understanding easier because they <i>force you to understand</i> and look at your notes."</li> <li>• "It made us go over our notes and you had to have an understanding of the concepts before you could complete the map."</li> </ul>
Concept mapping helped in the identification of key concepts	<ul style="list-style-type: none"> <li>• "It gives you an overall picture of each section. This helps you focus on the aspects that are important. Now you know what to concentrate on when it comes to studying for the exams."</li> <li>• "They made revision for tests much easier."</li> </ul>
Concept mapping helped in understanding quantitative genetics	<ul style="list-style-type: none"> <li>• "Concept mapping helped me understand clearly the relationships between concepts of quantitative genetics. This helps in the computation of population parameters."</li> <li>• "Concept mapping was wonderful, it helped a lot in understanding concepts in quantitative genetics. This is something I will keep from this university – not only for genetics but other disciplines also."</li> <li>• "Showing us your concept maps after giving ours back helped in the understanding of where we were going wrong. Your comments on our maps were also very helpful."</li> </ul>

Seven of the eight students interviewed at the end of the module felt that the concept mapping exercises had been beneficial in that they had forced them into finding the links between concepts and helped them to make a "story" out of the theoretical component of the course. These factors are illustrated in the following excerpts from the interviews with students.

One student said that the concept mapping exercises had helped her understand certain ideas by making her think of the relationships between concepts.

I: "Did the concept mapping help at all?"

S: "Yes, I think so."

I: "In what way do you think it helped you?"

S: "I think getting your feedback from the concept maps helped a lot, to see where we were going wrong. And the whole breeding value, additive gene action thing took me a long time to get. I'm not sure if I even get it now but its better."

I: "If you hadn't done the concept maps – if I had not made you do it, do you think you would have progressed so far?"

S: "I don't think I would have realised how concepts link up. 'Cause I wouldn't have gone and done a concept map by myself otherwise."

I: "And your brain would not have necessarily have connected things?"

S: "I wouldn't have made the connections."

Another student said that the concept mapping exercises had encouraged him to revise his work.

I: "And the concept mapping – did it help you at all?"

S: "Yes. It just helps you put concepts together because you have to sit down and go through your notes."

I: "So if I hadn't made you do that?"

S: "I definitely would not be as well off as I am."

One student commented that the maps summarised the data by "making a story" about the contents of the map. She said: "The maps made like a story for myself in a way. So even though they are just points linked with lines, it is done in such a way that you can link the concepts and just by having the concept map in front I could tell a whole story about it.

The only negative feedback, highlighted by the following quotes, was that a few students found the concept mapping exercises time-consuming and at times they became confused when constructing their maps. These results do however, also indicate that concept maps are powerful metacognitive tools which require students to spend time reflecting on the status of their own knowledge. These students would obviously rather have been doing something else!

- "Took some time to get used to them – not the way I would usually learn."
- "I found that the maps actually confused me even more."
- "I was usually just as confused after drawing the maps. Eventually, though I did find that some of the terms were getting firmly engrained in my memory from using them so much and thinking about them so much."
- "They would have been helpful if it was done as a class exercise. However, because we had to do them in our own time we didn't put the time and planning into them that would make them beneficial to our understanding."
- "I think they could have helped if we had enough time but we had so much other work."

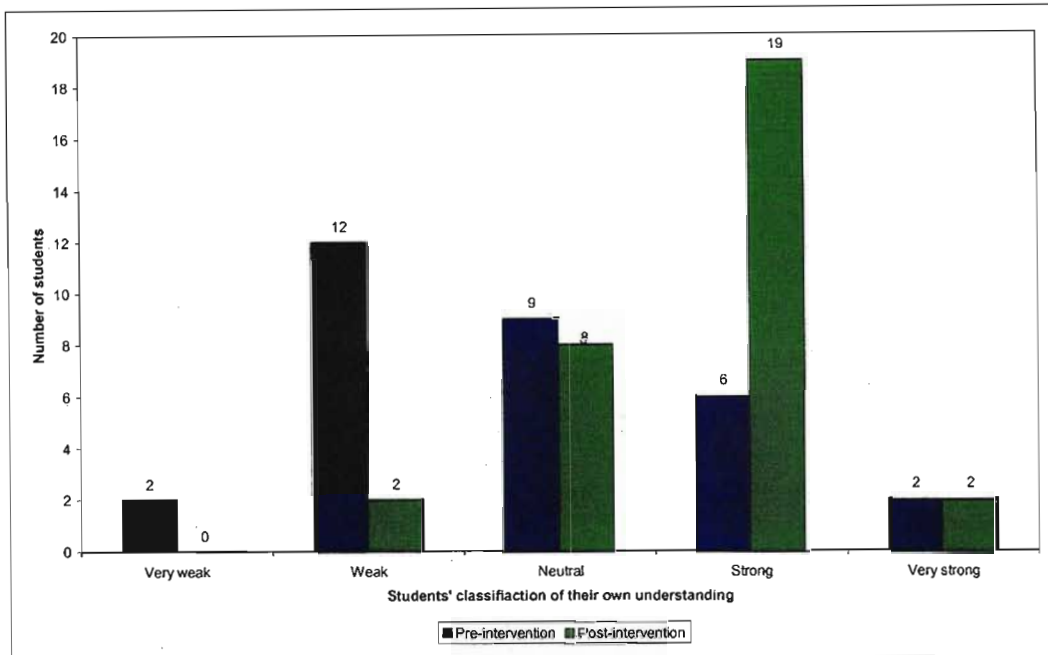
The fact that some students felt that they did not have the time for the concept mapping exercises is not surprising as Trowbridge and Wandersee (1994) reported a 37% increase in the time students spent studying for a module on evolution where

the students were required to construct concept maps throughout the course. These researchers felt this was very encouraging as students were reflecting on their knowledge, not just before tests and exams, but throughout the module. Briscoe and LaMaster (1994) also comment after conducting a study on college level biology students who were asked to construct a series of concept maps that some students initially found the move to concept mapping difficult. However, once they had mastered the technique the students felt that it had helped them identify concepts that they did not understand fully, it helped them organise their knowledge and as they revisited their maps the retention of their knowledge increased. Similarly, Allen and Tanner (2003) found over seven years of teaching cell biology to students with the aid of concept mapping exercises that even students who were initially reluctant to use the technique later enthusiastically participated in map construction. In fact Novak (1990) mentions that some research studies have noted that concept mapping ultimately reduced the level of anxiety of certain biology students to subjects of perceived difficulty.

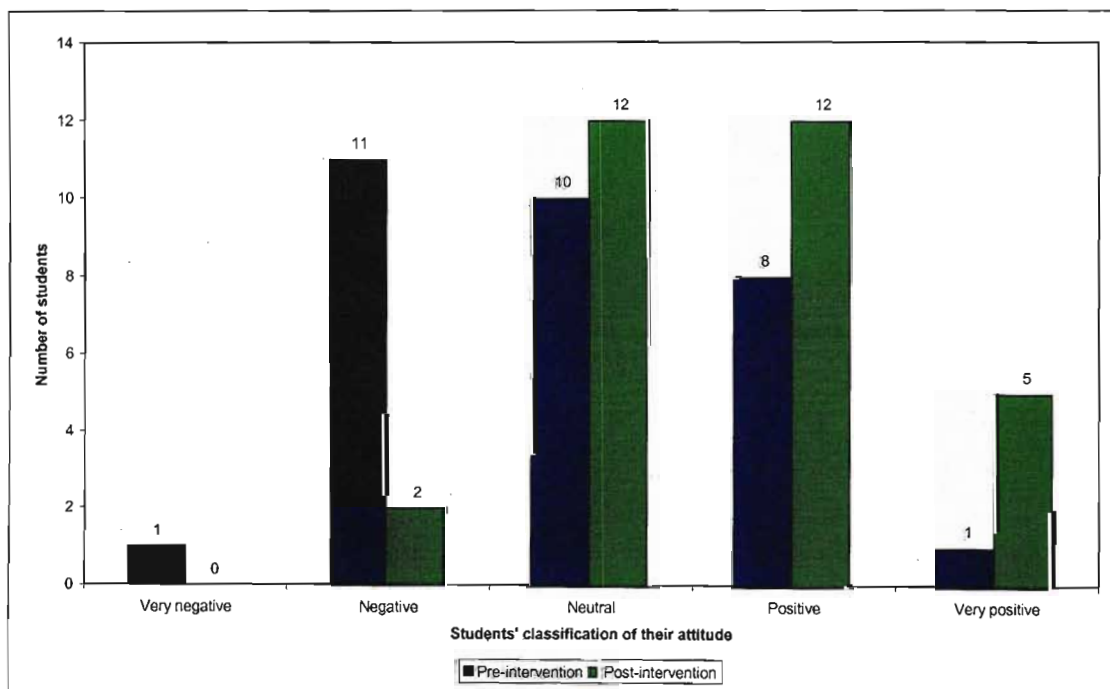
The students also indicated a more positive attitude towards quantitative genetics and an improvement in their perception of their understanding of the subject matter at the end of the module. A total of 31 students answered the Likert-style questionnaires both at the beginning and end of the module. Figure 8.15 highlights the fact that the majority of students rated their understanding of quantitative genetics as strong after the computer-based tutorials and after having constructed a number of concept maps covering the course content. No students thought of their understanding as very weak and substantially fewer students classified their understanding as weak.

Figure 8.16 illustrates that after the teaching of the module, many students felt positive about the subject of quantitative genetics. No students classified their attitude as very negative, substantially fewer students classified their attitude as negative and an increased number of students rated their attitude as very positive.





**Figure 8.15:** Student responses to questions on their feelings about their understanding of quantitative genetics before and after the intervention. (n=31)



**Figure 8.16:** Student responses to their attitude towards quantitative genetics before and after the intervention. (n=31)

#### **8.4 CONCLUDING REMARKS**

The results presented in this chapter indicate that conceptual change was examined from three perspectives. (1) An epistemological perspective where most changes were of the *evolutionary* form. Furthermore, many students' perceptions of the concepts of variance and heritability changed from *intelligible* to *plausible* and for some students the conceptions became *fruitful*. (2) An ontological perspective where many students' conceptions changed from *passive* to *active*. (3) An affective perspective where the majority of students expressed the view that both the computer-based tutorials and the concept mapping exercises had been beneficial and that their attitude towards and understanding of quantitative genetics had improved over the semester.

## CHAPTER 9

# GENERAL DISCUSSION AND IMPLICATIONS OF INVESTIGATION

### 9.1 INTRODUCTION

This investigation was motivated by the observation by the researcher that students have traditionally found the field of quantitative genetics particularly difficult to understand. The researcher thus aimed to gather empirical evidence on students' conceptual frameworks and their ability to link key concepts in quantitative genetics. It further aimed to ascertain what difficulties and alternative conceptions were held by students in the context of quantitative genetics. Once this diagnostic phase had been completed, the researcher developed an intervention which consisted of a series of computer-based tutorials and concept mapping exercises which were designed to address the previously identified difficulties and alternative conceptions. The results of the investigation have shown that students do in fact have difficulty with this subject area and many students hold alternative conceptions of concepts learnt during a quantitative genetics module, particularly the concepts of *variance* and *heritability* as well as the construction and interpretation of histograms. The results of the remediation phase of the investigation showed that the intervention used was successful and, in many cases, addressed students' difficulties and alternative conceptions in this field. Furthermore, the results suggested that conceptual change occurred in the cognitive frameworks of several students when viewed from an epistemological, ontological and affective perspective.

### 9.2 SUMMARY AND DISCUSSION OF RESEARCH FINDINGS

#### 9.2.1 Research question 1

What is the nature and extent of students' integrated knowledge and their ability to link key concepts of quantitative genetics?

Student-generated concept maps as well as concept maps generated by the researcher from student interview transcripts were used in the diagnostic phase of

the investigation to ascertain whether students were able to integrate their knowledge of, and to link key concepts of, quantitative genetics in the module under investigation. Two concepts were identified by the researcher in the *Introduction to Quantitative Genetics* module as being of particular importance. These were the concepts of *variance* and *heritability*. Knowledge of *variance* was seen to be important as a sound knowledge of this concept was required before students could comprehend why it is that the phenotypic values of most quantitative traits are normally distributed. Students also had to fully understand the meaning of the phenotypic variance before they could appreciate that this value is made up of a number of components, those that are influenced by the genetic make-up of individuals (additive and non-additive variance) in the population in question and those which are influenced by environmental factors (environmental variance), the ratio of the additive variance and the phenotypic variance giving the heritability of a trait. *Heritability* was identified as a second important or key concept as knowledge of this concept was required before students could understand that this population parameter allowed them to decide whether, on average, the phenotypic values of individuals were a good indication of their breeding values. This knowledge being required by geneticists as the breeding values of individuals, which are not readily measurable, provide an indication of what the average value of the individual's offspring will be and thus indicate whether any individual will produce offspring with a particular phenotype. Knowledge of the *heritability* of a trait is thus needed before students are able to apply many of the principles of quantitative genetics.

As in this investigation, other researchers have used student-generated concept maps to identify the level of integration of students' knowledge in statistics modules (Schau and Matter 1997), marine biology (Martin *et al.* 2000) and physics (Van Zele 2004). The results of these studies suggest that good integration of knowledge is necessary before full understanding of the subject area could be achieved. In addition, missing relationships and a lack of cross-linkages between concepts in student-generated concept maps indicate a lack of knowledge integration and the possible presence of concepts, known as *critical concepts*, knowledge of which is required for the learning of higher order concepts. Kinchin (2001) moreover suggested that the structure of the student-generated concept maps would indicate the level of knowledge integration where the *spoke* and *chain* map types show little integration. Building on the findings of these researchers the concepts of *variance* and *heritability* were identified as *critical concepts*. The criteria used for the identification of *critical concepts* in this investigation included a classification of the map type (*spoke*, *chain* or *net* type) as well as the identification of *missing* or *incorrect* linkages which consistently occurred in many different students' maps.

Furthermore, an analysis of the student-generated concept maps indicated that knowledge of the concepts of *variance* and *heritability* was required before students were able to practically apply their knowledge of quantitative genetics.

Trowbridge and Wandersee (1994) used student-generated concept maps to identify the presence of critical junctures or stages in a module where students must have an understanding of *critical concepts* before they can grasp new concepts. These researchers identified critical junctures by students' choice of the superordinate concept at different stages in a module. However, in this investigation the researcher merely suggested that the beginning of the module represented one critical juncture as it is at this time that students must have knowledge of *variance* before they can learn the principles of quantitative genetics. The second critical juncture would occur at the time the concept of *heritability* is introduced to students as knowledge of heritability is required before students are able to apply the principles of quantitative genetics in practice.

Once *variance* and *heritability* had been identified as *critical concepts*, the next cycle of the research focused specifically on the difficulties students had with these concepts as well as any alternative conceptions held by students with regard to these and other related concepts.

### 9.2.2 Research question 2

What concepts in quantitative genetics do students find difficult?

Two multiple-choice diagnostic tests and interview protocols were developed by the researcher to gather data on student difficulties and alternative conceptions at two consecutive stages in the teaching of quantitative genetics. The first assessment of students' knowledge occurred at the beginning of the module where students were assumed to have some knowledge of *prior-knowledge concepts* such as variation, variance and frequency distributions. The second assessment took place near the completion of the module once all the basic principles of quantitative genetics had been covered in lectures. Students' knowledge of *quantitative genetics concepts* such as breeding value, additive variance and heritability were investigated at this time.

With regard to students' understanding of *prior knowledge concepts* on entry to a quantitative genetics module, four major difficulties or alternative conceptions were identified.

- (a) Students confused the concepts of variation and variance, primarily because they did not understand the concept of variance.
- (b) Students thought that heterozygous individuals must be present in a population before variation could be observed in the population.
- (c) Students associated the ideas of equilibrium and fully inbred populations with values of zero and one.
- (d) Students showed difficulty in the construction and interpretation of histograms.

An analysis of the data from the multiple-choice diagnostic tests conducted with the *Winsteps software* (2003) and utilising the Rasch model indicted which concepts students found most difficult. Of the items tested at the start of the module, students found the concept of variance and its application most difficult, followed by the interpretation of frequency distributions. Most students seemed to have a sound understanding of the concept of variation and its application.

DelMas and Liu (2005) suggest that measures of variation, such as the concept of variance, are very difficult for students to understand. This is because students must: (1) have a graphical understanding of how the values of the variable in question may be summarised according to the frequency of its values, (2) have a conception that the variable that is under consideration relates to the manner in which values deviate from the mean and, (3) be able to relate descriptive statistics to graphs such as histograms. Students in this investigation were shown to exhibit difficulty with all three of the above-mentioned factors. The results of this investigation thus provide empirical evidence for the claim made by Delams and Liu (2005).

At the completion of the module it was noted that students exhibited difficulty in understanding some *quantitative genetics concepts*. Difficulty was observed in three primary areas.

- (a) Students frequently confused individual values such as breeding values with population parameters such as heritability. Some students thus thought of breeding values, additive variance and heritability as all being individual measures. In addition, some students held the alternative conception that additive variance is something that can be transferred between generations. Other students thought of heritability as being an indication of the proportion of genes passed from parents to offspring.
- (b) Students seemed to confuse the terms *heritability* and *inheritance*. These students tended to associate heritability with bringing about some form of change in a population or of having a particular function.



- (c) Students were not able to link statistics such as variance and heritability to graphical representations. Thus, many students were unable to comprehend *why* the phenotypic values of a population, when plotted in a frequency distribution, are normally distributed. Furthermore, some students could not recognise which of two populations, depicted graphically, would have the higher heritability value for the trait in question.

At the completion of the module students still seemed to find the concept of variance difficult along with that of heritability. Many students showed that they were unable to interpret extreme values of heritability and that they thought of heritability as being an individual measure. The majority of students had a good grasp of ideas such as “what is inherited?”

The results of students’ understanding of *quantitative genetics concepts* cannot be compared with results from other research as they are novel to this investigation.

### 9.2.3 Research question 3

What is the nature of the difficulties experienced by students taking a module in quantitative genetics?

Students seemed to experience difficulties with quantitative genetics because they: (1) inappropriately associated certain terms and topics and (2) had difficulty in the construction and interpretation of histograms.

In this investigation students confused the following terms:

(a) Variation and variance

Many students had an intuitive idea of the concept of variation but did not understand the concept of variance. As suggested by Hammerman and Rubin (2004) and Makar and Confrey (2005) this may be because students attempt to memorise statistical formulae and algorithms and do not fully understand the meaning of statistical concepts.

(b) Heritability and inheritance

Many students confused the terms heritability and inheritance and thought of the heritability as an *individual’s ability to inherit a trait*.

It is not surprising that students in this investigation were found to confuse terms that look and sound-alike such as variation and variance and heritability and inheritance

as Bahar *et al.* (1999a) similarly found that genetics students confuse terms such as homologue, homologous, homozygous and homozygote.

Students taking part in this investigation also confused individual and population measures such as the breeding value of an individual and the additive variance or heritability of a population. This confusion between individual and population measures has been noticed by other researchers working in the field of statistics education. For example, Hancock *et al.* (1992) noted that school children taking statistics modules often showed difficulty thinking on a population level. Konold *et al.* (1997) also found that the students they interviewed had not been able to make the transition from thinking on an individual level to thinking about populations. Ben-Zvi (2004) similarly, noted that students preferred to reason with individual data points on graphs rather than with the entire distribution.

Finally, students seemed to confuse the numerical values of zero and one with the absence and presence of certain phenomena in the context of quantitative genetics.

Students showed difficulty with the construction and interpretation of histograms. When considering students' ability to construct histograms it was observed that:

- (a) Students confused the X and Y axes.
- (b) Students confused histograms and scatterplots.
- (c) Students often tried to plot a point for every individual instead of grouping values according to their frequency.

These results confirm those obtained by Meletiou and Lee (2002) who suggest that transforming raw data into a different form, such as according to frequency in a histogram, is difficult for students. They also noted in their investigation on statistics students' understanding of certain ideas, that students needed assistance in recognising the functions of the X and Y axes.

Many students not only had trouble constructing histograms, but were also not able to interpret histograms correctly. The difficulties observed in this investigation included:

- (a) Students confused the X and Y axes.

Confusion between the X and Y axes has also been noted by Meletiou and Lee (2002), Lee and Meletiou-Mavrotheris (2003) and Ben-Zvi (2004) who all studied students' ability to correctly differentiate between different graphical representations.

- (b) Students had difficulty relating descriptive statistics such as variance and heritability to histograms.

Other researchers such as Makar and Confrey (2005) and Bakker (2004) have recently started research programmes directed towards improving students' ability to link descriptive statistics such as variance with graphical distributions as they have also recognised that students have difficulty in understanding this area of statistics.

- (c) Students had difficulty in understanding why quantitative traits are normally distributed.

Lawson (1996) also noted that students did not know why quantitative traits are normally distributed. He suggested the use of assorted sea shells to assist students in understanding the concept of variation and the manner in which individuals may be grouped according to the occurrence of a certain variant of a trait. He advocated that once students have completed such exercises and constructed frequency distributions, they will be more able to understand why a normal distribution results. In this investigation computer-based tutorials, where students constructed frequency distributions from simulated populations, were used to assist students in their understanding of why quantitative traits are normally distributed.

#### **9.2.4 Research question 4**

What are the possible source(s) of students' alternative conceptions about quantitative genetics?

The modelling framework of Justi and Gilbert (2002) was utilised to model the source of student difficulties and alternative conceptions in the field of quantitative genetics. The genetics curriculum of most South African universities was postulated as a possible source of the alternative conceptions noted during the diagnostic phase of this investigation. In particular, it was thought that the crosses between individuals, which are used by lecturers to illustrate how one may ascertain the degree of dominance of alleles at a locus, may put emphasis on certain ratios which are observed in offspring generations. It was thought that students may rote learn many of these ratios and thereby not realise the random nature of inheritance. Once students then have to start thinking about what happens on a population level they may still think of the deterministic ratios learnt in Mendelian genetics and start to confuse individual and population measures. The researcher also hypothesized that students may associate certain terms and topics with the absence or presence of variation, which may lead to the development of alternative conceptions. The results obtained from the multiple-choice diagnostic tests, interviews with students and a word association study revealed that this was indeed the case and that students associated the idea of a population without variation with values of zero or one, equilibrium, homozygosity, inbreeding and a normal distribution. In contrast, students

associated variation with, values greater than one, change, heterozygosity, outbreeding and discontinuous distributions. The *initial model* which accounted for students' preconceptions on entry to a quantitative genetics model was thus constructed on the premise that the genetics curriculum may have encouraged students to associate certain ideas and that this may in turn have led to the development of alternative conceptions. It was found that the data gathered from the diagnostic phase of the investigation supported the *initial model*. The *initial model* was then extrapolated to account for the alternative conceptions which were identified as being held by students at the completion of a module in quantitative genetics thereby creating the *final model*.

The *final model* indicated that the sequence in which ideas are introduced to students may cause them to inappropriately associate certain terms and topics. This may, in turn, lead to difficulties and alternative conceptions regarding *quantitative genetics concepts*. Genetics educators should thus take cognisance of the model presented in this thesis when designing genetics curricula.

### 9.2.5 Research question 5

What is an appropriate intervention strategy for use in a quantitative genetics module?

An intervention was designed and developed to address students' understanding of quantitative genetics. Particular emphasis was placed on ideas with which students had demonstrated a high degree of difficulty during the diagnostic phase of the investigation. These included students' understanding of the *critical concepts* of *variance* and *heritability* and their ability to construct and interpret histograms. In addition, the design and development of the intervention was informed by the principles of constructivism, conceptual change and metacognition. Furthermore, a review of the literature on theory-driven intervention strategies was carried out during the development of the intervention.

Due to the abstract nature of concepts in quantitative genetics, computer-assisted learning formed one component of the intervention. Computer-assisted learning was included as previous research indicated that students' ability to: (1) use realistic data sets, (2) make and test predictions, (3) visualise abstract ideas in terms of graphical representations and, (4) work at their own pace, would assist students in overcoming their anxiety regarding the mathematical and abstract nature of the discipline and to improve their attitude towards the subject matter.

Concept mapping exercises formed the second component of the intervention. This learning tool was utilised as previous research in statistics and biological education indicated that concept mapping aids students in the organisation of their knowledge, provides a link between the working and long-term memory and acts as a metacognitive tool.

Other researchers in the field of quantitative genetics have tried to assist students in their understanding of quantitative genetics by using computer simulation tools. However, researchers such as St. Martin and Skavaril (1984), Partner *et al.* (1993), Michaels (1993), Tinker and Mather (1993) and Podlich and Cooper (1998) created simulation tools which illustrated the response of quantitative traits to different breeding strategies and did not specifically address students' understanding of foundational concepts such as *variance* and *heritability*, as was the case in this investigation.

Concept mapping has previously been used by other researchers such as Schau and Mattern (1997) in statistics education and Okebukola (1990) and Esiobu and Soyibo (1995) in genetics education in an attempt to assist students in the organisation and integration of their knowledge in a systematic and meaningful manner. However, concept mapping has never before been documented as being used for this purpose in the field of quantitative genetics.

Notwithstanding that computer-assisted learning and concept mapping have been used by other researchers in statistics and biological education, the intervention which was designed and developed for use in this investigation was unique in that it consisted of both computer-assisted learning and the metacognitive activity of concept mapping and addressed students' understanding of quantitative genetics.

#### **9.2.6 Research question 6**

To what extent did the intervention assist students in the understanding of quantitative genetics?

Various statistical tests performed on data from the results of the multiple-choice diagnostic tests administered to the 2004 (control) and 2005 (experimental) student groups verified that the intervention was highly successful in improving students overall understanding of quantitative genetics.

As the intervention was specifically developed for use in the field of quantitative genetics and for this investigation, the results could only be compared to other studies which used computer-assisted learning or concept mapping in the fields of statistics and biological education.

With regard to the use of concept mapping as a metacognitive learning tool, researchers such as Schau and Mattern (1997) in statistics education and, Hienze-Fry and Novak (1990), Okebukola (1990) and Esiobu and Soyibo (1995) in biological education, found, as in this investigation, that the academic performance of students was enhanced after they had constructed concept maps for the subject under investigation.

When considering computer-assisted learning and the use of computer-based tutorials, this investigation differed from others in the field of genetics such as those conducted by Browning and Lehman (1998), Slack and Stewart (1989), Slack and Stewart (1990), Johnson (1990), Stewart *et al.* (1992), Hafner and Stewart (1995), Johnson and Stewart (2002) and Thomson and Stewart (2003) who considered students' understanding of transmission genetics, and St. Martin and Skavaril (1984), Michaels (1998), Partner *et al.* (1993), Tinker and Mather (1993) and Podlich and Cooper (1998) who developed software to be used by students studying quantitative genetics, in that it specifically evaluated whether students' *conceptual* understanding of quantitative genetics had improved. However, the positive results of this study are supported by studies conducted by Simmons and Lunetta (1993) and Cooper (1998) where the researchers deduced that computer-assisted learning had improved students' conceptual understanding of transmission and quantitative genetics respectively.

The results from this investigation revealed that the intervention successfully addressed many of the previously identified difficulties and alternative conceptions held by students. With regard to *prior-knowledge concepts*, most students who had participated in the intervention illustrated a sound understanding of the concept of *variance* and an ability to construct and interpret frequency distributions, an ability to relate descriptive statistics to graphical representations. These results are supported by those of Meletiou-Mavrotheris and Lee (2002) who also found that when they emphasized the concept of *variation* during their teaching, students' understanding of frequency distributions improved. In addition, DelMas and Liu (2005) found that a computer-assisted learning environment improved students' understanding of the standard deviation by improving their understanding of the relationship of the standard deviation to the mean and the relationship between the standard deviation



and the shape of a histogram. Similarly, Bakker (2004) found that software tools helped statistics students to better understand statistical concepts such as the mean and the range and their relationship to the “shape” of distributions.

After participation in the intervention used in this investigation, students demonstrated a good grasp of *quantitative genetics concepts* such as the concepts of breeding value, additive variance and heritability. However, some alternative conceptions were still held by a small group of students and a number of students indicated that they did not fully understand the concepts of frequency, additive gene action and covariance. These results have not been reported by other researchers, although Soderberg and Price (2003) did comment that the use of specialised software had assisted students to think on a population level, a requirement for the understanding of concepts such as additive variance and heritability.

### 9.2.7 Research question 7

What was the nature of the conceptual change which occurred during the teaching process?

The sequentially constructed student-generated concept maps created by students who had participated in the intervention and attitudinal questionnaires were used to investigate the nature of the conceptual change which occurred during the teaching of a quantitative genetics module. Conceptual change was investigated from three perspectives: (1) epistemological, (2) ontological and (3) affective.

An analysis of the student-generated concept maps indicated that most of the epistemological changes in the cognitive frameworks of students could be classified as *conceptual development* or *conceptual capture* and that a limited degree of *conceptual exchange* had taken place. This finding confirms those of other researchers working in the field of science education such as Treagust *et al.* (1996b), Pearsall *et al.* (1997), Venville and Treagust (1998), Hewson and Lemberger (2000) and Martin *et al.* (2000) who all found that when examining changes in students' conceptions over time, students' conceptions were usually only elaborated, and not entirely replaced, during the learning process.

When an in-depth analysis of changes in students' conceptions of the *critical concepts* of *variance* and *heritability* was performed it was found that many students' conceptions had changed from being *intelligible* to being *plausible* or *fruitful* to the students. As no other research has been conducted on epistemological changes in

students' conceptions of *variance* and *heritability* over time, these results are novel to this investigation.

The conceptions held by students after participating in the intervention were in many cases classified on an ontological level as *active* (students had knowledge of the application of the concepts) whereas it was previously classified as *passive* (students had rote-learned equations and definitions). This result is not surprising as in the field of genetics education, Venville and Treagust (1998), when considering students' conceptions of a gene, also found that students' conceptions changed from a *passive* view of a gene as a particle passed between generations, to an *active* view of a gene as a sequence of instructions which control the expression of characteristics.

An analysis of attitudinal questionnaires completed by the students indicated that the students enjoyed the computer-based tutorials and benefited from the concept mapping exercises. The students also felt that their knowledge of quantitative genetics was greatly improved and they also had a more positive attitude towards the subject. Other studies in statistics and biological education such as those conducted by Schuyten and Dekeyser (1997), Eichinger *et al.* (2000) and Tsui and Treagust (2002) also reported that computer-assisted learning helped to motivate students to learn and improved students' attitude towards the subject being taught. Furthermore, students in this investigation and in a study conducted by Liu (2004) reported that students enjoyed using the *Inspiration* software to assist them with their concept mapping exercises.

### 9.3 POSSIBLE LIMITATIONS OF THE INVESTIGATION

The generalisability of the results of this investigation must be considered within the constraints of the study. Possible limitations of the investigation include the fact that the researcher was also the lecturer involved in the modules used in the study, the sample size was dictated by the number of students registered for each module, students' understanding of a limited number of concepts was investigated and the study was conducted only at the University of KwaZulu-Natal.

The first possible limitation of the investigation is that there may have been researcher bias. As the methodology used in this investigation was action research, the researcher was also the lecturer of all the quantitative genetics modules which were used in this study. The researcher thus not only determined the aims of the study but also planned the research, decided which research instruments to use,

developed the multiple-choice diagnostic tests and interview protocols, decided what to incorporate in the intervention, developed the intervention, taught the modules concerned including the implementation of the intervention, conducted all the interviews with students and analysed the results generated from all the research instruments. The fact that the researcher may not always have been able to be objective in her approach to the teaching of the modules and the interpretation of the research findings must therefore be acknowledged. However, it should be noted that wherever possible other experts in the field were consulted to confirm the validity of the probes and the interpretation of the results obtained.

The second limitation was that the researcher had no control over the sample size. The researcher only had access to students registered for certain modules at the University of KwaZulu-Natal and the size of these classes determined the sample size. As a result the sample size was fairly small, ranging from 14 to 40 students in any one module. Consequently, when any quantitative analysis was conducted, such as the analysis of covariance (ANCOVA) that was preformed to determine whether the intervention had been successful in improving students' understanding of key concepts in quantitative genetics, the power of the statistical tests was reduced. Furthermore, it must be noted that the small sample size also meant that not all difficulties and alternative conceptions would be exhibited by all of the groups. The frequency of the difficulties and alternative conceptions observed would also be influenced by the random nature of the "sampling process". Therefore, the same frequencies were not consistently noted over all the student groups.

The final possible limitation of the study was that the researcher investigated students' understanding of a limited number of concepts in one context. A limited number of concepts, such as *variance* and *heritability*, were identified by the researcher as being fundamental to students' understanding of the foundational principles of quantitative genetics. It must however, be recognised that the concepts identified by the researcher are not fully comprehensive of all the concepts with which students may have had difficulty in understanding. Furthermore, the emphasis was on concepts which are introductory in nature and applicable to most animal breeding modules. In an applied plant breeding module students' understanding of concepts such as epistasis and genotype-environment interaction would have to be investigated. The investigation was also only conducted on students attending the University of KwaZulu-Natal and as such only certain South African students' understanding of the subject matter was investigated. It must therefore be noted that the results of this investigation may not necessarily be applicable in other contexts

where for example, the preconceptions held by students on entry to a quantitative genetics module may be different to those observed in this study.

## 9.4 IMPLICATIONS OF THE STUDY AND RECOMMENDATIONS FOR FUTURE RESEARCH

### 9.4.1 Genetics curriculum

The genetics curriculum followed at most South African universities was identified by this investigation as being a possible source of student difficulties and alternative conceptions in the field of quantitative genetics. The reason for this being that during the teaching of introductory modules in genetics students are often encouraged to focus on the deterministic ratios produced from crosses between two individuals. Consequently, students do not pay sufficient attention to the probabilistic and random nature of the process of inheritance. If introductory genetics modules consistently emphasized the variation present in a population for any trait of interest and the mechanisms by which this variation is generated, students may be able to more readily expand their understanding of genetic principles from an individual to a population level. This would also facilitate students' ability to expand their knowledge of the discontinuous variation observed in populations where the inheritance of traits determined by single genes to the continuous variation seen with quantitative traits determined by genes at numerous loci. Future research could thus investigate whether introductory genetics modules that focus on the concept of variation could positively influence students' understanding of population and quantitative genetics.

### 9.4.2 Use of correct terminology

The terminology used in the science of genetics is confusing and difficult for many students to understand. Future research should not only identify the concepts which are particularly problematic for students but also determine the nature of the conceptions held by students for these concepts. For example, it was noted during this investigation that students often confused the concepts of *variation* and *variance* as well as *heritability* and *inheritance* and students also held various alternative conceptions of these concepts. Other concepts which students may confuse and which science educators interested in genetics should investigate include *variance* and *covariance*, *codominance* and *no dominance* amongst others. Furthermore, this investigation showed that students also sometimes incorrectly associate certain ideas such as *variation* and *heterozygosity* and this may also lead to the development of alternative conceptions.

### **9.4.3 Focus on students' understanding of additional concepts**

This investigation paid particular attention to students' understanding of the concepts of variation, variance, graphical representations, breeding value, additive variance and heritability. However, it was noted during the study that students also had problems understanding the concepts of frequency, additive gene action and covariance. The researcher would therefore like to include these concepts in any intervention used in quantitative genetics modules which she may be involved with teaching in the future. The intervention described in this investigation would thus need to be altered to accommodate these concepts.

### **9.4.4 Focus on students' procedural knowledge and problem-solving ability**

The investigation described in this thesis focused specifically on students' conceptual understanding of foundational concepts in quantitative genetics. As students taking a module in quantitative genetics are also required to solve numerous problems and as such need to be able to conduct an initial qualitative analysis of a problem, formulate a hypothesis, design a strategy to solve the problem and analyse the results they produce. Future research could investigate the relationship between the conceptual and procedural knowledge of students in the context of quantitative genetics and the manner in which the problem-solving abilities of students could be enhanced.

## **9.5 EXTENSION OF RESEARCH PRESENTED IN THIS THESIS**

In line with the action research approach adopted in this investigation, the researcher has reflected on the results of the study and comments made by the examiners of this thesis. After careful consideration, she suggests that the research presented in this thesis be extended in the manner described below.

1. The multiple-choice diagnostic tests could be improved upon by including additional items probing students' understanding of concepts not fully investigated by this research.
  - (a) Very few students were able to correctly answer the item probing their ability to apply their knowledge of variance (cosmos example). This may be because it requires students to analyse a qualitatively measured trait (flower colour) in a quantitative manner. An item which utilised a numerically measured trait such as height could alleviate this problem and provide further insight into students' ability to solve problems relating to the concept of variance.

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- (b) Additional items probing students' understanding of concepts such as frequency, covariance, correlation, regression, additive and non-additive gene effects and the effects of genotype-environment interactions would provide an indication of the scope of students' knowledge of quantitative genetics, as well as their ability to apply this knowledge.
  2. Additional links could be analysed in the student-generated concept maps.
    - (a) Students' ability to link the concept of heritability with the response to selection could be analysed. This would provide some evidence of whether students understand the role of heritability in determining how a population will respond to selection and whether they could decide on an appropriate breeding strategy for the trait under consideration.
    - (b) As students' understanding of heritability was shown to be of utmost importance, students' ability to link the concepts of correlation and regression to the concept of heritability would provide evidence of students' understanding of the manner in which the heritability of a population is estimated.
  3. The interview protocols could be extended to probe not only students' conceptual understanding of the concepts of variance and heritability, but also their knowledge of the formulae used. This would give an indication of whether the students are able to use the formulae as a "toolkit" to quantify and partition the amount of variation in a population. However, care must be taken not to simply investigate students' ability to rote learn a definition or equation but rather their understanding of the structure of the formulae.
  4. The multiple-choice diagnostic tests, interview protocols and attitudinal questionnaires should be used to probe students' understanding of quantitative genetics at other tertiary institutions (different contexts) and on larger student groups. This would indicate the generalisability of the results presented in this thesis.
  5. The remediation strategy could be improved and extended upon by inclusion of the following:
    - (a) The use of concrete examples that could assist students in the understanding of concepts such as frequency. Students could then analyse the variation in a population by actually counting and



- categorising the number of different phenotypes in a given population.
- (b) Additional spreadsheets, and the Tinkerplots software, could be used to provide graphical representations of concepts such as covariation, correlation and regression. In this way students' understanding of heritability and the manner in which it is estimated could be enhanced.
  - (c) Practicing plant and animal breeders could be asked to talk to students about the practical implantation of breeding programmes. They could include some discussion on the estimation and application of concepts such as heritability and the manner in which statistics assist breeders to make decisions. Students may then become more motivated to learn as they realise they are not merely learning about abstract ideas, but rather about relevant concepts used in the development of improved plant and animal species.
  - (d) Academically stronger students could be extended by providing them with access to computer simulations that illustrate the effects of applied concepts such as intra-locus interactions (dominance), inter-locus interactions (epistasis) and genotype-environment interactions.
6. Genetics educators should be encouraged to re-examine the genetics curricula used at their institutions. Cognisance should be taken of the manner and sequence in which students are introduced to concepts to ensure that:
- (a) The random nature of inheritance and the concept of variation are emphasized.
  - (b) Students are aware of the distinction between individual and population measures.
  - (c) Students do not inappropriately associate terms or topics and thereby develop alternative conceptions.
7. It would enhance the results presented in this thesis to look at students' knowledge of quantitative genetics from not only a conceptual, but also a procedural perspective, thereby extending the work of researchers in the field of transmission genetics.

## 9.6 CONCLUDING REMARKS

This investigation was able to identify the areas of quantitative genetics that certain groups of students found difficult and numerous alternative conceptions held by these students in the field of quantitative genetics. The remediation phase of the investigation was further able to show that an intervention, which included the use of computer-based tutorials and concept mapping exercises, was effective in addressing many of the difficulties and alternative conceptions identified during the diagnostic phase of the investigation. The intervention was also able to improve students' attitudes towards the subject. The results of this investigation suggest that students respond well to interactive, visual learning tools such as computer simulations and that metacognitive tools such as concept mapping are effective in encouraging students to learn in a meaningful manner. Based on these successes the researcher recommends that the intervention described in this thesis be used in modules which focus on teaching the foundational principles of quantitative genetics.

The researcher would in future like to improve on and utilise the diagnostic tests developed in this investigation on student groups at other universities to ascertain whether the results of the investigation may be considered to be widely applicable to different contexts. In addition, she would like to continue working on the development of other tools and strategies which could enhance students' understanding of and enjoyment of the learning of quantitative genetics.

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## **APPENDICES**

**APPENDIX 1**

**Summary of research studies conducted into student difficulties with genetics and documented alternative conceptions in this discipline.**

Author(s)	Year	Location	Sample	Methodology employed	Relevant results
Longden	1982	England	(1) 114 A-level students. (2) 10 motivated students, academically sound in biology but experiencing difficulty with genetics.	(1) Multiple-choice questionnaire. (2) Interviews with students completing four genetically orientated tasks. (3) Questionnaires given to teachers asking their opinion on the source of student difficulties.	Confusion between alleles, chromatids and chromosomes. Difficulty understanding meiosis. 69% of the original 114 students associated both mitosis and meiosis with DNA replication. Difficulty with the mathematical elements of genetics. Difficulty with the symbols used in genetics. (Incidence of problems from individual interviews not given as data).
Radford and Bird-Stewart	1982	England	A-level biology textbooks, exam questions and syllabuses.  (Details not given).	Analysis of textbooks, exam questions and the syllabuses for A-level biology.  (Details not given).	The authors comment that: <ul style="list-style-type: none"> <li>• Genetics of quantitative traits not included in the syllabus.</li> <li>• Students seem to equate differences between individuals for continuously varying traits with environmental influences and discontinuous variation with genetic differences.</li> <li>• Students seem to confuse meiosis and mitosis, possibly because of sequential teaching of the two topics.</li> <li>• Students must simultaneously understand segregation, diploidy and dominance when studying Mendel's laws.</li> <li>• Some students think that every gene has two and only two alleles.</li> <li>• Students have difficulty with the mathematical component of the Hardy-Weinberg model.</li> <li>• Textbooks and the wording of exam questions maybe a source of difficulties due to ambiguous and incorrect use of terminology.</li> </ul>
Brumby	1984	Australia	150 1 <sup>st</sup> - year university students.	Written probes and structured interviews	Most students believed that evolutionary change occurs as a result of some need and that individuals and not the composition of populations change over time.

Hackling and Treagust	1984	Perth, Australia	48 10 <sup>th</sup> grade students (15 years of age) from 6 different schools and 13 different science classes.	Semi-structured interviews with individual students.	<ul style="list-style-type: none"> <li>• 40% thought one trait is controlled by one, a few, many, 23 or 46 genes. Only 1 student understood that some traits are controlled by many pairs of genes.</li> <li>• 48% believed gametes contain both chromosomes and both genes from the parent's body cells.</li> <li>• 27% stated that <math>\frac{3}{4}</math> of the children from an F<sub>1</sub> cross will have the dominant trait.</li> <li>• 38% thought dominant genes are more powerful than recessive genes.</li> <li>• 65% believed that cells contain only the genes required to perform their function. They did not relate growth and mitosis.</li> <li>• Only 8% understood the role of chance in the process of fertilization.</li> </ul>
Cho <i>et al.</i>	1985	Not specified	3 of the most widely used high school biology textbooks.	Analysis of textbooks.	<ul style="list-style-type: none"> <li>• All books treated meiosis and genetics separately. Chromosomal division discussed in meiosis and allelic segregation in Mendelian genetics.</li> <li>• "Heterozygous" and "homozygous" used to describe alleles.</li> <li>• Definitions of terms varied between books.</li> <li>• 1 book did not explain the relationship between allele, gene, chromosome and trait.</li> <li>• All books used allele and gene interchangeably.</li> <li>• All referred to mutations as rare, harmful and recessive.</li> <li>• None related punnett squares to meiosis.</li> </ul>
Browning and Lehman	1988	Purdue University, U.S.A.	135 undergraduate education majors taking a biology module.	Analysis of students' problem-solving ability using a genetics tutoring programme in which the computer recorded incorrect and correct responses.	<ul style="list-style-type: none"> <li>• 37% confused genotypes and phenotypes.</li> <li>• 27% of students assumed a 3:1 ratio for monohybrid crosses.</li> <li>• 48% could not determine the parental gametes.</li> <li>• 72% thought both parental alleles would occur in the gametes.</li> <li>• 20% did not realise that gametes must contain one allele from each pair, when considering dihybrid crosses.</li> </ul>

Lawson and Thompson	1988	Phoenix, Arizona, U.S.A.	131 7 <sup>th</sup> grade students at a modern high school.	Essay test on the principles of genetics and natural selection.	Concrete operational students (21% of student group) believed in the inheritance of acquired characteristics.
Greene	1990	U.S.A.	322 undergraduate education students taking a biology module.	Responses to a problem on natural selection.	<ul style="list-style-type: none"> <li>• 3% showed a meaningful understanding of selection.</li> <li>• 43% had a functional understanding within a typological framework.</li> <li>• 17% gave a Lamarckian explanation.</li> </ul>
Mertens	1992	U.S.A.	Secondary school biology teachers.	Observations during teaching of in-service teachers.	<ul style="list-style-type: none"> <li>• Student teachers felt threatened by the simple algebra used in population genetics.</li> <li>• Did not realise that a 3:1 ratio is not always found in populations. Students do not realise that genotypic frequencies are dependent on allele frequencies.</li> </ul>
Pashley	1994	Surrey England	96 A-level students from 4 educational establishments	Test booklet containing 21 pairs of genetic terms. Students were required to describe the relationships between terms.	<p>Three major alternative conceptions were observed:</p> <ul style="list-style-type: none"> <li>• 60% of students thought genes contain alleles.</li> <li>• 27% of students believed alleles contain genes.</li> <li>• 13% of students considered genes and alleles as equivalent.</li> </ul> <p>The researcher believed that these alternative conceptions could have led to the confusion students also showed between the concepts of homozygous and heterozygous and recessive and dominant.</p>
Sanders and Sebege	1995	Batswana	300 high school students.	Survey style instrument.	<p>Use of everyday English words was not always accurate. For example, “weak” and “les” were used as synonyms.</p>
Moletsane and Sanders	1995	South Africa	185 1 <sup>st</sup> -year biology students.	Written test of students’ understanding of certain diagrams.	<ul style="list-style-type: none"> <li>• 19% illustrated a sound understanding of chromosomes.</li> <li>• 1/5 understood what a chromatid was.</li> <li>• 1/3 understood the meaning of homologous chromosomes.</li> <li>• 1/5 could not explain the concept of a “gene”.</li> <li>• 1/3 could not explain the concept of an “allele”.</li> <li>• 47% gave correct answers of the relationship between DNA molecules and chromosomes.</li> <li>• Some students confused the terms “strand” and “helix”.</li> </ul>

Cavallo	1996	Midwestern suburban school in the U.S.A.	189 10 <sup>th</sup> grade biology students.	Multiple-choice questionnaires and open-ended essay giving a written description of their understanding of a topic.	When considering the relationship between punnett squares and meiosis. 44% showed no understanding, 11% rote learned, 43% were midrange and 2% showed meaningful understanding.
Sanders <i>et al.</i>	1997	South Africa	26 1 <sup>st</sup> - year university students.	Structured interviews conducted over three years.	Students showed a propensity for rote learning. Students had difficulty with genetics vocabulary e.g. confusion between meiosis and mitosis. Only knew both had something to do with cell division.
Venville and Treagust	1998	Western Australian	Three classes, at two schools. Grade 10 high school students.	(1) Completed worksheets given before and after the module were analysed (83 completed the first and 79 the second). (2) 29 students were individually interviewed. (3) Relevant lessons were videotaped.	Student's conception of genes changed during instruction in the following manner: 70-44% considered genes to be passive entities passed from parents to offspring and 42-76% an active sequence of instructions.
Lewis, Leach and Wood-Robinson	2000	England	482 school students between the ages of 14 and 16.	Written responses to written questions supported by interview data. Probes designed to probe conceptual understanding.	Findings indicated that: <ul style="list-style-type: none"> <li>• Students did not appreciate the relative sizes of the concepts of: organism, cell, nucleus, chromosome, DNA and gene.</li> <li>• 10% of students believed that organisms can contain chromosomes but not genetic material.</li> <li>• 25% of students thought that genes only occurred in certain organs or tissues such as the reproductive system or the blood.</li> <li>• Only 1/3 of the sample said that they had heard of alleles and the majority of these students viewed alleles as being interchangeable with genes or chromosomes.</li> <li>• Not one student explicitly linked a gene with a gene product.</li> </ul> Educators cannot assume that older students have a sound understanding of basic genetic structures and concepts. This could impact on students ability to understand the basic principles of selective breeding.



Soderberg and Price	2003	Not specified	(1) 7 professors from 6 undergraduate institutions – focussed on one. (2) Two classes on evolution. (2) Five students.	(1) Interviews with professors and students. (2) Class observations. (3) Audio-tapes of think-aloud problem-solving sessions.	<ul style="list-style-type: none"> <li>• Evolution was seen as changes in individual organisms and not populations. (Frequencies not given).</li> <li>• Students thought of adaptation as a conscious process dependent on an organisms needs.</li> </ul>
Lewis	2004	England and Germany	Combined findings from two studies into students' understanding of genetics. Students were nearing the end of school education.	<p>(1) English study: written probes and recorded group discussions.</p> <p>(2) German study: problem-orientated interviews with individual students.</p>	<ul style="list-style-type: none"> <li>• Students held the conception that genes and characteristics are equivalent and that the inheritance of a trait is due to the transfer of unchanged features (traits or genes) between generations.</li> <li>• 73% of students did not understand the determination of traits (mechanism of inheritance).</li> <li>• 59% believed that cells contain only the genetic information required for their own function.</li> <li>• Some students believed chromosomes are male or female.</li> <li>• Students did not use terminology such as allele, gene and chromosome accurately.</li> </ul>

**APPENDIX 2**

**Summary of research studies conducted into students' problem-solving abilities in genetics.**

Author(s)	Year	Location	Sample	Methodology employed	Relevant results and conclusions drawn by researchers
Stewart	1983	U.S.A.	27 high school students divided into 2 groups.	Transcribed audiotapes of students thinking aloud during problem-solving (procedural knowledge). Clinical interviews (conceptual knowledge).	17/27 students could only solve dihybrid problem using algorithmic methods, showing limited conceptual understanding. Researcher stated that students need to know how concepts are related.
Smith and Good	1984	U.S.A.	11 undergraduates (novices) and 9 graduate students (experts).	Videotaped while problem-solving. Asked to "think aloud".	Successful problem-solvers show hierarchical organisation of knowledge, engaged in qualitative planning, possessed strategic knowledge, used a knowledge development approach and were motivated. Unsuccessful problem-solvers just sought an answer, used a backwards, means to end approach and had disjointed knowledge structures.
Lawson and Thompson	1988	Phoenix, Arizona, U.S.A.	131 7 <sup>th</sup> grade students at a high school	Analysis of problem-solving ability using a genetics tutoring programme. Computer recorded incorrect and correct responses.	Formal reasoning patterns were necessary for the elimination of some alternative conceptions. Concrete-operational students failed to reject naïve theories (e.g. Lamarckian inheritance) when introduced to principles of genetics and evolution because they lack the necessary reasoning skills.
Slack and Stewart	1989	University of Wisconsin, U.S.A.	Summary of studies looking at students solving text book problems and using Genetics Construction Kit (GCK). High school students, university students and PhD geneticists.	Transcribed audiotapes of students thinking aloud during problem-solving. Computer printouts of initial data and sequence of crosses made by students.	Researchers postulated that students must be made aware that: <ol style="list-style-type: none"> <li>(1) A single trait may be caused by one gene.</li> <li>(2) A single trait can be caused by many genes.</li> <li>(3) One gene may affect more than one trait.</li> <li>(4) The number of variations of a trait may hint at the inheritance pattern.</li> </ol>
Gipson, Abraham and Renner	1989	U.S.A.	71 college general biology students.	Problem-solving test and Piagetian task interviews.	Formal thought was necessary for solving some types of Mendelian problems.

Author(s)	Year	Location	Sample	Methodology employed	Applicable results
Stewart and Hafner	1991	U.S.A.	Not specified Looking at past research	Analysis of previous studies	Researchers postulated that students should be encouraged to (1) Generate and develop new models. (2) Revise models (3) Learn how to generate data. (4) Recognise that all models have constraints (5) Link models (pleiotrophy and epistasis) (6) Link models to produce larger models
Smith and Suthern Sims	1992	U.S.A.	11 undergraduates (novices) and 9 graduate students (experts).	Videotaped while problem-solving. Asked to "think aloud" whilst solving classical genetics problems and three Piagetian tasks.	Researchers stated that formal reasoning abilities are not an absolute requirement but are conducive to successful problem-solving in genetics. They commented that many genetics concepts are formal or abstract in nature and that formal thought is required to work from effects to causes. They noted the formal nature of the principle of Hardy-Weinberg equilibrium.
Cavallo and Schafer	1994	U.S.A.	140 high school students.	Meaningful learning orientation evaluated using Likert-style questionnaires or teacher observations. Aptitude tests conducted. Likert questionnaire regarding motivation. Students comprehensive written description of knowledge of a topic.	Researchers illustrated a direct relationship between meaningful learning orientation and students' understanding. Researchers commented that an understanding of science is not restricted by aptitude but by how students learn.
Hafner and Stewart	1995	U.S.A	20 high school students.	Transcribed audiotapes of students thinking aloud during GCK problem-solving. Computer printouts of initial data and sequences of crosses and, written materials produced by students.	Researchers concluded that: Successful problem-solving involves "searching the model space". Testing the model and evaluating the model. Students should be encouraged to construct and revise models – perhaps through a process of cognitive apprenticeship (help from the teacher and other students).

Author(s)	Year	Location	Sample	Methodology employed	Applicable results
Finkel	1996	U.S.A.	25 high school students taking a genetics module	Transcribed audiotapes of students thinking aloud during problem-solving.	Researchers found that students used 3 types of knowledge while problem-solving and revising models. (1) Genetics knowledge (2) Knowledge of the process of model revision (3) Knowledge of own problem-solving strategies – metacognitive knowledge.
Cavallo	1996	Midwestern school in U.S.A.	189 10 <sup>th</sup> grade biology students	Multiple-choice questionnaires and open-ended essay giving written description of a topic.	Researchers concluded that a meaningful learning approach was not related to reasoning ability and high reasoning ability led to successful problem-solving. Meaningful learning orientation related to students understanding of the relationships between concepts.
Johnson and Stewart	2002	U.S.A	Two groups of high school students, one successful and the other not.	Students provided with a GCK problem and had to propose a model – co-dominance, multiple alleles or X-linkage.	Researchers concluded that successful problem-solvers detected anomalies in data by comparing the expected data with known models and used model revision to explain the results.
Thompson and Stewart	2003	U.S.A	6 geneticists (transmission, molecular and population).	Solved 4 GCK problem types. Solution protocols were analysed and participants interviewed. Transcribed audiotapes of students thinking aloud during problem-solving.	A framework for solving transmission genetics problems was proposed by the researchers: (1) Identify the problem. (2) Produce ideas (3) Explore data (4) Construct hypothesis (5) Analyse data (6) Assess hypothesis (7) Revise hypothesis
Martinez-Aznar	2005	Spain	Two groups of high school students. (n=30 and n=33)	Researchers classroom diary and students answers to problems.	Researcher stated that there are two types of problems: (1) Closed – cause to effect. (2) Open- effect to cause. The steps that should be used to solve open problems: (1) Qualitative analysis of problem (2) Emission of hypothesis (3) Design of resolution strategy (4) Resolution (5) Analysis of results

**APPENDIX 3**



## Research into students understanding of concepts in Quantitative Genetics

### REQUEST

The research is part of a bigger project that investigates students' understanding of quantitative genetics. The ultimate aim of the project is the development of teaching strategies to assist with any problems students may have with the subject. You are requested to participate in this research by answering certain questionnaires. Interviews (which may be video-taped) will also be conducted with selected students. Participants will remain anonymous in the study and it will not affect their course grade in this class.

### CONSENT

I, \_\_\_\_\_,  
do hereby give the researchers Mrs. C. Hancock and Miss C. Lindsay permission to use the questionnaire data and interview data (if applicable) towards the completion of this project.

I understand that my participation is voluntary. By signing this form, I release the said information for her to use with the understanding that it will be kept confidential and at no time will my name be used or connected with any information.

Name of participant:

\_\_\_\_\_

Contact telephone/cell number:

\_\_\_\_\_

E-mail Address:

\_\_\_\_\_

\_\_\_\_\_  
Signature of participant

\_\_\_\_\_  
Date

\_\_\_\_\_  
Signature of researcher

\_\_\_\_\_  
Date

**APPENDIX 4**

**Prior knowledge questionnaire:**

1. What do the following mean?

Variation:

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Variance:

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Name a practical use for the statistic – variance.

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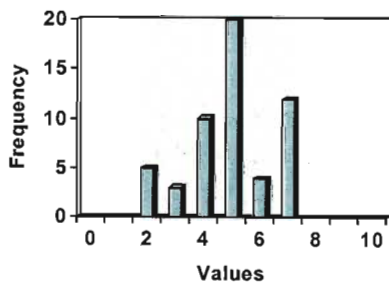


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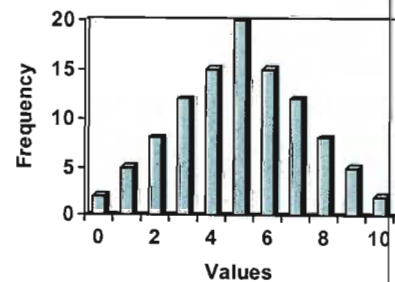
Circle the **one** answer which you think is **the most** correct and give a reason for your choice.

2. Which one of the following distributions shows more variation?

**Population 1:**



**Population 2:**



a) Population 1

b) Population 2

Give a reason for your answer:

---

3. Inbreeding leads to a loss of heterozygosity and an accompanying increase in homozygosity.

If an initial population consists of AA, Aa and aa individuals, the completely inbred population will consist of only AA and aa individuals. This means that inbreeding leads to: (assume there is no dominance)

- a) An increase in the phenotypic variation.
- b) A decrease in the phenotypic variation.
- c) There is no change in the phenotypic variation of the population.

Reason for answer:

Does a population consisting of only AA and aa individuals have variation?

- a) Yes
- b) No

Give a reason for your answer.

Does a population consisting of only Aa individuals have variation?

- a) Yes
- b) No

Give a reason for your answer.

4. Petal colour of cosmos is determined by two alleles with intermediate gene action at one locus. Population 1 has red ( $R^1R^1$ ) and white ( $R^2R^2$ ) flowers, whereas population 2 has red ( $R^1R^1$ ), pink ( $R^1R^2$ ) and white ( $R^2R^2$ ) flowers. Which population has the greatest phenotypic variance in flower colour?

(Assume the frequency of the  $R^1$  allele = frequency of the  $R^2$  allele = 0.5).

- a) Population 1
- b) Population 2
- c) Neither

Reason for answer:

5. There will be no variance in a population when:									
a) There is no dominance or epistasis.									
b) The population mean is equal to zero.									
c) The population mean is equal to 1.									
d) All the individuals have the same phenotypic values.									
e) There is complete dominance.									
f) The population is in Hardy-Weinberg equilibrium.									
Reason for answer:									
6. Consider a larger population of 100 chickens which was monitored and the following information on egg production obtained. 6 chickens produced 5 eggs, 22 chickens produced 10 eggs, 50 chickens produced 15 eggs, 12 chickens produced 20 eggs and 10 chickens produced 25 eggs. Draw a suitable graph that represents this information. (Label the axes).									
7. Forty of the chickens were also weighed and the following weights obtained.									
5.14	12.23	13.35	13.96	22.07	24.69	17.54	15.43	10.07	11.09
14.26	6.15	19.74	14.15	14.14	10.14	15.07	13.6	26.98	19.48
14.91	13.88	9.98	20.15	25.15	8.76	14.97	13.13	16.19	21.00
10.56	15.95	16.79	11.81	18.99	15.58	16.10	20.57	15.99	11.04
Draw a suitable graph to summarise this information. (Label the axes).									

The propositional statements of the scientifically correct answers to the prior knowledge questionnaire are given in table 3.2.

**Propositional statements of scientifically correct answers to each probe relating to students' prior knowledge.**

Question number	Propositional Statement
1	<p>Variation may be defined as the departure from a normal condition or standard type.</p> <p>Variance may be defined as the sum of the squared deviations from the mean.</p>
2	Population 2 shows more variation as the values range from 0 – 10.
3	<ul style="list-style-type: none"> <li>• Variation at the phenotypic level remains constant if the assumption of complete dominance is made. With no dominance the phenotypic variation will decrease as the number of different phenotypes reduces from three to two.</li> <li>• Variation decreases at the genotypic level in the inbred population.</li> <li>• Variance at the allelic level is the same in both populations.</li> <li>• A population consisting of AA and aa individuals represents two different genotypic forms (probably two different phenotypic forms) and therefore does show variation.</li> <li>• On the phenotypic level a population of Aa individuals will not show variation (unless variation is induced by the environment). On the allelic level the population does contain variation.</li> </ul>
4	<ul style="list-style-type: none"> <li>• Population 1 shows greater variance at the phenotypic and genotypic levels as the sum of the squared deviations from the mean (pink) will be greater..</li> <li>• Variance at the allelic level is the same in both populations.</li> </ul>
5	There will be no variance in a population when all the individuals in a population have the same phenotypic values i.e. the population is uniform.
6	A bar graph with the chicken number on the X-axis and the number of eggs produced per chicken on the Y-axis.
7	A histogram with weight, divided into classes, on the X axis and frequency on the Y-axis. Continuous distribution.



**APPENDIX 5**

**Post teaching questionnaire:**

Circle the **one** answer which you think is **the most** correct.

1. Quantitative traits are normally distributed because:
  - a) The genes have an additive or cumulative effect.
  - b) Many environmental factors and many genes affect them.
  - c) The population is undergoing random mating.
  - d) Many genotypes give rise to an intermediate or average value.
  - e) Genes exert a positive or negative effect on the trait, leading to positive or negative deviations from the mean.

Give a reason for your answer:

---

2. A high heritability does not necessarily mean an individual will have a high breeding value because:
  - a) There will be a range of breeding values in the population, most of which will be high.
  - b) Breeding values are a function of gene frequency.
  - c) The trait may be highly heritable, but undesirable, causing breeding values to be low.
  - d) A high heritability indicates that generally the phenotypic values of individuals are a good indication of their breeding values.
  - e) A parent only passes on half of its breeding value.
  - f) A high heritability indicates that  $V_A$  (additive variance) is large.

Give a reason for your answer:

---

3. What is passed from parents to offspring?
  - a) Non-additive gene action
  - b) Additive variance
  - c) Average effect of alleles
  - d) Variance due to common environment

Give a reason for your answer(s):

---

4. Heritability can be improved by:
- a) Increasing the breeding values of individuals in the population.
  - b) Increasing the range of breeding values of individuals in the population.
  - c) Increasing the range of environmental deviations in the population.

Give a reason for your answer(s):

---

5. If the heritability of a trait is equal to zero it means:
- a) The genes have no effect on the trait.
  - b) There is no genetic influence on the trait.
  - c) The individuals are genetically identical.
  - d) There is no genetic variance, thus no genes are passed onto the next generation.

Give a reason for your answer:

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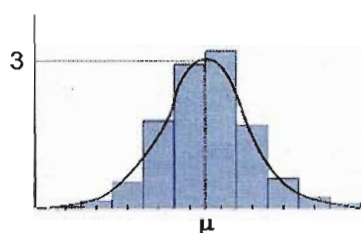
6. If the heritability of a trait is equal to one it means:
- a) All of the breeding value of an individual is transferred to the next generation.
  - b) There is no environmental influence on the trait.
  - c) There is no variance due to the environment and gene interaction.
  - d) All individuals in the population will have high breeding values.

Give a reason for your answer:

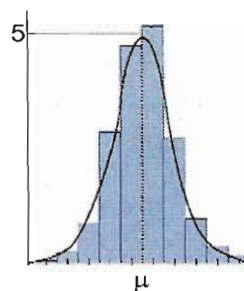
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7. Which of the following two populations will have the highest heritability for the trait under consideration?

**Population 1**

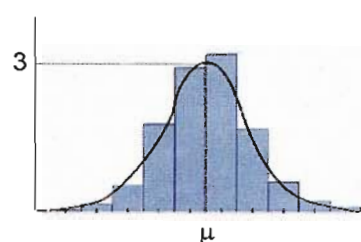


Distribution of phenotypic values

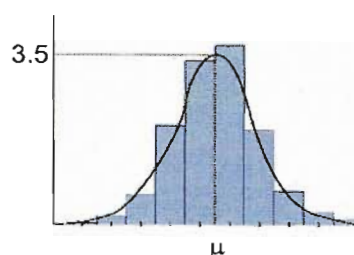


Distribution of breeding values

**Population 2**



Distribution of phenotypic values



Distribution of breeding values

- a) Population 1
- b) Population 2

Give a reason for your answer:

---

**Propositional Statements for questions asked in the post-teaching questionnaire on foundational concepts in quantitative genetics.**

Question number	Propositional Statement
1	Quantitative traits are normally distributed as many genotypes give rise to the intermediate or average value, whereas few genotypes give the extreme values.
2	A high heritability indicates whether the phenotypic values of individuals are generally a good indication of their breeding values for a particular trait.
3	The average effects of alleles are passed from parents to offspring.
4	Heritability can be improved by increasing the range of breeding values in a population i.e. increasing the additive variance.
5	If the heritability of a trait is equal to zero it means that the individuals are all genetically identical i.e. the additive variance equals zero.
6	If the heritability of a trait is equal to one it means that there is no variance due to the environment or non-additive gene action.
7	Population 2 has the highest heritability as the distribution of the phenotypic values (phenotypic variance) in the population is similar to the distribution of breeding values (additive variance).

**APPENDIX 6**



## Prior-knowledge Interview Questionnaire

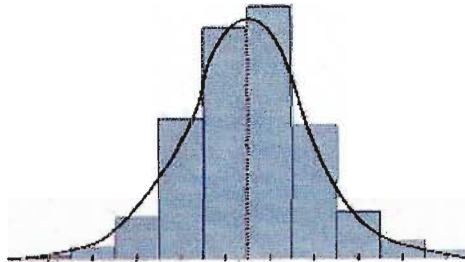
1. Is there a difference between an allele and a gene?
  - If so what is it?
2. Are the descriptions qualitative and quantitative inheritance two ways to describe the same thing? If not what is the difference between these two terms?
3. Using an example from daily life, explain the concepts of :
  - qualitative
  - quantitative.
4. Can you use the following pictures to explain the terms:
  - a. Homozygous
  - b. Heterozygous
  - c. Dominance
  - d. Absence of dominance



5. What is the primary difference between complete dominance and absence of dominance?
6. If you look at a population of people, how can you be sure that it is a population of people?
7. Are the people in a population of people all identical?  
If not, how are they different?
8. How would you identify variation in a population of people?
9. How would you describe a population with no variation?
10. Are the words variation and variance synonyms?
  - If not what is the meaning of each of these terms?
  - What is the primary difference between variation and variance?
11. How would you go about measuring the variance of a particular trait in a population e.g. weight in the human population?
12. Describe what a population without variance would look like.
13. Is it possible to represent the variation of a population on a graph? How?
14. Consider a group of people going to a Genetics conference in Durban.
  - If 45 of them were from South Africa, 35 from America, 15 from England and 5 from France. Could you draw a graph which could represent the delegates at this conference?
  - If all 100 of the delegates were from South Africa, how would this change your graph?

- All of the delegates were weighed and a survey conducted on the influence of diet on levels of obesity at the start of the conference. Could you draw a graph representing the weights of all the delegates?

15. This is a graphical representation of height/weight in a human population.



- a. Label the axes.
  - b. What does each bar represent?
  - c. Why is the tallest bar in the middle?
  - d. Are the people all equally tall? If not, how did you come to this conclusion?
  - e. What is a mean?
  - f. Place a mark on the graph that indicates the position of the mean.
  - g. Redraw this graph with less variance.
  - h. Will this graph have the same mean as the other? Give a reason for your answer.
16. Is there a relationship between:
- The mean and the variance of a population?
  - The variance of a population and a normal distribution? If so what is the relationship?

## Post-teaching Interview Questionnaire

1. What do you understand by the terms:
  - Variation
  - Variance
  - Why do we have this statistic variance?
  
2. What do you think causes variation?
  
3. Inbreeding leads to a loss of heterozygosity and a corresponding increase in homozygosity. If an initial population consists of AA, Aa and aa individuals, the completely inbred population will consist of only AA and aa individuals.
 

How would you describe the change in:

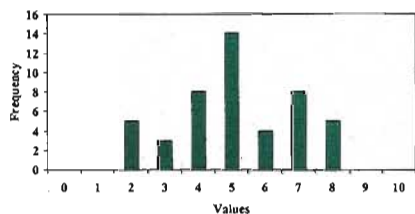
  - Variation?
  - Variance? (on both the genotypic and allelic levels.)
  - What is the mean?
  - Are heterozygous individuals necessary for variation to be present?
  
4. If I cross a red flower with a white flower, what will I get?
  - What type of individual will I have?
  - Do you have variation? What type?
  - Do you have variance?
  
5. If I have red and white flowers in a field and cross pollination occurs, what will the offspring look like?
  - Will you have variation? What type?
  - Will you have variance?
  - Will the parent or offspring generation have more:  
Variation?  
Variance?
  
6. If I tell you I have a population of individuals:
 

AA	Aa	aa	
Freq	0.2	0.5	0.3
Value	2	1	0

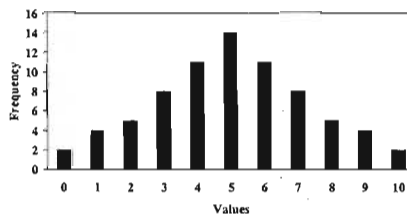
Would you be able to draw this on a graph? How?
  
7. Plot the yield of apples in a population e.g. one farm.
  - What would you put on the X axis?
  - What would you put on the Y axis?
  - What type of distribution results?
  - What does this graph tell you?
  - Do you think yield of apples is a quantitative trait? Why?

8. Which of the following distributions shows more variation? Give a reason for your answer.

Population 1



Population 2



9. If I tell you that  $G = E$  how does that affect  $P$ ?
10. If  $VE = VG$  how does that affect  $VP$ ?
11. If I told you that there was no  $VD$  and  $VI$ , what would that tell you?
12. How do you calculate heritability?
- Why do you think we work with variances and not values?
  - What does it mean?
  - How can you change it?
13. If the heritability is high, does it mean that the breeding values will be high? Why?
14. If I tell you the following:

Population 1:

<u>BV</u>	<u>P</u>
-4	-6
2	4
9	12
-1	-3

Population 2:

<u>BV</u>	<u>P</u>
-4	6
2	8
6	4
-3	9

Which has the highest heritability? Why?

**APPENDIX 7**

## **Introduction to concept mapping and the Inspiration Software**

The construction of concept maps will allow you to think and learn visually. Inspiration allows you to create a picture of your ideas or concepts in the form of a diagram. It also provides an integrated outlining environment to develop your ideas into organised written documents. Inspiration's combination of visual and linear thinking helps deepen understanding of concepts, increase memory retention, develop organisational skills and tap creativity.

When you work with visual representations of ideas, you easily see how one idea relates to the others. Learning and thinking become active rather than passive. You discover where your deepest knowledge lies and where the gaps in your understanding are. When you create a visual map of ideas, you can recall details better than if you read a paragraph. That is because you can see it in your mind.

### **What is a concept map?**

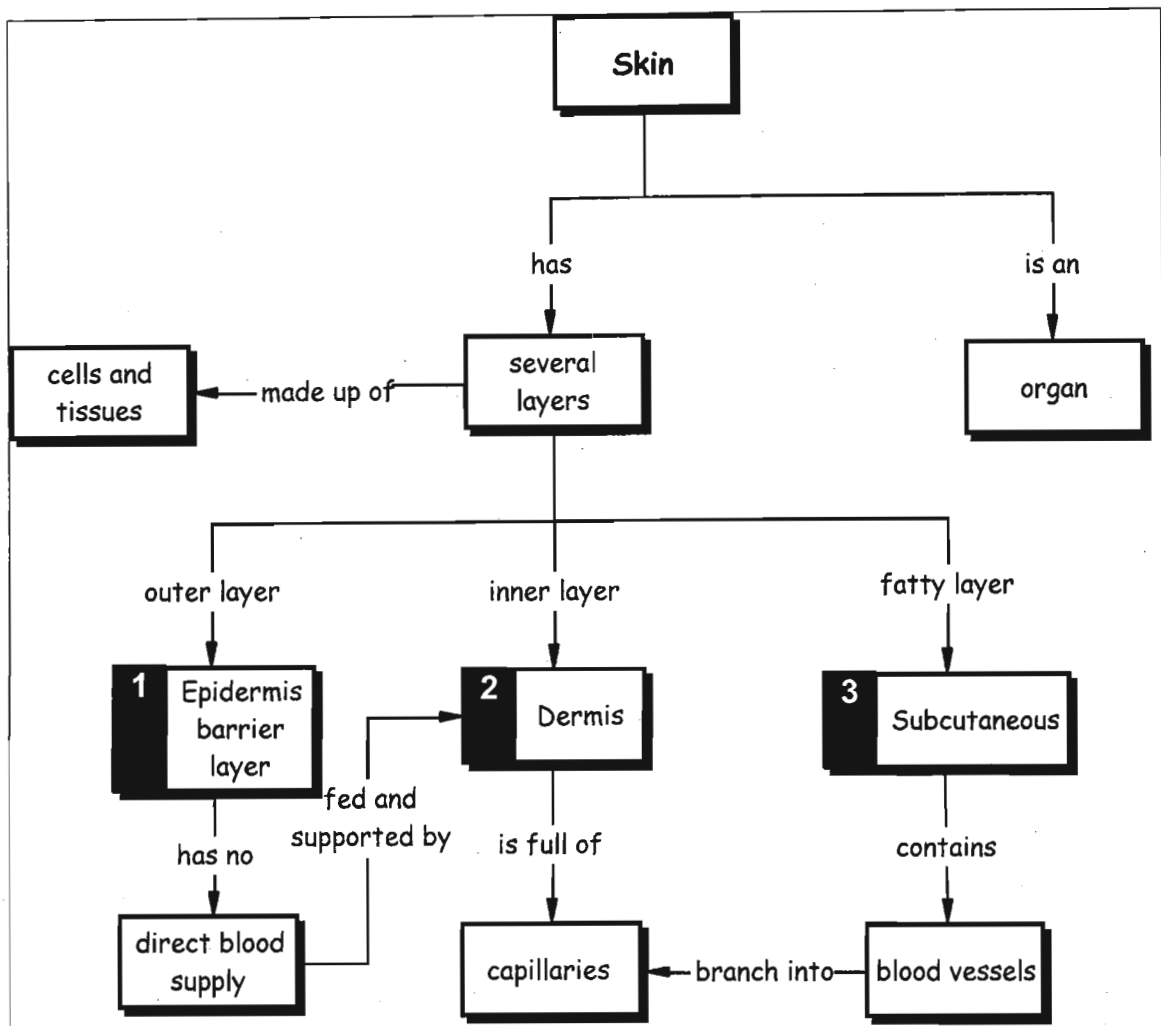
A concept map is a hierarchical diagram used to represent a set of concepts beginning with the most general or most important, and then working down to more specific detail. Key concepts are connected by links that have descriptive words on them explaining the relationship between the concepts.

The basic framework of a concept map is as follows:

- Made up of concepts and linking words
- The linking words describe how the connected concepts are related to one another.
- Two connected concepts make up a propositional linkage which describes a piece of knowledge.
- Concepts are usually arranged hierarchically, i.e. the most general or most important concepts are at the top of the map.
- Cross-links connect different segments of the concept hierarchy.



The following “skin” diagram is an example of a concept map.

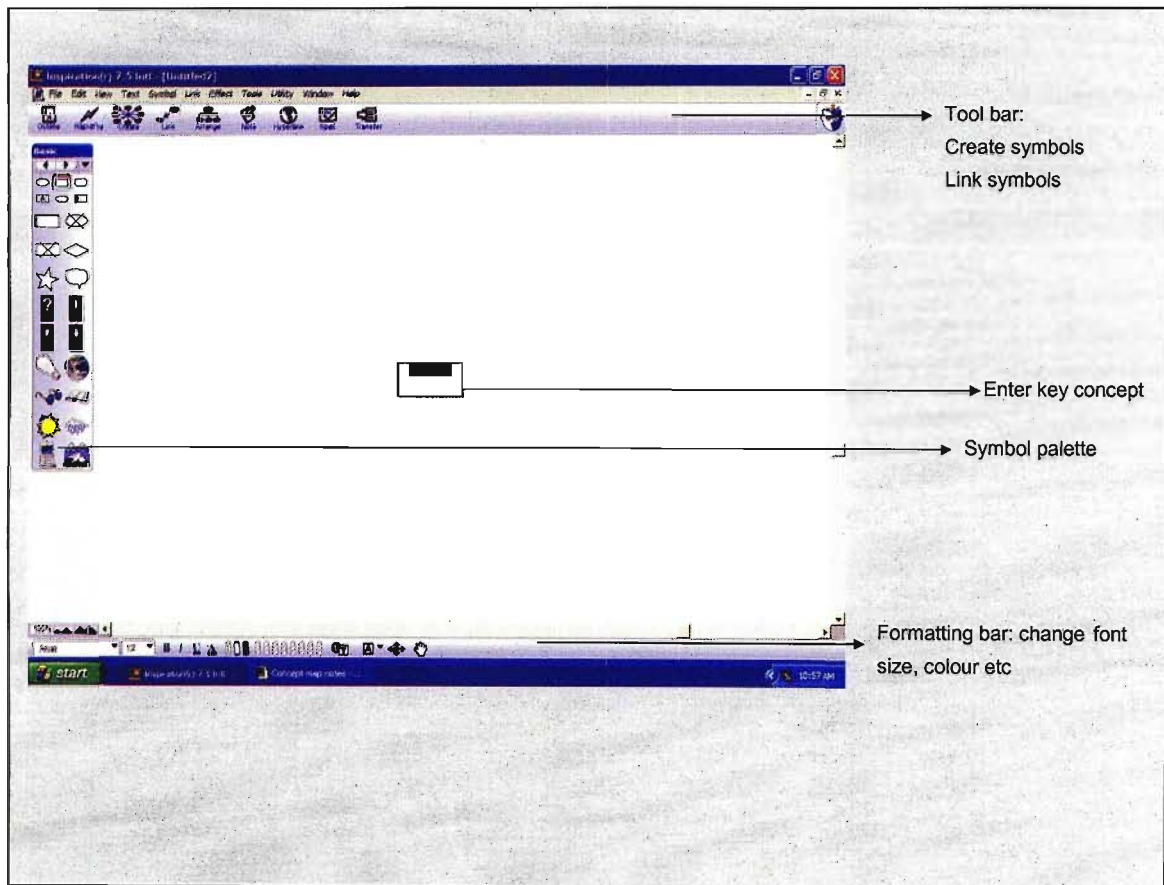


How to construct a concept map:

- Read through your notes
- Highlight the main concepts
- Write down the concepts on a piece of paper (in this module, you will mostly be given a list of concepts).
- Place the most general or all- inclusive concept at the top of the paper.
- Arrange concepts from top to bottom (from most general at the top to most specific at the bottom) so that a hierarchy is indicated. In constructing this hierarchy, place concepts next to each other horizontally if they are considered to have equal importance or value.
- Relate concepts by positioning linking verbs and connecting words on directional arrows.
- Support the concepts with examples.

## Diagram and Outline Views

Inspiration has two main views or environments: Diagram view and Outline view. As you work both keep track of your ideas. You will mostly work in diagram view to create a graphic organiser or map showing how ideas or concepts interconnect.



### To start Inspiration in Windows:

- Click the start button, point to programs, and click on Inspiration.

### Introducing diagram view:

Inspiration opens in diagram view where you process, organise, and prioritise information visually. Key functions are right at your fingertips with the **Diagram** tool bar along the top, the **Formatting** toolbar at the bottom, and the **Symbol** palette on the left.

### Entering the main idea or topic:

When you open Inspiration a symbol appears in the centre of the screen, with the placeholder text, *Main Idea*, selected. It's easy to get started – just enter a topic.

- Type the diagram topic, *Career thoughts*, into the main idea symbol.

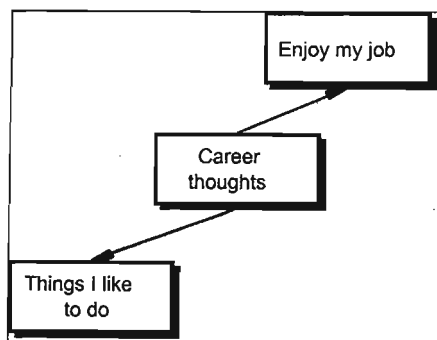


### Using the Create tool to add a new linked symbol:

There are many different ways to create new symbols in Diagram view. An easy way to add a symbol is to use the **Create** tool. The create tool adds a new linked symbol in the direction you choose.

- Select the “Career thoughts” symbol. On the Diagram toolbar, position the cursor over the upper right point on the create button. When you roll over a point on the Create button, it highlights to show the direction in which the new symbol will be created.
- Click the upper right point. A new symbol appears connected to and diagonally above the “Career thoughts” symbol. This symbol is selected and ready for you to enter an idea.
- Type “Enjoy my job” into the symbol.
- Create another symbol linked to career thoughts and type “things I like to do”.

This is what your diagram should look like:



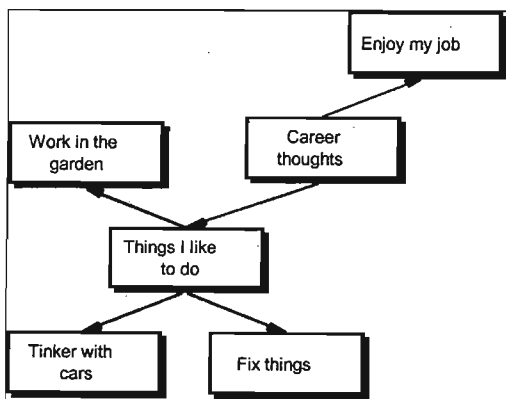


### Using the Rapidfire tool to quickly capture ideas:

You're going to use the **Rapidfire** tool to brainstorm things you like to do. The Rapidfire tool adds a series of linked ideas to a symbol. This allows you to concentrate on entering information, rather than creating symbols one at a time.

Rapidfire places ideas in a freeform structure. There is no need to think about organising yet; you're still getting ideas down to "see" what you think.

- Select the 'Things I like to do" symbol. On the Diagram toolbar, click the Rapidfire button.
- Type " Fix things" and press enter.
- Type "Tinker with cars" and press enter.
- Type " work in the garden" and press enter.
- Click the rapidfire button again to turn the rapidfire tool off.



### Adding an unconnected symbol using point and type:

Sometimes you want to add an idea, but you're not exactly sure where it fits. You can easily add an unconnected idea to a diagram using point and type.

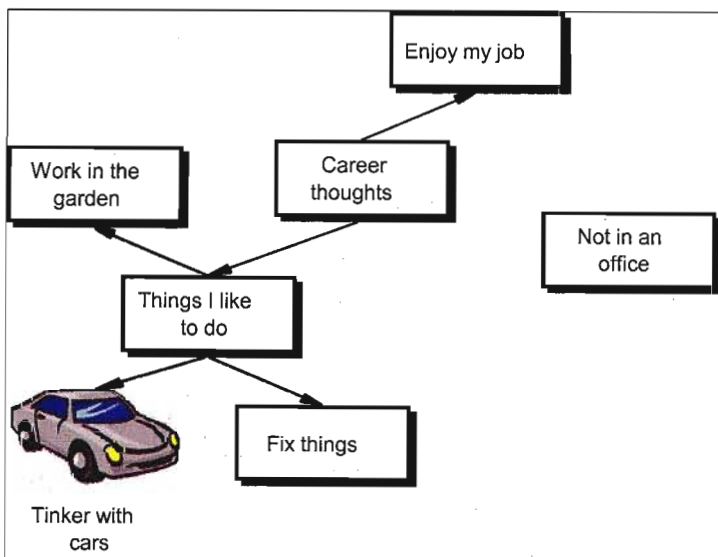
- Click on an open area in the diagram directly to the right of the "Career thoughts" symbol.
- Type " Not in an office"  
Inspiration automatically creates a symbol to hold the text. This symbol is not linked to any other symbol.
- Click away from the "Not in an office" symbol to deselect it.

### Replacing a symbol with one from the Symbol palette:



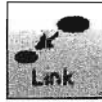
Once you get some ideas down, it's easy to replace a symbol already in the diagram with one from the Symbol palette. The symbols are organised into categories and libraries.

- Select the "Tinker with cars" symbol.
- On the symbol palette, click the **Select library** button to navigate to the Everyday category. Choose the Transport category.
- Click the grey car. The "Tinker with cars" symbol automatically changes to the shape of the car.
- You may also add any other pictures and symbols and create your own library.



You can also use drag and drop to add a symbol from the Symbol palette to represent a new idea.

- On the symbol palette, click on the select library button to navigate to the Geography category. Select the landforms category.
- Drag the "Mountains" symbol until it is positioned above the "work in the garden" symbol and release the mouse button.



### Linking symbols:

Now it is time to add links. Links show the connections and relationships between ideas.

- Select the “Career thoughts” symbol. This is the symbol where the link will start.
- On the Diagram toolbar, click on the **Link** button to turn on the Link tool.
- Click on the “not in an office” symbol. This is the symbol where the link will end.
- A link with the arrowhead pointing to the “not in an office” symbol appears.
- Click the Link button again to turn off the link tool.

### Adding text to the link:

Each link has a text box that appears when the link is selected. Adding text to this box defines the relationship between the symbols.

- Select the link between the “Career thoughts” symbol and the “mountains” symbol.
- Type “out of the city”.
- Click off the link to deselect it.

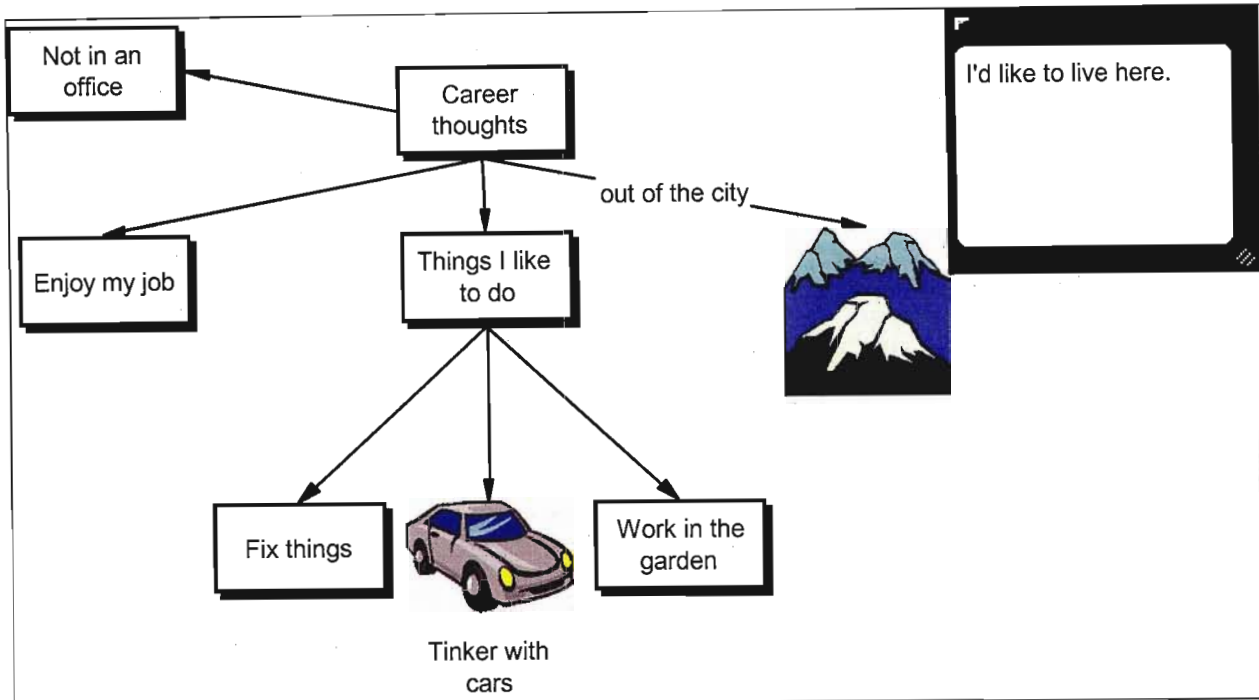


### Adding a note to a symbol:

For each symbol in a diagram, a note is available. Notes allow you to expand ideas.

- Select the “Mountains” symbol. On the Diagram toolbar, click the **Note** button.
- Type “I’d like to live here” into the note.





### Moving symbols:

You can also move a symbol to another place in the diagram.

- Select the “Work in the garden” symbol.
- Drag the symbol so it is directly below the “things I like to do”, and between the “Tinker with cars” and “Fix things” symbols.
- Release the mouse button.

Inspiration keeps the link attached so you never lose the connection between ideas when rearranging the diagram.

### Changing the colour of symbols:



Colour is great for customising the look of symbols. It helps to distinguish items in a diagram and is often used to identify a group of related ideas.

- With the “work in the garden” symbol selected, also select the “things I like to do” and “fix things” symbols.  
To select more than one item, press the shift key and click each item, or click and hold down the mouse to drag a selection box around the symbols.
- On the Formatting toolbar, click the Fill Colour button and choose a colour from the palette.  
When you change the fill colour of a symbol, the colour inside the symbol changes.

You can also change the colour of the writing in a symbol by selecting the text first and then altering the colour on the Formatting toolbar.



### Arranging the Diagram:

The **Arrange** tool arranges the diagram into various formats.

- On the Diagram toolbar, click the arrange button.
- On the Links list, choose *Standard*.
- In the Diagram List, choose *Top Down Tree*.
- Click OK.
- The diagram automatically rearranges in the new format. (Save your work before making any changes in case you are not happy with them).

### Printing the Diagram:

When you print from Diagram view, the default is to fit to one page, which automatically sizes the diagram to fit on one page. If desired, this can be adjusted so that the diagram prints full size on multiple pages.

- On the File menu, choose page set up. Here you can set up the diagram layout, determine margins, headers, footers, and preview your diagram before printing.
- Make your selections; choose Print Preview to preview your work.
- Click print to print your diagram.

### Saving your work:

Whenever you are working on a document it is a good idea to save it on a regular basis. To save a document for the first time or to save a document you have already saved, use the Save command.

- On the file menu, choose Save. The dialog box appears with the main idea as the name of the file.
- If necessary, navigate to the folder in which you want to save the diagram.
- Click save

**Transferring to a word processor:**

If required, you can transfer your work to a word processor.

Click the **Transfer** button on the toolbar. Inspiration automatically launches your preferred word processor and transfers your work.

**Quitting Inspiration:**

To close your file and quit Inspiration, on the File menu choose Quit.

## **Class Exercise**

*Use the following extract from notes on evolution to create your own concept map.*

Evolution is the progressive increase in the degree to which a species becomes genetically adapted to its environment. A principal mechanism of evolution is natural selection, in which individuals superior in survival or reproductive ability in the prevailing environment contribute a disproportionate share of genes to future generations, thereby gradually increasing the frequency of the favourable alleles in the whole population. However, at least three other processes can also change allele frequency: mutation (heritable change in a gene), migration (movement of individuals among subpopulations), and random genetic drift (resulting from restricted population size). Spontaneous mutation rates are generally so low that the effect of mutation on changing allele frequency is minor, except for rare alleles. Migration can have significant effects on allele frequency because migration rates may be very large. The main effect of migration is the tendency to equalise allele frequencies among the local populations that exchange migrants. Selection occurs through differences in viability (the probability of survival of a genotype) and fertility (the probability of successful reproduction).

Populations maintain harmful alleles at low frequencies as a result of a balance between selection, which tends to eliminate the alleles, and mutation, which tends to increase their frequencies.

Random Genetic Drift is a statistical process of change in allele frequency in small populations, resulting from the inability of every individual to contribute equally to the offspring of successive generations. In a subdivided population, random genetic drift results in differences in allele frequency among the subpopulations. In an isolated population, barring mutation, an allele will ultimately become fixed or lost as a result of random genetic drift.

*List key words:*

## Concept mapping exercises

### Concept map 1

*Construct a concept map using the following terms:*

Allele

Gene

Polygenes

Quantitative inheritance

Qualitative inheritance

Observed value

Phenotypic value

Normal distribution

Frequency

Population mean

Variance

Genotypic value

Environmental deviation

Dominance

Epistasis

**Concept map 2**

*Construct a concept map using the following terms:*

Allele

Gene

Polygenes

Quantitative inheritance

Qualitative inheritance

Observed value

Phenotypic value

Normal distribution

Frequency

Population mean

Variance

Genotypic value

Environmental deviation

Dominance

Epistasis

Average effect of an allele

Breeding value

Additive gene action

Non-additive gene action

Selection

**Concept map 3**

*Construct a concept map using the following terms:*

Individual

Population

Mean

Variance

Phenotypic value

Genotypic value

Breeding value

Dominance Deviation

Epistatic interaction

Environmental deviation

Average effect of a gene

Gene

Allele

Quantitative inheritance

Phenotypic variance

Genotypic variance

Additive variance

Dominance variance

Epistatic variance

Environmental variance

Heritability

Genotype-environment interaction

Genotype-environment correlation



**Concept map 4**

*Construct a concept map using the following terms:*

Breeding value  
Phenotypic value  
Additive variance  
Phenotypic variance  
Covariance  
Variance between groups  
Pairs of data  
Groups of data  
Heritability  
Resemblance between relatives  
Regression coefficient  
Correlation coefficient  
Breeding strategy

**Concept map 5 (Summary of module)**

*Construct a concept map using the following terms:*

Individual  
Population  
Mean  
Variance  
Normal distribution  
Frequency  
Additive gene action  
Non-additive gene action  
Phenotypic value  
Genotypic value  
Breeding value  
Dominance Deviation  
Epistatic interaction  
Environmental deviation  
Average effect of a gene  
Gene  
Allele  
Quantitative inheritance  
Qualitative inheritance  
Phenotypic variance  
Genotypic variance  
Additive variance  
Dominance variance  
Epistatic variance  
Environmental variance  
Covariance  
Variance between groups  
Pairs of data  
Groups of data  
Resemblance between relatives  
Regression coefficient  
Correlation coefficient  
Heritability  
Breeding strategy  
Selection

**APPENDIX 8**

**Pre-tutorial questionnaire**

Name: \_\_\_\_\_

Sex: male  female 

Home language: \_\_\_\_\_

Degree programme: \_\_\_\_\_

Year of study: \_\_\_\_\_

Would you have done Gene 350 if it was not compulsory for your degree?

Yes  No 

Have you had any prior computer experience?

Yes  No 

Please indicate your response in the appropriate block.

Question	Response				
	Strongly agree	Agree	Neutral	Disagree	Strongly disagree
My computer skills are strong.					
My mathematical skills are strong.					
I understand foundational concepts in genetics.					
I have a good understanding of statistics at this time.					
I have a good understanding of quantitatively inherited traits at this time.					
I feel positive about statistics at this time.					
I feel positive about quantitative genetics at this time.					

## Post-tutorial questionnaire

Name: \_\_\_\_\_

Please indicate your response in the appropriate block.

Question	Response				
	Strongly agree	Agree	Neutral	Disagree	Strongly disagree
I feel positive about quantitative genetics and statistics at this time.					
I have a good understanding of quantitatively inherited traits and the concept of heritability at this time.					
I am more enthusiastic about computer tutorials than conventional pen and paper tutorials.					
The computer tutorials have helped me understand statistical concepts.					
The computer tutorials helped me to understand the relationship between descriptive statistics and graphical representations.					
The instructions given for the tutorials were clear enough.					
The language was at a level that I could understand.					
The lectures and tutorials were well synchronised.					

Please add any comments or suggestions you may have about the computer-based tutorials which you have completed. E.g. Did you enjoy them – in what way were they helpful? If not how could they be improved?

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**Please comment of the concept mapping exercises which you have done.**

Do you think concept mapping helped you understand the relationships between concepts in quantitative genetics?

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Did you enjoy using the Inspiration software or would you have preferred to draw the maps on paper yourself?

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Any other comments?

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**APPENDIX 9**



**Tinkerplots Tutorial**

Name: \_\_\_\_\_

**How can data be summarised?**

Data should be organised and summarised in a form which allows further interpretation and analysis. One way in which large amounts of data may be summarised is in the form of a frequency distribution/table. As values occur more than once in the dataset they may be grouped together into class intervals. The table will then consist of a number of classes and the frequency of observations (counts) in each class. The manner in which frequencies are distributed between the frequency classes is described as a frequency distribution. In a graph the **class intervals** (values) are plotted on the **X axis** and the **frequency** on the **Y axis**.

A histogram is a graphical representation of a frequency distribution for observations of continuous variables. If the midpoint of the top of each block in a histogram is joined by a straight line, a frequency polygon is produced. When the number of observations of a continuous variable is large and the unit increments are small, the “steps” in the histogram tend towards a smooth, symmetrical, continuous bell-shaped, curve, called a normal curve.

Open up **Tinkerplots** (start-programs-tinkerplots). Tinkerplots will be used to get an idea of how discrete and continuous data can be summarised in the form of a histogram.

Click on “**File**” then “**Open**”. The “**Sample data**” folder should automatically be opened and in it double click on the “**Cats**” file. If the “Sample data folder is not automatically opened then use the following pathway:

**C: / Program files/Tinkerplots / Sample data / Cats**

- You will notice two boxes, the small one on the left is called a “**card**” and the large one on the right with a number of cats is called a “**plot**”.
- On the Card click “**Eye colour**”. Now click on the plot. A number of buttons should appear on the upper toolbar.
- Click in the “key” button. A key will appear in the top right hand corner. You will notice that there are three discrete classes, green, yellow and blue. This is because eye colour is a discrete trait.

- Now click on the blue cat and drag it towards the right. Notice now that the blue cat is separated for the other cats. Now click on another cat and drag it to the right notice now that the three classes are separated.
- Click on the **“Stack vertically”** button on the top toolbar. On the bottom of the plot you will notice the words **“image icon”**, click on the little arrow next to these words and from the resulting list select **“fuse rectangular”**. The resulting plot is now a simple histogram representing a discrete distribution.

### Questions

1. How many green-eyed cats are there?

---

2. How many yellow-eyed cats?

---

3. How many have eyes that are a combination of yellow, green and blue?

---

- Now click on the **“vertical stack”** and **“separate”** button on the top toolbar and the **“image icon”** on the bottom toolbar so that the cats are no longer stacked and no longer separated.
- On the card click on **“weight”**. Notice now that the cats in the plot have changed colour.

4. What do you notice now about the key in the top right hand corner of the plot?

---

5. How is it different from the eye colour key?

---

6. Why is there this difference?

---



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- Now separate the cats out as described earlier, keep dragging a cat until they don't drag anymore. Stack them vertically.

7. What do you notice about the number of classes (the X-axis) this time?

---

8. What do you notice about the resulting histogram?

---

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To get a better idea of a continuous, normal distribution a larger population or sample size is needed.

- Open the file "**Chickens**" in the "**Sample data**" folder. You will notice that this population is much larger (500).
- Select one of the traits on the card and follow the procedure explained earlier to create a simple histogram of the chicken population.

10. What do you notice about the distribution now?

---

11. Why is this?

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- Now click on the "**average**" button.

12. Where does the mean occur?

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13. What happens on either side of the mean to the frequency of the classes?

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- Use the "**pencil**" tool to join the top centre of each block.

14. What shape appears?

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**What are descriptive statistics and why do we need them?**

Descriptive statistics are used to organise, summarise and describe measures of a sample.

The **mean** is a descriptive statistic which is the arithmetic average. The mean is a statistics which tells us what a “typical” member of the population is like. For normally distributed traits the mean occurs at the centre of the distribution – the point on the horizontal axis where the bell-shaped curve is the highest (most of the individuals in the population will have a value close to this mean value).

The mean indicates the population average, but indicates nothing about how individuals deviate from the average. It tells nothing about the uniformity or **variation** in the population. The most commonly used mathematical measures of variation are the **variance** and the square root of the variance or **standard deviation**. These statistics tell how the values vary from the mean value. The variance is measured in squared units, which does not have much practical meaning. The standard deviation is better in this respect. A standard deviation is just what the name implies – the “standard” or “average” deviation of values from the mean. The variance and standard deviation are statistics which tell us how spread out the members of the population are around the “typical” member.

The shape of the normal curve for a particular trait indicates the amount of variation in the value in the population. A relatively flat, broad distribution indicates a high degree of variation. A tall, narrow distribution, on the other hand, indicates a high degree of uniformity (the values do not differ much from the mean value). The shape of the normal distribution and the standard deviation are closely related. On the graph of a normal distribution, the standard deviation appears as the distance between the mean and the point of inflection of the normal curve.

- Open spreadsheet 1. You will use spreadsheet 1 to learn how to plot a frequency table and a histogram in Microsoft excel.
- Column 1 represents the average egg weight values (grams) of a population of 500 chickens. Scroll down and note that all these values vary, even if only by a few decimal places. The values range between 40 and 70.
- Column 2 represents the range.

The farmer of this group of chickens has the problem of trying to analyse the population. The difficulty is that the values do not fall into discrete classes, but instead there is a continuous range of egg weight values, which vary slightly from bird to bird.

In order to analyse and summarise these differences/variations the farmer has to use statistical measures.

Two descriptive statistics may be used to describe the population are:

- a) **Mean** (average or central value)
- b) **Standard deviation and variance** (the spread of the data from the mean)

The farmer may calculate these statistics using a calculator or statistical package. One such statistical package is Microsoft excel.

These statistics may be calculated as follows:

- In cell A502 calculate the mean by entering in the following formula:  
**"=average(A2:A501)"**.

3. What is the approximate mean of this population?

---

4. What does this value tell you about the population?

---

- In cell A503 calculate the variance by entering in the following formula:  
**"=var(A2:A501)"**.

3. What is the variance of this population?

---

4. What does this value tell you about the population?

---

- Calculate the standard deviation ( $f_x$  – **statistical – sdev**)

5. What is this value and how does it differ from the variance?

---



---

6. Is it more useful to the farmer? Give a reason for your answer.

---



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The farmer may also represent the chicken population graphically. Firstly a frequency table must be constructed, from which a histogram may be produced.

- Plot the histogram of this chicken population by clicking on “**Tools**” then “**Data analysis**” and in the resulting dialog box click on “**Histogram**” then click “**OK**”.
- The 500 egg weight values now need to be entered into the “**Input range**” space. First click on the red arrow in the “**Input range**” space then select the 500 egg weight values in column 1 and then click on the red arrow in the small dialog box named “**Histogram**”.
- Using the same method, enter the values from column 2 into the “**Bin Range**” space. These values represent the X-axis on the histogram (average egg weight).
- Now click on the small box to the left of “**Chart output**” (at the bottom of the dialog box) so that a tick appears in that box, click “**OK**”. Another sheet will appear containing a frequency distribution/table and a histogram chart.
- Interpret the frequency table.

7. What range of egg weight values do most of the individuals have?

---



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- Right click on the histogram and select the “**Location**” option. Then select the “**As new sheet**” option in chart 1. The title of the X-axis will say “**bin**” you can change that to “**Egg weight**”. You can now use this histogram to analyse the population.

11. Make a note of where the mean egg weight value is on the graph. What do you notice about the frequency of this part of the graph?

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12. Explain the variation, i.e. How spread out is the data from the mean? Is there a lot of variation or is there very little variation?

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13. How does the value you calculated for the standard deviation relate to the distribution?

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The next year the farmer will be working with the progeny of these birds, which will have slightly different values to these birds. You can change the population by pushing F9. Recalculate the statistics and redraw the histogram. Note, that different samples will have slightly different values for the statistics. The larger the sample, the smaller the differences that will be observed.

- Create another histogram of the first 100 individuals. The procedure to follow is exactly the same as before except that instead of selecting all 500 individuals just select the first 100 individuals.
- Repeat this with the first 50 individuals and then the first 20 individuals.

14. What happens to the bell shaped curve of the histogram as the population size decreases?

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The next year the farmer will be working with the progeny of these birds, which will have slightly different values to these birds. Note, that different samples will have slightly different values for the statistics. The larger the sample, the smaller the differences that will be observed.



### How do different populations vary?

You will use spreadsheet 2 to compare the variances of different populations.

- The first 4 columns represent 4 different chicken populations each with a different variance. Using the method explained in part 1, create a histogram for each of these four populations. Remember always use the same bin range which is in column 5.
- Place the 4 graphs on the same spreadsheet (sheet 2) and print out a copy of the four graphs.

Use the four histograms you have created to compare the variances of the four populations.

1. Which population has the most variation? Give a reason for your answer.

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2. Which population has the least variation? Why?

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You can test to see if your answers were correct by calculating the exact variance of each population using the formula explained in part 1.

3. Do the results obtained from the statistic agree with your inferences from the graphs?

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The aim of the farmer is to change and improve the mean value of egg weight.

4. Which of these populations, do you think, would enable him most successfully to alter the mean and why?

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Summarise what you have learnt about descriptive statistics.

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## Genup Tutorial

Name: \_\_\_\_\_

**Why are quantitative traits normally distributed?**

- Open up genup (**Start – programs – Genup – Genup**).
- Open up the “**Modules**” option and then select “**Loci**” – “**From genes to genetic variance**”.
- Firstly change the population size to 500.
- The number of loci should still be 1. Now click on rerun.

1. What do you notice about the distribution of the population?

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2. How many phenotypic classes are there?

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3. Which genotypes do you think correspond to these phenotypic classes?

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4. What do the X and Y axes represent?

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- Now change the number of loci to 2.

5. What happens to the distribution now?

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6. How many phenotypic classes are there now?

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- Keep increasing the number of loci; try 3 loci, then 10 loci, then 20 loci then 50 loci, then 100 loci and finally 500 loci.

7. What happens to the population and the number of phenotypic classes as the number of loci increase?

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- Keeping the number of loci (20) constant now, change the population size. Firstly, change it to 1000. Note the resulting distribution; now change the population size to 100 then 20, then 5 then 1.

8. What happens to the distribution and the number of phenotypic classes as the population size decreases?

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9. Why is it that the greater the number of loci affecting a single trait, the greater the chance of obtaining a normal distribution?

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**Excel Spreadsheet Tutorial** Name: \_\_\_\_\_

## Heritability

Imagine that you take a black and white photograph of people you know and you “score” the darkness of their hair with a single value. The lightest-haired people would receive a zero and the darkest-haired people 100. Everyone else would have values between 0 and 100. For almost any trait that we can measure in a population the individual values will vary i.e., there will be variation. This variation may be caused by either genetic or environmental effects. The phenotypic value of each individual, (value that can be measured) may be represented by the following formula:

$$P = \mu + G + E$$

P: The phenotypic value, e.g. a performance record. This value is directly measurable.

$\mu$ : The population mean

G: The genotypic value, i.e., the effect of an individual's genes, singly and in combination. It is the value of an individual's genes to its own performance and is not directly measurable.

E: The environmental value. This value includes all non-genetic factors affecting the performance of a trait.

Note: The genotypic and environmental values are all expressed as deviations from the population mean i.e. they are all relative to the population being considered.

However, not all of the genotypic value is heritable. The breeding value of an individual (BV) is that part of the genotypic value that is due to independent gene effects that can be transferred from parents to offspring. The breeding value is then the value of an individual's genes to its progenies performance (the mean value of its progeny).

The remainder of the genotypic value is due to the effects of genes in combination i.e. dominance and epistasis (GCV: gene combination value). These effects are broken up and reformed each generation and are thus not transmitted from parents to offspring.

The phenotypic value may thus be represented as follows:

$$P = \mu + BV + GCV + E$$

The variation in each of these components may be described by the statistic, variance. For example, individuals differ in their hair colour for different reasons. One is that they inherited different kinds of genes for hair colour, and the other reason is that they have experienced different environments e.g. hair dye or time spent in the sun. Theoretically the variance in hair colour (abbreviated  $V_P$  for the phenotypic variance) can be divided into the variance due to genetic differences between individuals ( $V_G$ ) and differences due to the environment of individuals ( $V_E$ ).

Thus  $V_P = V_G + V_E$ .

$V_G$  may be further subdivided into  $V_{BV} + V_{GCV}$ , where  $V_{BV}$  represents the variation in the breeding values of individuals in the population.  $V_{GCV}$  represents the variance due to the non-additive action of genes (how they perform in combination).

The heritability of a trait tells us to what extent the **differences** we observe in animal performance are due to inheritance. The heritability thus measures the proportion of differences in phenotypic values for a trait that are attributable to differences in the genetic values for the trait. It answers the question "Are the differences that we observe in animal performance, primarily due to differences between the breeding values of individuals in a population?"

The heritability therefore measures the proportion of the total phenotypic variance present in a population that is the result of genetic factors. It is the proportion of genetic variance ( $V_G$ ) to the total phenotypic variance ( $V_P$ ) (broad sense). Or it is the proportion of additive genetic variance (variance of the breeding values,  $V_{BV}$ ), to the total phenotypic variance ( $V_P$ ) (narrow sense). The narrow sense heritability can therefore be worked out as follows:

$$h^2 = V_{BV}/V_P$$

Heritability is also a measure of the strength of the relationship between the phenotypic values and the breeding values for a trait in a population. The heritability therefore, measures the degree to which offspring can be expected to resemble their parents for a trait. When a trait is highly heritable, the performance of animals reveals a lot about their breeding values i.e., the performance of their offspring. A trait with a high heritability implies that high performing parents will have high performing progeny and low performing parents will produce low performing progeny.

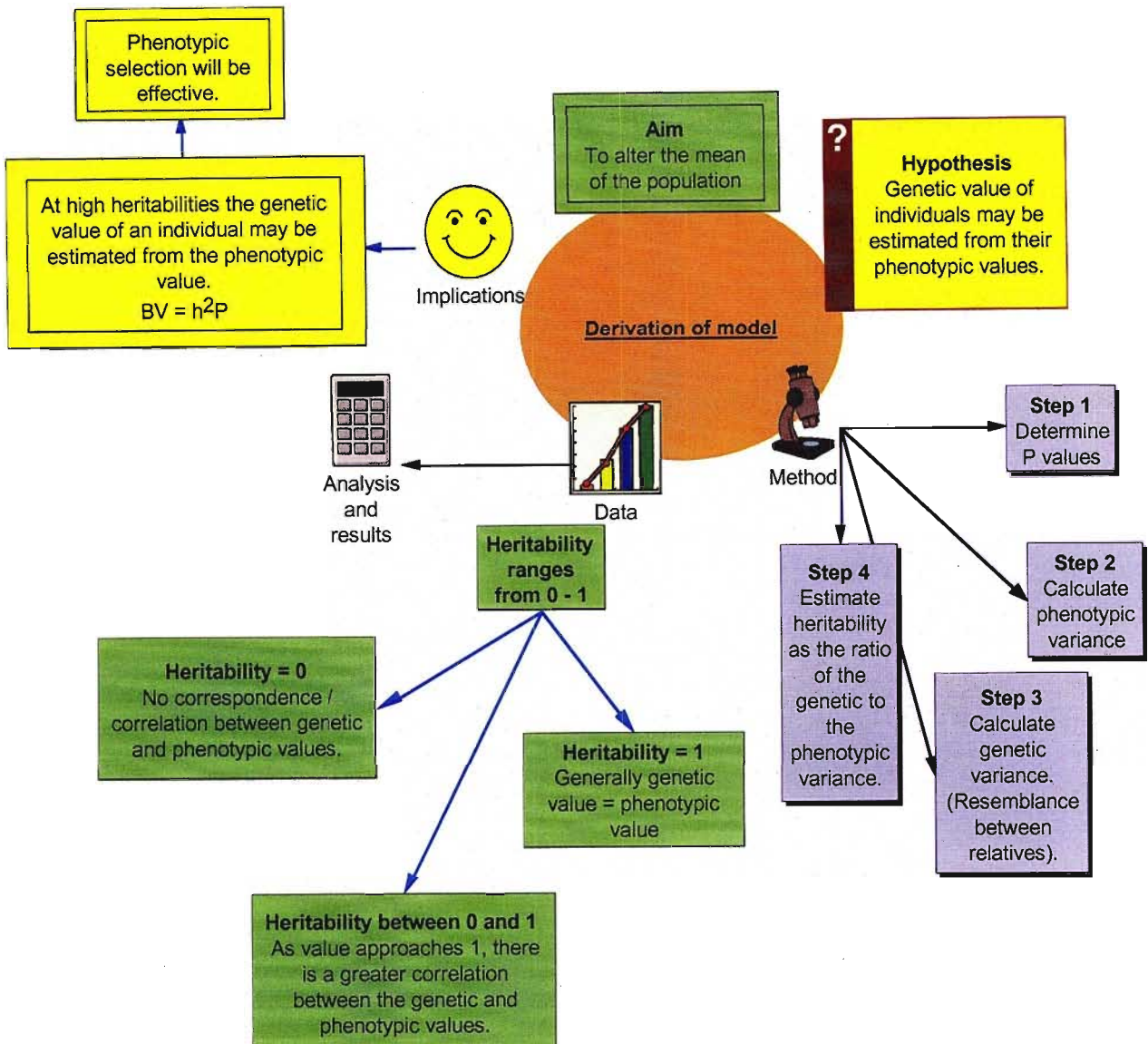
It must be emphasised that heritability is a population parameter, in other words it is a parameter that describes **a population not an individual**. It can, however, be used to **ESTIMATE** the breeding value of an **individual within that population** as,

**$h^2 P = A$ .** The reason for this is as follows: if the phenotypic variance is similar to the additive variance ( $h^2$  close to 1), then the phenotypic values must differ from the mean in the same way as the breeding values; this implies that the phenotypic values must be similar to the breeding values! Therefore, in a population with a high heritability the phenotype will be a good estimator of the underlying breeding value (which is difficult or impossible to calculate). In such circumstances, selection of animals to breed (identification of individuals with the best breeding values) can therefore be made based on phenotypic values. In contrast, when considering a trait with a low heritability, the phenotype will be a poor estimator of the breeding value and selection based on phenotypic values will not prove very accurate.

Heritability is not fixed. It depends on the genetic variation in a population and the environment in which the population occurs.

The following diagram shows how knowledge of the heritability of a trait enables one to make decisions on a breeding strategy.





In the following exercise, we will assume that there is no variation due to **non-additive gene action**. We will do this by constructing individuals with genotypes for two genes (A and B) i.e., we are working with a polygenic or quantitative trait. For these genes, there will be two alleles (a “1” allele and a “2” allele, each with a frequency of 0.5). Each allele will have an effect on the phenotype of the individual regardless of what other allele occurs at that locus and regardless of what alleles occur at other loci. The  $A_1$  and  $B_1$  alleles will always be worth +1 and the  $A_2$  and  $B_2$  alleles -1 unit from the mean in terms of the phenotype. The genotype  $A_1A_1B_1B_2$  will thus have a value of 2, representing the breeding value of that individual.

How can one go about estimating heritability if you cannot measure  $V_G$  and  $V_E$  directly? Probably the most conceptually simple way is to compare offspring to their parents. The more closely the offspring’s phenotype is predicted by their parents’ appearances, the more variation among individuals is due to genetic variation.

Specifically, you can measure the trait in an offspring and graph it against the mean of the trait of the two parents (the midparent value). The slope of that plot represents the narrow sense heritability. When an offspring's trait is perfectly matched to the average of its two parents,  $h^2 = 1$ . Small parents will have small offspring and large parents will have large offspring. When an offspring's trait cannot be predicted by the traits of its parents,  $h^2 = 0$ . Parents of any size can have offspring of any size.

In this exercise, you will explore the theoretical definition of heritability. At the same time you will see that the practical method of constructing a regression of offspring against midparent values can also be used to estimate heritability. Two consequences of the theoretical definition of heritability; that it is a population level phenomenon and that it depends on both the genetic composition and the environment of the population, will be illustrated.

Firstly, note the **model inputs**:

The alleles; their values and frequencies are given, along with the mean value and the environmental variance of the parental and offspring generations.

The population consists of 1000 individuals. The genotypes of the parents have been randomly generated and the breeding values of each genotype calculated as the sum of all the contributing alleles. Each individual experiences its own set of environmental conditions that cause its phenotype to deviate from the population's average phenotype. In this model a low initial score of 0.01 suggests that the deviation from the mean phenotype is very low, i.e., most individuals occupy the same type of environment. High numbers such as 10 suggest individuals occupy dramatically different environments. The phenotypic value of each individual has been calculated as the sum of their breeding value and their environmental effect.

The offspring genotype is generated by simulating gamete formation and independent assortment so that each parent contributes a single A and B allele. The environmental effects and phenotypic values are calculated as described above.

The **model outputs** give the variance components for the offspring generation, along with the heritability estimate and slope of the regression line.

1. It is necessary to determine the additive variance and the phenotypic variance before the heritability can be calculated. How do you think the additive variance ( $V_{BV}$ ) was estimated from this data set?

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2. Why does the slope of the line not exactly equal the heritability?

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3. How does the population mean affect the heritability?

a) Change the mean of the parents and offspring to 10. Does this alter the heritability estimate? Give a reason for your answer.

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b) Press F9 and see how the values change with a different sample of individuals.

4. How does the environmental variation affect heritability? Change both mean values to 50 and then complete the following table. The heritability estimate is altered by changing the environmental variance to the value given in the table.

Trial (Push F9 to obtain a different population of individuals.)	Heritability with environmental variance = 0.01	Heritability with environmental variance = 1	Heritability with environmental variance = 5	Heritability with environmental variance = 20
1				
2				
3				

5. Return the environmental heterogeneity to 0.01 and change the frequencies of the alleles to  $A_1 = B_1 = 0.001$  and  $A_2 = B_2 = 0.999$ . How does heritability change if there is very little genetic variation in the population?

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6. Try allele frequencies of 0 and 1 i.e. there is no genetic variation.

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6. What does a heritability of zero indicate to you?

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7. What does a heritability of one indicate to you?

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The following section allows you to graphically visualise the effects of the environmental variance of a population on heritability. Keep the genetic variation constant by setting all the allele frequencies to 0.5.

- a) Chart 2 is a scatterplot of the **midparent** versus the **offspring trait size**. Alter the environmental variance and thus the heritability and comment on the scatter of the points around the regression line.
- b) Chart 3 is a **column graph** of the **breeding values, environmental deviations** and **phenotypic values** (expressed as deviations from the population mean) for 20 “parent 1” individuals. Alter the environmental variance and thus the heritability and comment on the similarity between the phenotypic deviation, breeding value and environmental deviation of individuals.

$h^2$	$V_E$	<b>Column graph</b> Comment on the similarity between P, BV and E.	<b>Scatterplot</b> Comment on the scatter of the points around the regression line.
0	20		
0.3	3		
0.5	2		
0.7	1.5		
1	0.01		

- c) Chart 1 is a **histogram** of the **frequency of phenotypes in the parental and offspring** populations. Alter the environmental variance and thus the heritability and comment on the change in the shape of the distributions.

$h^2$	$V_E$	<b>Histogram</b> Comment on the shape of the distributions.
1	0.01	
0.7	1.5	
0.5	2	
0.3	3	
0	20	

Summarise what you have learned.

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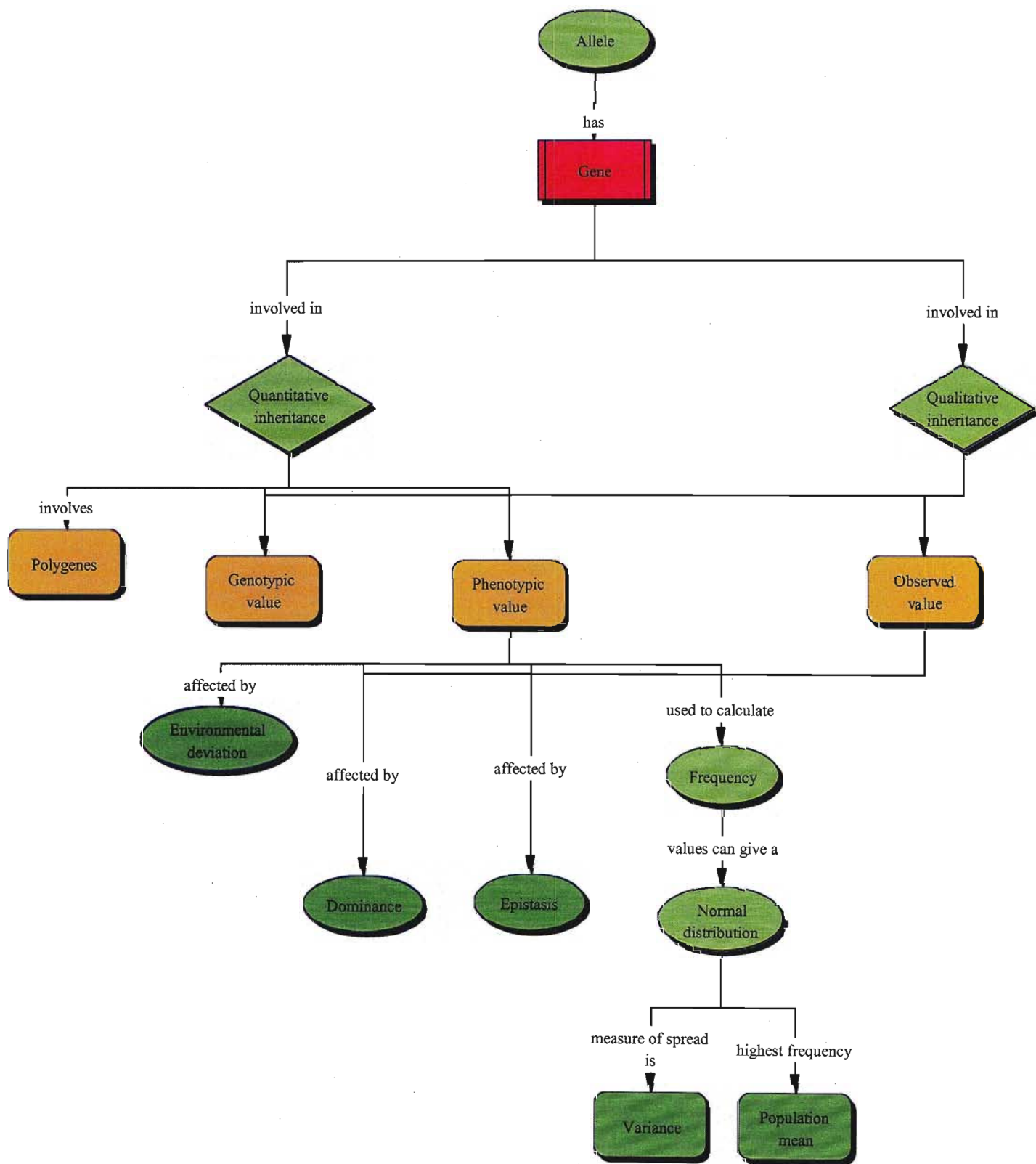


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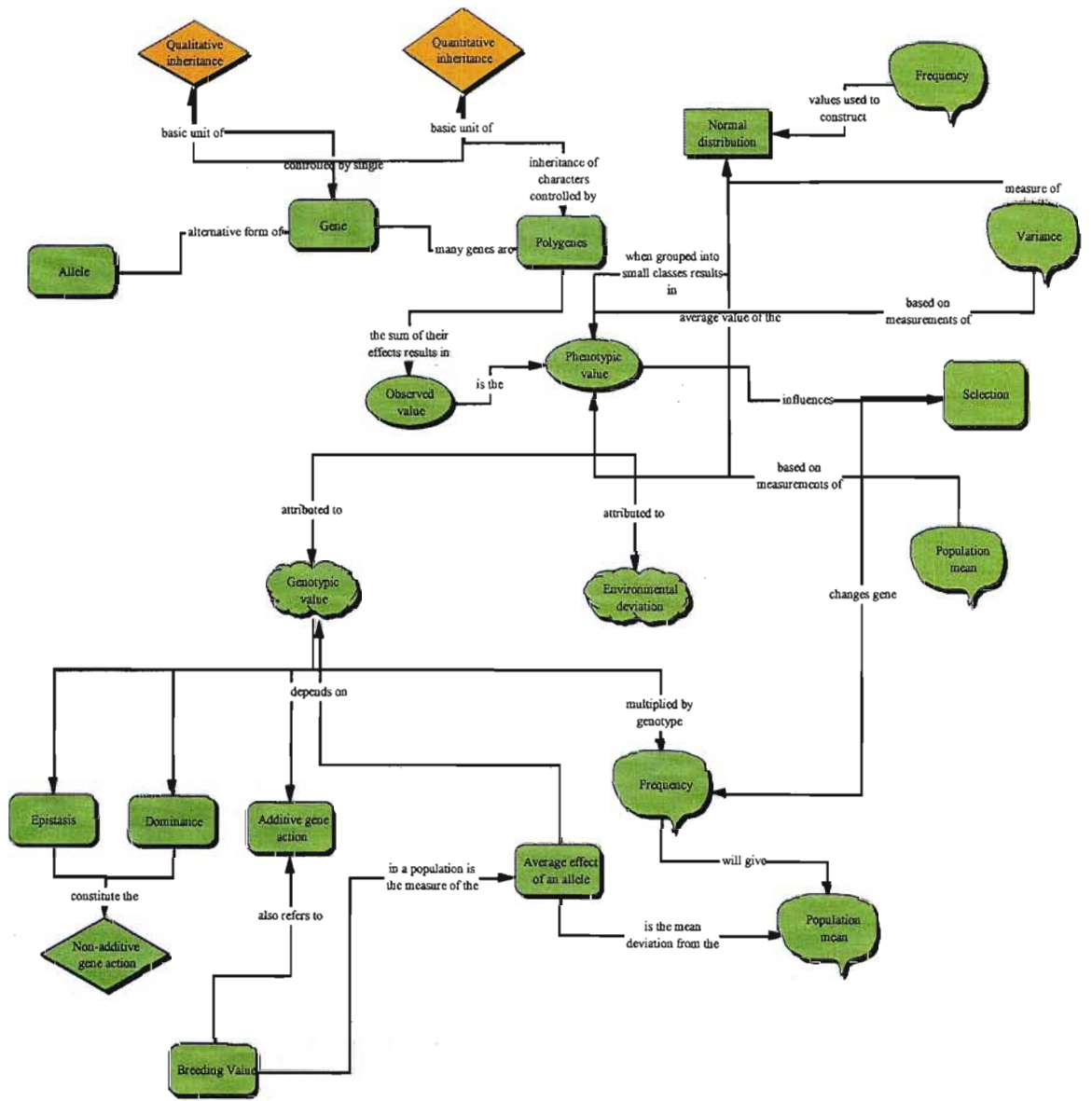
**APPENDIX 10**

Consistently good set of concept maps

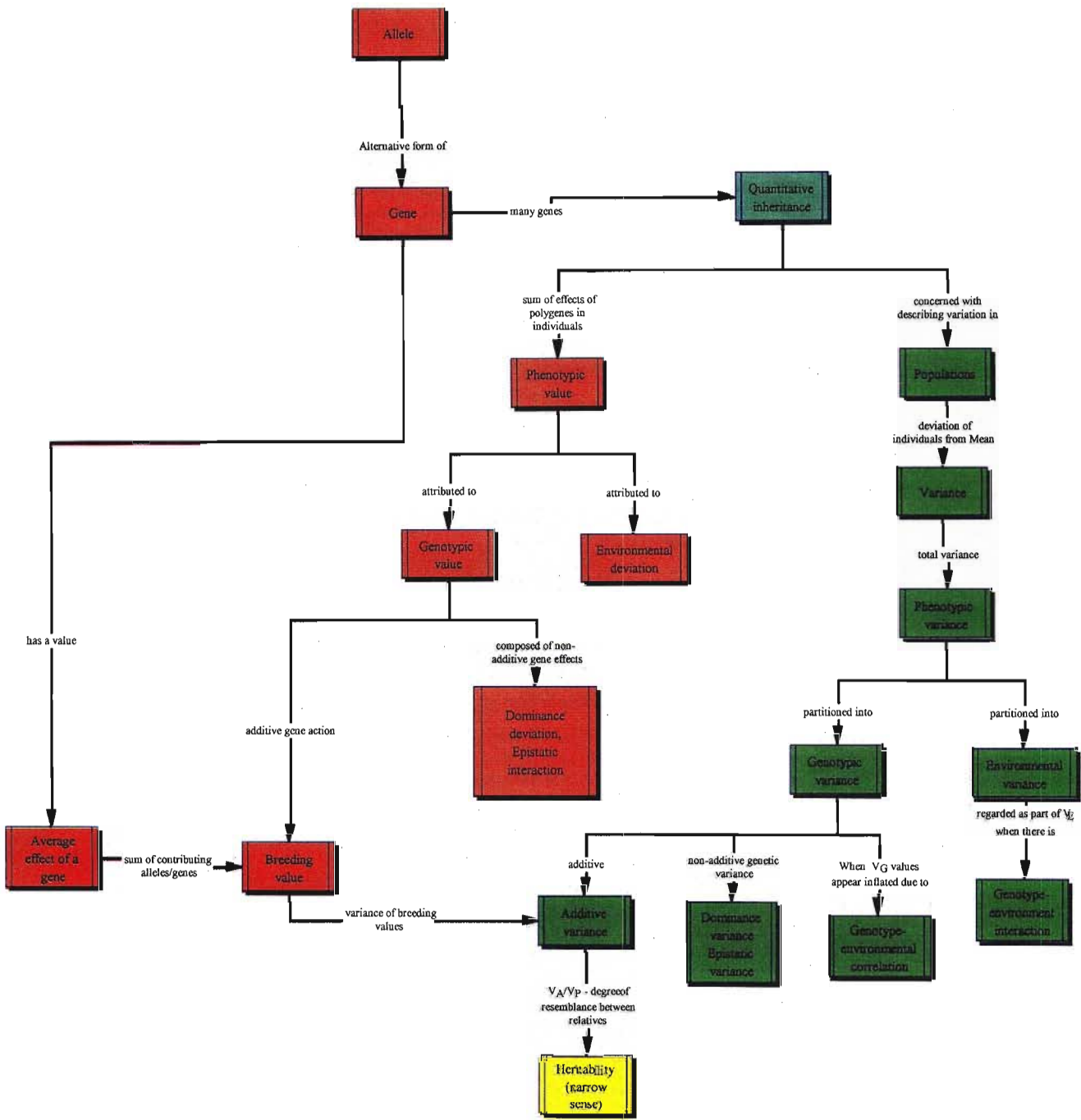
Map 1





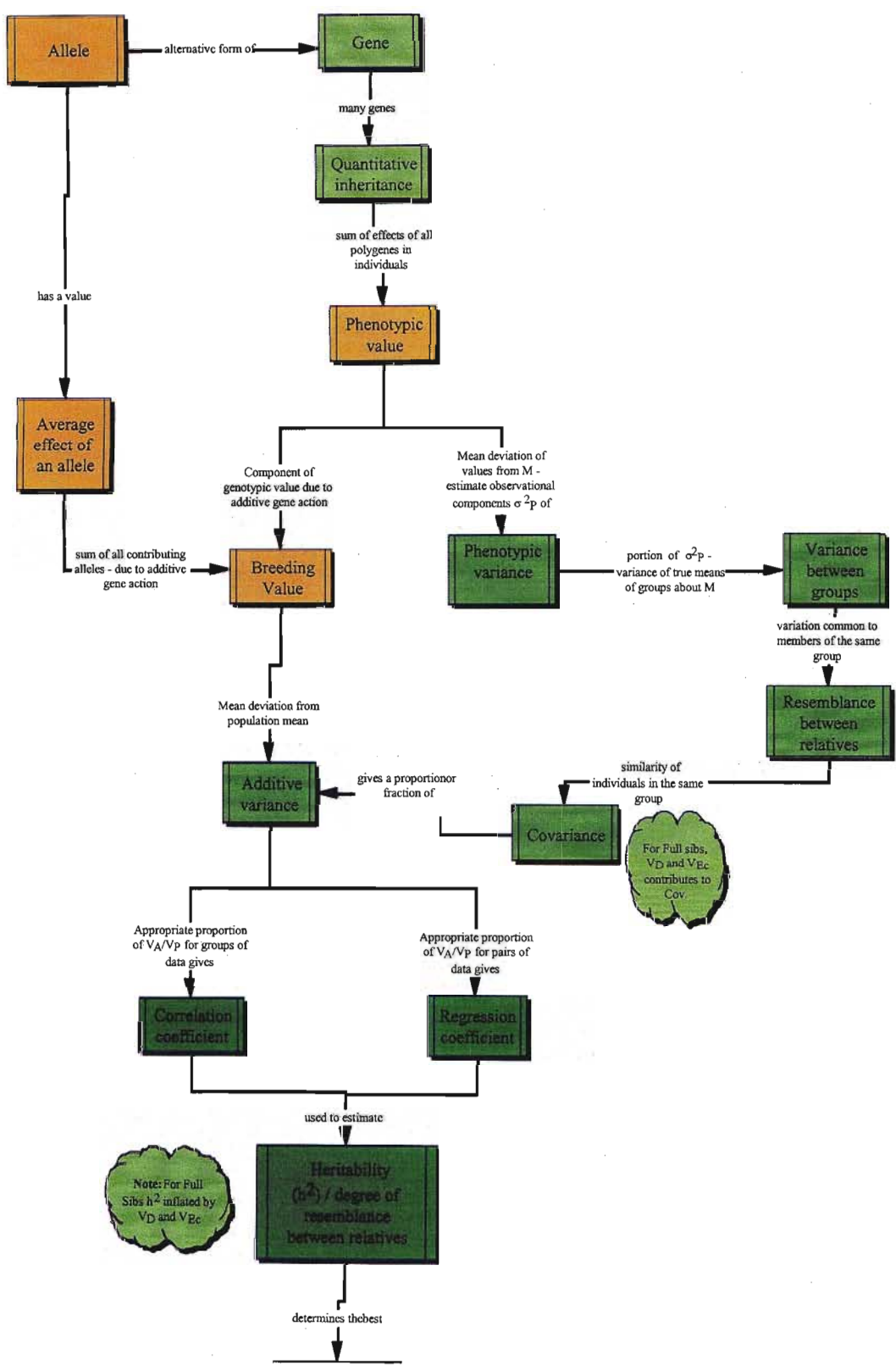


Map 2

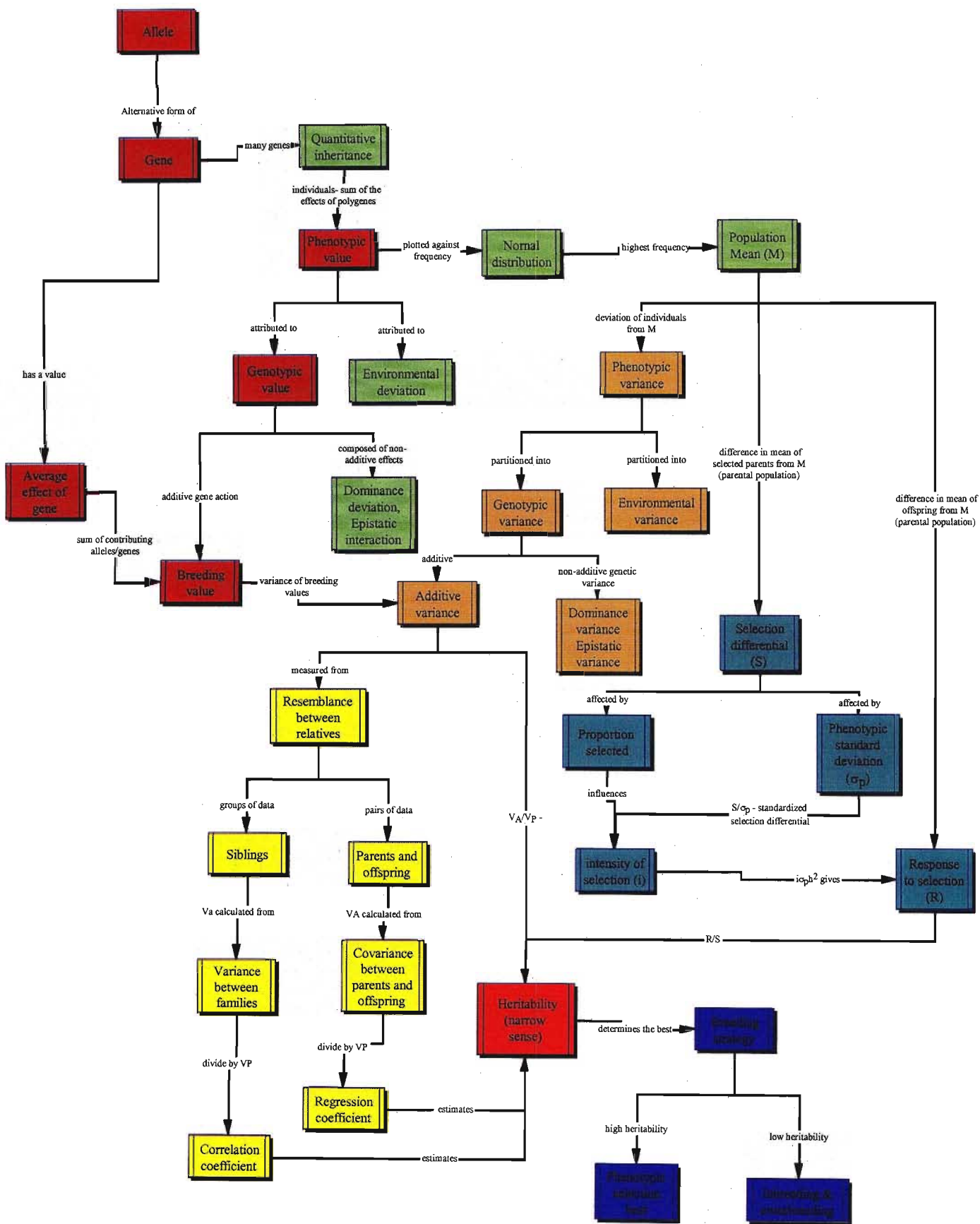


Map 3

Map 4

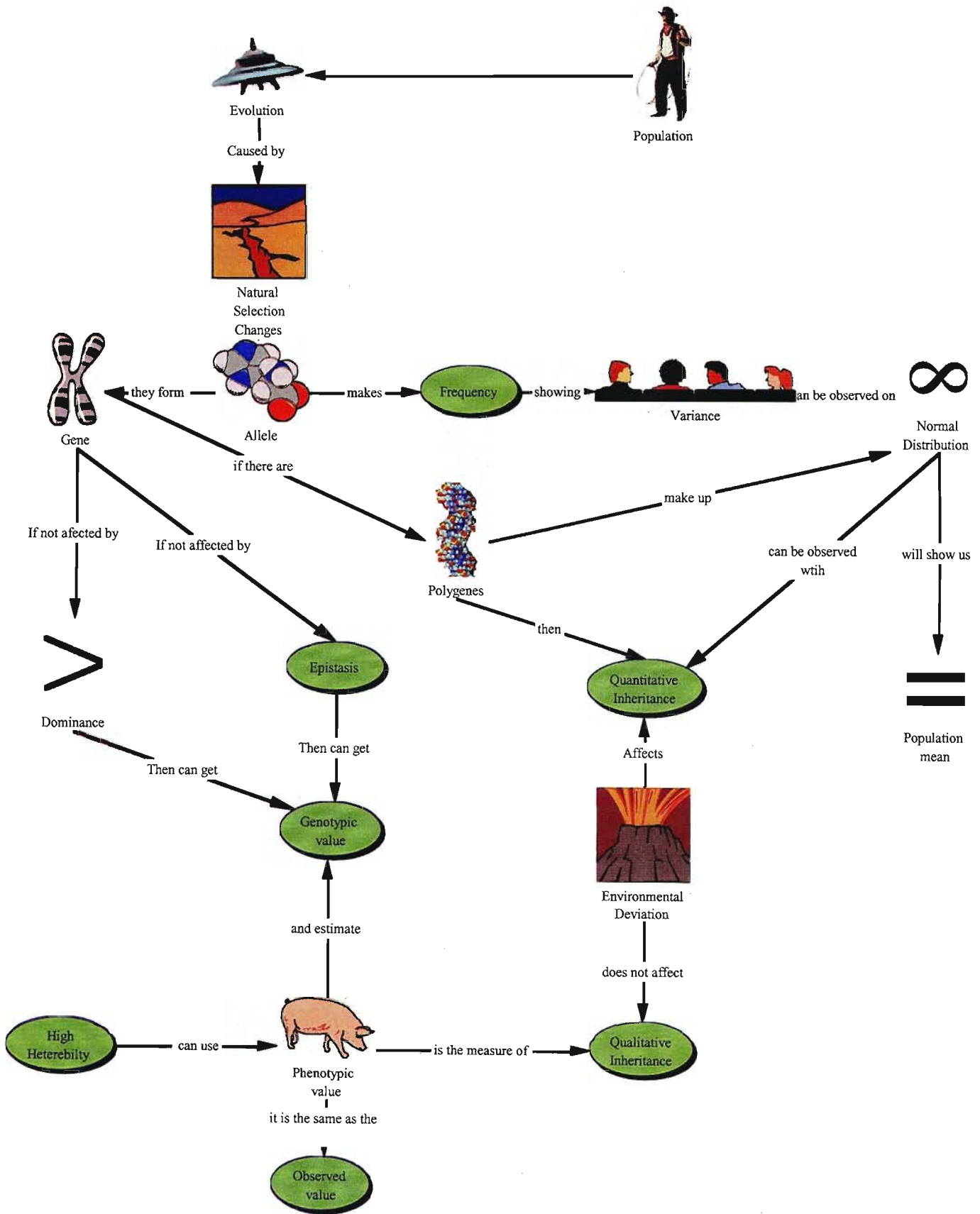


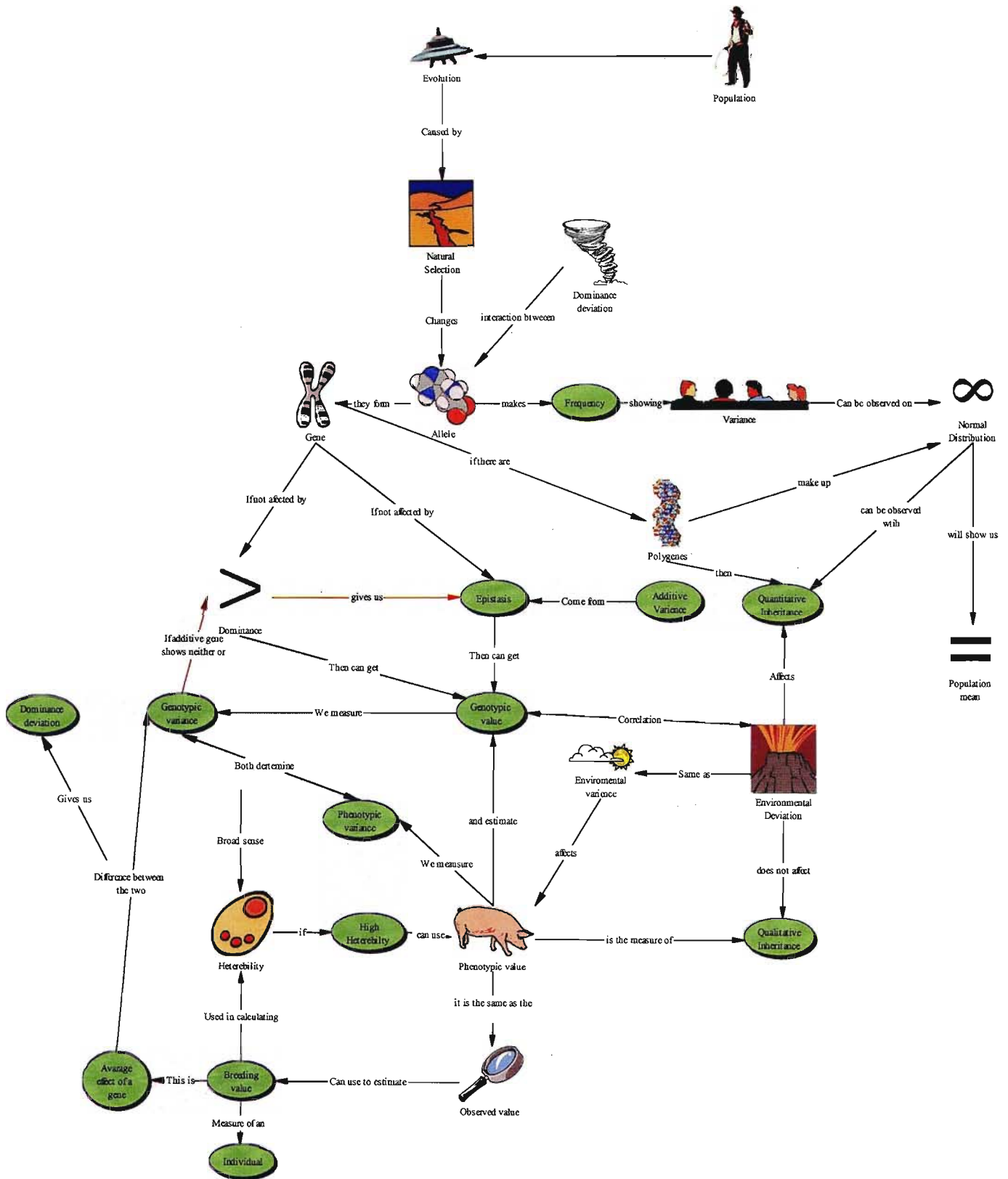
Map 5



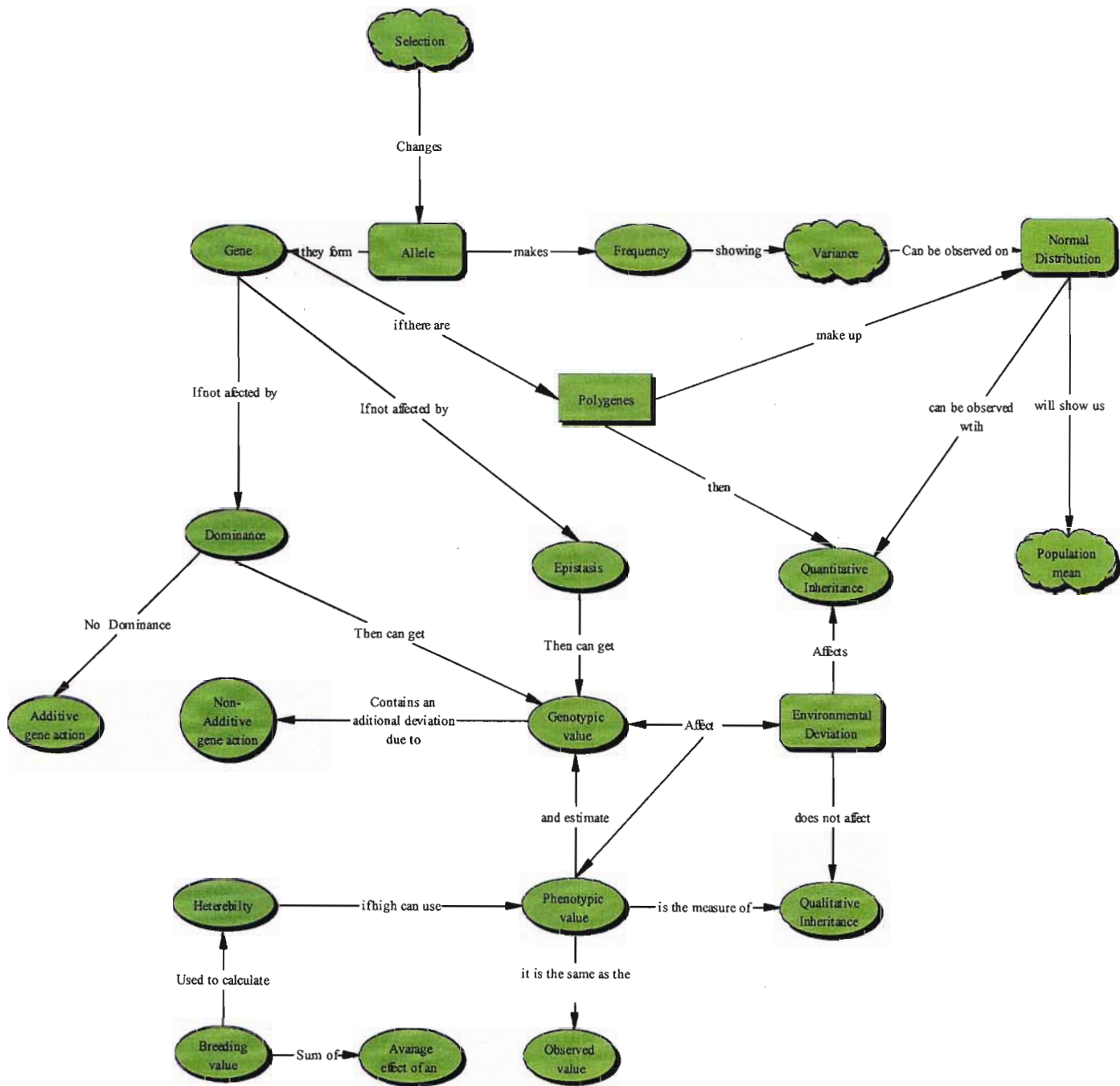
### Consistently poor set of maps

### Map 1



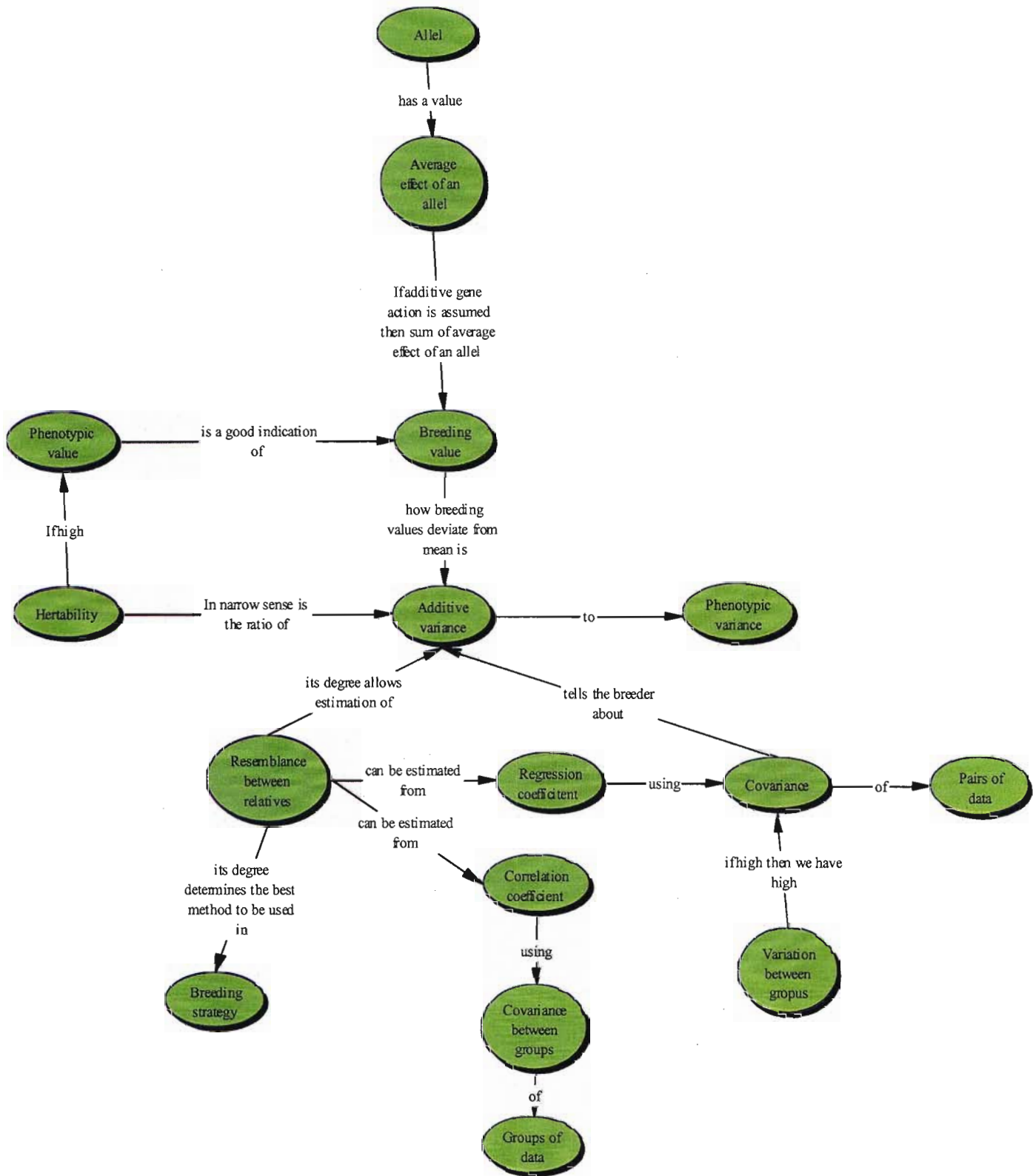


Map 2



Map 3





Map 4



Map 5