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An exploration and validation of computer modeling of evolution, natural selection, and evolutionary biology with cellular automata for secondary students.

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AN EXPLORATION AND VALIDATION OF COMPUTER MODELING OF EVOLUTION, NATURAL SELECTION, AND EVOLUTIONARY BIOLOGY WITH CELLULAR AUTOMATA FOR SECONDARY STUDENTS

A Dissertation Presented

by

GEORGE R. COLLISON

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University of Massachusetts in partial fulfillment
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School of Education

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DEDICATION

To Ben and Grace

ACKNOWLEDGEMENTS

Thanks to Judith, my wife, my inspiration and my editor. Special thanks to my friend and colleague, Kevin Mertes, who took my clumsy code and turned it into something that could execute in less than a lifetime.

ABSTRACT

AN EXPLORATION AND VALIDATION OF COMPUTER MODELING OF EVOLUTION, NATURAL SELECTION, AND EVOLUTIONARY BIOLOGY WITH CELLULAR AUTOMATA FOR SECONDARY STUDENTS

MAY 1992

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The Evolutionary Tool Kit, a new software package, is the prototype of a concept simulator providing an environment for students to create microworlds of populations of artificial organisms. Its function is to model processes, concepts and arguments in natural selection and evolutionary biology, using either Mendelian asexual or sexual reproduction, or counterfactual systems such as 'paint pot' or blending inheritance. In this environment students can explore a conceptual "What if?" in evolutionary biology, test misconceptions and deepen understanding of inheritance and changes in populations. Populations can be defined either with typological, or with populational thinking, to inquire into the role and necessity of variation in natural selection. The approach is generative not tutorial. The interface is highly graphic with twenty traits set as icons that are moved onto the 'phenotypes'. Activities include investigations of evolutionary theory of aging, reproductive advantage, sexual selection and mimicry. Design of the activities incorporates Howard Gardner's Theory of Multiple Intelligences. Draft of a teacher and student manual are included.

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CHAPTER 1

INTRODUCTION AND STATEMENT OF THE PROBLEM

Introduction

Experts in both the history of science and practitioners of the life sciences do not doubt that evolution by natural selection, evolutionary biology, and its sister science, population genetics are the key ideas to understanding modern biological thought (Futuyma, 1983; Ghiselin, 1969; Margulis, & Sagan, 1986; Maynard Smith, 1986; Mayr, 1988; Mayr, 1991; Ridley, 1983). Unfortunately these unifying topics generally have occupied a minor role in practical pedagogy in secondary science. One reason may be that the great 'evolutionary synthesis' that was achieved by the Darwinians, geneticists, paleontologists, naturalists, and geneticists from the 1920's to the 1960's was seen by educators, and perhaps by professional researchers, as very largely a technical matter with many supporting arguments expressible only in dense technical prose, often accompanied by pages of highly abstract mathematical analysis. The older modeling strategies in evolution and population genetics depended on algorithms with roots in either iterated finite difference mathematics or differential calculus and the modeling of continuous variables (Maynard Smith, 1974a; Maynard Smith, 1982; Morrison, 1991; Murray, 1989; Partridge, Lopez, & Johnston, 1984; Wilson, & Bossert, 1971).

The work of seminal researchers in this field like Fisher, Wright and Haldane are "incomprehensible to the average biologist, even to many of those interested in the processes of evolution . It is doubtful whether the majority of those who read mathematically-oriented papers on population genetics to gatherings of geneticists realize that many of their audience will have little understanding of what is said, and that few will understand it thoroughly (Crosby, 1973)."

In the late 60's Jack Crosby at the University of Durham pioneered the use of computers in modeling genetics and evolutionary biology. Crosby was among the first to explore computer models both for research and as pedagogical aids. He stated that "sometimes the arguments have forgotten the biology and been about the mathematics (Crosby, 1973)." "The consequence of this is that most biologists are often in no position to be able to judge for themselves the validity of the mathematical representations of evolutionary systems in which they are interested." He cites a vehement argument between Fisher and Wright on the evolutionary importance of random fluctuations, "a problem which could be solved quite easily using a non-mathematical model." Crosby's 1973 book, Computer Simulations in Genetics, is a landmark in the field. Almost all computer modeling of genetic systems draw on his insights.

Unfortunately, for the general reader, and certainly for the secondary educator, Crosby's work poses barriers as high as that of the mathematical formalism of earlier researchers. The computers and software environments available at the time he did his work were not at all friendly by today's standards. Crosby's algorithms are written in either assembly language for machines that no longer exist or in a higher level language he devised for his modeling called MENDOL. It is not easily accessible to the modern reader or computer user.

Since Crosby's pioneering work research in this area has been quite extensive. Over the last thirty years, new tools and new methods have been explored by many biologists and evolutionary theorists, as well as some life science educators (Avers, 1989; Axelrod, & Hamilton, 1981; Ayala, 1978;

Barricelli, 1962; Bowler, 1989; Conrad, 1970; Eldredge, 1989; Futuyma, 1983; Mani, 1984; Maynard Smith, 1982; Mayr, 1988; Price, 1985; Raup, 1991; Rizki, & Conrad, 1985). Generally stated, the method these investigators used involved finding numerical solutions to linked non-linear partial differential equations. Stochastic elements often were introduced to simulate the random effects of the selection process. Populations were treated as numerical quantities and incremented or decremented over time intervals. Various rates of natality or mortality were determined at each time interval based on auxiliary functions dependent on the states of other populations or initial conditions. As one might expect, analysis of this sort requires considerable mathematical preparation to comprehend, and more than considerable mathematical gifts to creatively apply to new situations and arguments.

This highly technical mathematical method of analysis poses an insurmountable barrier in presenting the important ideas of natural selection, evolution, and evolutionary biology at the secondary level. These are very important fields, necessary components of a student's understanding of the living world. They are also the threads that tie together the diverse areas of biological thought. Waiting till late in secondary school, or perhaps at the post secondary level, to introduce these topics until students have mastered the rudiments of algebraic probability and differential calculus is just not good enough. It is too late. Currently a very low number of students are exposed to these ideas; fewer understand them. Our society depends on a consensus of well informed citizens. Some science educators have tried to use modeling on micro-computers to circumvent this methodological bottleneck.

Some talented science educators have made very innovative adaptations of mathematical modeling once done on mainframes for educational purposes (Hodgson, & Murphy, 1984; Jungck, & Calley, 1985; Kinnear, 1986; Murphy, 1984; Murphy, 1986; Price, 1985; Slack, 1989; Slack, 1990; Thomson, & Stewart, 1985). Some have even abandoned the mathematical formalism that formerly carried these ideas, even in the computer models, and created graphic interfaces usable at the secondary level. In genetics education, the work of Kinnear, Jungck, Slack, and Stewart has made significant impact. Some of their work is available from educational software houses or commercial distributors.

Another approach was taken by General Systems Dynamics of Old Lyme, New Hampshire in the creation of Stella, a generalized graphic modeling language. Stella is based on the work of E. Forrester at M.I.T. Stella users place graphic 'primitives' of boxes (representing populations or stocks), valves (representing rates of change, positive or negative), and circles tied to either boxes or valves (representing auxiliary relationships or constants governing rates, or population interactions) at various points on the screen. Stocks are given initial values; rates of increase or decrease from valves are defined algebraically or by point and click charts referring to values of populations, auxiliaries, or other rates. The modeling engine within Stella automatically constructs differential equations, invisible to the user, that drive the output screens. Non-linear multiple linked differential equations are modeled with the same ease as graphing straight lines. Users of Stella can model quickly an astounding variety of processes, including biological ones.

Stella is a remarkable product. Its sole drawback from the point of view of modeling evolutionary phenomena is the nature of the modeling process itself. Stella uses differential equation methods to extrapolate from properties of whole systems to properties of systems as a whole; it is not based on properties of individuals. There is no 'genotype' or 'phenotype' possible for an individual organism in a Stella model. One can say 10% are heterozygous for trait X; but which individuals have this property cannot be determined. There are no individuals. For modeling of natural selection in any attempt to show it as a process dependant on variation within the individuals of a population, the drawback is severe.

Another type of system modeling using objects called cellular automata, one not based on difference equations or continuous variables, paralleled these efforts. It was based on some ideas set out by John von Neumann in the mid 50's. Automata modeling became more widely used in the 70's and 80's (Collins, & Jefferson, 1991; Jefferson, et al., 1991; Kauffman, & Levin, 1987; Langton, 1989; Langton, 1991; Murray, 1989; Pagels, 1988; Rizki, & Conrad, 1986; Toffoli, & Margolus, 1989).

What are 'Cellular Automata'? They are 'creatures' that occupy cells in a grid that is modeled in the memory of a computer. Rules govern the manner in which each automata changes through time. The rules can depend on conditions of neighboring automata, or on global conditions for the whole grid, or on internal conditions specific to that automata. Initially automata modeling was used on physical systems such as fluid flow, annealing of metals, or atmospheric modeling. The mathematics of each of these applications is notoriously very difficult. If conditions are changed even slightly, the new phenomenon is totally different than that which preceded it. Recent studies have shown that many systems studied in these fields are chaotic in behavior; it is theoretically impossible to obtain general models for phenomena in fluid flow, metallurgy, and atmospherics for other than very simple cases (Briggs, & Peat, 1989; Gleick, 1987; Langton, 1991; Morrison, 1991; Stewart, 1989).

Von Neumann attempted to bypass the problems presented in finding differential equations that would predict global properties of these dynamical systems from initial conditions by attempting to model them locally using objects called cellular automata. The automata cells would represent regions of a flowing liquid, a cooling metal, or a small region of the atmosphere. Based on these local 'events', and known physical laws, each cell would interact with neighbors, and the global pattern of interaction could be extracted by massive computation integrating effects at the cellular level. In general the effort was successful. Much climatic modeling is based on von Neumann's insights. Automata modeling also is subject to chaotic behavior under certain conditions, but it is more easily understood and modeled than current alternatives.

In the early to mid 1980's research in cellular automata took a turn that even von Neumann had not predicted. Scientists began to use automata to model natural systems (Barlow, 1991; Barto, 1975; Burks, 1975; Hogeweg, 1988; Langton, 1986; Margolus, 1984; Preston, & Duff, 1984; Wolfram, 1983; Wolfram, 1986). Cellular automata had properties, or could be defined to have properties, much like natural organisms. Each automata could be set up with a 'genetic code', a packet of data, analogous to a genome. The information in the code determines the physiological or social behavior or physical properties of the automata, its 'phenotype'. Each automata would interact with other automata, or its environment according to the rules set up by the programmer. The modes of inheritance of information from one 'generation' to another can be modeled by rules governing the cellular automata. Mutations in the pseudo-genetic code can be provided by a random number generator. Some modelers used self modifying neural nets in place of the 'rules' to determine what automata would do.

Based on research in this new area, a new discipline sprang up called "Artificial Life" (Brockman, 1988; Langton, 1986; Langton, 1991; Packard, 1987; Pattee, 1987). With the new discipline also came more questions (Augros, & Stanciu, 1987; Barlow, 1991; Margulis, 1988), "Is this life at all?" "Is this biology or computation?" For an educator the question is a side issue. If these artificial organisms have properties and behaviors analogous to living organisms, they can be very useful indeed. With micro-worlds based on these models students can have complete control over environment, inheritance mechanisms, mutations, agents and effects of natural selection, long range studies of effects of mutations, and many more key constructs of modern evolutionary theory.

The first of these cellular automata algorithms that was widely known was Conway's GAME OF LIFE in the late 1960's (Casti, 1989; Langton, & Kelley, 1988; Rucker, 1988). Conway's game happened in a square grid with automata showing up as lighted squares. They would "die" if there were too many neighbors with all edges occupied. If there were too few neighbors (only one), they would "die" of loneliness. With two or three neighbors, the automata would reproduce in an empty square. Lovely, complex patterns were produced under these simple rules. Some initial patterns were cyclic, recurring after a fixed number of generations. Others would always die out. A few would replicate to fill the entire board.

Analysis by Rucker and Wolfram demonstrated the power of the concept of cellular automata (Rucker, 1988; Wolfram, 1986). The creatures of Conway's LIFE, together with the generalized rules that govern them are

"Universal Computational Machines". This technical term means that any problem that can be programed and solved in a digital computer can be solved by a cellular automata model with correctly chosen rules and a space large enough to contain all its operations. Principles of cellular automata modeling are becoming very important in the designs and algorithms of the newest parallel processing computers.

Dewdney, in several articles in "Scientific American" popularized a simple ecological model called Sharks and Fishes based on cellular automata (Dewdney, 1988; Dewdney, 1989b). It had circled among hackers for several years before that. The cellular automata and the rules that govern the sharks and fishes are not intrinsically difficult to understand. These automata "live" in either two or three dimensional worlds; their interactions with other automata, such as motion, or breeding are determined by rules like: "If Energy > minimum, then Move one square at a random direction,." or "If Energy > minimum and Age > Breed Age, then Breed." There is no need to invoke calculus based mathematics to describe their interactions. The plots produced by the simulations resemble very closely natural predator/prey plots including natural limits of carrying capacity, as well as potential approximations of gene frequency ratios. In this regard cellular automata simulations are easily applicable to life science instruction in the secondary schools.

Unfortunately very little research has been done by educators on the pedagogical applications of these newer evolutionary and genetic models used by professionals. There is only one short report on application of the technique (Sepe, 1988). Some have speculated about the educational potential of this new form of modeling (Resnick, 1989; Taylor, Jefferson, Turner, & Goldman, 1987). One reason for the lack of educational literature may be that the material is so new. The first conferences on cellular automata and artificial life were held at Los Alamos in 1987. A second was held at the same site in 1989. Much of the material still remains in primary, technical sources. This inquiry will attempt to take some of the most recent results of research scientists in evolutionary biology, computer science, and artificial life, and translate their ideas and methods into working simulations and models, suitable for instruction at the secondary level.

Central to the design of this effort will be an adaptation of the 'conjecturing' technique pioneered by Judah Schwartz and Michal Yerushalmi in mathematics instruction with the Geometric Supposer (Schwartz, & Yerushalmy, 1987). Cited by many mathematics educators as "the first change in geometry instruction since the publication of Euclid's Elements" the Geometric Supposer approaches geometry in an inductive, student centered way.

Going far beyond the electronic geo-board, the Geometric Supposer provides a new learning environment and challenges students to actually "do" mathematics, to think like mathematicians. As the title of Schwartz's article states, it does restore the sense of invention to the field of geometry education. Rich formulations, called conjectures, are given to students to investigate. Each conjecture may contain many different "proofs", some deeper than others. Using the measuring tools of the Geometric Supposer the students probe the relationships of elements of the conjecture construction, doing "what if's" at any point on the way. When they are satisfied that any proposition is true (or false), they attempt to construct a standard two-column proof for it. The rationale for the seemingly artificial deductive form of the proof is supplied by the intellectual investment that the student has in the problem through his or her inductive explorations. The Geometric Supposer provides normally passive students with an active way to interact with geometry and mathematics, a way to develop intellectual commitment to solving a mathematical problem as mathematical researchers. This new modeling technique using cellular automata, combined with the conjecturing pedagogical strategy of the Geometric Supposer shows great pedagogical promise in life sciences.

Statement of Purpose

The Nobel Prize winning physicist, Murray Gell-Mann once remarked that education in the 20th century is a most remarkable and exciting experience. It is like being invited to a world class restaurant staffed by the world's finest chefs. With great relish one sits down to begin a meal that promises to be most memorable, except the only thing you are offered to eat is the menu.

Unfortunately this analogy to current educational practice is all too accurate. In a world where there is an information explosion, where there are more active writers, scholars, researchers, and scientists than at any time in the history of our planet, our students are provided educational experiences with all the nutritive value of cardboard. Offerings of this sort may be enough to provide real sustenance if the student's mental apparatus contains the analog of the busy micro-fauna in a termite's gut. Cellulose is digestible with the right enzymes. If you don't have them, all one can do is contemplate a string of finely printed words. In many classrooms students just get the menu read to them. The real question is "Where's the meal?" As committed educators we can, and must, do better. I feel we can give all of our students, not just those with special enzymes, a basic understanding of the great ideas of this century. This shared understanding is necessary for our species and the richness of life on this plant to survive into the next century (Ehrlich, 1986; Ornstein, & Ehrlich, 1989; Thornburg, 1991).

The core of this dissertation centers on a serious consideration of Gell-Mann's remarks when applied to teaching in the life sciences. Much like the investigation of the mysterious beast called the elephant by the fabled blind men, many students' approach to life science commonly yields confusing and conflicting interpretations. The unity of the life sciences, provided by the insights of evolution, natural selection, and evolutionary biology eludes them. I wish to explore the opportunities offered by micro-computers and cellular automata modeling, combined with innovative pedagogy, that will fill this need for a vision of the unity of the life science. My investigation will explore this potential in three areas: Accuracy and Appropriateness of Content, New Methodology, New Ways of Thinking.

Accuracy and Appropriateness of Content

The micro-worlds populated by cellular automata exhibit many of the properties that communities of living organisms exhibit. Cellular automata themselves exhibit many properties similar to those of living organisms. I wish to make no arguments that cellular automata, no matter how complex, are 'living' systems. This is a field for experts; some of whom have answered in the affirmative (Brockman, 1988; Hogeweg, 1988; Langton, 1991; Langton, et al., 1988; Ray, 1991; Rizki, et al., 1986). Other strongly argue against this position (Harris, 1991; Margulis, 1988; Mayr, 1988). I will treat cellular automata models as powerful tools, very useful heuristics for science educators for investigation of relationships and concepts in evolution and population genetics for "possible" living organisms at levels and in ways that were not possible before.

New Methodology

The ease of manipulation of these micro-worlds provides a powerful pedagogical tool to explore the unifying ideas of evolution and population genetics at the secondary level, with possible extensions to the middle grades. Much like the micro-worlds of Logo and the Geometric Supposer the worlds populated by cellular automata permit personal interaction of the learner with the subject area. In life science education cellular automata modeling provides a remarkable potential for student centered learning that is constructive, not instructive. Students can appropriate their own knowledge, rather than be the passive recipient of the knowledge of others.

Beyond providing a platform for a much needed constructivist approach in this discipline, cellular automata modeling also provides an opportunity to mold instruction to individual learning styles. Howard Gardner's Theory of Multiple Intelligences gives a framework for restructuring curricula for individual learning. Gardner set out seven modes by which humans learn and interact with their surroundings: Linguistic, Logico-Mathematical, Intrapersonal, Spatial, Musical, Interpersonal, and Kinesthetic (Gardner, 1988; Gardner, 1989). Gardner believes that all of us have a dominant mode with capabilities in the other six.

Unfortunately most classrooms and instructional techniques rarely go beyond the first three, with much science instruction assuming a Logico-Mathematical mode continually. Limiting educational practice to these modes fails students in two ways. First, it ignores the needs and abilities of students whose dominant intelligence is not one of these three. Secondly, it fails other children in the class whose intelligence and experience are not validated in these modes. Computers offer educators an invaluable tool in opening up their classrooms to multiple paths to learning. Ways to include other individual learning styles in science instruction will be explored.

The approach will also build on the research done on student misconceptions in the sciences in the last decade. Gardner calls this "the smoking gun" in the indictment our educational practices (Gardner, 1991). The "venerable subject of physics" provided the first evidence that "even when our schools appear the most successful, even when it elicits the performances for which it has been designed, it typically fails to achieve its most important missions." In several carefully designed investigations it was found that the majority (in some cases over 80%) of undergraduate physics majors and engineering students, even some graduate students, at M.I.T. (DiSessa, 1983), Johns Hopkins (McCloskey, 1983), the University of Montreal (Faucher, 1983), and the University of Massachusetts (Clement, 1982b; Mestre, 1989) do not demonstrate a qualitative knowledge of Newtonian mechanics even slightly outside a textbook context.

Gardner cites other studies in the biological sciences that reveal similar startling gaps in understanding in genetics (Browning, & Lehman, 1988; Martin, 1983; Simmons, 1987; Slack, 1990; Thomson, et al., 1985), meiosis (Brown, 1990; Stewart, Hafner, & Dale, 1990) and natural selection (Bishop, & Anderson, 1990; Brumby, 1979; Brumby, 1984; Clough, & Wood-Robertson, 1985b; Greene Jr., 1990; Jungwirth, 1975). Brumby's pioneering 1979 study discovered that over 80% of the second year medical students interviewed preferred Lamarkian or teleological explanations of evolutionary processes. Bishop found, among other distressing discoveries, that years of instruction in biological science made no difference in students' acceptance of teleological or Lamarkian explanations. The other studies, their findings, and ways that The Evolutionary Tool Kit can practically approach the problems they have found will be discussed latter in this paper.

In both physical and biological sciences the world views that students' brought to classes are remarkably robust and resistant to change. The conclusion of all these researchers was that students' preconceptions must be addressed if educators can expect instruction to bring about any meaningful conceptual change. The Evolutionary Tool Kit using microworlds that students construct themselves, populated by cellular automata attempts to provide life science educators a new tool to challenge these naive world views and assist students in accommodating to conceptual change.

New Ways of Thinking

The computer is very much a part of our world. Its virtues as data collector, analyzer, predictor, quantifier are extolled in all forms of media. It is a good thing that this machine has such potential, as we certainly will need its services to solve the problems that face our species and the planet as a whole in the coming decades. The problems are such that our minds and sensory apparatus do not even perceive them as problems at all: toxic chemicals, nuclear waste, ozone depletion, green house gases, urbanization. Psychologist Robert Ornstein attributes this difficulty to "old mind" mental mechanisms like "fight or flight", among others, that have dominated our thought patterns since our Hominid ancestors found them so useful (Ornstein, et al., 1989). The newer challenges require "new mind" mechanisms, new ways of seeing. Evolutionary biology and population genetics, as I noted before, are particularly difficult to teach because the disciplines are fundamentally dynamic, long-term processes, all but invisible to the eye. Our educational medium is generally a 40 minute lecture. Our perceptual and conceptual frameworks are not attuned to see change on a long term scale.

The point Ornstein makes is an old one; it is also a profound one, well worth exploring. Emmanuel Kant stated three hundred years ago that all perception is interpretation. The world is changing in a decade more than it changed in a millennium; the rate of change is ever increasing. "Adapting to change must be the center of any new kind of teaching (Ornstein, et al., 1989) ." Disciplines like Evolutionary Biology and Population Genetics where dynamic change are central elements are most important in forming the perceptions that will aid a student in understanding the world they must live in. Students investigating with computers through cellular automata modeling can gain precious insights that can help mankind solve the problems in the next century.

There is also a fourth theme running through this investigation: Critical Thinking and Biology Education. It is a central concern certainly, but it is not of the same quality as the other three. Matthew Lippman's defines critical thinking as "skillful, responsible thinking, that facilities good judgement because it (a) relies on criteria (b) is self-correcting, and (c) is sensitive to context (Lippman, 1988)." There are many who say that this is what is done in their classrooms. This is nothing other than the scientific method. The second statement may be valid. The results of the cognitive researchers in science education belie the general validity of the first. A curriculum that is inflexible, teacher centered, knowledge based, and ignorant of the deeply rooted misconceptions that our students bring to school cannot be said to practice critical thinking.

It is through the exercise of critical thinking the Lippman sees the classroom developing into a "community of inquiry." The Geometric Supposer has managed to do this for a curriculum as venerable as Euclidian geometry. Geometry classes using The Geometric Supposer are alive with inquiry; students are working as mathematicians exploring and discovering their own mathematics.

It is most important to note that mathematics is not science, nor science mathematics. The core ideas in geometry, the nature of induction and deduction require different pedagogical strategies than core ideas in science. Contrary to much popular lore in books on science education, the central method of science is not induction or deduction but analogical thinking. It is the central analogies, models, *gestalts*, that define the connections and extensions of a discipline in science. The harmonic oscillator in physics is applied from the level of atomic particles to motions of galaxies.

Life science brings very different analogies. In genetics, the particulate nature of inheritance is a central theme, as is the role of randomness in genetic recombination. Evolutionary biology poses a particularly difficult problem. As Ernst Mayr states, the first, and most important change in Darwin's thinking was "The gradual replacement of the assumption that all individuals of a species are essentially alike by the concept of the uniqueness of every individual (Mayr, 1991)."

This is a very difficult step to make indeed. It is a change in paradigm from essentialist thinking (thinking in terms of types) to population thinking (thinking in terms of individuals defined by variety). Essentialist thinking had dominated Western (and Eastern) thought for thousands of years. Plato's ideas, Aristotle's categories, and all their descendents are still very much with us. Our language itself is essentialist in formulation. We use the word 'dog' to define a class of organisms, not to describe the variations of individuals in that class. Language ignores these differences. The problem is much deeper than recognition of simple stereotyping.

Essentialist thinking has shown remarkable success in other scientific areas like mathematics or physics. All triangles, all circles, pendula, all harmonic oscillators are to be treated in a similar fashion. Galileo's brilliant insight in dropping the weights from the tower was to realize that what was important was not that the times were different, but that the time it took to fall was almost the same. He specifically stated that he thought the difference was due to some other factors (which we now call air resistance) that made the heavier fall slightly faster. It was a remarkable typological insight. Even much of the biological cannon, theories of classification and taxonomy are based fundamentally on essentialist thinking.

Evolution and natural selection are not based on typological insights. "Variation, which had been irrelevant and accidental for the essentialist, now became one of the crucial phenomena of living nature (Mayr, 1991)." Once organisms are viewed as members of a population, each with individual differences, then competition between them has some real meaning. "Indeed the concept of competition among individuals would be irrelevant if all these individuals were typologically identical - if they had the same essence (Mayr, 1991)."

A great deal has been written about Darwin and the origin of populational thinking and his first insights into the process of natural selection. The application of Lippman's definition and the creation of a community of inquiry in the biology classroom demand that the students own minds be the subject of inquiry into the nature of individuals and populations. To achieve the conceptual change required, the teacher must create an environment which can demonstrate the power of populational thinking and, at the same time, the inadequacy of essentialist thinking.

The Evolutionary Tool Kit attempts create an environment in which the students can experience the same cognitive dissonance that Darwin experienced, and then, through directed discussions and guided inquiry, uncover the advantages and insights possible with populational thinking. From the studies already cited by Brumby, Bishop and Anderson, Clough, Greene, Hatano, and Jungwirth, reading about it, or being lectured about it is completely insufficient, even for our brightest students. One reading of Malthus (in which populational thinking is not explicit at all) was sufficient for Mr. Darwin; but this was a special case.

The target population for The Evolutionary Tool Kit is not upper level, advanced track students. It is aimed at general students in the early years of secondary schooling. It is during these years that the basic questions, the fundamental metaphors of the study of life science are formed. The design is qualitative; it is intended to model concepts, not mathematical models. If the effort in secondary life science is classificatory or essentialist to the exclusion of other kinds of thinking, it is little wonder that students later have a great deal of difficulty understanding concepts based on populational thought.

I am suggesting that introductory life science students pose and investigate 'the big questions' as an essential part of their studies. Mark Ridley in The Problems of Evolution (Ridley, 1983), masterfully frames for the general reader the main lines of inquiry of evolutionary biology in the form of ten 'Great Questions'. The first four are: "Is evolution true?", "What is the nature of heredity?", "What is the mechanism of evolution?", and "How does natural selection work in nature?" Other questions explore the nature of molecular evolution, principles of classification, 'What is a species?', forces that drive speciation, rates of evolution, and problems of macro-evolution. Professor Ridley asserts that almost all biologists are firm in their belief that the answers to the first four questions are settled. The answers to the last six are less certain; some even lend themselves, even in professional circles, to heated discussion and very diverse opinions. Others may certainly have a different set of questions (Mayr, 1988).

The problems faced by secondary educators attempting to teach natural selection and evolutionary biology are certainly very different than those of the researcher in seeking answers to any of them. Clearly, in the minds of many students, the answers to the first questions are not settled firmly at all. Indeed they may be settled quite firmly, but not in the direction of evolution or modern evolutionary biology. It is not the intent of this inquiry to convince creationists of the validity of Darwinian theory. I am seeking a method to increase accurate understanding of evolution by natural selection. Results by Bishop and Anderson show that for university students a course specifically designed to produce conceptual change can increase by 50% the number of students understanding of the fundamentals of the theory evolution by natural selection. The number of students who 'disbelieved' the theory after 'successful' instruction remained unchanged. This result may not be comforting to science educators, but it does give an indication of the robustness of students' preconceptions.

The intent is to provide an learning environment that is theoretically and pedagogically sound, in which students can explore interactions of artificial organisms, operating under rules that are closely analogous to those constraining living organisms. They can then modify the rules, make hypotheses, and refute or verify them. In the course of their investigations seminal terms like, population, mutation, population sample, natural selection, selected for, selected against, advantageous, gene pool, and gene frequency will appear in their natural context, as descriptions of phenomena they encounter.

Within the confines of the computer simulation, I wish to make the arguments in favor of evolution plausible. The experience should bring the student to a level of cognitive dissonance at which they can begin to feel uncomfortable with their naive view of organisms and typological thinking. I wish to provide a platform on which students can build for themselves a knowledge of the interaction of organisms, genetic information, and the environment that supports them. This experience with the core metaphors of the discipline will lay the groundwork for inductive argumentation and content familiarity so that students can follow and assess inductive arguments in favor of evolutionary theory using evidence from fossils or living organisms for interpretation and support.

Once an understanding of populational thinking has been forged, students can approach the problem of seeking the mechanism of evolution is to find a theory that can explain evolution, that can explain adaptation, and fit the facts of heredity. Darwin, Huxley, Weissman all faced the same difficulty. Examples of evolution and adaptation are plentiful from the paleontological record and from the observations of naturalists: multi-toed horses, Galapagos finches, pepper colored British moths, and many others. It is most important for educators to note that none of these examples are dynamic. This fact was noted by the pioneers at the turn of the century also.

Yes, one can parade photos of fossils of many sorts, slides of finches and moths; all, conclusive "proof" of evolution and its traces in time. Yet the student is very much the passive recipient of all of these "illustrations". One really must ask "What has the student proven, or can prove to him or herself?" Simulations using cellular automata provide just this platform for exploration.

Beyond this pedagogical difficulty in convincingly presenting support for evolutionary theory, there is a major problem integrating Mendelian inheritance as a support for evolutionary theory. The heated arguments from the pages of the history of biology attest to the difficulty of this synthesis (Futuyma, 1983; Ghiselin, 1969; Gillispie, 1960; Mayr, 1988). Demonstrations of the underlying algebra of Baysian probabilities by drawing colored marbles from jars are insufficient. It didn't convince the last few generations of scientists, why should it convince our students? The natural process is dynamic, not algebraic. Under Mendelian inheritance there is no directing process that could bring about evolution. Students sense this problem immediately: how can randomness bring about any change other than some organic smearing? The relationship is not obvious; but it is exactly this random change, random mutation that is required by natural selection to bring about adaptive states (Futuyma, 1983; Ridley, 1983).

The key insight is that the randomness of heredity provides only the raw material; the particulate nature of Mendelian inheritance actually conserves variation while natural selection operates on it. Mendelian particulate heredity is an all or nothing affair, the traits produced by the genes do not blend. It is very easy to hold the idea that, in a large population, one mutation, advantageous or not, will naturally "wash out";

this idea is also quite wrong. Cellular automata permit students to experiment with systems of heredity not found in nature (like blending of characters) but which are found in their own naive views, and those of scientists of former generations. Why was the theory of blending characteristics discarded? Saying that "it is wrong" is circular; it does not answer the question. Why is it wrong? What results does it predict?

Conjecturing with cellular automata can be a strong first step in providing a student with hands-on experience that particular inheritance will actually preserve variation. Using automata operating under alternative models of heredity, for example, "paint-pot" genetics, students can explore the counterfactual environments. As an example, students can explore the conjecture that under "paint-pot" genetics: "If heredity is a mixing of qualities (as most assume), then any variation or mutation, even a very highly advantageous one, will wash out, leaving little or no effect on the population." This conjecture, interestingly, is true.

Guessing at the meaning of photos of fossils or trying to extrapolate population changes from bean bag genetics is just not enough. With the resources at our disposal, science educators can do much better than attempting to teach natural selection and evolutionary biology with educational techniques little changed since the last century. There is such a thing as "evolutionary pressure". How can a student experience or believe in the effects of natural selection, or become convinced of its validity, unless he or she can actually see these forces drive changes in organisms before their eyes? A powerful pedagogical advantage of modeling with cellular automata is the concreteness of the conjectures and the associated experiments. Students need "hands-on" time to manipulate and work with complex ideas before they can really be said to believe them. The cellular automata experiments are dynamic, not subject to the vagaries of interpretation of the incomplete fossil record. They actively involve the student from inception of the conjecture to the design of the experiment, to the interpretation of the results.

Implementation of the Rationale

I propose to design and construct a general cellular automata modeling environment for life science students called The Evolutionary Tool Kit that will simulate many of the processes of biological natural selection and evolutionary biology. Cellular automata are ideal to demonstrate the interaction of these two great ideas of modern biological thought: natural selection and evolutionary biology.

The data structure of the automata model sets up a 'genetic code', a 'genotype' for each automata as well as an environment in which they 'live' and interact. The code determines the physiological or social behavior or physical properties of the automata, its 'phenotype' according to the rules of the traits assigned to the organism by the student experimenters. Inheritance can be governed strictly by Mendelian laws, or, alternatively by other hypotheses such as "paint pot" genetics. Mutations in the pseudo-genetic code can be provided by a random number generator.

Most importantly, adaptation of the individual organism is determined by the interaction of the automata with each other, with the environment, and by other auxiliary calculations based on size, shape, and physical law. It is important to note that modeling of natural selection at the individual level is not possible using models based on finite differences or differential equations. Cellular automata are local phenomena, locally determined. What is truly remarkable is that these simple digital beings do evolve, at a rate of hundreds of generations per hour, much like living organisms would at a significantly slower rate.

In the field of education, no research has been done in this area. I have found several professional references that extend cellular automata to evolutionary and ecological modeling (Brown, 1987; Collins, et al., 1991; Conrad, & Strizich, 1985; Goel, & Thompson, 1987; Hogeweg, 1988; Langton, 1991; Lovelock, 1991; Niklas, 1986; Ray, 1991; Rizki, et al., 1985; Taylor, et al., 1987). Models studied by these professionals include mosquito control, evolution of language, lek formation, evolution of molecular self-reproducing systems, and models of punctuated equilibria.

Clearly the The Evolutionary Tool Kit is a much simpler model than any of these; it will permit qualitative modeling of inheritance and evolutionary processes. Reproduction is modeled through particulate (Mendelian) or alternative continuous ("paint-pot") models. Students may also select (under Mendelian inheritance) either SEXUAL or ASEXUAL genetics, dominant or recessive traits, multiple allele (in series), adjustable mutation rates, and adjustable penalties for some traits (say multiple births). Predation can also be modeled.

Students will also be able to control the interaction with the environment with the substrate in some regions specified as "fertile", "average", "poor" or "seasonal". In future models the environment will be time variant. Also there will be the possibility of setting up time dependant barriers impassible by organisms to investigate rates of speciation from isolated populations. Also catastrophic declines can be explored to investigate the effect of drastic reductions in population on the gene pool. It is also possible to extend the interaction with the environment to include metabolic reactions and the effects on the substrate. Interactions between organisms will also include social interactions such as hunting strategies, camouflage, flocking or cooperative or altruistic behavior.

All experiments will be constrained by physical laws. The automata will move, live, or die using first order estimates of gravitation, tensile strength, or drag (laminar flow) of genetically determined shapes derived from physiology or fluid mechanics. Students will be able to change some physical constants such as gravitational acceleration (to try out life on another planet , for example). Extensions to considerations of metabolic functions of the organisms and their affect on the environment will also be explored.

All of the above investigations appear in various research literature on automata modeling using super-computers, Connection Machines, or high powered work stations. A further constraint is that The Evolutionary Tool Kit fit comfortably in the confines of the type of computer that most secondary educators are likely to see in classrooms over the next decade.

Before going on to a review of automata literature and a description of the algorithms used by The Evolutionary Tool Kit let us consider some sample investigations of modeling with cellular automata, much in the spirit of the approach taken by the Geometric Supposer, in which the student to explore the world of evolutionary genetics in a semi-concrete way, making conjectures, designing experiments and verifying or disproving hypotheses on the way.

In a sample conjecture, a student would first select the inheritance pattern (we will assume Mendelian for these examples). They would then select ASEXUAL or SEXUAL inheritance. Sexual populations present a particularly interesting counter-intuitive result. It is very tempting to conclude that an advantageous mutation, once it has reached a certain low percentage in a population, will go on to propagate through the entire population. Most people guess that it will probably take over 100% of the gene pool. Similarly, one is very tempted to believe that recessive traits could never propagate through breeding populations. Even if advantageous, they would always occupy a small percentage of the population. Both of these propositions are false. The cellular automata model can demonstrate that quite easily. Sample hypotheses or conjectures students can make and explore with cellular automata are:

Conjecture one: "In a sexually reproducing population, an advantageous trait expressed by a dominant allele will eventually propagate through the entire population." This is false. Such a trait will always be expressed over the recessive allele in the phenotype. This means that the trait will always remain part of the gene pool, even though it may be heavily selected against. An equilibrium will be reached after a sufficiently large number of generations. It is NOT dependent on the Mendelian ratios, rather on a 'fitness' measure of the trait.

Conjecture two: "In a sexually reproducing population, an advantageous trait expressed by a recessive allele will never propagate through the entire population." This also is false. Oddly enough, an advantageous trait expressed by a recessive allele will take over all of the population. In order for a recessive trait to manifest in the phenotype, the individual must have two copies of the recessive gene (homozygous recessive). It will take considerable time for sufficient numbers of homozygotes to build up. When this happens the take over of the population is very rapid. It approaches 100% quickly.

Conjecture three: "In a sexually reproducing population, a disadvantageous trait expressed by a dominant allele will eventually be eliminated from the population." This is also false in general. There are many examples of this phenomena in human genetics: Huntington's syndrome, several forms of dwarfism, polydactyly. Students can find conditions that make the conjecture true also - early lethality or impaired fertility.

Conjecture four: "In an asexually reproducing population, a disadvantageous trait will not propagate through a population." This is false. In fact disadvantageous traits propagate readily. Haploid inheritance patterns are not limited to lower animals. All mammals have haploid inheritance patterns in the male chromosome (it comes from one parent only) or in mitochondrial DNA (passed on by the ovum). The laws of probability guarantee that after a sufficient time the decedents of one ancestor comprise the whole population (one all female generation kills any one line of X chromosomes). The mutation rate is relatively constant over this time. Therefore X chromosomes have a tendency to accumulate disadvantageous traits. The high rate of infertility in African cheetahs seems to be an example of accumulation of genetic defects.

The Evolutionary Tool Kit will permit students to explore conjectures like these in evolutionary biology in a highly dynamic and creative way under a wide range of environments and genetic constraints. Such a program will be a most useful addition to life science classes at the secondary level. It will put into the hands of students and teachers alike a tool to explore the core ideas of the life sciences using the results of contemporary researchers without the heavy burden of abstract mathematical formalism which dominated exposition of these topics in older literature. Notes on staff development for teachers and departments planning to use this approach should also be included in discussion of educational applications of The Evolutionary Tool Kit . Without the pedagogical mechanism of cellular automata I see no way to provide students a "hands-on" feel for the relationship of random mutations at the molecular and the phenotypic world of classification and morphology (Pickover, 1990; Sheppard, Turner, Brown, Benson, & Singer, 1985; Thompson, 1942).

The approach taken in The Evolutionary Tool Kit is very flexible. Many extensions are possible. Of particular interest is use of cellular automata modeling to include inclusion work done by Sheppard and Owen on Mullerian rings in butterflies (Owen, 1980; Sheppard, et al., 1985). It is possible to have cellular 'genes' that govern wing patterns (Owen, 1980). Owen's formal work gives algorithms for generating patterns of butterfly wings. With a cellular automata approach, one can integrate these formal pattern generating algorithms with an analog of the natural selection process. The distasteful butterflies with one pattern would co-evolve with the tasty mimics with another pattern right on the screen. Through random mutations and the pressure of selection, the patterns of the tasty butterflies will "evolve" to similar patterns to the distasteful butterflies. It is an important pedagogic point to note the effects of non-random transitions, those that give rise to the Mullerian or Batsean rings. Yes, the changes at the molecular level are random, yet direction to the changes is produced by the filter of natural selection. Changes at the molecular level may also force other changes in populations in non-random fashion. The randomness in the process of natural selection occurs only at the final step. Natural selection is the final filter that shows us the observable phenotypes. The role of randomness in the process of natural selection, from a Neo-Darwinian viewpoint, may be considerable.

Naturally The Evolutionary Tool Kit should be pilot tested in actual classroom environments, and its evaluation based on the experience of students and teachers. Afterwards a revised edition should be made available to a wider range of schools and student populations. Unfortunately on-site piloting is not possible at the current time. Three obstacles must be overcome before on-site trials of The Evolutionary Tool Kit can begin.

First, the methods and algorithms used by the cellular automata models are very demanding on the hardware platform. The most powerful commonly available machines like Mac II's or 386 based processors and several megabytes of memory are still too slow for many of the computations posed by the tool kit. Stronger machines are not generally available at the secondary level now, but in a few years they will be. The Evolutionary Tool Kit will provide a prototype for modeling evolution, natural selection, and evolutionary biology for these new generation of computers.

Second, the underlying assumptions behind all of the models in The Evolutionary Tool Kit are Neo-Darwinian (Cho, Butler, & Nordland, 1985; Futuyma, 1985; Mahadeva, & Randerson, 1985; Margulis, et al., 1986; Maynard Smith, 1989; Mayr, 1988). The Neo-Dawinian synthesis, developed over the last 40 years, recognizes the important role of randomness in natural evolutionary processes. This recognition brought about some fundamental changes in the way biologists conceive of the process of natural selection. As set out previously explanations in The Evolutionary Tool Kit strongly depend on the development of populational thinking. The program's design encourages students to construct "What if?" scenarios to confirm or even dispute these findings. Few secondary teachers are currently prepared to present these views. There are strong indications that very few of our potential teachers understand the nature of natural selection, and the populational thinking that underlies it s (Bishop, et al., 1990; Greene Jr., 1990; Jungwirth, 1975).

A desired result is for students themselves to construct the Neo-Darwinian synthesis, or even find ways in which it must be modified. It is for this reason that the first use of The Evolutionary Tool Kit may be in teacher training programs in schools of science education. This issue of confirmation of the teacher's understanding of the discipline will be explored in the section on validation. Mathematics educators learning to use software like The Geometric Supposer worked very hard to developing a pedagogy and curriculum that is student centered; many stated that they learned more mathematics while learning to use these student centered programs than they did at university.

There is preliminary evidence from genetics education of a similar phenomenon (Jungck, et al., 1985; Simmons, 1987). The simulations by Jungck (The Genetics Construction Kit) and Kinnear (Catlab) require teachers to work more on a level with their students, as facilitators, even as colleagues in investigating a problem. Many find the experience unsettling; they are uncomfortable with inquiries in which there may be no 'right answers'.

I feel that prototype software like The Evolutionary Tool Kit used in schools of education can partially pave the way to a student centered curriculum in evolutionary studies. In the current environment in secondary schools, the model advocated by The Evolutionary Tool Kit would prove very difficult for many science teachers, given the current state of integration of computers in science instruction. Much staff development is needed.

Third, The pedagogical model advocated by the design of The Evolutionary Tool Kit much like that of The Geometric Supposer, goes far beyond what educators normally conceive as CAI (Computer Assisted Instruction). As one seasoned geometry teacher said of her own experiences in geometry classes, "I felt like I had been trained to perform some one else's mathematics. With The Geometric Supposer students actually become practicing mathematicians". With The Geometric Supposer mathematics teachers went a long way to developing a pedagogy and curriculum that is student centered. I feel that prototype software like The Evolutionary Tool Kit can partially pave the way to that laudable goal. The model advocated by The Evolutionary Tool Kit would prove very difficult for many science teachers, given the current state of integration of computers in science instruction.

Since at this time The Evolutionary Tool Kit cannot be validated in practice, I will seek out the help of expert practitioners in science education and pedagogy to validate content soundness, use in teacher preparation, and applicability to performance based assessment. I have contacted and received confirmation of their willingness to review and comment on The Evolutionary Tool Kit from the following experts: Soundness and appropriateness of content by Richard Wickender, Ph.D., Paleobiology, University of Massachusetts and Paul Deal, Research microbiologist, NASA, author of the only other automata based simulation on evolution; Potential for new directions in pedagogy by Seymour Itzkoff, Professor of Education and Philosophy, Smith College; and Potential for use in classrooms and in staff development programs by Neil Davidson, State Sci-

Net Coordinator, and Science Staff Developer, Massachusetts Department of Education.

These experts' comments and suggestions will be incorporated into the instructional design of the program, and in its documentation. Although each is associated with a single topic in the above schema, each expert will be encouraged to comment on the other two topics, to the extent that they feel themselves qualified to do so.

CHAPTER 2

REVIEW OF LITERATURE

For clarity of exposition, the review of literature is broken into four parts: education research on misconceptions in evolution and natural selection; commercially available software in natural selection and evolutionary biology, commercial software based on cellular automata modeling, and current research on modeling with cellular automata that has immediate applications for middle and secondary educators.

Research on Misconceptions in Evolution and Natural Selection

The pioneering work in this field was done by British researchers, Margaret Brumby, J. A. Deadman and P. J. Kelly in the late seventies as part of the educational reform that swept that country at that time. Before the 1960's evolution as a phenomena, the process of change and adaptation, natural selection, randomness, and inheritance had not been part of the secondary curriculum. After the 1960's heredity and evolution assumed a central place in biology textbooks with passages on the importance of these concepts for both society and the individual.

The introduction of these ideas was a matter of considerable debate. In their studies on misconceptions of secondary students on evolution Deadman and Kelly (Deadman, & Kelly, 1978) cite studies by Kelly and Monger (Kelly, & Monger, 1974) that show both teachers and students find aspects of evolutionary theory such as heredity (Hardy-Weinberg, DNA studies, genetic code, and the gene-enzyme hypothesis) difficult. In evaluation studies of the Nuffield project the students performance on this section of the course was poor compared to other units. They also cite a theoretical study by Shayer (Shayer, 1974) based on a Piagetian framework in which Shayer suggests that "... a reasonable structure, based on Nuffield content, might be arrived at by abandoning the evolutionary picture objective of Year V (with its implied distorting constraint of the content of previous years), regarding the environmental approach of Year IV as the end objective instead...". Deadman and Kelly strongly dissented. "We should accept the challenge of finding suitable methods of presenting these topics (heredity and evolution) to the under 16's (general biology students)." Evolution and heredity are important at this level; we have not yet established what methods and sequence is appropriate.

In an attempt to discover the problems that may lay at the root of difficulties students have with these topics Deadman and Kelly proceeded to interview 52 boys, ages 11-14, from an all male secondary school to ascertain their understanding of seven key concepts: evolution as a phenomenon, why evolution occurred, the process of change, adaptation, natural selection, chance, and inheritance.

All boys were aware of evolution as a phenomena but the form of the concept varied considerably. Some saw it as a series of disconnected episodes. Much fewer showed awareness of a time dimension. Almost all described evolution as associated with primitive life forms. They showed no reference or "apparent understanding of relationships between groups of animals."

Explanations of why evolution occurred tended to be naturalistic (associated with 'needs' or 'wants', or 'making them better') or overtly environmentalistic (associated with specific changes in animals and the environment, such as the Ice Age). In older boys, though a few used biotic factors in their explanations, explanations were still naturalistic.

The explanations for the process of change invariably elicited explanations similar to that of why evolution occurred. "Some were phenomenistic ('It just happened.')" Others were naturalistic. Still others were explicitly Lamarkian. Deadman and Kelly noted a very interesting conceptual shift that occurred when boys who explained with great certainty starting off in terms of mutations, progressive changes in cells or chromosomes but then were faced with difficulties. "They invariably started to refer to the 'needs' of the organism."

Adaptation was central to all of their explanations. Younger boys almost always associated the term with a naturalistic view described earlier. It was seen as an subconscious 'trying to improve.' There was no evidence of the idea of pre-adaptation and very few were aware of the evolutionary implications of 'survival.' Of the boys who did understand the evolutionary meaning of survival, "the concept of survival became dominant in their explanations and their concept of adaptation took on a new dimension" expressed as an aspect of change instead of an end product.

All were aware that some species of earlier times had descendants today and some did not. Their explanations were generally inter-specific. They did not relate the process to adaptive change. Clarity of the idea varied widely. A few older boys were aware of intra-specific selection. No boy had a full concept of selection.

Chance was rarely used in their explanations. They appeared "to be virtually unaware of the probabilistic aspects of the evolutionary process." Interestingly the idea of other hypothetical outcomes of selective processes or alternative breeding patterns appeared to be absent. A few boys provided explanations in which the environment "was seen as a guiding force in evolution."

All showed a singular lack of understanding of any valid concept of inheritance as a source of variation among organisms. They understood that heredity involved the transmission of characteristics from generation to generation. But changes in animals were explained in Lamarkian terms. With few exceptions explanations of the appearance of new characteristics used folklore ('mistakes can happen.' 'grandchildren can look like grandparents.') or plausibility arguments relating to everyday occurrences. There was much confusion on the mechanism of inheritance as well. "Some believed that certain essential characteristics, such as teeth, bone, and eyes, are not controlled by any physical mechanism but just happen."

Deadman and Kelly's interviews revealed that the concept of variation was not central to their conceptual structure. They very rarely used it as a subsumer in their explanation of other concepts. The authors speculated that it may have been inadequately covered in previous studies and that it is "important to introduce studies of variation early in a biology course... to serve as a basis for understanding evolution and heredity."

Two problem concepts were identified by Deadman and Kelly. The first is the naturalistic or Lamarkian interpretations that students use for many concepts. The second is their inability to understand probability. A hopeful insight was gained on deeper probing of some students who gave naturalistic explanations. It may be a way of saying 'I don't know.', "a colloquial abbreviation for a poorly understood concept." The student readily abandoned the naturalistic answer with subsequent probing.

Deadman and Kelly attribute the seeming intuitive nature of naturalistic or Lamarkian explanations to the anthropocentric world view of adolescents. Being conscious of his own needs and abilities he "intrudes these into his explanations." Change is conceived within individual organisms rather than between generations of organisms. Likewise the young person "feels more comfortable with certainty and will look for firm and simple explanations." Explanations that are probabilistic in nature are resisted. "The absence of a broad concept of chance, and a simple concept of Mendelian inheritance to act a subsumer was a major bloc on the development of more elaborate concepts."

Initially Deadman and Kelly assumed that they were dealing in the study with concepts that were derived from incidental learning. Some, like knowledge of the phenomenon of evolution, were of that type. But there were others like adaptation, naturalistic and Lamarkian processes, were "of a more intuitive kind". Students were infrequently unable to define them or link them with discernable facts. "This prompts us to suggest that a number of key biological concepts may have an intuitive form or counterpart in the minds of children." They also suggest that some of these concepts may be robust and long standing and dominate students thinking during and after the student's schooling. Prior knowledge of these structures is a great value to teachers.

Margaret Brumby's 1979 publication, an outgrowth of her doctoral work, examined the nature and origin of misunderstandings of natural selection of first year university students (Brumby, 1979). The population consisted of 63 university students, 49 of which had passed either A-level biology or zoology. The remainder had not studied biology at the A-level. Students responded in writing to three questions in an open response format. The same three questions were translated into multiple choice format where students would circle the most appropriate responses. Distractors in that section were taken from responses given by students in pilot testing of the questions and were selected to reveal specific misunderstandings.

There was a remarkably consistent pattern of introduction of incorrect responses to the written test. The terms 'good' and 'poor' were defined in relation to Bloom's higher levels of application and analysis as applied to the concept of natural selection. "'Good' students (14% of the sample) all mentioned that individual variation exists in all populations by chance mutations, and correctly explained that with a change in the environment only some individuals will survived by natural selection (Brumby, 1979)." The 'poor' students (86%) accounted for change in simple Lamarkian terms. They saw adaptation as a process in which individuals became immune to changes in the environment. Few students attempted to introduce any concept of heredity.

The origin of their misunderstandings Brumby found particularly significant. She notes four central problems in the misunderstandings exhibited by the 'poor' students. First, the conception that populations contain individual variation which arises from spontaneous mutation was totally absent. Second, "adaptation is described as a positive process rather than an the end-result of selection of the better adapted." She attributes some of this difficulty to inconsistent usage in textbooks. "The difference between an adaptive process and a selective process must be emphasized by teachers." Third," students so not take into account the time scales of evolution. They extrapolate from the idea of changes to individuals occurring within a lifetime to explain changes seen in populations over many generations." Even though most of them had passed A-levels in life science, they did not understand the significance of Weissmannian inheritance. Fourth, they often introduced the concept of immunity to explain natural selection. One of the questions involved the development of resistance to a pesticide by an insect population. Students commonly described it as a case of 'insects getting more immune'. They did not see this as a case rather of descendants of particular insects who were less affected by the pesticide increasing in the population.

"The pattern of misunderstandings was consistent with the results reported by Deadman and Kelly." Of the students who had passed A-level biology, 82% exhibited either partial or poor understanding of natural selection. Of these 59% had exhibited poor understanding. Of students who had not taken university level biology, 86% exhibited poor understanding of the concepts, with the rest exhibiting partial understanding. There is a bright side to this result; though not statistically significant, it may be that university level biology does increase understanding of natural selection over students who have not formally studied it. But the 82% showing little or no understanding is clearly disheartening.

Brumby states that "Together with Deadman's report, this finding suggests that pre-existing (Lamarkian) beliefs have acted as a barrier, which blocks the formal learning of Darwin's theory." She also notes that running "Lamarkian type experiments" runs the risk of enforcing the intuitive misunderstandings. "Teachers have to 're-teach' this concept, in order to overcome students' misconceptions which block their understanding." No specific pedagogy or practical suggestions are given. In response to an educator who had vigorously attacked the curricular change as 'virtual indoctrination in Darwinism in our classrooms', Brumby whimsically replied that, in light if this research, "it is a theoretical, rather than a real problem."

Brumby's 1984 work caused considerable stir in science education circles. Its results were stunning (Brumby, 1984). She studied misconceptions about natural selection of 150 first year medical school students in Australia. Certainly these were able science students; their backgrounds showed years of course work in biology and other sciences. Written responses to a series of problems were taken. Also individual interviews presented further problems with students taped 'thinking aloud.' The problems were of greater difficulty than those in her previous study or that of Deadman and Kelly. In the interviews ninety percent showed poor or partial understanding of natural selection (59% showed poor understanding). They showed confusions between immunity and selection, the action of antibodies and antibiotics, as well as on other concepts. In the same time frame that the interviews were conducted students were attending lectures on Darwinian evolution including evidence of fossil 'links'. No student correctly referred to these ideas in any of their explanation of homologous structures. Some did refer to them but implied a 'master mind' role for natural selection.

Brumby states that "these results clearly demonstrate that the majority of these very able science students leave school believing that evolutionary change occurs a s a result of need (Brumby, 1984)". The lecture material given in progress with the interviews did not influence their conceptions. "The 'intuitive Lamarkism' in biology problems appears similar to the intuitive Aristotelian explanations in mechanics problems.... They are far more than simple errors of knowledge which can be simply corrected. The entire pattern of reasoning is faulty." "Indeed it is more surprising to consider, not how little these students knew, but how much they knew incorrectly, for their answers were give with assurance, not hesitatingly."

She goes on to consider the implications for pedagogy. "Lamarkian and Aristotelian ideas had scientific acceptance in earlier centuries. Perhaps intuitive scientific reasoning mirrors a kind of 'recapitulation theory' of the history of scientific thought (Brumby, 1984)." Should this be consistently found for other basic concepts then such information can be very useful for predicting and perhaps designing curricula to uncover and re-educate around major misconceptions.

She sees a second problem in the way science is generally taught, a series of lectures. It is too often seen as "a body of absolute knowledge... recorded in books or yet to be discovered by experts." The danger of this approach is that it encourages students to view the learning of science as an exercise in rote learning. "They are learning the 'What' not the "How'." Brumby states that passive learning is "insufficient to bring about sufficient conflict in students' minds to alter their existing understanding." We must create curricula in which "students begin to use, rather than recite their understanding."

In a study centered around the conceptual and philosophical foundations of evolution by natural selection E.Jungwirth of Jerusalem University revealed similar problems (Jungwirth, 1975). In the 1975 study he cites an article by the great historian of biology M. T. Ghiselin, "On the Semantic Pitfalls of Biological Adaptation" (Ghiselin, 1967). Ghiselin states that "Different basic assumptions about the nature of the universe are mirrored by conflicts about the definition of terms." Jungwirth paraphrases this quotation by "The verbal formulations of the science teacher, and pupil, mirror different basic assumptions about the nature of the universe." This observation would seem to tell authors, editors, as well as teachers to be very mindful of the effects of language on the effect of their content communication.

Jungwirth continues with some quotations from highly regarded several sources describing evolutionary processes that demonstrate anthropomorphic and even outspokenly teleological mechanisms. Bacteria "showing ingenuity". Cacti "transforming" their leaves. Limbs "developing for ......" Is the danger of high school and university students understanding their instructor's loose locutions very literally? Jungwirth thinks 'Yes'.

To ascertain high school pupils succeed in the formation of certain basic biological concepts, and if they can differentiate between philosophical implications relating to these concepts, Jungwirth constructed the Test on Understanding of the Language of Science. It was administered to ten 4th form classes and ten 6th form classes and 48 third year university students in Israel. Lists of 4 statements were given to the students. The form of the test was simple. They were asked to read each statement and circle the ones that represented acceptable 'scientific' explanations.

The test revealed considerable distortion in students' minds about the concepts of 'adaptation' and 'evolution'. 'Cart before the horse' evolution was quite popular in all groups (from 26% to 69%). A sample 'Cart before the horse' evolution statement would be : "When primitive plants had reached a certain size, additional growth would have raised the problem of efficient distribution of water and nutrients, so the were provided with transport systems." Or, "Certain plants grow in hot and dry regions and for that reason features developed in these plants which enable them to reduce water-loss". Teleological statements were also commonly accepted as scientific. A sample teleological statement is: "Certain plants, which grow in hot and dry regions try to develop features, which will enable them to reduce water-loss." On average, less than one third of the university students were able to detect the scientifically acceptable explanation.

University students interviewed by the author after the examination were asked what contributed to their poor performance. "One of the most frequent replies was that, in essence, university studies had contributed very little, if anything, to a deeper, philosophical understanding of the concepts under discussion here, so that the respondents had based their choices on their high school experience i.e. their teacher's formulations and locutions". The prospects are chilling for persons preparing for a teaching career. "The danger of a vicious circle must seriously be considered." Instructors and text book writers should not assume that "loose formulations by their pupils are meant metaphorically, but rather, that they actually 'mirror different (and faulty) assumptions about the nature of the universe."

In a pair of well designed parallel studies Elizabeth Engel Clough and Colin Wood-Robinson explored students understanding of inheritance and adaptation (Clough, & Wood-Robertson, 1985a; Clough, et al., 1985b). In "Children's Understanding of Inheritance" Clough and Wood-Robinson interview of 84 British students from 12-16 years old with two series of tasks relating to inheritance of acquired characteristics (chopped mouse tails, athletes' training, and gardner's rough skin) and inheritance of intra-specific variation (spotted markings on dogs, twin similarity, brother/sister similarity, and mating of a mouse born with no tail with a normal mouse).

Results of this study were thoroughly consistent with the studies by Brumby and Deadman and Kelly. There was a well developed and coherent set of ideas about inheritance that children brought to school. Much of it was either naturalistic, teleological, or Lamarkian. From age 12 to age 16 the number of students believing that acquired characteristics over time would be inherited remained constant at about 45% of the group. Over that frame, the number of students using some form of genetic inheritance increased from 10% to about 50% for 16 year olds. An intuitive idea of particulate inheritance through a genetic entity rose from 13% to 63% in that time.

Clough and Wood-Robinson noted that the results showed some improvement towards a better scientific understanding of inheritance. Nevertheless, some alternative conceptualizations, representing ideas far removed from scientifically accepted ones, were held by 16 year old students. "The present study alerts teachers to a number of commonly held viewpoints which do not conform to currently accepted scientific theory, and may constitute 'blocks ' in later understandings." Clough and Wood-Robinson endorsed the idea that open discussion of students conceptions about inheritance in a non-threatening atmosphere. The explanations put forward here can serve as a starting point for discussions in biology classes. Most importantly, from the viewpoint of the unique design of The Evolutionary Tool Kit they specifically stated the need for the development of new pedagogical strategies to aid teachers in clearing up students' misconceptions. "The creation of this atmosphere and the devising of strategies for open exploration of ideas are real challenges for science teachers. It seems obvious that we must find ways of incorporating ideas from 'everyday experience' into our biology lessons and that extended discussion will be an essential component of any strategies developed."

In "How Secondary Students Interpret Instances of Adaptation" Clough and Wood-Robinson interviewed the same 84 students from ages 12-16 using two tasks involving predicting and explaining outcomes about colored caterpillars on colored tree trunks, and the length of hair on arctic foxes.

Again results were consistent with previous studies by Brumby and Deadman. From the 12 year old population to 16 year old population there was an increase in students who responded in a 'scientifically acceptable' manner from 2% to 30% for both the fox and caterpillar tasks. Naturalistic and Lamarkian responses were very popular. Additionally there was no indication of any better scientific understanding from 12 to 14 year olds. There was a clear improvement at 16 years.

Clough and Wood-Robinson also strongly disagreed with the suggestion by Shayer that ideas about evolution are too difficult for this age level. "Evolution is of such central importance in modern biological thought that we must surely instead think of ways of teaching it more effectively." They do remark that students find it much more difficult than many teachers realize.

As with their suggestions on teaching inheritance, Clough and Wood-Robinson state that "It seems clear that a way forward would be to start with students' ideas and to devise teaching strategies which take some account of them." They state, also, that perceived teleological or anthropomorphic responses may reflect language related difficulties, rather than consistent misunderstandings in some cases. Citing Jungwith (1977) they ask "Is it fair to attribute these interpretations to students when many educators (and television programs) describe evolution in stridently teleological and anthropomorphic terms?"

The authors suggest a strategy in which teachers assist students to clarify what they do believe "to provide them more structured opportunities for them to talk through ideas at length". Alternative ideas should definitely be included in these discussions. These, as well as scientifically accepted ones, should be discussed and evaluated by both the teacher and fellow students. The authors remark that "Some alternative theories mirror theories which preceded new-Darwinian theory. A deliberate link with the historical development of thought on evolutionary processes might be a useful strategy." I cannot help but comment that this is exactly the model proposed in <u>The Evolutionary Tool Kit</u>; only with this computer program the class now has a common environment in which to explore and comment on their observations and theories.

Finally Clough and Wood-Robinson note that "rather than delaying the teaching of evolution beyond 16 years, we need to include it much earlier in the secondary science curriculum. It may be better, rather than ignoring it, to draw this out-of-school knowledge into our classrooms and laboratories and make use of it."

J. Murphy and B. K. Hodgeson describe a university level course in evolution taught to 446 students at The Open University during summer session (Hodgson, et al., 1984; Murphy, 1984). The course used a CAL and distance learning format quite advanced for that time. Students did a computer project as one of a four part course assignment. The program used was EVOLVE a direct descendant of the work of Crosby (Crosby, 1973). EVOLVE modeled the genetic and evolutionary consequences of two populations of flowering plants coming together after a period of genetic isolation. The driving force behind the evolutionary aspects of the model is that, though the plants freely intermix, hybrids have impaired fertility (F1 hybrids have a fertility of .25). Nine genes are studied, no linkage, no epistasis. Genes affect the time, during the 10 week 'summer' that the plants flower. The program, running on a mainframe, provided printouts of allele frequencies for each year of the experiment. A version of EVOLVE, marketed by CONDUIT, is now available for micro-computers (see the following section). Hodgson (Hodgson, et al., 1984) reports that the curricular experiment was generally very successful (70-82% responded positively to the course, irrespective of their grade).

Clearly such a program is not easily adaptable for secondary students. In all the screens and printouts there is nary a flower anywhere, only tables of alleles. Its significance, as Hodgeson states, is that this innovative approach shows that "CAL was not chosen selectively by computer enthusiasts or avoided by those with limited experience of computing. It is most important that simulation CAL be regarded by both students and teachers not as something 'special' but as complementary to traditional work.

Frank Price in "<u>EVOLVE</u>: a Computer Simulation for Teaching Labs on Evolution" describes a computer simulation he authored for modeling microevolution for university level students (Price, 1985). <u>EVOLVE</u> is also currently available from CONDUIT for micro-computers. In this article he eloquently addresses some concerns of biologists attempting to use computers as teaching tools. "Many people regard biology laboratories as 'wet' places where you cut up frogs ... or mix colored beakers.... Learning about evolution is made more difficult because students cannot 'get their hands dirty' by doing experiments." He states that a lab should not merely demonstrate, this is too cook-bookish. The goal of a lab should be "to help students see what professionals in the discipline do.... But what does an evolutionary biologist do?"

One cannot apply the standard approach of experimenting and testing hypotheses very easily in this discipline. Many of the models of evolutionary processes are highly mathematical rather than observational. "In essence we simulate some aspect of the real world in mathematical form, and then experiment with the simulation.... The concept of Hardy-Weinberg equilibrium and the mathematical population genetics that evolved from it are excellent examples."

EVOLVE is such a model. It is a Monte Carlo simulation; it uses random numbers to simulate complex processes and events. It is based on a hypothetical organism with characteristics that make it useful for the simulation. One gene is studied with alleles + and 0. There are three genotypes: ++, +0, and 00. The alleles can affect any of four characteristics: survival, emigration rates of juveniles, and reproductive and immigration rates of adults.

Price notes that "rates of survival, reproduction, immigration and emigration are not, strictly speaking phenotypes in the sense that color of a petal is for a flower." The rates used by EVOLVE are "statistical characteristics of populations of organisms. "EVOLVE incorporates the statistical effects of phenotypes not the phenotypes themselves."

The model makes no assumptions about "the mode of inheritance of the characteristics." The user sets parameters for the pattern of inheritance of the two alleles. Setting survival rates at 80%, 80%, 0% for the genotypes will simulate a recessive lethal gene. The life cycle of the organism is simple. It hatches, matures over a period of time, during which it may die or emigrate. At the end of the juvenile period, "surviving individuals become adults. Additional adults may immigrate. During breeding season all adults mate, produce offspring, and die." EVOLVE is not a cellular automata simulation. The data structure holding the population is a simple list. There is no environmental interaction.

"If the population of adults exceeds an upper limit set by the student, the number of adults is randomly reduced to a lower limit". This artificial mechanism prevents overflow of memory. The reduction or population 'crash' is independent of genotype so that surviving populations are representative of the initial gene pool. It is possible to drive a population to extinction depending on choice of reproduction and survival rates.

The design and parameters of the simulation satisfy the Hardy-Weinberg conditions. All individuals are identical with respect to sex and age. There is no mutation and mating is random. "Because students may specify values for all of the other assumptions, they may 'design' a population that fits any experiment your want them to do on selection, genetic drift, and gene flow." In the article Price goes on to illustrate the potential of EVOLVE with several experiments on selection of dominant or recessive alleles. It is a remarkably versatile and well crafted package. Several of the experiments in The Evolutionary Tool Kit manual are and modeled after Price's suggestions.

There is one informal study of the effectiveness of EVOLVE and some of the Chelsea science simulations on high school students (Ybarrondo, 1984). Ybarrondo conducted a 3 week summer seminar in population genetics and evolution for AP biology students. The treatment group received CAI labs in lieu of a traditional laboratory experience received by the control group. There was no significant difference in content comprehension between the groups. There was no quantitative measure attempted of affective areas. The written student responses reviewing their CAI experiences were very positive.

Ola Halldén describes a very rich and penetrating study of the different perceptions and perspectives of secondary students and their teachers in the study of evolution (Halldén, 1988). It is the most involved and conceptually complex study done in this area. I will attempt to provide only a skeletal outline of his method and results.

Halldén notes that many previous researchers remark that "understanding the significance and meaning of diversity of organisms within a species is a major stumbling block for pupils attempting to explain evolution." He noted the work of Longden, Radford, and Stewart (Longden, 1982; Radford, & Stewart, 1982; Stewart, 1983) recognizing genetics as an area of particular difficulty for secondary students. He suggests that "although instruction in genetics usually precedes instruction in evolution, it does not give pupils a means for understanding the mechanisms of evolution." Including those cited by Halldén there are many studies citing 'successful' students lack of comprehension of material in genetics even after attaining good grades in their genetics courses (Brown, 1990; Browning, et al., 1988; Marek, 1986; Martin, 1983; Radford, et al., 1982; Simmons, 1987; Slack, 1989; Slack, 1990; Stewart, et al., 1990; Thomson, et al., 1985). Even 'good' instruction in genetics fails to provide students with an understanding of variation in a population. Halldén designed an observational study of instruction in genetics and evolution to probe students understanding and perspectives on the content and the instruction.

The study was carried out in a 11th year Swedish secondary school with 27 pupils averaging 17 years of age. A seven week, 30 lesson, unit on genetics and evolution was given. Instruction was in standard lecture, discussion, demonstration, laboratory format. No computer simulations were used. Students understanding of the materials was observed and analyzed in two forms, written and oral explanations. Before and after the instruction students were asked "to write an essay explaining the development of species." At the end of the instruction, two groups of three students were asked to give an oral presentation "of how traits and genetic predispositions are inherited". Presumably these were the most able students; no selection information was provided. The groups met and discussed for an hour to discuss and arrive at a consensus for the presentation. The discussions were taped.

Both the essay explanations and oral presentations contained mountains of confusion. There was very little content difference between the pre and post instruction explanations in the essays. The only pronounced difference was that seven students who had previously written nothing, now produced an essay. The same confusions and misconceptions about typological populations, teleological and naturalistic 'causes', and Lamarkian inheritance filled their writing, much in agreement with earlier researchers. Halldén concluded that "the conceptual problems encountered by pupils arise independently of their studies of genetics."

The problems were very deep seated. In responding to the inquiry of "Why do students adapt a surface approach, rather than a deep approach?" Halldén found that it was very much the case that they did not get 'the point' because they were not looking for it. The instruction appeared to be disjointed to the students. The framework had been logically set out: an experiment on mice breeding, introduction to genetics in the context of evolution, the mechanisms of inheritance, cell division, traits appearing in offspring, and ending with deviations from the normal. "The sequence made the content of the instruction inaccessible to the pupils, preventing them from forming a coherent picture of the mechanisms of genetics and their relationship to evolution." To understand "DNA and cell division, one must know something about how it is constructed." Understanding gene distribution during cell division one needs to know about cell division and phases. They did not understand the 'chain of events'

Beyond the problem of the whole becoming lost in the detail Halldén noted another significant difficulty relating to the domains of knowledge presented. The initial questions touched on in the opening of the course made sense on a commonsense level. "How is inheritance passed on?" "How do species evolve or change?" When answers were explored within the context of the course material and the phenomena dealt with in the course "a major gap" appeared between the students' understanding and classroom experiences and course-specific questions. This change from "commonsense questions to course-specific questions .... also put a limitation on what type of explanation appeared to be appropriate." The students did not understand the kind of explanation that would be appropriate at this different level. The students persisted in asking their "own questions, whether or not they are relevant." The explanations or concepts presented in the material will then "be incomprehensible or lack real value as explanations to his questions."

Beyond considerations of students alternative frameworks Halldén argues for the existence of a meta-level, "conceptions of the subject field as a whole, and what counts as an explanation within the subject field as a whole." Understandings determined in this meta-level determine "the relevance of the information presented in the teaching." Schools should try to clarify beyond what questions are being asked, but also what kinds of explanations are needed, as well as "what questions we are not providing answers to."

Lawrence Scharmann study "Enhancing an Understanding of the Premises of Evolutionary Theory: The Influence of a Diversified Instructional Strategy" (Scharmann, 1990) builds on premises and observations similar to those of Halldén but he incorporates a practical pedagogical tool and studies its effectiveness. The subjects were members of two sections of a concurrent, summer session college biology course for non-majors (n=30). The course duration was three weeks; the format was 150 minutes of lecture, and 120 minutes of laboratory each day for six days. The unit on evolution was introduced early in the course; it lasted one week. One the control group received standard lecture, demonstration, lab work. The treatment group received what Scharmann called 'diversified instructional strategy'.

The diversified instructional strategy consisted of group discussion of students' written responses to four questions "regarding the potential controversy between evolutionary theory versus creation origins." The questions were as follows: "(1) From what you have been taught in science classes, explain how you feel about the theory evolution. (2) From what you have read or been taught, explain how you feel about creation origins. (3) Do you perceive there to be a conflict in your feelings or responses to questions 1 & 2? (4) Do you believe that science teachers should present creation as well as evolutionary origins in their classes? Why or why not?"

Students in the test group were then assigned into random groups and discussed their responses as an exercise in critical thinking. They were asked to find the best reasons for teaching one view only (evolution or creationism), both, or neither. They were then asked to make a judgement on their discussions and arguments in each of the three positions. After the group work the instructor provided an interactive lecture/demonstration attempting to "resolve the misconceptions that arose as a consequence of the small group sessions." Students were finally asked to reflect individually on their feelings on these issues.

A pre and post test in Likert format was given to assess content knowledge and understanding of science and its methods. The instrument was constructed by Johnson and Peebles (Johnson, & Peebles, 1987). No difference was measured in content understanding of evolutionary items between the groups. The experimental group did show "greater understanding of the nature of science and attitude toward evolution ($p < 0.05$). In commenting on the null result for difference in understanding versus the positive result for understanding science and evolution, Scharmann suggests that "non-major biology majors are less concerned with learning the specific content of a course in general biology." Since there was no difference in content understanding, he further suggests that general biology instructors be aware "that the factual content taught is potentially less important than the development of learner attitudes regarding biology and the application of biological concepts on both a personal and social level."

Edgar Greene Jr. in his article "The Logic of University Students' Misunderstanding of Natural Selection" enquired into the misconceptions about natural selection among 322 university sophomores (education majors) at Appalachian State University (Greene Jr., 1990). Students were in 11 classes spread over 8 years (1977-1984). The vast majority were sophomores taking the course in fulfillment of a requirement for an education degree; 90% were white females.

Greene narrowed the inquiry focus of other researchers in an attempt to find any patterns in the misconceptions students consistently showed. Evolution problems used as measures were part of the final assessment process of the course. Greene was the instructor. A sample problem is: "The ancestor of the modern day bat could not fly, resembling a shrew or mouse. Assume that the bat evolved wings from the arm and paws of shrew-like ancestors. Explain how this could have happened using the idea of natural selection (Greene Jr., 1990)."

Citing Ernst Mayr (Mayr, 1988), Greene set out two major assumptions that are necessary to understand natural selection. The first is the recognition of populational thinking. If students assume that "a population is a collection of individuals representing a common type, then variations among individuals will have little importance in the change process of the population." This is typological thinking. Student responses to the questions were categorized as typological focus or populational focus.

Greene attempted to see if there was any relation between the kind of population thinking used and the kind of change process students used in their explanations. He defined two views for change: 'closed' or 'open. 'Closed' change processes would create changes without reference to any outside information. Also 'closed' change would not be linked in any way to 'need' or changing environments. Darwinian selection needs a closed change process such as mutation at the molecular level. Other closed change processes have appeared in the history of ideas; orthogensis is one.

Orthogensis explains change by stating that it is the result of patterns within the organism constantly unfolding generation after generation (Bowler, 1989; Greene Jr., 1990). The changes could be positive or negative, accounting for survival or extinctions. No students advocated this line of thought, however. A closed process also creates a range of variations.

Open change processes are those that are not closed (Lamarkian, teleological, naturalistic). A process that used the 'need' of the organism, or a 'need' set by the environment was termed open. An open process could create variation also.

Student responses were also classified, beyond the population focus, or the kind of change process used, and by the type of selection chosen. Green categorized student selection processes as Darwinian, non-functional, and non-selection. If the selection process has a mechanism for judging which individuals live or die it is Darwinian. If a trait is deemed already advantageous, and that trait is used to confirm that individuals possessing it will survive, then the student is using non-functional selection. "No judgement is made between individuals with different traits." "If the student did not make a logical connection between survival and death and the definitions of advantageous or disadvantageous or the response does not mention survival or death" the response is deemed non-selection.

Greene hypothesizes that there are specific patterns in student responses. Students using a teleological thinking will use a more directed change process and a less functional selection process on an evolution problem. A common assumption that students make is that "When nature changes, it is not at random." This is teleological thought. This is at odds with the random nature of variation in Darwinian natural selection.

Greene hypothesizes that students using teleological thinking will use a more directed change process and a less functional selection process on an evolution problem.

Student responses were scored and tabulated. Reliability of the classification was tested by having other biology instructors analyze 10 responses randomly chosen. The reliability estimate from this procedure is 96%. Null hypotheses were formulated and checked against data from the scoring of the student responses.

The results of the study again were in agreement with previous studies by Brumby, Deadman, and Clough. Only 3% of the students showed a 'true' understanding of natural selection. By this Greene meant: a populational focus, a closed change process; and a Darwinian selection mechanism. However 43% demonstrated a functional understanding within a typological framework. By contrast 17% of the students used Lamarkian explanations: typological focus, open change process, and non-functional selection or non-selection.

There is a structure to students misunderstandings Greene's study clearly shows. The greatest stumbling block is the development of a population focus for the students' thinking. Green's study shows that if a student views a population as a repository of many variations, then the student will also view the change process as closed. It seems that Mayr is correct. If one can get a student to think with a populational focus, rather than a typological one, more than half the battle is won.

If the student thinks typologically "there is a relationship between the degree of the directedness of the change process and the use of less functional selection processes." Highly directed change implies choice of a less functional selection process. Less directed change implies a choice of selection process that is more functional in a Darwinian sense. This result suggests "that the change and selection process are chosen by the student so that they are compatible." Students are trying to make sense of the ideas, but they are fitting them into an existing conceptual framework. "The logic between the change and the selection processes suggests that the student tries to fit the change and the selection process into the whole rather than using each part independently." "Students starting with the assumption of non-random change will not grasp the meaning of selection." For them "survival or death" is the product of natural selection, not part of the process. Also students using the idea that acquired characteristics are inherited (Lamarkism) will also use non-selection.

On the meaning of this study for biology teachers, Greene states, "Students are trying to make the idea of evolution make sense." Biology teachers should be mindful of the probable roots of students' misconceptions. It is important that topics be integrated around the principle involved in the assumptions. "The idea of populations filled with variations as nature's way to insure against an unpredictable future makes sexual reproduction and meiosis, which ensure variations, fit tightly together rather than separate and independent processes as is often taught." The weakness of directed evolution and Lamarkian ideas must be openly addressed. Lamark's explanation just doesn't work; one must not just take the teacher's word for it. "It is through the understanding of students' misunderstandings that effective instruction can be created."

Beth Bishop and Charles Anderson published a recent study titled "Student Conceptions of Natural Selection and Its Role in Evolution" (Bishop, et al., 1990). It builds on the work of Novak, Brumby, Clough, and parallels that of Greene and extends it to practical pedagogy. The results are most illustrative. Bishop and Anderson studied the effects of instruction specifically designed to bring about conceptual change in evolution and natural selection on 110 college students, mostly juniors and seniors in a one term non-majors course in biology. "We used techniques of research on conceptual change in order to understand better the nature of our students' difficulties" "On the basis of this understanding we hoped to develop teaching materials and techniques that better helped students to overcome their difficulties".

Using principles of conceptual change learning, the authors attempted "to develop instructional materials, including, lecture overheads, laboratory activities, and problem sets that would result in students' a) becoming dissatisfied with their existing conceptions, b) achieving minimal understanding of the scientific conception, and c) seeing that the scientific understanding is useful and plausible in a variety of situations (Bishop, et al., 1990)." The full module is available from the Institute for Research on Teaching, Michigan State University, East Lansing, Michigan. No computer simulations of evolution or natural selective processes were used.

The initial concepts and beliefs of the students were assessed by instruments piloted as a post test on pilot groups. "Patterns of student responses which appeared to differ from correct understanding as we had defined it were identified and used as the basis for hypotheses concerning the nature of students' conceptions." The revised instrument, including open written questions, and multiple choice items was administered to 110 pre-test students and post test students. Using a description of the student reposes devised in the pilot study, student responses were coded, and conception scores assigned to each on the basis of test responses. Also data was taken on the number of years of biology studied prior to the biology course. Students were also asked "Do you believe the theory of evolution to be truthful?"

Student responses on the tests were tabulated by percent of the population comprehending three basic issues. The first issue was the origin and survival of new traits. Its associated scientific conception was that random processes are responsible for the appearance of traits, and that natural selection accounts for the survival or disappearance of the individuals with these traits. This is a clear statement of the two fold nature of Darwinian natural selection. The second issue was the role of variation within a population. Its associated scientific conception was that variable population is essential for evolution. The third issue was evolutionary change. Its associated scientific conception was that evolutionary change involves changing proportions of individuals with discrete traits.

Analysis of both the pre and post tests of conceptual understanding revealed remarkably low scores all round. Even with students who had three or more years of biology instruction only 31% demonstrated an understanding of the second issue. That was the highest score. These same students scored 3% and 17% on issues one (random processes and natural selection) and two (nature of evolutionary change).

Another remarkable result was that "previous biology instruction did not "seem to have any effect on the the students' ability to learn the scientific conceptions during the biology course." Also there was no significant association of belief in any of the scientific conceptions on the post test with any number of biology courses taken on any of the issues.

On the positive side, the effect of the instruction was to increase the number of students able to use scientific conceptions to explain evolutionary changes from 25% to over 50% on all three of the issues. Corresponding naive beliefs decreased. Bishop and Anderson plainly state: "These results indicate two things: First, the concepts of evolution by natural selection are far more difficult for students to grasp than most biologists imagine. Second, many students can change their naive conceptions on the subject if instructors are aware of them and are prepared to confront them." They also admit that even with specially prepared materials they were not able "to help a significant number of students."

Results on belief in theory of evolution were also interesting. In the pre-test the believer/non-believer/undecided ratio in percentages was 59: 11: 30. In the post-test the results were 49: 26 : 27. Sixty seven percent did not change their beliefs after instruction. "Of the 11 who did change their belief, it was into the unsure category. There were no changes from believer to non-believer or visa versa." Interestingly "student conceptions of the process of evolutionary change were not associated with the belief (or lack of belief) in the truthfulness of evolution." In fact the percentage of non-believers who understood the theory of evolution (73: 73: 80, quoted as percentages understanding the three issues previously), as measured by Bishop and Anderson's instrument, was slightly higher, though not significantly so, than the percentage of believers in the theory (50: 57: 57).

There implications for educators of this study are considerable. First, if the sample of students taken in this study are "representative of college educated non-scientists', then it appears that a majority of people on both sides of the evolution-creation debate do not understand the process of natural selection or its role in evolution." It seems that the college students in East Lansing are not alone. Some men in black robes sitting in high places share some considerable confusions on this topic as well (Gould, 1991b). Bishop and Anderson, in seeming resignation, state that much of "the debate is reduced to, as creationists argue, a dispute between two different kinds of faith." Approximately half of the students claiming to believe in the theory do so based on an acceptance of the authority or prestige of science, rather than on any understanding of the reasoning that led to acceptance of the theory.

Biologists may find disturbing the lack of appreciation of the public toward the central theory of the discipline. Perhaps in open sympathy with Brumby's comment on the effectiveness of instruction in natural selection, Bishop and Anderson remark, "it should be comforting to those who fear that instruction in evolution will cause students to abandon religious beliefs." The results do indicate that over half the 'well-educated' population possess naive conceptions about this central idea of modern biological thought.

Bishop and Anderson, at the end of the article, speculate on why the population holds these beliefs. First, they suggest, the simplicity and logic of the naive ideas are attractive. "It would be much simpler if organisms could simply acquire those features necessary for survival; but nature does not operate in this manner." They posit a second potential reason as inaccurate language in popularizations of evolutionary history. "As the climate changed, the plants and animals had to adapt or face extinction." A biologist may hear and understand these statements much differently than "a member of the general public for whom the program was intended."

The alternatives offered by Bishop and Anderson are, I feel, a bit simplistic. The problem cannot be laid at the feet of script writers of educational documentaries. The roots of naive 'biology' run deeper. Even 'conceptually honed' conventional pedagogy designed to produce conceptual change is not effective. Perhaps unconventional pedagogy is more in order. With The Evolutionary Tool Kit I propose to permit students to build and experiment with their own micro-worlds. They can do "what if's" with systems of inheritance and reproductive strategies. One of the problems with presenting the central ideas of evolution and natural selection, as pointed out by Clough, Greene, and Mayr is the typological nature of language itself. If students can experiment with an non-verbal systems such as worlds defined through cellular automata and rules that govern them, perhaps a new level of understanding can be reached.

A recent study by Don Ploger of UC Berkeley (Ploger, 1991), though not on instruction in evolution or natural selection, shows the possibilities of such an unconventional approach. Ploger describes the use of Boxer a computational medium based on Logo described by A. DiSessa (DiSessa, & Abelson, 1986). Boxer is a concept simulator much like The Evolutionary Tool Kit. It simple, more general, but it is not dynamic, and, I feel, not as easily adaptable for specific investigations into the nature of variations, inheritance, and randomness in populations as is The Evolutionary Tool Kit.

Boxer permits students to draw boxes on the screen and label them at will. These are really Logo sprites, capable of limited movement. Several layers of diagrams are permitted. Ploger used Boxer to permit high school students to model for themselves the uptake of glucose by muscle cells. Using Boxer students constructed a narrative that described a muscle cell (represented by a large rectangle). Sprites representing glucose (composed of a simple pattern of smaller boxes) and insulin (again a different pattern of boxes), the cell receptor, and the carrier protein. The representation of insulin and the cell receptor schematically indicated the 'key in latch' nature of the interaction. In a more advanced model the student indicated whether the insulin was bound or not. The student wrote in the Boxer medium simple routines that permitted the sprites to move and demonstrate the function of insulin and the cell receptor. The student later "became interested in what happened to the glucose after it entered the cell."

The student continued the process to make a more detailed model of glycolysis "which simultaneously presents the cellular and molecular views of the process." Flipping through 'cards' in the Boxer medium permitted the student to zoom in and out of the levels. The student advanced through a series of models, the first being very crude, the later ones more sophisticated, though still not advanced as the 'right' way according to modern biology. In another article Ploger explores extensions of this idea in a historical context (Ploger, 1990). Students used Boxer to "investigate Sanger's technique for determining the sequence of amino acids in a protein." Students built their own models describing initial work, then improved on the models to illustrate finer and finer detail in their representations.

Mitchel Resnick and Brian Silverman, in Dewdney's new recreational computing magazine Algorithm described an informal investigation in genetics using Logo on a work station class machine (Resnick, & Silverman, 1991). These authors were surprised to find that the pattern of trait inheritance of their creations followed precise mathematical lines. On reviewing the literature they found that they had 'rediscovered' the Hardy-Weinberg equilibrium. The design and implementation of interface of The Evolutionary Tool Kit was begun a year before the publication of the ideas of Resnick and Silverman.

The Evolutionary Tool Kit is intended to provide a similar computational medium for early secondary life science students to explore the fundamental ideas of evolution, natural selection, and evolutionary biology.

Available Commercial Programs On Evolution and Natural Selection

Dr. Harold Modell of the University of Washington at Seattle, Editor of the newsletter *Computers for Life Science Educators*, maintains a listing of available software for life science educators. In the January 1991 edition of the newsletter Dr. Modell listed 23 programs as resources for educators in evolutionary biology (Modell, 1991). The following discussion describes and offers a brief critique of programs in Dr. Modell's list relevant to middle and secondary school science educators. Only programs that focus on student interaction with material are discussed; tutorial programs are omitted.

Of special note is a very recent resource article "Resources for Teaching Evolutionary Biology Labs" published in The American Biology Teacher (McComas, 1992). After discussing common lab activities on evolution in textbooks and lab manuals, McComas noted "a certain uniformity in the activities commonly provided in these published sources." McComas, in an attempt to "bridge the gap between what is readily available in previously mentioned sources (texts/lab manuals)" lists 18 "non-textbook laboratory exercises dealing with aspects of evolution. None of the entries contain any computer simulations. Price's EVOLVE or the simulations by the Chelsea Science Series are not noted.

Oh, Deer! by the Minnesota Educational Computer Consortium (5-9). First published in 1985 Oh, Deer! received glowing reviews by educators (Willis, Hovey, & Hovey, 1987). Based on a real life model, Oh, Deer! challenges students to manage a herd of white-tailed deer in a residential area. It fosters an understanding of population dynamics while giving students a feeling for the effects of controlled and uncontrolled variables. Following the innovative design of many M.E.C.C. products, Oh, Deer! utilizes several levels of interaction with students. Much of the information and feedback from decisions made by students running the simulation is in a written format, fitting well with Gardner's "linguistic intelligence". Reading level is appropriately set at the 4th grade level.

Considerations of costs of each of the actions suggested as well as costs of the damage done by the deer must also be part of the students' decision processes. Students track the size of the herd off the computer by plotting information given in textual form on the screen. Students construct their own graphs from data collected from experiments or surveys done in the program to evaluate their progress. At each option a random element, a 10% chance of a viral infection, forest fire, or construction project, impacts the size of the herd. The program is driven by a finite differences model of a deer population. A limitation of the program is that no opportunity is given to explore other animals, or to investigate other related topics such as gene pools, and dynamic inheritance. The "deer" are fundamentally a static collective entity. There is no way for students to gain an understanding of the importance of variation in a population from models constructed on this line. This same modeling system lies at the core of many other designs.

Mendelbugs by Focus Media (7-12) explores the fundamentals of genetics and heredity. It includes a tutorial and several simulations. Students breed generations of 'bugs' through monohybrid and dihybrid crosses. The program summarizes in Punnet Squares the results of their experiments. There is an animated Punnet Squares program that provides a fine illustration of this genetic bookkeeping heuristic.

In general Mendelbugs is an excellent introduction to Mendelian genetics. A minor inconvenience is caused by the fact that the shapes of the bugs, as well as the pattern of inheritance is fixed by the program. More serious pedagogical difficulty arises when trying to integrate treatments of genetics as in Mendelbugs with evolutionary theory or with a sense of dynamics of the genes in the population. The problem resides not in the program but in the nature of Mendelian inheritance and its relation to change. There is no way for students to include a fitness function on any of the crosses. It is very difficult for the student to get a feel for why the Mendelian patterns have anything to do with evolution or change.

Natural Causes by Q.E.D. Educational Computing (7-12) is based on predator-prey-environment relationships on the nearly closed moose/wolf ecosystem on Isle Royale, Michigan. It is based on difference equations models, giving students limited control over variables like immigration, emigration, mortality, natality, carrying capacity and the effects of severe weather and disease on the moose or wolf populations. Students running the simulation can vary any of the above quantities for either of the populations and try to predict and explain the outcome. Output is almost exclusively quantitative or graphical expression of quantitative population data.

Population Ecology and Genetics by Edutech of Cambridge MA (10-College) explores population genetics covering topics like Hardy-Wienberg equilibrium, and simulations of natural selection, genetic drift, inbreeding, mutation , migration, and gene flow. The program also includes modules on population ecology that can test hypotheses about systems in nature for making future predictions of population sizes and values of variables. Population Ecology and Genetics also permits exploration of exponential logistic, discrete, geometric, Leslie, Lotka-Volterra competition, as well as Volterra predator-prey and MacArthur predator-prey models of population growth. Output is generally quantitative graphics.

This two disk set is a clearly potent brew. Considerable class work and mathematical training is needed to understand and run the simulations intelligently. The underlying model again is a set of linked difference equations in which the student has some control over various coefficients selected from various menus. Population Ecology and Genetics is by far the most comprehensive offering in this area. One problem does surface after running this simulation for a while. One cannot help feeling that this simulation (perhaps it is the general method of using computers to teach topics in this manner) somehow fundamentally begs the question. One can easily see students asking "What is being studied: life or mathematics?" "Where are the genes that are mutating or 'flowing' or 'drifting' anyway?" It is certainly true that the implementation of the various theoretical models is cleverly done. Unfortunately, because of the modeling strategy chosen, there are no 'populations' composed of individuals, nor are there any individual 'genes'.

PopGen: Population Genetics Simulation (9-College) explores Hardy-Weinberg Law and concepts of genes in populations. Students can select cases that violate any of four conditions and observe effect on the gene, genotype and phenotype frequencies over time. Output is solely tables of gene frequencies. No graphics are employed. Current technology and general 'computer literacy' of average students is such that the whole simulation could be set up in Excel. Excel, or other general spreadsheets, also have built in powerful graphical display utilities permitting users to share, manipulate and display data in any way he or she sees fit. This simulation, as well as Popgrow, Balance: Predator-Prey Simulation, Moths: Peppered Moth Evolution, and even complex simulations EVOLUT, could be set up by students in a spreadsheet format, including graphical displays of results surpassing those in the original programs.

Popgrow: (9-12) Population Growth Simulation by Diversified Educational Enterprises permits students to experiment with three population growth models manipulating variables. This is the weakest of the simulations listed.

Balance: Predator-Prey Simulation by Diversified Educational Enterprises (9-12). Students manipulate variables of food supply, carrying capacity, environmental conditions and external pressures to explore effects on population. Tabular and graphic output of students' experiments are produced. Though control of emmigration and immigration and natality rates is permitted, there is no real 'gene pool'. Mutation is not permitted

Moths: Peppered Moth Evolution: by Diversified Educational Enterprises (8-12) students examine effects of changing environment on the numbers of light and dark colored peppered moths in a population. The model is virtually identical with that in Balance: Predator-Prey Simulation except that there are two linked populations undergoing predation. Output is given as quantitative graphics. This could be done, with a few well chosen equations, in any standard speadsheet. In fact this type of problem, with this form of global modeling, is ideal for a program like Stella.

EVOLVE by Frank Price, available from COMPRESS, has already been partially described. It is a fine simulation for its intended purposes. It does not permit mutation in any temporally extended sense, nor does it permit the modeling of fitness other than setting survival rates for various genotypes. If the student has a firm grasp of populational thinking in his/her first meeting with the organisms in EVOLVE they can learn a great deal. If the student thinks typologically, the simulation cannot easily help a student overcome that problem.

EVOLUT: A Unit on Natural Selection (10-college) by S. McCormick, available from Conduit Software, University of Iowa, is a simulation based on linked difference equations. First published in 1980 by the Chelsea College Science Project, EVOLUT demonstrates the beginnings of a trend in science education in which computer simulations were designed to involve students actively in the learning process. It is a direct descendant of the modeling done by James Crosby on the genetics of the evening primrose in the 1960's. It shares some of that previous model's brilliant insights as well as some of its pedagogic difficulties. Experiments in evolution or population genetics in EVOLUT take minutes instead millennia, clearly a pedagogical advantage.

With EVOLUT students can select several scenarios to run: Mendel's experiments with mixing, counting, and breeding peas; sickle cell anemia with its condition of heterozygous advantage; color banding on snails; differential allele selection in plants growing on slag heaps (similar to Crosby's models); and the selection process of the gray and black forms of the British Peppered Moth in the 19th century. For its time frame this package was quite forward looking. Students can interact with the material in a more meaningful manner than if the ideas were taken off the printed page. Limiting the potential for this product were some of the examples, as well as many of the supporting materials. Unfortunately there is not a pea, snail, plant, or moth to be seen in any of the runs. A great number of graphs keep the user informed about the allele frequencies and their time dependant evolution. The printed support materials were unavailable outside Britain. Many of the examples would be familiar only to inhabitants of those isles. The limited use of graphics and presentation of data solely through highly structured tables on the screen or in print unfortunately confines this program to being a specialist's tool in a general science curriculum.

Similar criticisms, from the view point of use as a tool in developing populational thinking in secondary students, can be made of another program from the Chelsea Science series. LINKOVER. Understanding of the basic issues is assumed before the program starts. As the above research shows, the assumption is not generally warranted.

Beyond the lack of concreteness and a clear analogy to what is being modeled, a very important pedagogical idea missing. With global computational structures like those in EVOLUT there is no way for students to see the feedback from the micro or local level to the macro or global level of conditions effecting both the organism and the environment (Langton, 1991). The unit of selection must be the individual gene (Dawkins, 1976; Dawkins, 1983; Maynard Smith, 1982; Ridley, 1983); yet genes are not at the center of any of these models. It is the gene that affects the growth, development, and function of the organism, which, in turn affects other organisms and the environment, which, in turn, effects, through the process of natural selection, the populations of genes. Models based on cellular automata can provide that necessary link.

Steven Sepe describes a program called EVO (Sepe, 1988); it is not commercially available. Organisms in EVO resemble the world of Dewdney's sharks and fishes. Like Resnick and Silverman, Sepe has gone beyond the typological definition of Dewdney's world so that each organism has particular characteristics. It is written in C for an MS/DOS environment. It possesses a limitation of 640K for the grid and data. Reproduction is asexual. The simulation runs very slowly; several hours are needed for a single run. Characteristics include: lifespan, number of offspring, adaptive index, and dispersion of young. Interaction with the substrate is not modeled. The 'adaptive index' measures "the chance of survival when competing with other organisms. The greater the adaptative index, the better the organism is adapted to the current conditions." The user can also vary the mutation rate.

Although EVO does have some pedagogical potential I find the 'adaptive index' variable confusing and even circular. The definitions of adaptation, natural selection, fitness, and survival potential should be external to the variables of the program. The student should be the source of these analytical concepts in his or her attempt to understand the analogs of natural processes in the simulation. EVO does not clarify the fundamental concepts behind natural selection that the previous studies have shown to be so confusing to students.

A final evolution simulation came to my attention during the final draft of this paper. John Jungck and a group of biology educators has announced a series of new simulations titled BioQuest (Wright, 1992). His Genetic Construction Kit is one of them. The simulations are intended for college students. One of the simulations titled Biota addresses evolution and population genetics. The program was not available to me for review at the time of publication.

Available Commercial Packages Using Cellular Automata

There are six packages based on cellular automata currently available for educators. Three are marketed at the national level.

Life and Cellular Automata Technisoft Engineering, Bremerton, WA. This Macintosh based program, published in 1985 incorporates Conway's GAME OF LIFE, as well as several other more complex cellular automata simulations. The review of Life and Cellular Automata by Willis, Hovey, and Hovey (Willis, et al., 1987) gives some idea of the reaction of life science educators to the educational possibilities and pitfalls of cellular automata. "Life and Cellular Automata differs drastically from most simulations reviewed . . . because the program simulates abstract concepts instead of 'real world' events." The authors further state that "Another 'problem' with this simulation is the fact that it can be used in many different classes - from a high school biology class to a graduate level computer science course." Later the authors state that "Life and Cellular Automata thus requires more careful planning, and often much more preparation, than many simulations." Willis, Hovey, and Hovey set the audience for the program as "Advanced or accelerated high school classes in computer science, math, botany. and college classes in computer science, math, botany." The Macintosh interface makes the program easy to use and the concepts it addresses very easy to understand.

It seems that while simulations based on cellular automata pose significant problems for reviewers, the same may not true for students. One wonders what 'real world event' is captured in the coefficients of Lotka-Volterra predator/prey equations. Of particular interest is the reviewer's concern about the general applicability of the cellular automata modeling. A decompartmentalization of science is very much underway in the halls of research (Clark, 1989). The Human Genome Project will require the combined resources of thousands of geneticists, molecular biologists, mathematicians, and computer scientists for several decades (Lander, Langridge, & Saccocio, 1991). It is estimated that there is a serious shortage of computational biologists needed for this type of work (Frenkel, 1991). Much planning and careful preparation will be required for this most important project. New ways to capture massive amounts of data from the estimated three billion base pairs of the human genome are being planned. Designs for teams of biologists, microbiologists, geneticists, and computer scientists are being formulated to start preliminary compilations of the data (Lander, et al., 1991). Why not ask the same careful interdisciplinary planning and concern from science educators attempting to restructure their own curriculum?

The response to Life and Cellular Automata shows that a great deal of work must be done over the next decade by science educators and schools of education. A massive quantity of new knowledge is being created by a synergy of many disciplines. The Human Genome Project is but one example. Our students, and most importantly, our future science teachers must know about these developments if they are to prepare students to understand the world and century in which they will live. The current compartmentalized curriculum is not well suited to receive, much less teach this new knowledge. New ways of structuring and teaching must be found.

In defense of Willis, Hovey, and Hovey's criticism of Life and Cellular Automata, the software indeed may have limited application in the life science curriculum. The rules by which the cells interact are restricted. Many are seemingly "non-biological", or so abstract as to be biologically meaningless. The model itself holds a great deal of potential that deserves exploration.

Phantom Fish Tank: An Ecology of Mind by Logo Computer Systems Incorporated, published in 1987, provides a similar approach to automata as Life and Cellular Automata for younger students. It is also available in a variety of machine formats. Students can explore automata by seeding the screen with organisms that live or die according to global rules defined by the user. The full range of automata behavior described by Wolfram is possible in this microworld (Wolfram, 1986). Students can make rules and seedings that are static, periodic (returning to one configuration after a finite number of moves), complex (having arbitrarily long periods), and chaotic. The manual describes how the "fish" and their rules can be made to model AND and OR gates. One can build a simple binary counter with automata. The exercise can be extended to building parts of larger automata 'computers'. Wolfram and Langton have offered proof that automata are capable of Universal Computation, meaning that if a problem can be solved by any computer, then it can be programmed into a cellular automaton, if one has a large enough grid (Langton, 1991; Wolfram, 1986).

This is all very interesting, but is it life science? Is it biology? Perhaps some boundaries between disciplines have been crossed. Are the rule governed dynamical patterns of the cells in the Phantom Fish Tank representative of any sort of ecology? There isn't even a substrate to support them, other than transistors changing states. Are there really populations here? Lynn Margulis and Dorian Sagan take strong exception to this computational view of life (Margulis, 1988; Sagan, 1988). Phantom Fish Tank, delightful as the program is, has a very limited audience. It is predicated on a very profound insight: VonNeuman's cellular automata in which exchange of information between localized neighborhoods can be seen as a model for change of all kinds. One of the characteristics of life is change. Langton goes as far as describing life itself as 'wetware' (as opposed to hardware and software) that maintains itself against the disorder of entropy in its environment by operating constantly on the boundary between complexity and chaos (Langton, 1991). Perhaps the real question to be asked is "Why are the boundaries there in the first place?" An exploration of cellular automata may provide some insight on this fascinating question.

Simulated Evolution by Life Science Associates (Bayport, NY, 1989) uses a true cellular automata genetic algorithm. The program was written by David Palmitre, a high school biology teacher from Temple City, California. It is quite similar to the sharks and fishes in the WA-TOR world of Dewdney (Dewdney, 1988; Dewdney, 1989a; Dewdney, 1989b). In Simulated Evolution two species of "microbe", a predator and a prey, inhabit the screen move through a grid based on specific rules. The rules that govern their motion are simple. The prey wanders randomly on the screen. Each move consumes a fixed amount of energy. The predator has an eight bit genetic "code" that determines its motion. The first four bits code the probabilities that the organism will move one square up, down, right, or left. The next four bits code the organism's probability of making a "hard right up", "hard left up", "hard right down", "hard left down". These "hard" moves are defined as two steps in one direction and one to the side, much like a knight's move in chess. To calculate the move of the organism at any one turn, the probabilities are summed and normalized, then results of a random number generator select what move the organism will make. For example, an organism with the genome (1,1,0,0,2,0,0,0) would have a 25% chance of going up, with the same chance of going down, and a 50% chance of making a hard right up. The sum of the probabilities is 4, of which 2 units are in the hard right up gene. Initially the genes of all predators are seeded randomly. Motion of all organisms is random.

A particularly interesting and novel feature of Simulated Evolution is the predator microbe's ability to evolve. This feature is possible only because of the use of a cellular automata algorithm; each automata is treated individually. When the microbe is old enough, and has gained sufficient "energy" by capturing enough food microbes, it reproduces. The "genetic" code that determines the probabilities of the parent microbe's turning in any given direction (up, down, right, left, hard right (like a knight's move in chess), or hard left) is passed onto the daughter. When a specified age is reached, or the parent runs out of energy, it dies. The "daughter" microbes receive a copy of the parent's motion probabilities plus a random mutation placed on one of the probabilities of motion. According to Darwinian theory, the "probability" genes that obtain the most food for the organism should have a reproductive advantage and increase in the population. Effective genes should propagate through the population.

Palmitre's organisms begin to evolve slowly as the program runs. The random mutations of the direction probabilities begin to show their effect on the behavior of the organisms. The design is particularly clever in that the observable "phenotype" directly represents the unobservable "genotype" (the motion probabilities of each organism). Initial motion is random, but patterns of motion slowly begin to evolve after several hours and a few thousand generations of organisms. It seems that there is an advantage if the organism develops what is called a "looper" strategy. "Loopers" make wide, slow looping paths across the screen. This seems to provide the organism with a greater chance of meeting "food" organisms in its path. The "looper" feeding strategy is stable, once it evolves. The random mutations induced on the offspring seem to converge on the set of values that specifies a "looper".

How are Palmitre's organisms related to the "real world"? Clearly these "strategies" represent a kind of optimal behavior based on the limitation of the automata's world. Evolution of hunting behavior in the real world is clearly a very complex process dependent on a multitude of factors. The similarity of these artificial microbes to real motion patterns is remarkable. Some real microbes are loopers, others gliders. It is more than remarkable that such seemingly complex behavior can be mimicked by simple commands and rules of a simplistic cellular automata model.

I am very much intrigued by the possibilities offered by Simulated Evolution. Clearly it was written by an educator with a firm grounding in classroom dynamics. Yet the program is too narrowly conceived to be used as a general pedagogical tool or exercise. As the commercial version is formulated, I cannot see a use for it in any way other than as a limited demonstration of a system governed by a genetic algorithm. There is no easy way for the student to "play God" and fiddle with the variables. There are no "what if's" that the student can experiment with. The result is determined by stochastic processes. Oddly enough, it is the same every time: the evolution of "loopers". This point is well worth discussion in a biology class. Is evolution as we have it on earth, inevitable? There seems to be no natural follow up, within the limit of this program, to the beautiful conceptual problems posed by Palmitre's organisms.

The next three simulations all, by Maxis Corporation of Orinda, California, though primarily based on cellular automata models, build substantially on the concept of randomness and random walks. I must digress slightly to introduce these ideas within the context of computer modeling of evolutionary biology.

Random Walks and Simulating Evolution

Several articles appearing in paleobiological and evolutionary biological literature during the 70's and 80's explored the possibility that some, or indeed a good deal of what biologists have thought to be the result of natural selection or evolutionary pressures may be the result of random selection processes (Cairns-Smith, 1985; Dawkins, 1986; Gleick, 1987; Packard, 1987; Partridge, et al., 1984; Pattee, 1987; Raup, 1977; Raup, Gould, Schopf, & Simberloff, 1973; Taylor, et al., 1987) . An explanation based on random walks is just as plausible a theoretical framework as classical Darwinian evolutionary theory, if it can adequately explain the fossil record. Pioneered by David Raup, Steven Jay Gould, and Norman Packard, and others this approach represents a new view of biological process as possibly containing more random, non-deterministic elements that previously thought. It is a revision of the Neo-Darwinian perspective developed in the mid-century. These non-deterministic elements can be readily modeled on a computer. This new approach promises to change significantly the standard view of natural selection by evolutionary theorists (Augros, et al., 1987; Avers, 1989; Gleick, 1987; Mayr, 1988; Packard, 1987; Raup, 1977; Raup, 1991; Raup, et al., 1973).

The use of computer programs as tools to investigate theories is quite new in biology. More traditional methods were virtually Aristotelian in form: argument by analogy based on "type" cases or induction based on selected samples (Mayr, 1988). Minor changes in "type" or different or new information would change interpretations radically. The computer offers a new method of investigation and argumentation for biologists, one not available before the last decade (Augros, et al., 1987 ; Raup, 1991). It also provides educators models to explore some of the impact on genetics and evolutionary theory of new advances in molecular biology (Conrad, et al., 1985; Price, 1985; Thompson, 1988). Versions of these "older programs" which explore stochastic explanations of extinction and speciation, found in specialists technical journals, were made available to general audiences in the late 80's by A.K. Dewdney in *Scientific American* (Dewdney, 1984; Dewdney, 1985; Dewdney, 1989a; Dewdney, 1989b).

The topic of the cause of mass extinctions is certainly a fascinating one for career researcher and beginning student alike. It leads immediately to a discussion of some fundamental questions in biological science. Raup bluntly restates the problem as an inquiry into "bad genes or good luck?" (Raup, 1991) What caused the mass extinctions of the past? Are answers other than causal ones possible? The question was explored in the series of articles by Raup and Gould was "Can random processes explain the fossil record?" (Raup, 1977; Raup, et al., 1973). The evolutionary processes that lead some lines to new species, and others to extinction, can be modeled mathematically by a Markov chain. A Markov chain or process is a series of events, each manifesting as one of a finite number of states, the probabilities for transition to the next state in the chain are either fixed, or determined by previous sequences in the chain or by external conditions. The Markov chain explored by Raup and Gould is quite simple. There are four states considered: 1) branch to a new species, 2) continue without change, 3) branch to a new lineage, or 4) go extinct. A random number generator is used to create a model of an evolutionary process . The model starts with one species; monophylogeny is assumed. Each turn or cycle, every living organism has one of the four possibilities (states) open for it for the next move based on the results of the random generator. A random number is selected and that species has its state changed according to the interpretation of the value of the random number selected. A walk through of several cycles of the algorithm at the heart of the program will clarify this idea quickly.

The symbols and values for each of the probability states set out in Table 1 represent the probabilities of extinction, adding, branching, and remaining unchanged over some arbitrary time unit. These values represent an equilibrium condition as the sum of the new species and new lineage probabilities equals that of the extinction probability.

Table 1. Values of Probability States

P_e =	Probability of extinction of one species.	.15
P_n =	Probability of adding another species	.10
P_b =	Probability of branching to a new lineage	.05
P_s =	Probability of remaining unchanged.	.70

Set in a linear order these probabilities of changes in the state of any species at any one cycle are set out in Table 2.

Table 2. Ordered Probability States

Extinction	IF	0.00	≤	P	<	.15
Add a new species	IF	0.15	≤	P	<	.25
Branch	IF	0.25	≤	P	<	.30
Unchanged	IF	0.30	≤	P	<	.99

The probabilities chosen in Table 2 were used by Raup and Gould as general first order approximations to similar events in the real world as recorded in the fossil record. Clearly the probabilities of extinction (here P_e=.15) and speciation (here P_n=.10 and P_b= .05 for a total of .15)) should be about equal to have any chance at equilibrium. These probabilities are but one of many possible sets. Others can be arbitrarily generated under the conditions that the system should be at or near equilibrium.

Table 3 shows a sample run of the random number generator and the interpreted results following the speciation/extinction/branching rules outlined above. This stochastic process is applied to each species individually once for each simulated time unit. Please note that after the first cycle there is still only one species (as p1=.54). After the second cycle there are two species, as probability p2 was .19 meaning that the original species should add another species. The third cycle begins again with species one which adds another species (totaling three now). The probability on the second species was .28 meaning that a new lineage should be added (totaling four species now with two separate lineages). The fourth cycle brings an extinction and another new species.

Table 3. Sample Markov Process to Generate Clade Data

Time	RND#	Result	Total Species	No. of Lineages
1	.54	Unchanged	1	1
2	.19	Add species	2	1
3.1	.22	Add species	3	1
3.2	.28	Branch	4	2
4.1	.56	Unchanged	4	2
4.2	.10	Extinction	3	2
4.3	.69	Unchanged	3	2
4.4	.24	Add a species	4	2

In this example the rates of branching, extinction, speciation, and no change are constant during the run. It is possible to modify each probability to model "speciation blooms" that can occur after a random event that lowers the number of species below a specified level (Raup, 1977).

The output of this process can best be illustrated using a diagram of a 'clade' or cladogram or spindle diagram. A cladogram is a representation of an evolutionary tree or lineage with time on a vertical axis and the arbitrary horizontal axis showing the number of species extant at that particular time. Figure 2.1 shows what the associated cladogram for the above sequence would look like.

Species are represented by boxes. Time is increasing in the vertical direction. Additions of species increases the number of boxes at a certain level. Likewise extinctions decrease the number. Branching to a new lineage is indicated by horizontal lines.

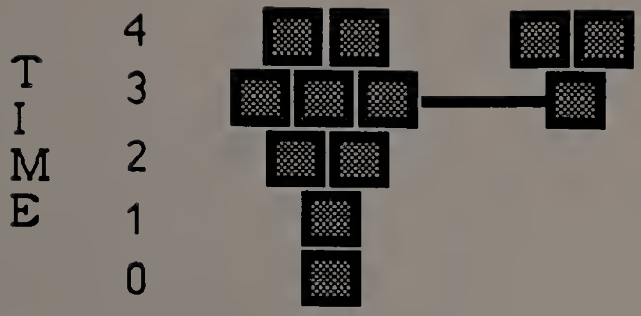


Figure 2.1 Simple Computer Generated Cladogram

The articles by Raup and Gould (Raup, 1977; Raup, et al., 1973) give more details on models in which rates of speciation are variable in time. This extension of the model is in line with their interest in punctuated equilibria. Modifying the probabilities based on the number of species is certainly a valid modeling technique, one that may approximate more accurately the fossil record, but it is not needed to appreciate the fundamental approach to modeling evolution by a stochastic process.

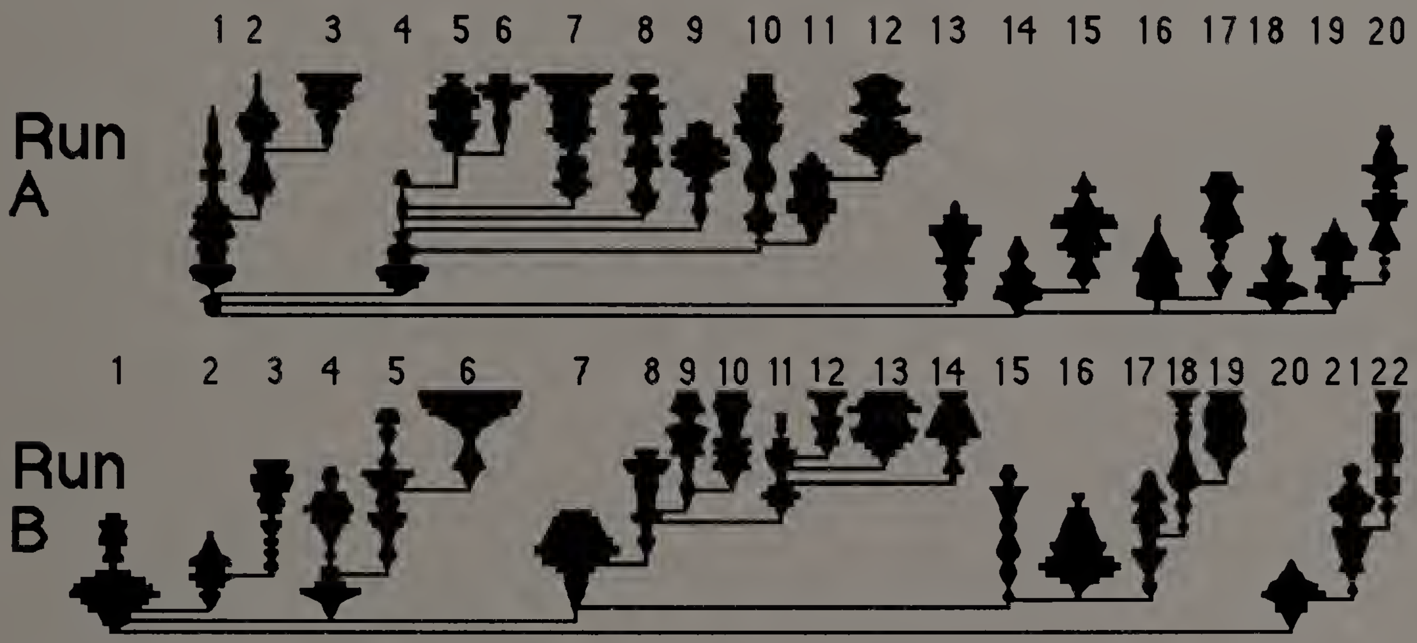


Figure 2.2 Two Runs of a Computer Generated Cladogram.

The result of a run is stored internally in a large matrix with the i_{th} row holding the number of species in i_{th} lineage. The j_{th} column contains the data for all lineages in the j_{th} time period. As such the matrix is almost impossible to read and interpret. It is much more helpful to translate the matrix into a clade or spindle diagram as shown above.

Figure 2.2 is a computer generated clade diagram after Raup (Raup, et al., 1973). Two runs are shown, plotted as cladograms. It is surprising indeed to see how similar these artificial clades are to real clades from the fossil record. Some clades like B6 or A7 start about the time mid point and expand vigorously, much like the class insecta or phylum arthropoda of earth's fossil record. Others like B7, B16 and A16 or A17 show much initial "success" and then gradually die without issue, much like the trilobites. Some show initial success, then almost go extinct, only to have a second bloom before final extinction. Clades B1, B4 show this pattern, much like the ammonites.

Figure 2.3 is a clade diagram of 17 reptilian families taken from the best data to date of the fossil record (Raup, et al., 1973).

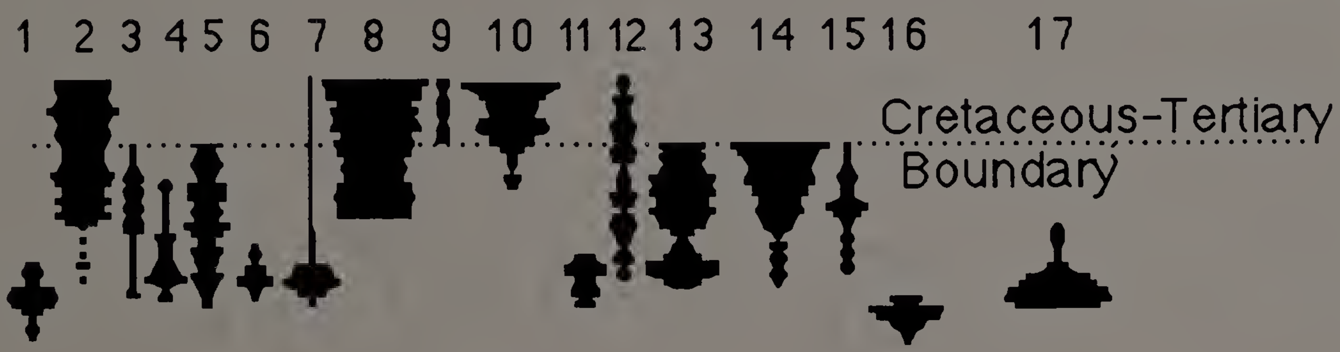


Figure 2.3 Diversity of 17 Reptilian Clades from the Carboniferous to the Present.

The clades in the above diagram are as follows: (1) Cotylosauria (primitive reptiles from the late Permian), (2) Chelonia (turtles and tortoises), (3) latipinnate ichthyosaurs, (4) longipinnate ichthyosaurs, (5) Sauropterygia (plesiosaurs), (6) Placodontia (aquatic reptiles from the early

Triassic), (7) "primitive" lepidosaurs (of which the tuatara is the last extant), (8) Sauria (lizards), (9) Amphisbaenia (blind snakes), (10) Serpentes (true snakes) (11) Thecodontia (Triassic socket toothed reptiles) (12) Crocodilia, (13) Saurischia (lizard-hipped dinosaurs), (14) Ornithischia (bird-hipped dinosaurs), (15) Pterosauria (flying reptiles), (16) Pelycosauria (primitive Permian and Triassic reptiles), and (17) Therapsids (primitive mammal-like reptiles). The Cretaceous-Tertiary boundary is marked.

Some comments on this graph are in order. Clearly, extinction is not uncommon. After the Cretaceous only turtles (Chelonia), the tuatara, lizards (sauria), blind snakes (Amphisbaenia), true snakes (Serpentes), and crocodiles survived. At the Cretaceous-Tertiary boundary five of the 11 living reptilian clades at that time went extinct (two clades of ichthyosaurs, the Saurischia, Ornithischia, and Pterosauria). Two of the clades show a distinct flat topped shape (#13 - the lizard-hipped and #14 - bird-hipped dinosaurs). Vertical dots in #2 represent missing elements in the fossil record. The long column in #7 represents the persistence to the present of one species, the tuatara from New Zealand, the last of the lepidosaurs.

The general similarities between the computer produced clades and the clades from the fossil record is striking. Is there any difference between these two diagrams? Is it possible that massive extinctions such as those at the end of the Permian, or at the Cretaceous/Tertiary boundary have no 'cause', but are statistical in nature? The query posed in the Raup, Gould articles is in the form of a null hypothesis: "There is no difference between observed clade diagrams and diagrams produces by stochastic processes".

The idea behind the investigation is quite intriguing. It strikes at the core of a critical thinking investigation in the natural sciences. Is there only randomness in nature? How much of what we observe as natural process or the product of natural law is really the result of stochastic processes. Clearly the shapes of snowflakes, river drainage patterns, and biological mutations call on randomness as their origin. Is there more such randomness in nature? The "Argument from Design" is brought into inspection; all things do "seem" to have a purpose under heaven. But how much of this is our own minds projecting order where there is none? The question here is coldly put to both scientific theorists as well as creationists. Conversely, how much of what we consider random is, in fact, according to one pattern or another?

The mathematics behind the test of this Null hypothesis is beyond secondary students. One must use the Kolmorogov statistic to test randomness in Markov processes (Raup, 1977). The result from Raup and Gould is that, interestingly, the null hypothesis cannot be disproved based on the data we have. We only have one example, our earth; and the fossil record is very incomplete.

It is not necessary, I feel, to introduce such elegant mathematics as Kolmorogov statistics on Markov processes to guide secondary students to analysis of this data. Nor is such an approach pedagogically fruitful. One can approach it in a concrete and pedagogically sound fashion by performing many trials obtained by pooling data from the whole class' efforts, then simply counting it. Several hundred "alternate worlds" can be produced in the space of one hour even in a small class. The results of these "alternate worlds" can be analyzed and tallied. During this process students learn a great deal about the fossil record, geologic time, extinctions, mass extinctions, and principles of phylogony. All of these topics are dry as dust without a context that connects them and brings them to life. Use of a random walk program can do that. Students compare their "worlds" with clade diagrams of real fossil families. They come up with conjectures about the relationships between the fossil record and the computer generated clades.

Six conjectures that can be investigated by this method are: (1) What is the probability that a massive extinction (50%) like that at the end of the Cretaceous would occur as a random event? (2) What is the probability of a "speciation bloom" like the one that occurred at the start of the Cambrian? (3) What is the probability of a flat topped clade like that of the dinosaurs? (4) What is the probability of a random occurrence of two extinctions of 30% to 50% of species. The fossil record on earth shows at least two such massive extinctions. Do we really need to invoke meteor collisions to explain these events? (5) Several specialized shapes of extant clades do not appear often in the computer produced clades. An example is the *Coelocanth*. It is a genus of only one species that has remained unchanged for 300 million years. Another is the tuatara of New Zealand. What is the chance of such an event? (6) What percentage of extinctions can be explained by random events as opposed to more standard causal explanations?

This process of student involvement with the subject through manipulating and conjecturing shows clearly how technology can open new exciting methods of approaching previously difficult areas of the curriculum. The method I have set out here also shows clearly that the computer is a powerful tool. It is important to build up students reasoning abilities if they are to use the insights made possible through technology. Here is a fine example of use of the statistical argument as well as the argument from analogy like the Argument from Design: The world is like a fine watch, the work of the Master Watch Maker (Barrow, 1988; Botkin, 1990; Dawkins, 1983; Dawkins, 1986).

One commercial program employs a modeling strategy much like that in Raup and Gould. It is The Blind Watchmaker by Richard Dawkins. The Blind Watchmaker is a program distributed by Norton with the purchase of a copy of Dawkin's book, The Blind Watchmaker (Dawkins, 1986). Dawkins presented the program at the first conference on artificial life at Los Alamos (Langton, et al., 1988). The 'chromosome' of the organisms in The Blind Watchmaker contains 16 elements that control horizontal and vertical gradients, number of segments, scale, symmetry, and mutation rates. Each element controls some aspect of a recursive routine that generates the images of the biomorphs in the world governed by The Blind Watchmaker. Below is a figure showing some of the biomorphs created by Dawkins program. Some resemble insects, others plants, still others starfish. The diagram is from Dawkins' book.

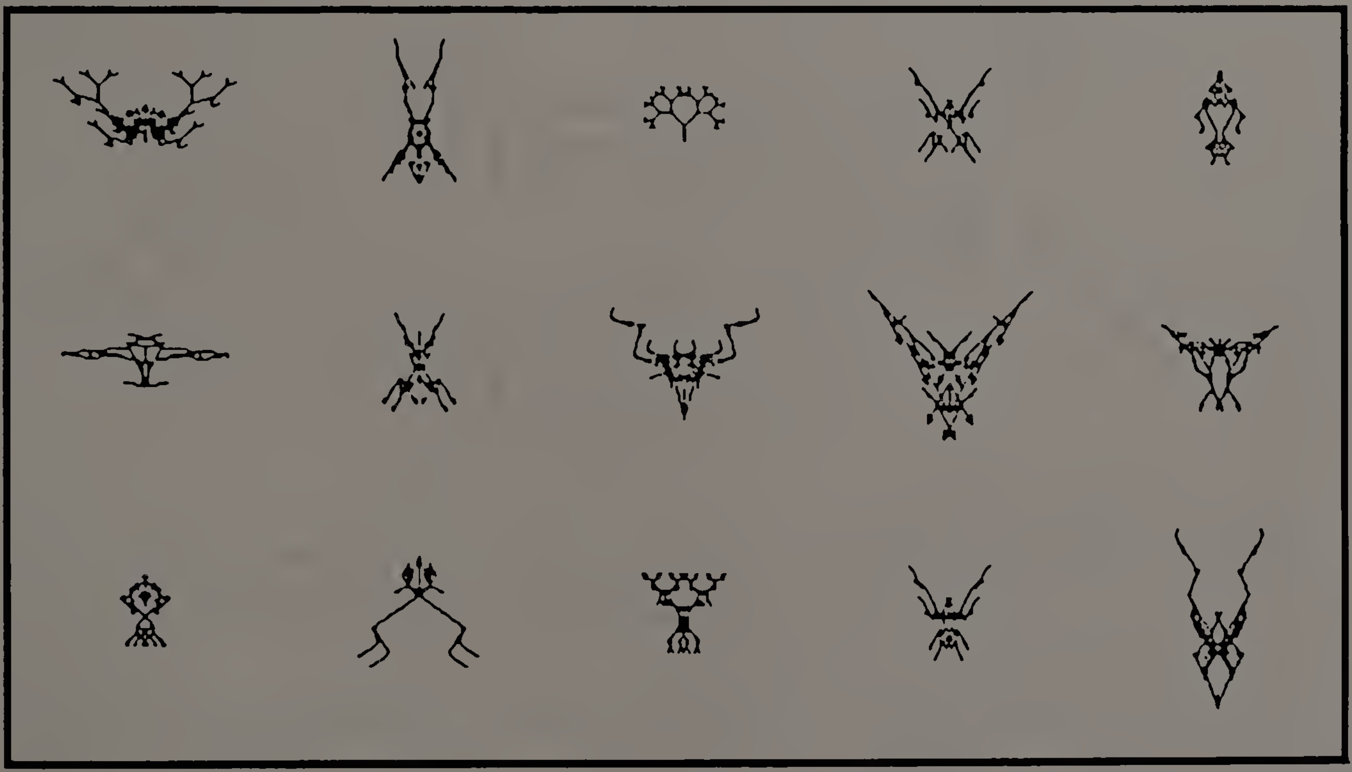


Figure 2.4 Sample Biomorphs from *The Blind Watchmaker* by Richard Dawkins.

One can also randomly generate biomorphs and then select any one to selectively breed it. This is done through the 'Pedigree Screen' shown in Figure 2.5. The ancestor of all the biomorphs on the screen is the arachnid-like beast at the center bottom. Varying any of the 16 parameters in the chromosome produced the effects on the biomorph shown. The parameters can be varied by choice of the user (genetic engineering) or by a random drift for each of the parameters from a mechanism in The Blind Watchmaker program itself, the analog of genetic drift in biomorphland. Playing with these biomorphs can be very addicting. Asserting a British sense of the absurd, Dawkins even offered a prize for any player who, through random mutation, or genetic engineering could come up with the best image of the Holy Grail. Two years later a second prize went to anyone who could breed the best 'human' biomorph from the 16 biomorph genes.

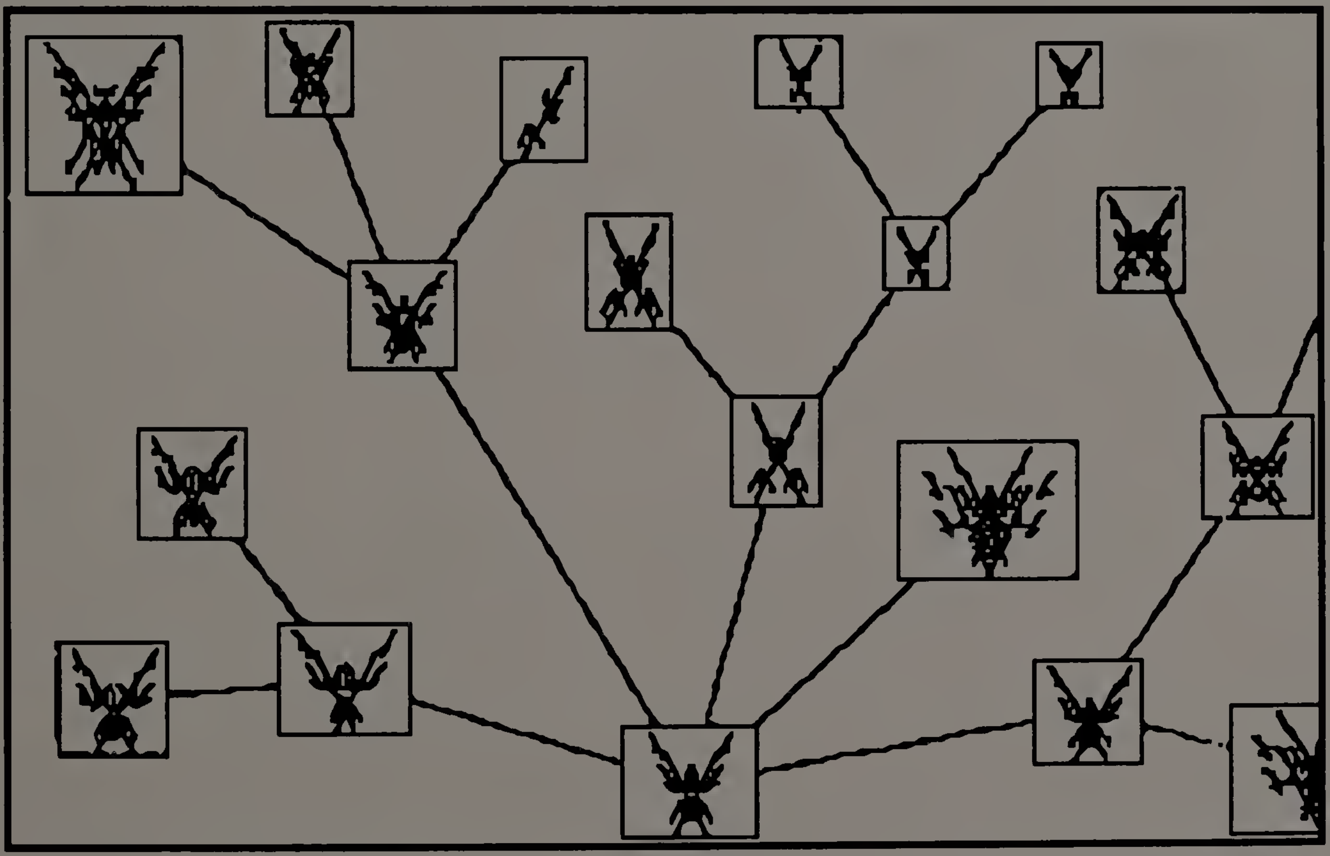


Figure 2.5 Pedigree Screen from *The Blind Watchmaker*

Dawkins' book is a delight to read. Bold, carefully argued, it explores the argument from design from many aspects. The computer program is an aid, and a fascinating supplement to the ideas in the text; it is not an essential part of the exposition. The title and central theme derive from the famous argument in Thomas Paley's *Natural Theology* (1802) in which the great theologian formulates an argument for the existence of good by considering a walk in the heath. Kicking a stone he notes that it could be there by some random action. Paley then finds a watch and marvels at its intricacy and craftsmanship. Paley concludes that watch must have had a maker (Dawkins, 1986). Likewise the works of nature are a manifestation of a design "in a degree which exceeds all computation." Dawkins takes the "Argument from Design" apart piece by piece and concludes that the natural world can be explained by Darwin's mechanism natural selection and there may be a watchmaker, but he or she is blind.

Of note in commenting on Dawkins' program in comparison with that of other researchers at the conference is its intentional lack of any mechanism for selection. There is no fitness function. Dawkins' biomorphs do not interact with their environment or each other. They are not really cellular automata, the biomorphs are really points in a state space described by the data structure of the 'chromosome'. Dawkin's text in The Blind Watchmaker extensively discusses natural selection and the multiple meanings of fitness and relationships to evolutionary theory.

The Evolutionary Tool Kit takes many elements of Dawkin's work and adds ways to define the fitness of each organism. As set out in the introduction to this dissertation, these functions can be based on reproductive success, or on physical, social, or metabolic constraints, all under the control of the user.

Simulations by Maxis: SimEarth and SimAnt

SimEarth, SimAnt, and the unnamed, unpublished simulation on fish, by Maxis Corporation of Orinda, California, have incorporated the Markov process modeling into the cellular automata models in a most skillful way. First I shall discuss SimEarth.

Published in late 1990 and distributed through Broderbund, SimEarth represents the first commercial package to use cellular automata as an instructional medium. Its predecessor by one year, SimCity, is designed in a similar manner, with a focus on urban planning. The general design of the program borrows heavily from James Lovelock's work on the Gaia Hypothesis (Lovelock, 1979). The prototype of SimEarth was "DaisyWorld", a model made by Lovelock in the mid 80's to demonstrate the interconnection of life on the planet and the environment (Lovelock, 1991).

"DaisyWorld" is a spherical body populated by daisies of different reflectance. They have shades from white, through gray, to black. The solar source for "DaisyWorld" is a star that is gradually maturing to a red giant phase. Its energy output is increasing. Randomly seeded daisies on "Daisyworld" cover the planet, changing its albedo to maintain an acceptable temperature range for daisies to grow. When output is low, in the youthful age of the star, it is advantageous to have black daisies cover the planet. As the sun heats up lighter shaded daisies evolve that reflect more sunlight. Darker daisies remain near the poles. In the final stages white daisies cover the planet. "DaisyWorld" is an elegant model for natural selection under a simple fitness function. As the energy output increases whiter and whiter daisies evolve to reflect more of the sun's heat. The process stabilizes the planet for a considerable time until the solar output becomes too great and all life dies.

Similarly the planet in SimEarth starts out lifeless. Life develops when the planet has cooled sufficiently. Evolution proceeds to develop a variety of creatures to populate the planet, changing its atmosphere and climate by their interaction with the environment. The source of energy for the planet is a star much like our sun. It is getting increasingly hotter. SimEarth is a game whose goal is to guide one of the sentient life forms that evolves to a stage where they have both the technology and energy for inter-stellar travel to colonize another world before their home world dies. It is a remarkable intricate, accurate, multi-disciplinary model investigating and evolving ecosystem on a planetary scale (Derrick, & Derrick, 1991).

SimEarth is also targeted at the home market; not the educational one. There is much to be learned by educators from this marketing decision. Investigations on SimEarth lead the user through inquiries in paleobiology, climatology, atmospherics, geology, ecology, social interactions, plate techtonics, and astronomy. Each discipline is approached by the student, this is most important, in a context that makes sense in relation to other disciplines and the specific problems with which each discipline concerns itself. The approach taken by SimEarth, a world view that is really a world view, may not neatly fit into science curricula as currently conceived. It certainly won't fit into the bells of forty-five minute time blocks that drive our current instructional system. Investigations take several hours in SimEarth.

In spite of these draw backs, it has remained in the top 5 of educational software sales since its introduction almost two years ago. It ranked #1 for the last quarter of 1991. There is a market for a quality educational product, it seems. Many parents and students have already bought it and enjoy it. Its approach is very non-linear and unconventional from the point of view of standard pedagogical software. I strongly feel that educational specialists, curriculum planners, and textbook developers must rework their conception of the format of education and the use of computers and multi-media tools in it. I have no doubt where the current 'chalk-talk' presentation of these topics would rank if it were reduced to a talking screen (probably a relatively easy job), shrink wrapped, and marketed on the shelves of bookstores or software emporia. I suspect that in two weeks it would hit the remainder bins, discounted and sold by the pound to clear the shelves for something buyers really want. There is no lack of citations of the failure of our standard curriculum and presentation formats. SimEarth shows that there are viable alternatives.

Unfortunately the marketing of educational software and textbooks follows very different rules. Review and selection by committees, as well as review and editing by publisher's staff with an eye to a national market, produces a much different product and perceived buyer profile. I suspect that, given the choice, the vast majority of educators would choose the shrink wrapped version of the same materials and methods they are currently using, and then claim to utilize the "new" technology and "new" methods to "restructure" their curricula in light of the much publicized national goals. Deep rooted change in education is so badly needed. With very few exceptions, it is not done.

In parallel with SimEarth's entry into the home market, The Evolutionary Tool Kit attempts to provide for young people, through the educational market, a quality multi-disciplinary, student centered learning environment for life science in the 21st century.

In SimEarth, cellular automata are used at six concentric shells or levels: plate tectonics, landforms, the hydrosphere, atmospherics, planetary biomes, and the life forms shell. The first level, that of plate tectonics, divides the surface of the planet into tens of thousands of cells each stationary or moving in one of eight compass directions. These cells interact with each other and heat and magma upwellings from the core to form ocean basins or continental masses. They can collide to form mountains on land masses above them, as well as earthquakes and tidal waves. The user can also control the motion of these cells to literally make mountains, ocean trenches, land bridges, or new continents with a "Terra-Former Tool" to aid the development of SimEarth's inhabitants.

The automata shell above the plates are the landforms. This can be either ocean plain, continental shelf, shallow bay, sea shore, swamp, forest, grassland, rocky, or polar region. Each landform automaton also has an elevation and climate associated with it. Elevations can be changed by the user, either by earthquakes or direct manipulation. The landform automata have a global influence. For example, a world with too much swamp will produce an excess of methane and heat will build up rapidly.

The hydrospheric cells occupy areas above landforms that have the lowest elevations. The amount of water available for oceans is determined by the mean temperature of the planet. Under bad management and a run-away greenhouse effect, the oceans can evaporate. Hydrosphere cells also carry information about ocean currents. The currents flow around the planet under constraints imposed by the landforms, incoming energy from the star and the planet's atmosphere.

The biome cells hold information about the particular geologic condition of the cell at each location, such as barren rock, arctic, boreal forest, desert, temperate grassland, forest, jungle, or swamp. The state of the landform cells are determined by states of neighboring cells in the tectonic, hydrospheric, and atmospheric layers.

The atmospheric cells hold information about temperature of the cell, direction of air flow, and moisture content. This information, along with feedback loops dependent on information from cells in the hydrospheric, landform, and tectonic cells determines the amount of rainfall at that particular region.

The life form automata hold information about what kind of life form occupies each cell. There are fifteen classes of life represented in SimEarth. The classes are: Prokaryote, Eukaryote, Radiate, Arthropod, Trichordate, Mollusk, Insect, Fish, Amphibian, Reptile, Dinosaur, Avian, Cetacean, Mammal, and Carnifern (Derrick, et al., 1991). Each class has a preferred climate and landform. Fish like open ocean, or continental shelves. Amphibians like swamps but will not live in polar regions, etc. Trichordates are a long extinct group of three chorded creatures that the designers of SimEarth decided to give a second chance. Carniferns are mobile carnivorous plants that may or may not evolve after the appearance of insects. Eight classes are land dwelling, seven live in the seas.

Each class on SimEarth has sixteen species. The species are not true species as taxonomists would define them. Each is really a level of development. The sequence of development within a class are fixed, as is the sequence of appearance of each species within the class. If a class has reached the sixteenth level, it is said to have attained sentience. At the level of sentience civilization can develop in any class except prokaryotes or eukaryotes.

There are seven levels of civilization: stone age, bronze age, iron age, industrial age, atomic age, information age, and nanotech age. Any class, other than prokaryotes and eukaryotes can evolve intelligence. Once civilization has developed it is the job of the user to guide the beings to wise use of the planet's resources to permit inter-planetary migration. It is possible to speed this process up by employing the "monolith", after Arthur Clarke's movie *2001.* At considerable expense to the energy budget of the user, a monolith can be placed near any biome. The monolith has a 30% chance of accelerating that life form to sentience or to a much higher level of civilization.

The development of the life forms in SimEarth cannot be said to model evolution or any natural selection process very closely. The units of life are not individuals, rather they are considered to be ecosystems. There are no genetic elements to the life forms, only properties assigned to each. These properties are very general, such as habitat likes or dislikes, potential for evolution. The algorithm governing the time sequence development of the life is fundamentally not adaptive. It is a Markov process much like that used by Raup and Gould (Derrick, et al., 1991). Probabilities for evolution within each class, or probabilities of the development of a new class from existing ones are fixed by internal constraints of the program. For example, the class Arthropod can evolve from any of the first eight species of Radiates. The next four species of Radiate can possibly mutate into Trichordates. The first four species of Arthropod can mutate into Mollusks, the next eight can mutate into Insects. The last species of these classes are reserved for sentient forms of that class. It is possible to have intelligent Mollusks or Trichordate cities in the Atomic Age on SimEarth. The Monolith is simply a subroutine that alters the probabilities of mutation for a very short time in favor of leaps to sentience for organisms encountering it. The rate at which species can evolve is determined by a global variable called the "mutation rate". It can be modified by the user.

Graphs of the Life Class Ratio are available from a MAP WINDOW that provide counts of the numbers of classes and numbers of species in each of 16 classes of life. These maps are bar graphs of numbers of species of each of the 16 life forms. No evolutionary history for any class is provided. Under the stochastic conditions that the life forms evolved, such information would make little sense. Because there is no passing of any genetic information, this really is not evolution in any conventional sense, rather it is successive replacement of ecosystems.

Modeling evolution by a random walk in SimEarth is certainly very elegant, and probably accurate. In agreement with the work of Raup and Gould there is not enough information to determine if the fossil record, as we currently know it, is different from a sequence produced by a Markov process. The model is adequate, but not instructive. Some important elements of evolutionary theory are omitted. There must be some form of natural selection.

The cellular automata in my design, The Evolutionary Tool Kit do not use of Markov processes to model evolutionary change, and the biological unit in the Tool Kit can be either the gene or the organism. This marks a significant difference between SimEarth and The Evolutionary Tool Kit . Because the unit of selection is neither the individual or the gene in SimEarth, it is not possible to define a fitness function at the level of the organism in SimEarth. The Evolutionary Tool Kit does permit the definition of fitness, as well as a model for natural selection. It can provide a platform for a student to explore possible definitions of such a function and examine the feedback through global consequences of the individual's action on the population and the environment. As such it provides a powerful complement to the educational potential of a program like SimEarth.

The user of SimEarth is provided with a bewildering variety of pathways and interactions to explore. One can add, at some energy expense, nitrogen, oxygen, or carbon dioxide generators to correct atmospheric problems. One can change the tilt of the planet to explore the effect of modifying the angle of insolation has on thermal regulation. Meteors can be made to impact to create lakes or lagoons. Ice meteors can provide needed water. Earthquakes or volcanic eruptions can be manufactured to release some atmospheric or tectonic bottleneck.

Several scenarios are provided to more experienced user of SimEarth to test their skills as planetary managers and their understanding of the intricate feedback mechanisms involved. One is a model of Earth in the Cambrian era. The tectonic cells follow a fixed course of development, starting with the first multi-cellular life in the seas around the super-continent Pangea, ending in the present day distribution of land masses.

In another, more difficult scenario, the user is assigned to be the planetary manager of Mars. One has 50 years to make the planet habitable. The landforms on the model are those on the real red planet, constructed from NASA maps. In the most difficult scenario, one is set the challenge of making Venus habitable. Venus' surface in SimEarth is also a state of the art facsimile. The run-away greenhouse effect must be brought under control. The atmosphere consists of almost totally of green house gases and the surface temperature will melt lead.

In general SimEarth is an absolutely stunning package. The amount of planetary science, ecology, and paleobiology that a student can simultaneously learn from this package is remarkable. Perhaps "learn" is the wrong term. Most importantly, the package is constructive, rather than instructive. The ideas from all these disciplines are presented in a context that supports the need and utility of each. Also, it is important to note, it is the student who defines the problems, makes the connections, draws the conclusions in all of these disciplines while planet managing in SimEarth. Students build and deepen their understanding instead of digesting already existing knowledge from books.

The SimEarth manual is an aid to students' learning in this environment, but it is not intended as a bible. The program serves as a dynamic inquiry vehicle for ideas in planetary science from any resources the student wishes to use. One hopes that such a novel and powerful instructional design can find a place in school curricula. SimEarth does not lend itself to a linear "table of contents" approach so common in many classrooms.

The approach taken in SimEarth represents a quantum leap from the previous generation of software simulations on natural selection and evolutionary biology. The difference, I feel, deserves comment. The technical differences stem from two sources. First, the power of modeling with cellular automata became evident through the work of Christopher Langton and others at the Institute for the Study of Complexity at the Los Alamos National Laboratory. This work was disseminated to a larger audience through two conferences on the developing field of artificial life held at Los Alamos in 1988 and 1990 (Langton, 1989; Langton, 1991).

Second, the general style of programming changed from a linear style fostered by languages like BASIC, Fortran, to an object oriented style made possible by C, Lisp and other more specialized languages.

Programs, instead of being confined to linear executions, were able to define computational objects, with variable properties and relationships with other objects permitting very complex interrelationships to be the focus of the algorithms. Pedagogical changes in the decade of the 80's, a movement toward student centered instruction, individualized learning, seem to coincide nicely with this newer programming style. SimEarth exploited both changes quite well.

A second program by Maxis, SimAnt, was released in mid-November of 1991. Its theme is taken from the work of Harvard Sociobiologist E. O. Wilson. It is not a simulation of either evolution or evolutionary, but its content and method do deserve discussion. In SimAnt, the user is the mastermind behind several species of ant that populate a back yard. The user is personified as one of the ants, not as a god-like creature outside the simulation. The goal of the simulation is to gain access to the inside of the house of an increasingly desperate suburbanite. The "objects" manipulated are behavior patterns of the red and black ant colonies. There is no explicit attention paid to Mendelian inheritance in the sense of manipulating a gene's dominance, recessiveness, number of alleles, linkage etc. Non-genetic inheritance by shared, group behavior "mimetic" inheritance is a major focus of exploration (Dawkins, 1976; Dawkins, 1983). It is a very successful implementation in an educational, commercial package of some of the research done by Taylor, Jefferson, Collins, and Werner of the artificial life group at UCLA (Collins, et al., 1991; Jefferson, et al., 1991; Taylor, 1991; Taylor, et al., 1987; Werner, & Dyer, 1991).

"In SimAnt you are the intelligence of the ant colony. The individual ants are like the individual brain cells of your being. You will hop into and out of individual ants, using them as tools."(Bremer, 1991) The user, perceiving danger from one of many sources such as spiders, ant lions, lawn mowers, humans with insecticides, can lay down pheromone trails to guide other ants to safety. Ants can also be recruited by the user by sending pheromone signals to bring groups of ants together to accomplish jobs that one ant could not do alone.

Images of the ants and their movements in their burrows are very realistic. Considerable care went into rendering three dimensional images of the insects as they crawl through the burrows or engage in foraging, hunting, breeding, housekeeping, or communicating activities. The carapaces and thoraxes shine, as if they were reflecting real light. Each ant is cycled through a series of images so that a realistic simulation of motion and activity is achieved. One could definitely start 'thinking' like an ant after a few hours at this simulation. SimAnt certainly does fill a void in secondary curricula; the importance of the interaction between social organisms, their society as a whole, and the environment is too often left to 'chalk talk' techniques.

A particularly effective and innovative feature of SimAnt is the "yellow ant" construct. Ants that find large sources of food or enemy invasions "recruit" help. These ants that call for assistance are called initiators; they spur other ants to action. The yellow ant is the initiator for the black colony. The yellow ant is the user's way of communicating with and teaching the other ants in the black colony. "It is the ant you personally inhabit and control."(Bremer, 1991) It is the alter-ego of the user. The yellow ant is always of member of the black colony.

The "yellow ant" construction is a particularly clever pedagogical innovation. It permits the user to interact directly with the automata within the "rules of the system simulation", at the same time learning the constraints of the simulation and the rules on which it is based. While playing the simulation a very interesting sensation develops; one starts feeling like an ant. The simulation is designed to facilitate, in part, the insights enabled by a physio-kinetic learner in Gardner's multiple intelligence theory.

Similar algorithms to those in SimAnt for exploring how organisms and societies interact using models from sociobiology are open for direct manipulation in The Evolutionary Tool Kit. Pedagogical constructs like the "yellow ant" in The Evolutionary Tool Kit will be described in the discussion of the work of Karl Nicklas on forms of trees and extensions of the work of Werner and Jefferson on evolution of language, as well as in chapters three and four of this dissertation. Importantly the Tool Kit algorithms permit both genetic and mimetic flow of information.

At a conference at M.I.T. in October 1991, I was privileged to view the first demonstration of a new simulation from Maxis. This one is several years from release. It's theme is evolution and genetics. In the fish simulation beautiful multi-colored tropical fish swim around the tank (really the screen). The image is three dimensional, with the fish twisting their bodies and fins to propel themselves. They swim around, in front of, and behind other objects and fish in the tank. The illusion of a real fish tank is startling. The imaging process employed elegant ray tracing algorithms so that the surface of the fish had color and texture as a real organism would. The effect was not unlike some of the screen saver programs from After Dark except the images are very high quality and the illusion of depth is almost perfect.

It is possible to breed the fish. Parents are selected and some traits are selected with a percentage of dominance given to each. The new fish is hatched and swims with its parents. A problem surfaces, so to speak, when breeding two fish is attempted. The memory requirements for the program are quite large. The version demonstrated had a fish population of about a dozen. The program ran under OS/2 on a 33 mHz 386 processor with a requirement of 6 megs of RAM. Once a fish was bred, it took the program approximately ninety to one hundred and twenty minutes to create, render, ray trace, and shade the hundred odd views of the new fish that are needed to create the illusion of swimming in three dimensions. The rendering could be done in the back ground. Two hours per fish is quite slow. This time is only for one fish not a generation of them. Having seen the skill of the programmers at Maxis through their other work, I have no doubt that this fish simulation will be a fine product. There are considerable problems to be faced before a marketable version is available.

The approach taken in The Evolutionary Tool Kit, I feel, is more general. Organisms are not limited to an aquatic environment. The program does not spend a great deal of time or computer memory allocation on three dimensional renderings. Versions of The Tool Kit running populations in the tens of thousands can be piloted in classrooms in three or four years. As noted in the above discussion, it is also more faithful to the biological aspects of automata simulations.

The last commercial cellular automata simulation, BIOSIM was written by Paul Deal of Moriarty, New Mexico. It was first published in 1988. Paul Deal is a microbiologist at NASA. He markets the simulation as shareware. BIOSIM is unique in that it is concerned mainly with the interaction of organisms or systems of organisms with their substrate. It specifically addresses cellular biochemical pathways such as photosynthesis, respiration, and fermentation. The experimenter can observe the effect of each pathway, or combination of pathways in single organism systems or dual or triple organism ecosystems. It is also possible to introduce metabolic inhibitors or mutagens.

The simulation permits the experimenter to keep track of the mass flow in oxygen, carbon dioxide, soluble substrate, sediment, and biomass. It is possible to permit mutations of each organisms genome to study population dynamics and changes such mutations cause on the sample ecosystem. The number of organisms in the simulation is at most in the low thousands. It also takes place in a rectangular world with a top and a bottom. Gravity acts on non-soluble substrate to move it to lower layers.

Unlike other automata simulations, there is no control given over breeding times or maturation rates in BIOSIM. After each 'turn' all the organisms breed by fission, if they have enough energy, and pass genetic information to the daughter cells. Then they all die. In the next turn the daughter cells interact with the substrate biochemically, breed, and die. This model may be applicable to some microbial communities, but it is not generalizable.

The following description of the automata and their biochemical properties in BIOSIM draws heavily on the users manual. The interaction of the organisms with the substrate can be rather complex. The reader is referred to the BIOSIM manual for a fuller explanation of these mechanisms.

There are eight biochemical pathways available to organisms in BIOSIM . Using short hand notations of (C2/O) and (C2/O2) to represent a product with a fixed carbon/oxygen ratio, not any specific molecule, the pathways are shown in Table 4.

Table 4. BIOSIM's Metabolic Pathways

P1: light + 4 $\mathrm{CO2}$ ----> $3\mathrm{O2}$ + 2 $\mathit{(C2/O)}$ 'classical' photosynthesis
P2: light + 2 $\mathrm{CO2}$ ----> $\mathrm{O2}$ + $(\mathrm{C2/O2})$ 'classical' photosynthesis
P3: light + 2 $(\mathrm{C2/O2})$ ----> $\mathrm{O2}$ + 2 $\mathit{(C2/O)}$
P4: light + 3 $(\mathrm{C2/O2})$ ----> 2 $\mathrm{CO2}$ + 2 $\mathit{(C2/O)}$
P5: light + $(\mathrm{C2/O})$ ----> $\mathit{C2/O}$
R1: 3 $(\mathrm{C2/O})$ + 3 $\mathrm{O2}$ ----> 4 $\mathrm{CO2}$ + $\mathit{(C2/O)}$
R2: 2 $\mathrm{CO2}$ + 2 $(\mathrm{C2/O})$ ----> 3 $(\mathrm{C2/O2})$ anaerobic fermentation
R3: 2 $\mathrm{CO2}$ + 3 $(\mathrm{C2/O})$ ----> 3 $(\mathrm{C2/O2})$ + $\mathit{(C2/O)}$ anaerobic fermentation
R4: 6 $(\mathrm{C2/O2})$ + $3\mathrm{O2}$ ----> 8 $\mathrm{CO2}$ + 2 $\mathit{(C2/O)}$
R5: 2 $(\mathrm{C2/O})$ + $\mathrm{O2}$ ----> 2 $(\mathrm{C2/O2})$

It is important to note in the generalized pathways above that (C2O) can appear on either side of the equation. If it is on the right side of the equation, the substance is part of the living biomass (indicated by italics). If it is on the left side of the equation it is part of the substrate. After each generation all organisms die and their biomass (minus that given to daughter cells) is added to the substrate. It is possible for (C2O) as well as other waste products to accumulate in the substrate as a by product.

Pathways P1 and P2 represent the analog of classical photosynthesis. Pathways P3, P4, and P5 represent light mediated reactions of unspecified mediating steps in which carbon dioxide is taken from the substrate and fixed into the biomass.

Pathways R1-R5 do not require external energy. Certain of these must be combined with photosynthetic pathways to permit biosynthesis. Pathways R2 and R3 are anaerobic fermentive reactions. These result from the accumulation of soluble substrate. The byproduct could be oxidized through other pathways if oxygen is present.

Efficiency of light mediated pathways are dependent on the relative intensity of light. If more than one photosynthetic pathway is available, light is shared with order of priority as in the list above. The second pathway is more efficient at low light levels. The respiratory pathways are also not equally effective. For example, R4 is much more effective than R3, as one is an oxidative pathway, the other being fermentive. Twelve inhibitors, each targeting a specific pathway, or substrate component, are available for the experimenter. Inhibitors can be used singly or in combination.

The genome and its decoding in BIOSIM, unfortunately, is quite complicated. Organisms in BIOSIM have a 13 element genome. The elements are further organized into 6 determinant pairs. The thirteenth element holds morphology information. To decode the genome these pairs of each element are added together, base four, to determine the total weight of that pair. These pairs, together with the 13th element determine the organism's general biochemistry and morphology. The biochemical pathways are enabled, through this coding, by an algebra on the weights of these pairs. For example, pathway P1 is enabled if the total weight of pair 6 minus the total weight of pair 3 is greater than zero. Pathway R4 is enabled if the weight of pair 5 minus the total weights of pairs 2 and 1 is greater than zero. The amount by which a pathway rate exceeds zero also determines the efficiency with which the organism can utilize that pathway. Selective pressure to use the substrate more efficiently can be applied by introducing mutagens, or changing mutation rates during reproduction.

The result of this elaborate coding system is that, given the genome of an organism, it is not at all easy for a student to see what exactly its metabolic properties would be. I am reminded of the tale of King Alfonso the Wise of Castile and his astronomy instructor. Curious to see how the heavens were organized, Alfonso hired the finest astronomer in the land to tutor him. After several lessons, and the presentation of Ptolemy's five spheres with its 92 epicycles rolling on the spheres or on each other, Alfonso leaned back in his throne and remarked, "This is indeed a wonderful creation, but if I were around at the beginning, I would have advised something simpler."

Clearly the model set out by Dr. Deal has a great deal of potential. Very possibly BIOSIM can bring learning about metabolic pathways 'alive' for the student. Giving the student a grasp of the metabolic links between an organism and its substrate is a most important goal of life science education. The BIOSIM manual is quite helpful, even overcoming some of the problems caused by the arcane coding scheme. A sample investigation from the BIOSIM student manual can illuminate some of that potential.

Sample Investigation (condensed from BIOSIM student notes): Consider an ecosystem with two organisms, both phototrophs (the genome is explicitly given for both organisms). Organism one has only P1 available. Organism two has available pathways P2 and P3. Try experiments with one organism at a time, then try both together. Try varying the levels of light or carbon dioxide.

Commentary (condensed from BIOSIM student notes): Both organisms alone can continue alone indefinitely. When the two organisms are put together one observes a phenomenon called 'competitive exclusion'. With high carbon dioxide concentrations organism one gradually takes over the system. With low carbon dioxide concentration, it is organism two. The organisms do not form a balanced ecosystem. The shared substrate is carbon dioxide. Each differs in the rate of assimilation. Note that sediment, usable by neither organism, accumulates indefinitely. Processes similar to this have produced deposits of coal and peat.

Other BIOSIM experiments from the manual illustrate evolutionary adaptation, mutualism, commensalism, and parasitism. All in all the package is very well conceived. It is designed to run on a MS/DOS platform with VGA graphics. Execution time on commonly available machines, especially in more demanding experiments, can become rather long. Runs of many hours can be expected with evolutionary or adaptive experiments. Graphic output is also limited. No provision is given to export any data to a spreadsheet or database for further manipulation. The energetics of the reactions are also not explicit. There is no way to look at energy flow through the whole system. It may be possible to design the simulation so that the student is more "inside" the simulation, much like SimAnt.

A particularly useful model that is not explored with BIOSIM is the role of symbiosis in evolution. The data structure in BIOSIM is rather brittle. It will not permit properties of one organism to be assimilated to those of another. Given some of the remarkable work that has been done by Lynn Margulis on the origin of the eukaryotic cell, a simulation that can model the metabolic pathways enabled by this process, and the consequent selective advantage, would be a powerful instructional tool (Margulis, 1970; Margulis, 1981; Margulis, et al., 1986). The data structure in The Evolutionary Tool Kit is specifically designed to be flexible enough to permit modeling of symbiosis, as well as the modeling of metabolic pathways like the organisms in BIOSIM.

Professional Literature on Evolution and Cellular Automata

It is not within the domain of a dissertation on science education to review and analyze the work of the highly skilled researchers in the developing fields of simulated evolution and artificial life. In the proceedings volumes of the two international conferences on artificial life at Los Alamos Christopher Langton has provided an expert's overview of this fascinating and highly technical new area of research (Langton, 1989; Langton, 1991). The guide to discussion of the elements of the work of these researchers are the three themes in investigating automata modeling in life science education set out in the introduction to this dissertation: accuracy and appropriateness of content through the work of Thomas Ray and Mary Clark, new methodologies for teaching through the work of Charles Taylor, David Jefferson, Gregory Werner, and Kristian Lindgren, and new modes of thinking through the work of Christopher Langton, David Akley, and J. Doyne Farmer.

Accuracy and Appropriateness of Content

Appropriateness of the role of informatics in evolution education is openly discussed in the Project 2061 Panel Report on Biological and Health Sciences in a chapter called "A Conceptual Framework for Biology". Mary Clark writes:

> If we are to meet the goals of familiarizing all adults with the living world on which they depend, of making them feel at home with the workings of their own bodies, and of giving each a sense of humankind's evolutionary place in cosmic time, we shall need to develop a mental vision of reality, a conceptual framework for biology that incorporates several all-pervasive principles. Among these principles are the role of *information* in organizing matter into discrete living and reproducing entities; the need for energy to animate and maintain life; and the necessity for

> adaptive changes in organisms to meet new conditions, including changes in other life-forms with which they directly or indirectly interact (Clark, 1989).

The target population for the work of this dissertation, as for that of the conceptual framework for biology set out by the 2061 Panel, is all students. My goal is not to cleverly translate the recent work of theoretical biologists into a form digestible by some percentage of secondary students, putting our 'best' on "the cutting edge". Though not excluding the needs of a small group that will go on to professional work in this area, the duties of science educators are much broader. It is most significant that the first of the organizing principles cited by the 2061 panel was the "role of *information* in organizing matter into discrete and reproducing entities". The type of information cited (italics in the quote are Clark's) is specifically not classificatory or descriptive; rather it is information at the genetic level, information contained in individual cells.

This role, I feel, is beautifully illustrated by modeling with cellular automata, as in The Evolutionary Tool Kit. Flow of information is the core of its modeling structure. As Langton states, "biologists cannot rewind the tape of evolution, and are stuck with a single, actual evolutionary trace out of a vast, intuited ensemble of possible traces. Although studying computer models of evolution is not the same as studying the 'real thing,' abilities such as free manipulation of computer experiments, potential to 'rewind the tape,' to perturb the initial conditions, and so forth, can more than make up the their 'lack 'of reality (Langton, 1991)."

The pedagogic advantages of such computational tools are obvious. Use of tools like SimEarth or The Evolutionary Tool Kit will permit, as the Rationale for a new curriculum by the 2061 Panel states, "a curriculum that will clearly depart from the usual catalog of facts, with an occasional experiment thrown in for good measure. Not only will it build concepts as much as possible by using historical and inquiry methods; it will also apply those concepts to current issues, asking 'What does it *mean* to know this?' Biological understanding will become connected in students' minds to questions that are generally labeled 'social'; 'economic'; or 'ethical' (Clark, 1989)."

The question of accuracy or suitability of cellular automata modeling of evolutionary phenomenon has been a central concern for researchers in this field. The problem is generally restated as a concern for the problem of openness of the simulation process itself (Collins, et al., 1991; Jefferson, et al., 1991; Langton, 1989; Langton, 1991; Pattee, 1987; Ray, 1991; Taylor, et al., 1987). Computers are finite objects, their coding is digital, finite as well. How can they be said to permit anything like evolution? Can a computer simulation be truly open? Can it have sufficient freedom to model in any small aspect the phenomena of the real world? A related point is raised by philosopher Errol Harris (Harris, 1991) in asking whether even if a self-reproducing, self-programming computer is conceivable, "would it not have required a human (or divine?) programmer?" Harris claims that the contention that genetic machines could evolve by random processes fundamentally begs the question.

By asking such questions we are sailing into very deep waters indeed. It is very important to do so. Anyone with classroom experience of the questioning, authority-hostile mind of adolescents will know that the discussion will get to this level soon enough, with little or no directed inquiry. If we are to develop the "mental vision of reality, a conceptual framework for reality" spoken of by the 2061 Panel, this is exactly where the discussion should go. Central to the question being asked is: "What kind of framework for explanation can be accepted in biological science?" The question is legitimate and deserves exploration (Barlow, 1991; Collins, et al., 1991; Jefferson, et al., 1991; Margulis, 1988; Margulis, et al., 1986; Maynard Smith, 1986; Mayr, 1988; Rasmussen, Knudsen, & Feldberg, 1991; Ridley, 1983).

A tale from the a set of short stories called *The Aleph* by Brazilian writer Jorje Luis Borjes, cited in the context of discussions of evolutionary theory by both philosopher Dorian Sagan (Sagan, 1988) and mathematician Rudy Rucker (Rucker, 1988) can illuminate the central features of what could be a rather abstruse analysis.

The story is about a fabulous creature called Oomano, that was discovered on another planet in the first years of space travel. Oomano was a both a delightful and strange beast. It was highly intelligent, non-agressive, and friendly toward human kind. It had one very remarkable property: it's memory. Oomano could remember everything in its life exactly, not just the general details of where it went and who it saw or what it said or was said to it. Oomano remembered <u>everything</u>, including the color and shapes of the clouds at each instant, the feel of breezes, the scents it experienced, the lapses of its mind in daydreams, breaths it took, as well as exact words of conversations and feelings that accompanied them. Oomano had another remarkable property, if one held any of its hands, a visitor could experience, along with the creature itself, any one of these days from its long life. One could ask Oomano to replay any one of these days and the experience, exactly as the original would begin. There was only one problem. The replay of one day took as long as the day itself. The result of this wonderful capacity was also unusual: Oomano had no future. Its tomorrow was a yesterday.

Both Rucker and Sagan remark, from very different perspectives, of the similarity of Oomano with any theory or vision of the world. There is a necessary process of abstraction that must accompany any sense of memory, any characterization of events, or any theory. Some elements must be seen as important or determining, others are insignificant, therefore forgettable. Oomano's memory provides a mere exact copy of events, there is no transfer, no learning from them. The relative significance or insignificance of any happening is highly dependent on the mind set or theoretical perspective one brings to any situation. The drab finches of Galapagos, or the darkening moths of Birmingham were completely unnoticed until an individual with insight saw meaning in their appearances. It can even be argued that Captain Fitzroy of the *H.M.S.Beagle* and Charles Darwin did not visit the same islands in the Pacific; what each saw was entirely different (Gould, 1977). Fitzroy was horrified by the place. Its billowing lava flows, now cold and spottily covered by cactus and oddly colored, grotesque iguanas, reminded him of scenes from Dante's *Inferno*. Darwin was fascinated. An odd place, indeed, so different from his English homeland, yet one whose starkness revealed the beauty of natural law, ever present, but subtly hidden in the lusher climate of the British Isles.

From Borjes' subtle tale one can easily see that there is some thing fundamentally wrong with a "theory of every thing," even with a "complete" theory of a particular thing. Oomano's exactitude is caught in an infinite regress; today could be a copy of yesterday, or tomorrow even a copy of time long past. Even the naturalists' perception of the world around them is subject to this disconcerting observation. A total view of knowledge of the past precludes learning about both the present and the future. Ornstein's insistence that perception is, and needs to be, interpretation is with us at all times, in all disciplines (Ornstein, 1986; Ornstein, et al., 1989).

Simulating evolutionary processes in computer micro-worlds provides an ideal situation to examine this conceptual limitation and use it for pedagogical advantage. Micro-worlds must be fragments, abstractions from the real world, or, perhaps more properly, artifacts of our mind's perception of it. These computer worlds also have the advantage of a semi-independent existence. Through these computer micro-worlds we can watch the interactions of many of our ideas, "in real time" as it were. We can even examine counterfactual cases, impossible in the laboratory, to test ideas and their relationships. In the specific case of this study, the micro-world is an analog of stored coded information (the genotype) and its relation with the rules governing the interaction of the organism with its community and its environment (the phenotype) and the interaction of the natural and social environment on the organism through time (natural selection). To explore this concept further and its relation to the unfinished discussion of openness or necessary closure of computer evolution simulations, I must discuss more specifically the work of Thomas Ray, a biologist at the University of Delaware.

Trained formally as a tropical ecologist Ray has extended the micro-world of evolutionary automata modeling to where it has been referred to as "digital Darwinism" (Travis, 1991). Ray defines life in a most general sense, restricting it to carbon based forms. For him a system is living if it is "self-replicating and capable of open-ended evolution (Ray, 1991)." Without self replication the mechanisms of selection would be limited by the simulator. Most evolution simulations, including that in The Evolutionary Tool Kit, are specially designed data structures with certain pre-defined genes with various allelic forms (Dawkins, 1986; Dewdney, 1985; Dewdney, 1989a; Dewdney, 1989b; Jefferson, et al., 1991; Packard, 1987; Werner, et al., 1991). Importantly the organisms are not free to invent their own fitness functions. The model that Ray has constructed permits just that, an extremely flexible evolution simulation called the Tierra Simulator.

Most other simulations attempt to use data structures, machine codes, or operating systems to emulate organisms. Such approaches have many drawbacks. The first is that they tie the model to specific hardware. A second very important reason is that machine languages of Von Neuman type machines are very "brittle". The ratio of possible code written in them, to the number of viable programs is essentially zero. The slightest change in machine code causes programs to crash. Ray's ingenious method around this problem was to design a parallel virtual computer with each CPU as an organism. The Tierran virtual machine resides inside a very large computer, its CPU and operating system governing the changes in the Tierra Simulator. The Tierran organisms use a robust language, one tolerant of variations as their instructional code. The language of the virtual machine is very limited. It is intended to have similar structural and functional properties of RNA molecules. It uses 32 instructions, analogous to the 64 DNA codons.

Importantly, the Tierran language uses "address by template", a digital analog of the biochemical phenomenon wherein the surface of protein A, for example, must find the complementary protein A* with which it fits like a key, before any process can continue. In the Tierran dialect a jump instruction (JMP) followed by an address 0 0 0 1, would function for the organism (really a miniature parallel CPU) as an instruction to look in the local memory or in a neighboring cell for a sequence 1 1 1 0, and then begin executing there when it has found the match. If an error condition occurs, the JMP is ignored. Tierran organisms can rewrite their own code or read and execute that of any of their neighbors.

Tierra occupies a block of RAM in a large computer. The block of RAM is referred to as the "soup". The inhabitants of the Tierran soup are, in fact, computer viruses, separated from each other by "the semi-permeable" membrane of the memory allocation. Mutations occur at a rate selected for the soup as a whole (analogous to errors caused by cosmic rays), as well as a fixed rate copying errors common in any replicating process. The soup is seeded with an ancestor, a self replicating program 80 instructions long. The developments in Tierra parallel the second great event in the history of life, the origin of diversity. Ray makes the important distinction between an inquiry into the origin of life and the origin of diversity, which first occurred with Cambrian explosion of life about 600 million years ago. Modeling of the origins of self-replication is not attempted in Tierra.

The combination of the simplicity and robustness of the Tierran language, self replication, and address by template produces some remarkable results. As the soup evolves, many variations in the organisms are observed. Parasites develop that steal computer time from their hosts, or interfere with the replication instructions. Parasites in Tierra are programs in a neighboring space that do not have a self replication code of their own. Their instructions jump to the self-replicating code of one or more of their neighbors and use this to make copies of themselves. They are smaller programs than their hosts and therefore more efficient in using memory space (the analog of environment). Immunity to parasites also evolves. Later on, more complicated parasites circumvent the organisms' immunity. Hyper-parasites evolve that subvert the energy metabolism (here CPU and reproductive cycle time) of parasites. These, in turn develop hyper-hyper parasites. Of special interest is the observation of phenomena that look very much like the punctuated equilibria of Eldredge and Gould (Eldredge, & Gould, 1972). Quite often there are long periods of stasis or equilibria when one or several forms of organism dominate the soup. A random change introduces a new property that disturbs the balance and a period of rapid change ensues, followed by another period of relative stasis. Other researchers in artificial life have noted similar phenomena (Brockman, 1988; Conrad, et al., 1985; Farmer, Lapedes, Packard, & Wendroff, 1986; Jefferson, et al., 1991; Langton, 1991; Taylor, et al., 1987; Werner, et al., 1991).

Ray's Tierran model does provide an example of open evolution within a community of cellular automata. It has no direct application in life science instruction at the pre-college level. No secondary computer administrator in his or her right mind would permit a program like Tierra to run on a school system, no matter what protections the author could supply about the containment of its products. A program whose sole purpose is to breed thousands of generations of rapidly mutating computer viruses is too dangerous to be put in the hands of anyone but experts. Ray's work does show the requirements of a simulation that would permit an organism to evolve freely and even define its own fitness function. It does provide an answer to Professor Harris' question. Yes, such a "self-replicating", "self-programing" simulation does require a skilled programmer, but it is not in the same sense as the Divine Watchmaker from the Argument from Design (Dawkins, 1986). Given a simplified, robust language, "address by template", and a self-replicating seed, generation upon generation of unlimited complexity can evolve all by itself. The problem of the origin of diversity is separable from that of the origin of life. Ray's work seems to show that Harris' objection does not apply to the first problem; clues to the origin of diversity can be obtained through computer models. It remains unclear what his objection means for the second, the problem of the evolution of evolvability (Dawkins, 1986; Farmer, & Belin, 1991; Rasmussen, et al., 1991).

The data structure in The Evolutionary Tool Kit is much too brittle to permit open evolution in the sense of Ray's Tierra. The investigator with sufficient computer knowledge is not limited to options presented by menu screens. If a student has access to a C Developer's Tool Kit , it is possible for a user to append their own routines onto the Tool Kit shell and add their own designs for genes or their own fitness functions.

New Methodologies

New methodologies for science education is a popular topic these days. Professional educational journals are filled with articles on how to teach, package, or present science better, faster, or more effectively. Some of this effort is inspired by the numerous scholarly reports by one national committee or another on how bad the state of education really is. Others find inspiration in the unpreparedness of students in their classrooms and their own efforts to remedy the situation. My sympathy lies, admittedly, with the grass roots classroom innovator. The classroom teacher is where the rubber hits the road, as Carl Berger said. It is with these people and the students that they contact that any real innovation in education must begin. The metaphor I wish to employ to explore this topic of new methodologies in science education is that of the "knowledge hacker", first coined by David Thornburg (Thornburg, 1991).

Computer hackers have received a lot of press, mostly bad, in the last few decades. Unwashed, anti-social, and obsessive, these junk food addicts squirrel themselves away working on perfecting skill in the latest computer game or finding ways to break into other people's networks. They certainly do not fit the "brave, clean, and reverent" stereotype of youth of old. "A few did manage to become millionaires, put on clean clothes, and dine at elegant sushi bars." One feature does characterize their lifestyle: a dedication to the pursuit of knowledge. David Thornburg observes that what we need is "more hackers - not just computer hackers of course, but hackers in all areas of knowledge. We need to find ways to keep kids' intrinsic love of learning alive well into high school so that it never gets lost (Thornburg, 1991)." Computer simulations like SimEarth and SimAnt represent the beginnings of a new type of software and instructional design that encourages knowledge hackers in the life sciences.

Thornburg gives three advantages of instructional design of this sort (Thornburg, 1991). First, hackers are self motivated. They willingly spend hours interacting with these simulations, testing them in all sorts of ways, all for the pleasure of the experience, not for grades. Second, hackers are very often introduced to the subject by another. This gives room for a teacher to guide students to an understanding of why some subjects have a potential for excitement, ways in which they can love learning and not find it drudgery. Third, the acquisition of knowledge is constructive, not limited by instructional constraints. Hackers are very likely to chart their own course through the study, developing capacities perhaps far beyond a teacher's expectations. Clearly the role of the teacher in such an environment is much more that of a knowledge facilitator than master or expositor of what is to be learned.

With The Evolutionary Tool Kit students can investigate the potential of individuals and species, and their interactions with each other and the environment in worlds much like those studied in SimEarth but on a global scale. Sample investigations were described in the introduction of this dissertation. These can easily be generalized. "Is there an advantage (or disadvantage) to parthenogenic reproduction?" "Why is sexual reproduction so common in plants and animals?" "How does social behavior effect inheritance?" "How can altruism, which can be harmful to individuals but helpful to populations, evolve?" These are wonderful questions cutting right to core meanings in biological science. They have also all been asked in the context of cellular automata simulations by researchers (Barlow, 1991; Brockman, 1988; Collins, et al., 1991; Farmer, et al., 1991; Hofstadter, 1991; Jefferson, et al., 1991; Langton, 1989; Lindgren, 1991; Lovelock, 1991; Maynard Smith, 1978b; Maynard Smith, 1986; Maynard Smith, 1989; Packard, 1987; Taylor, 1991; Travis, 1991; Werner, et al., 1991). Why can't similar questions be posed and explored with automata of their own construction by "life science hackers" as part of their own investigations?

As a sample of the phenomena opened for investigation by secondary "life science hackers" by use of cellular automata modeling, I will discuss briefly the work of Kristian Lindgren, incorporating elements of game theory, and the work of Charles Taylor and the UCLA Artificial Life Group on modeling insect behavior.

Lindgren's work builds on the work of Axelrod and Maynard Smith in the application of Von Neumann's theory of games to models in the life sciences (Axelrod, et al., 1981; Maynard Smith, 1974b; Maynard Smith, 1982; Maynard Smith, 1989). The simplest model to understand the framework of this application is the Prisoner's Dilemma.

The Prisoner's Dilemma is a two person non-zero sum game. The original problem was stated in the form of two prisoners suspected of having committed a crime. There is not enough evidence to convict either, unless one confesses. Neither knows the choice of the other. If both stay quiet (called 'Cooperation'), they will be released. If one confesses (called a 'Defect'), he goes free and the other is imprisoned. If both confess, there is a short prison sentence for both. The interaction is generally quantified by assigning weights to each outcome. If both cooperate each receives a 3. If both defect, each receives a 1. If one cooperates, and another defects, the defector receives a 5 and the cooperator receives a 0.

Is there a strategy that is optimal for both players? In the case of a one game only, clearly the optimal strategy is to defect (inform on the other fellow). This won't work if one plays the same opponent again and again, as the opponent will begin to defect often and both will receive the low score of 1 per round. The problem gains greater depth with consideration of the Iterated Prisoner's Dilemma (IPD) where the same players meet again and again at the same game. The IPD problem was extensively analyzed by Axelrod (Axelrod, et al., 1981). From results of a computer tournament Axelrod found that "Tit for Tat" (TFT) provides both prisoners the optimal strategy, giving a score of 3.0 over long iterations. With TFT a player never initiates a defection; it is not an aggressive or 'hard' strategy. Also the player will defect only after the opponent has defected in the preceding round. The TFT player has no memory other than the last round. It is 'forgiving'. In general, strategies that were more 'forgiving', rather than 'punitive' or 'hard' performed the best (Axelrod, et al., 1981; Barlow, 1991).

A biological analog of the IPD can be easily found in hunting behavior. Cooperative hunting gives much greater chance at downing a prey, with both sharing a meal. Stealing the prey from the partner (Defecting) gives immediate personal gain, but at a cost of disrupting cooperative behavior. The analog of a dual defection would be a pair of hunters that trap a prey and argue over it until it escapes. In The Evolutionary Tool Kit the user populates the world with organisms of specified strategies and runs trials to see which strategies are stable over long runs, or beneficial to the population as a whole. The question asked is "Is it possible for cooperative behavior to evolve under Darwinian constraints?" The model can be constructed with a genetic inheritance of the behavior or a Lamarkian model, where newborn hunters take on the behavior pattern of those near to it.

Lindren's organisms do not move in the sense of organisms in The Evolutionary Tool Kit. Each round Lindgren's organisms play the IPD with each other based on rules from a genome each contains (Lindgren, 1991). The genome contains the game theoretic strategy used by the organism coded in binary form. For a one memory genome (meaning that the organism remembers only the last move of the opponent) there are four possibilities for the strategies;

I. Always Defect: This is encoded positionally in the genome as {0 0}. The first position in the bracket gives the response if the opponent defects. The second position gives the organism's response if the opponent cooperates. In the bracket symbolism cases are coded

{ action if opponent defects, action if opponent cooperates}

II. Follow the Opponent or "Tit for Tat" (TFT): If the opponent defects, the organism defects. If the opponent cooperates, the organism cooperates. The genome {0 1} encodes the Tit for Tat strategy. Note that TFT will not initiate a defection.

III. Anti-Tit for Tat or ATFT: ATFT does the opposite of what the opponent does. If the opponent defects, it cooperates. If the opponent cooperates, it defects. The genome {1 0} encodes the Anti-Tit for Tat strategy. Note that ATFT will *always* initiate a defection.

IV. Always Cooperate or AC: AC is a very forgiving strategy. If the opponent defects, the organism cooperates. If the opponent cooperates, the organism cooperates. The genome {1 1} encodes the AC strategy.

On each play, a parser reads the organism's genome and selects a response based on the genetic code and the behavior of the opponent it is playing. Lindgren's organisms can also mutate. A *point mutation* can turn a 1 in any area of the genome into a 0. The organism can also have a *duplication mutation* where {0 1} becomes {0 1 0 1} with a two step memory as a result. A two step memory codes, in binary form, appropriate responses for any of the 4 possible interaction histories. The genome {0 1 0 1} is basically "Tit for Tat" with a memory. A *split mutation* will randomly remove the first or second half of the genome. A two step genome sets its responses from the last two opponents it has played. Table 5 displays four possible strategies for a two step memory and the genome that encodes each.

In each run all Lindgren's organisms play the IPD against all others. The organisms receiving above average scores receive more offspring in the next generation. Population size is kept constant. It is during the reproduction that the mutations bring new strategies. The capacity to lengthen the genome and randomly vary the strategies give Lindgren's simulation an openness much like Ray's Tierra. Genomes can evolve to arbitrary length, thereby putting no limit on the number or kinds of strategies the organisms can use. These organisms do not self replicate, however. Table 5 shows sample genomes of memory length two.

Table 5 Strategies for a 2-Memory Prisoner's Dilemma Genome

HISTORY OF PLAY	Always Defect	TFT	Avg. Forgiving	Avg. Non-Forgiving
(Defect, Defect)	0	0	0	0
(Defect, Cooperate)	0	1	1	0
(Cooperate, Defect)	0	0	1	0
(Cooperate, Cooperate)	0	1	1	1
GENOME	{0000}	{0101}	{0111}	{0001}

The results of Lindgren's simulations are interesting. Populations evolve rapidly and then reach periods of stasis, much like Eldredge and Gould's punctuated equilibria. It is possible to have pair of mutually supporting strategies that dominate the population, an analog of polymorphism. The pair can resist exploitation by other strategies. This mutualism naturally emerges from the model. In general, strategies that dominate the periods of stasis are cooperative.

Explorations of such game theoretic models of cooperation are easily included in The Evolutionary Tool Kit. These are described in chapters two and three of this dissertation. Students are able to design their own strategies from buttons on pull-down menus on the gene menues. They could select 1, 2, or 3 level memories and determine the behavior pattern they wish for their organisms case by case. They can then see how their strategies fare against other strategies they construct, or against other students' strategies. It is possible, on a network, to have students play one another. Questions that can be explored are: "Are there optimal strategies?" "Which strategies are stable against invasion by others?" "Can cooperation naturally evolve?"

Modeling Plant Growth

In work begun in the '70's and early 80's Karl Niklas and others used computer models to investigate evolution and selective pressure in herbs and woody plants (Aono, & Kunii, 1985; Fisher, & Honda, 1977; Honda, & Fisher, 1978; Honda, & Fisher, 1979; McMahon, 1975; McMahon, 1976; Niklas, 1984). In a 1986 article in *Scientific American* Niklas gave an account of his work for a general audience (Niklas, 1986). Given a few very simple assumptions about the growth of plants and strengths of structures, some remarkable properties and evolutionary processes can be demonstrated.

Niklas assumed that only three variables (probability of branching, rotation angle, and branching angle) were needed to develop a very wide variety of models for woody plants. The three variables, and their physical associations are shown in the figure below. The rotation angle is γ. It determines the amount of rotation the branch undergoes before the growth of the next segment. The branching angle is ϕ. It determines the branching angle between two new segments. The probability of branching is simply a probability of bifurcation after a segment has elongated a specified amount. Figure 2.6 displays the two branching angles. The process of generating the tree is much like the Monte Carlo technique used by Raup and Gould in generating cladograms.

The simplified diagram in Figure 2.6 assumes axial symmetry of branching at each node. Niklas' model added another feature to include the possibility of apical growth (growth from the apex) as in a pine tree (Niklas, 1984). In a more realistic model here are two branching angles possible at each node, one which controls the secondary branch off vertical, another which controls the angle of the primary.

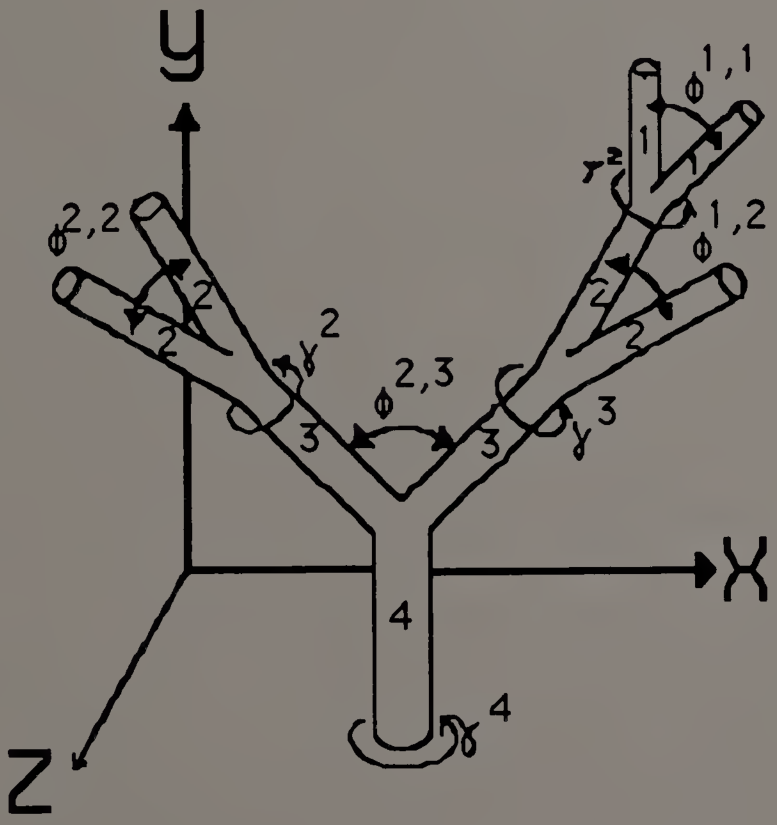


Figure 2.6 Parameters of Tree Growth after K. Niklas (1986)

The article in *Scientific American* describes the fitness function Niklas used, as well as his method of modeling the process of natural selection (Niklas, 1986). Niklas assumes that "the majority of plants can be seen as structural solutions to constraints imposed by the biochemical process of photosynthesis." Branched patterns gather more light. The plants must also be able to stay erect. Niklas also assumes "that the evolution of plants was driven by the need to reconcile the ability to gather light with the ability to support vertical branching structures." He also assumes that evolution of plants is also driven by "the extent to which they are successful at reproduction, placing a premium on branching patterns that allow for better dissemination of seeds or spores."

Early plants lacked leaves. They were basically vertical photosynthetic, branched, cylindrical frame structures (Scott 1984). The light gathering potential for such structures can be modeled easily by static three-dimensional branching structures in a computer. The structures generated by the stochastic processes look remarkably similar to early vascular plants like *cooksonia.* The computer can calculate the amount of light any rigid structure can gather as the sun goes over it in a daily arc. The computer can also calculate the first moment of inertia of these structures to give an estimate of the load inherent in any branching pattern.

Shading was certainly a factor in early evolution of vascular plants. Since there is a wide variety of modern shade tolerant plants, it is assumed that some early plants were also shade tolerant. Self-shading was also a factor. The issues of shading, and self shading are very difficult to handle computationally. Niklas' model did not address them; nor did it address any problems of fluid flow and capillarity.

The universe in which Niklas' plants evolved could be represented as a cube with its three axes representing one of the variables determining the plants structure. The 'world' would start out with a plant with a low angle of branching (much like a primitive plant would have had) and arbitrary values for the other two variables. Because of the random nature of the branching variable any unique number triplet would produce plants with different morphologies. The computer would generate a specified number of plants at each triplet and also a number of plants from local regions around the triplet. The size of the region investigated was constant throughout the run. It was initially set by the user. This 'investigation' region is analogous to a mutation rate in a natural system.

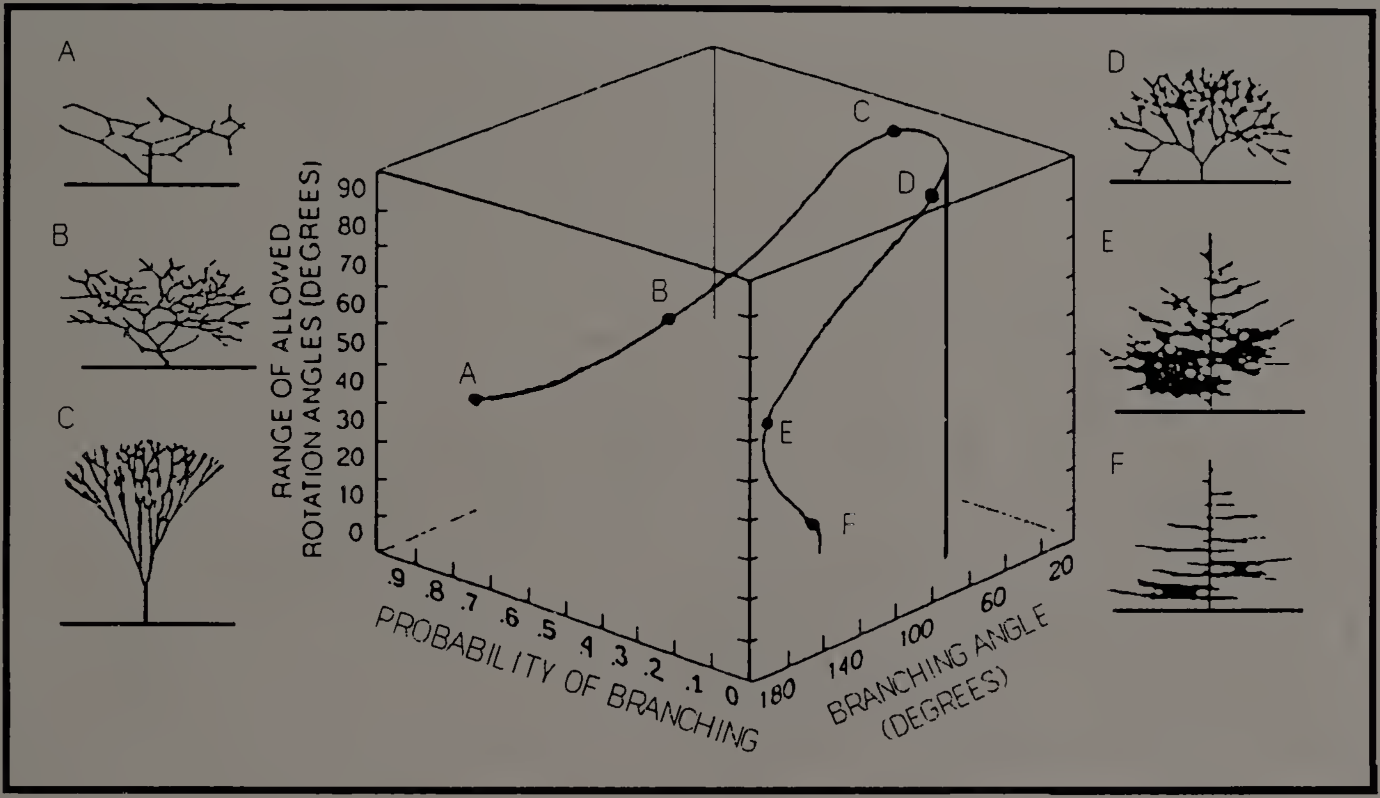


Figure 2.7 'Universe' of Possible Branching Patterns

Each of the hundred odd plants generated would be analyzed quantitatively for light gathering ability, strength, and reproductive potential (number of nodes for spore production). Natural selection was modeled by the selection of a plant in the region of 3-space that was the most successful as measured by the three criteria. This new plant would serve as a basis of analysis for the next round.

The model would describe a trajectory through the state space with each point representing a general plant structure. The trajectory and the associated plant structures are shown in Figure 2.7. The figure is from the 1986 Scientific American article.

Starting from what looks like a fungus (A), the path of natural selection (here, a type of optimization) leads to shapes not unlike the odd cycads (B) and fern trees (C) of the Carboniferous to shapes that look much like pine trees (E, F). It seems that, from the crude perspective of this model, pine trees, with apical growth represent an optimal form.

The Evolutionary Tool Kit will model vascular plant growth and selection much like Niklas' work. The automata in The Evolutionary Tool Kit can have motive or non-motive properties. A non-motive automaton with a gene structure that gives a branched morphology can be set up as the focus of an investigation. The Niklas model is not really based on cellular automata; it is a discrete Monte Carlo simulation. As the diagram shows his method really shows a solution to an optimization problem using a genetic algorithm. Only groups of plants around a special point in the phase space are considered at any time.

With the gene structure associated with an automata in an environmental grid much more realistic modeling can be attempted. Once can change environmental conditions, such as specifying periods of dryness, heavy snow, or low levels of light. It would be possible to vary latitude of the region in which the plant grows. Browsing by animals on lower branches could be modeled as well. The shape of African acacia trees is just as much a result of browsing by long necked herbivores as by demands for light and structural strength.

Using analyses suggested by Vogel (Vogel, 1981; Vogel, 1986), it is possible to factor in aerodynamic drag. Plants in windy regions may evolve very differently from those in calm air. All of these conditions can be set up and potentially investigated by the user of The Evolutionary Tool Kit.

A interesting experiment possible in The Evolutionary Tool Kit would involve a student setting up a spherical world, seeding it with primitive plants, setting polar regions with a heavy snow load, and then observing the effects of natural selection on plants in the different regions. The 'success' of each plant automata would be quantitatively measured much as in Niklas' model, photosynthetic capacity, structural strength, and reproductive success. In any automata neighborhood the lowest fitness score would die on that round. Its space would be taken by offspring of any automaton with above average fitness. "Does selection drive upper latitude plants to a different morphology than equatorial ones?" "What is the effect of prolonged periods of dryness, or snow?" "If the force of gravity were different, what plant shapes would evolve?" Questions of these nature could be investigated with automata modeling with The Evolutionary Tool Kit.

At this point it is possible to investigate a particularly useful pedagogical construct of The Evolutionary Tool Kit which I shall call "The Designer". It is similar in function to the "yellow ant" of SimAnt. The Designer permits students to alter the genotypes of single organisms or groups of organisms in the middle of a run. The mutations of groups or individuals under the Designer are totally under the user's control. Other organisms in competition with the Designer's organisms can evolve under a genetic algorithm. A sample investigation using the Designer in the 'tree world' will illustrate the constructs features.

After a period of experimentation in an 'explore mode' in a tree world in The Evolutionary Tool Kit a student would decide on initial values for "his or her" species of tree. The students would set their species tree in competition with other species of tree generated by the computer. The computer would seed the world with its species (with parameters chosen to lie in the same region of Niklas' cube as the student's choice, but closer to the trajectory curve). Students could see the morphology of both initial populations. The game would be to beat natural selection by evolving a 'fitter' tree. The competition between the two species would be shown by tallies and by displaying each in different colors on the world grid. The game is really "playing" the Argument from Design, with the student as the omnipotent Creator, against a Darwinian natural selection model. Mutations in the computer's species are random fluctuations in parameters.

A student's initial setup may perform well for a short time, but then the random changes, aided by selection, throw the advantage to the opponent's trees. The Designer must alter the 'recipe' for a successful tree, or see his or her species go extinct. In fact they must continuously improve their creation with considerable planning and foresight just to stay in even competition. It is a shock to find that the Darwinian model does quite well, thank you, with the Blind Watchmaker at the helm. The fact that random variations in these parameters can continually produce successful trees is an important point to learn. The analog of the mutation/breeding process embodied in the computer model produces cumulative selection, a powerful force indeed.

This Designer/selection experiment also provides students a first hand demonstration of a fascinating idea in modern evolutionary theory, the "Red Queen" hypothesis (Dawkins, 1986). It is so named after the famous queen from Lewis Carroll's classic. A confused Alice, while she was hurriedly dragged through the country side by the Queen, yet all the time remained in the same place, remarked, "In *our* country you'd generally get somewhere else - if you ran very fast for a long time as we've been doing." The Red Queen answered, "A slow sort of country. Now, *here*, you see, it takes all the running you can do, to keep in the same place. If you want to get somewhere else, you must run at least twice as fast as that." The process of natural selection is continuous. One good design just won't do, it seems; as the competition with tree design in The Evolutionary Tool Kit shows. One can evolve more and more successful life forms with little or no change in the success rate against any competition, as the competition is evolving at the same rate as the life form itself. Automata modeling puts the student right in the center of the process.

One of the most important aspects of Darwin's theory, and most difficult to get across to students, is the cumulative effect that very small changes can have on a group of organisms. Much like their carbon based counterparts, the automata are constantly changing. The dynamic nature of cellular automata modeling can provide a wealth of experiences from which the life science hacker can learn. Exercises like these also widen the front on which students can approach materials in life sciences. The intuitions needed in designing trees go far beyond the linguistic and mathematical and call upon resources from spatial and physio-kinetic intelligences in Gardner's model.

UCLA Artificial Life Groups

I shall briefly discuss the work of three groups at the UCLA Artificial Life Group. The work of these groups is very complex. The code is implemented on a large Connection Machine using a dialect of parallel C. One of the reasons for reviewing this technical material is to show the original sources that the designers at Maxis have adapted to write the commercial product SimAnt. The second reason is to explore some approaches, similar to those taken by these researchers, that have direct application in life science pedagogy. These technical sources also can give a hint at some of the potential for artificial life as a modeling and teaching tool in the classroom.

David Jefferson and other researchers at the Artificial Life Group at UCLA have developed a very interesting model of evolution in the Genesys/Tracker System (G/TS) (Jefferson, et al., 1991). The Genesys/Tracker System is a refinement on the earlier RAM evolution emulator built by Taylor (Taylor, et al., 1987). The creatures modeled in G/TS are ants that leave and follow pheromone trails. G/TS ants are the prototype for the SimAnt creatures created by Maxis.

In the attempt to model the evolution of behavior, the authors of the Genesys/Tracker system faced the same problem of openness as Ray's Tierra model. They solved the problem in a similar fashion. The automata in G/TS use a simplified language that is robust when subjected to mutations. G/TS ants have four behavior's coded in their genome: Move (the ant moves forward one cell); Right (turn 90° right); Left (turn 90° left); No-Op (stay in place, a null-state). The ant can 'see' ahead only one square directly in front of it. It has a sensor that tells it if that square is marked as part of the trail. The program of the ants themselves is subject to evolution, much like the viruses of Tierra. The behavior of the ant is encoded in the genome as either a cellular automata or a neural net. Which representation is used is determined at the start of the experiment.

The G/TS ants move on a 32x32 toroidal grid. Only one ant is on the grid at each trial. The 'test' ant is placed at the beginning of a pheromone trail, whimsically dubbed "the John Muir Trail". The trail winds round the grid, making several right and left turns. It is interrupted in several spots. Pheromone levels at some cells are faint.

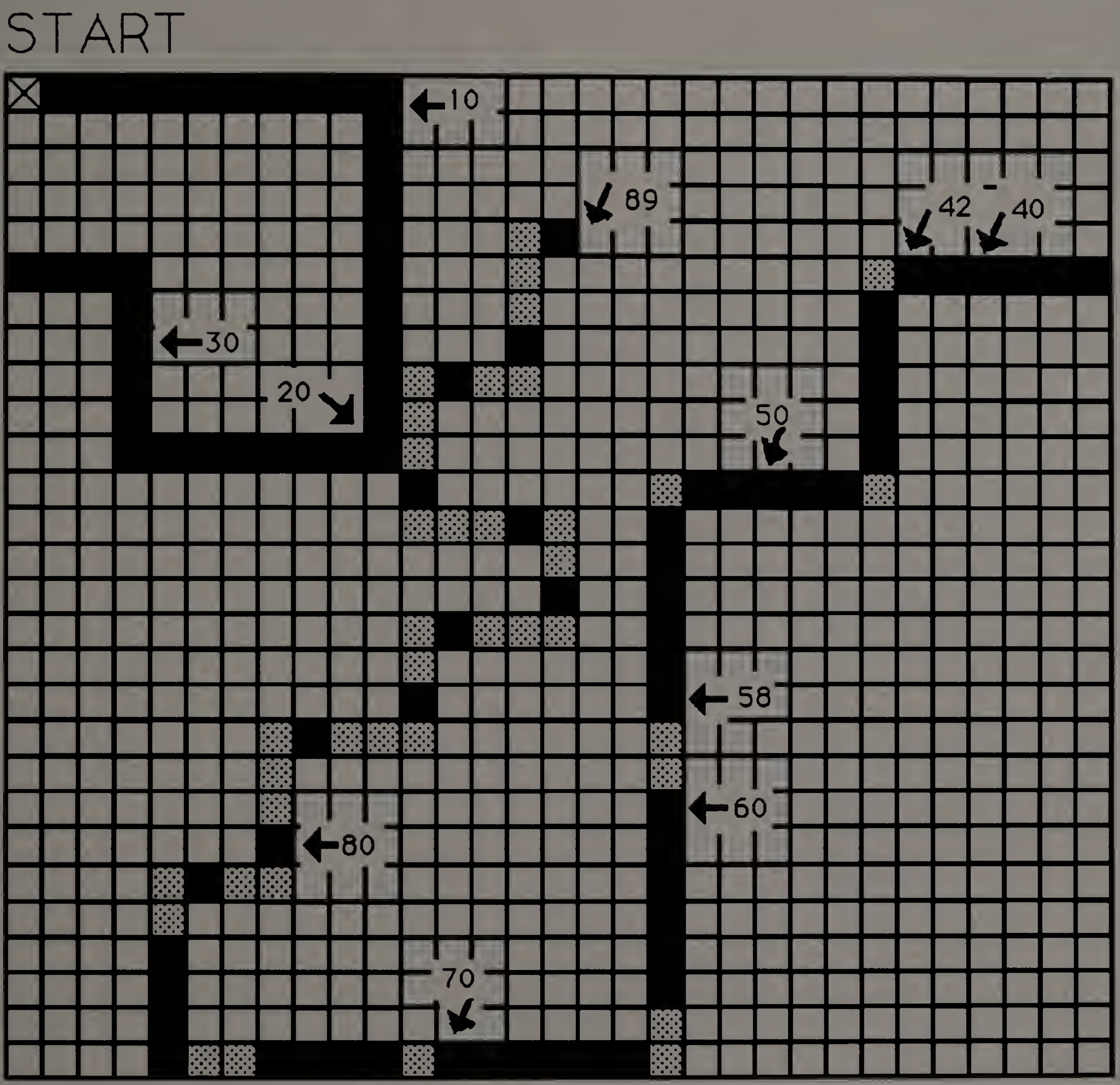


Figure 2.8 The "John Muir Trail" from the *Genesys/Tracker System*

The ant's task is to move from cell to cell and traverse as much of the trail as it can in 200 steps using the behavioral program in its genome. One point is given to an ant each time it reaches a cell on the trail. After an ant steps on a marked cell, its scent is removed to prevent the ant from circling and getting points for tagging the same square many times.

A G/TS ant has only one sense organ, a 'nose' that can only smell the cell immediately preceding it. The sensor returns a 0 or 1 depending on the absence or presence of pheromone in that cell. The sequence of moves coded by the genome evolves so that the succeeding ants can use the information from the one sense organ to follow the trail.

Figure 2.8 shows the "John Muir Trail" traversed by ants in G/TS . The numbers on the grid give the number of points that an ant has accumulated if it reached that spot. The black marks the trail. The grey spots are not part of the trail. They are visual aids to the reader to mark the fastest route of travel. These grey spots would appear white to the ants. Note that after the 70 marker the trail gets harder. There are many "Knight's" moves (two or three unmarked then left or right one cell).

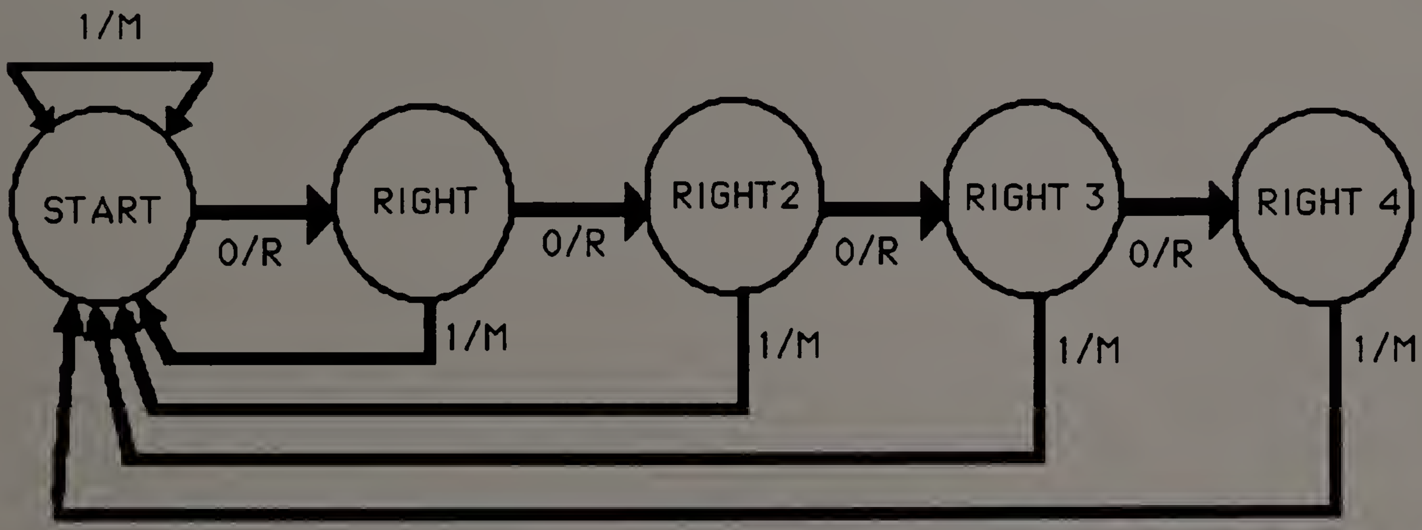


Figure 2.9 Five state automaton that can traverse the trail in 314 steps and gets a score of 81 in 200 time steps. (Jefferson, 1991)

The behavioral 'program' of a G/TS is not unlike a LOGO program. Pappert's LEGO/LOGO turtles move around the floor under programs much like that of G/TS ants. Below is a sample G/TS ant program expressed as a cellular automaton.

The notation in figure 2.9 encodes moves of the ant as follows. At the start, if the ant senses a trail in front of it (sensor input is 1) then it Moves onto that square (coded '1/M'). The automaton's condition then returns to the 'START' state. If the square is not a trail square (input code 0), then the ant's internal mechanism moves to 'State 2' and it makes a Right turn (coded '1/R'). Now in the second state of the five possible, it executes instructions given by its genome for this state. In State 2, for this automaton, it checks for the trail in front of it. If there is no trail, it makes a right (remember turns just affect direction, the ant does not move) and goes to the third state. If there is a trail marker in that direction, it moves onto it and the state of the automaton goes back to START. Programs very much like this one have been written in LOGO and programmed into LEGO/LOGO robots for use in middle school classrooms at the MIT Learning Lab (Resnick, 1989). The example given is a five state automaton. Automata of up to 32 states are permitted. The rules governing the automaton are stored as a look-up table in the genome. The look-up table gives the appropriate response after whatever condition the ant encounters. The ant's genome is long, 453 bits. How much of the genome is actually used is highly dependant on the code of the particular ant.

The initial loading of the ant's genome (rules governing its behavior) is random, so that over 40% of the first ants are non functional. They never find the first square. Another 20% only find square one. Over 90% get scores of under 10. The population evolves using a genetic algorithm in which the genotype's score determines its representation in the next generation. In each run there are 64,000 ants, each with a different genome. At the end of a run all ants are killed. Only the top scoring 10% are reserved for breeding. Mutations occur only at breeding. The mutations are always blind to the part of the genome on which they operate. Pairs of parents are chosen at random from the top scoring ants. These are bred to produce the next generation of 64,000 ants. From each parental pair an offspring is produced first by a crossover mutation (usually at a 1% rate) on each element of the 453 bit string. For example, consider parent A and parent B. The algorithm takes the first element of parent A's genome to construct the first element of the genome of the offspring. But 1% of the time it uses the first element of parent B instead. Parent B's genome is not disadvantaged in this process, as it could be the first parent in another random pair. A second point level mutation (usually again at 1%) will invert a 1 into a 0 or visa versa at each element of the 453 bit genome of the offspring. The new generation of 64,000 ants is tested on the trail. It takes the hardware approximately two hours to execute 100 generations of ants.

Even starting from initial random states, after one hundred generations the genome of the G/TS ants evolved to a level where they can exhibit the behavior of following accurately a "broken trail" in a grid environment, achieving mean scores in the 50's. A small fraction of ants actually reached a perfect score of 89 in this short time. The structure of some of the most efficient organisms was remarkable. "Such efficient logic seems exquisitely adapted to the features of this particular trail, and suggests that evolution has had the effect of 'compiling' knowledge of this environment into the structure of the organism (Jefferson, et al., 1991)." The meaning of theoretical studies of the evolution of behavior of individual cellular automata like G/TS for students of science educators can be best seen through the work of the successor to the Genesys/Tracker System, AntFarm.

AntFarm by Robert Collins and David Jefferson is a massively parallel, micro-analytic, evolutionary simulation. It focuses on the evolution of behavior of a whole colony of automata. Each colony of ants in AntFarm has a single chromosome with a 25,590 bits. There are 16,384 colonies of 128 ants each. Each colony occupies its own 16X16 grid environment. The genome of the ants in AntFarm differs from the structure used in G/TS in that each ant in the colony has the same genome (haploid genetics). Their behavior is encoded as a neural net, not a finite state cellular automata. The size of the genome, as well as the number of ants and the number of colonies gives the reader some idea of the computing power needed for this simulation. A run can take days to complete.

The AntFarm ants also wander around their world leaving or following pheromone trails, finding food and bringing it back to the nest. There is no fixed 'trail' to follow as in G/TS . Each ant has four options: 1) move to any of the eight neighboring locations, 2) pick up a unit of food, 3) drop a unit of food, 4) drop from 0 to 64 units of pheromone. The ant also has more senses. It can sense: 1) presence of food, 2) presence of the nest, 3) the amount of pheromone, 4) whether it is carrying food or not, 5) direction to the nest, 6) random noise that disturbs other signals. The response to sensory input is determined by the genome. Fitness is determined primarily by the number of bits of food that ants carry back to the nest. Because metabolism is included in the assessment of fitness, there is a pressure to evolve streamlined foraging strategies.

The genome of the initial population, like that of Genesys/Tracker is set randomly. A great many initial ants are non-functional. After 500 steps by each ant, a generation is considered complete. All ants die and a new generation is hatched. Frequency of a genome in the new population is determined by its success in the last generation. Mutations occur in the genome during reproduction. As in G/TS they can be both point mutations, or crossovers. Over the course of a run the ants in AntFarm evolve very complex search and foraging behaviors. Like the ants in G/TS these ants 'learn' to follow pheromone trails to food, but to become more efficient at foraging they also 'learn' to leave trails that may aid other ants. The word 'learn' may not carry the proper meaning in this context. It is the neural nets in the 16,000 different ant colonies that is evolving after each generation.

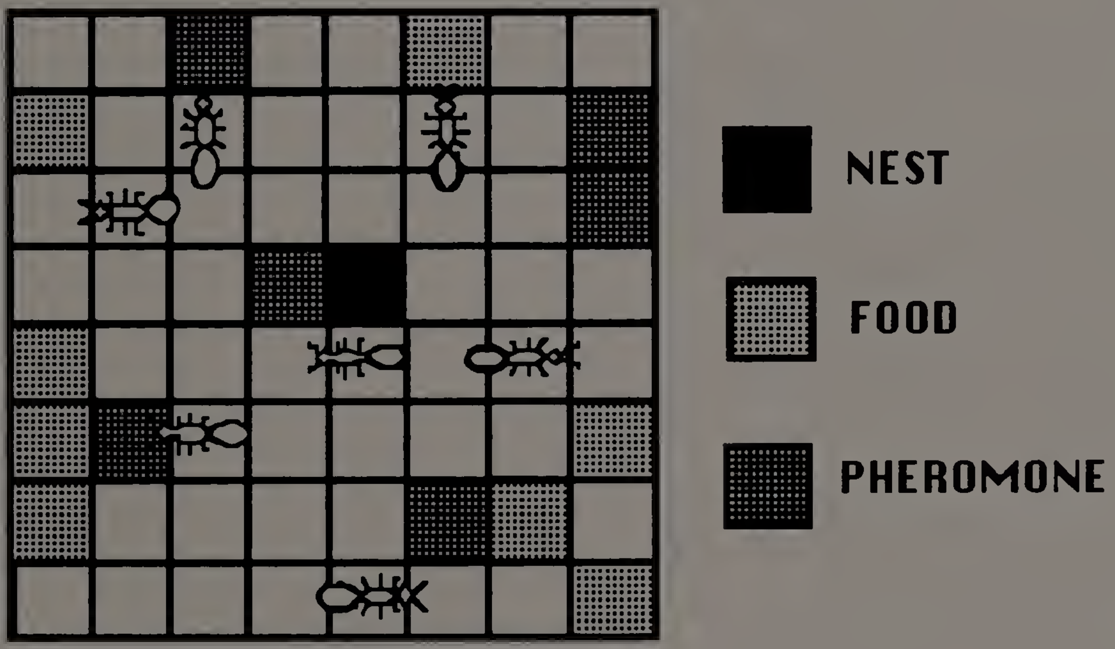


Figure 2.10 Section of a Grid from *AntFarm*

Collins and Jefferson chose not to attempt to model navigation in AntFarm. The ants are provided with a "sense organ" that performs some tasks of navigation. The organ indicates the direction back to the nest. They still must evolve the ability to use it. Real ants use a very complex system of tracking the sun or moon, polarized light, and perhaps magnetism to determine the direction to the nest. It was not realistic to attempt to model this behavior in such a simple simulation. Figure 2.10 is a schematic of a section of one colony of ants in AntFarm.

Each run of AntFarm lasted 500 generations. The time for a run on the Connection Machine was one or two days. The ants developed very complex, and reasonably efficient foraging behaviors. The evolution of cooperative foraging has not been observed as yet. The programmers at Maxis have taken some of the more successful genomes from AntFarm and used them to represent the behavior patterns of the ants in SimAnt. The ants in SimAnt don't evolve like those in AntFarm. The genomes (neural nets) that govern the behaviors of workers, queens, and soldiers are fixed over time. While playing SimAnt these artificial creatures do show the seemingly purposeful behavior exhibited by these 'evolved' neural nets. As stated previously the 'yellow ant' construct is a very clever method of introducing the human player into the world of these neural net ants, as well as a chance for the human to explore ways in which cooperative behavior may be initiated. The human now becomes the initiator ant, the element of the colony that precipitates cooperative behavior. SimAnt is a very successful adaptation of the technical work done by the Artificial Life Group at UCLA to a home/educational environment.

Gregory Werner and Michael Dyer, also of the UCLA Artificial Life Group, used another variation on the Genesys/Tracker System to investigate the evolution of communication in artificial organisms (Werner, et al., 1991). Their work does bear directly on pedagogical use of modeling in The Evolutionary Tool Kit.

Werner and Dyer's organisms (W&D) occupy a 200x200 toroidal grid. Females of the species are non-moving; they emit calls that are heard by the males. Females also have limited 'vision'; they can see males up to two squares away horizontally or vertically. The eye can detect the location and orientation of a male. Males roam about listening for females. The males share the condition of Eros in legend; they are blind. They do have an 'ear' which can hear the signals of nearby females. The male's hearing is not directional; it can only sense the signal. The problem that the W&D organisms set out to solve is the age old one of mating. Can a type of communication between the organisms evolve that will assist in this process?

The females can produce eight different signals. The male has only five outputs: forward, back, left, right, and still. When a male in the visual field of a female that is one right turn and two forward moves away, the female may emit sound 4. The neural network genome of both males and females determines initially what sound is emitted, or what movement is taken, in response to any condition it encounters. To that female, sound 4 carries the meaning of "right, then forward two". Other females may use different signals for the same condition. Furthermore the neural networks of the males are also arbitrary. The neural network of the male that receives that signal may interpret it as "go left then forward two" or some other arbitrary pattern. The networks are initialized randomly. The environment puts evolutionary pressure to evolve efficient communication. The best strategy for two animals to find each other is for the female to direct the male to herself. "As the males evolve a search strategy, the females will have to evolve a corresponding signalling protocol for the males to follow."

When a male finds a female, the two mate and produce two offspring, one male, one female. The genome of the offspring is produced by combining the neural networks of the parents, using crossover and mutation as described previously. The offspring and the parents are then moved to random locations in the grid. Mutation rates are set at about .01% per gene, with crossover at 2% per gene. Organisms have a fixed time in which to reproduce or they die. Reproduction is asynchronous, permitting overlapping generations. This procedure differs from more traditional genetic algorithms, but it is suited to studies in the evolution of language where inter-generational communication is important. The task may be restated as a co-evolution of populations of males and females who agree on a dialect or protocol to interpret the signals sent and received. The dialect may be completely arbitrary. A control group of totally deaf males was sometimes used for comparison purposes.

Results of Werner and Dyer's work were very interesting. Up to 1500 cycles the 'deaf' males reproduced more efficiently than 'hearing' ones. Presumably confusing signals from females with random dialects caused confusion. After 1500 cycles the hearing males reproduced with double the frequency of their deaf brethren. In all runs one particular communication protocol eventually took over the entire population. Werner and Dyer also tried introducing barriers in the grid. The barrier could be impermeable or semi-permeable. As one would expect, if the barrier was impermeable, different dialects evolved on each side. Interestingly, if the barrier was semi-permeable (up to 80% chance of crossing when approached) separate dialects could be maintained on each side. At rates higher than the 80% permeability one of the protocols would consistently take over the population.

Werner and Dyer wish to extend their model to include metabolism and deaths by starvation, predation, and more detailed modeling of vision and listening. The random placement of the parents and offspring is also unrealistic. The authors plan to have offspring placed nearby parents. This may encourage "both speciation and altruism." Werner and Dyer note that several species of frogs that can interbreed in nature, never do. Their calls are so distinct as to insure such cross species mating never happens. Calls of male frogs attract only females of that species (Blair, 1958; Blair, 1964). Werner and Dyer also state, "We believe that communication protocols could provide a natural way of establishing genetic barriers that spontaneously emerge. This could be useful in exploring a wide variety of biological problems in the origin and maintenance of distinct species in an ecological setting, including kin selection, altruism towards kin, genetic drift, gene flow, mimicry, and parasitism."

It is investigations of this sort that The Evolutionary Tool Kit is setting out to facilitate at the secondary level. Werner and Dyer believe that modeling with artificial organisms can play a role in theoretical understandings of these phenomena. I am convinced that modeling with cellular automata has great pedagogical potential in the life sciences. As set out in their 1991 paper, the inaudible digital chirping (the calls were all in binary, no real sound was made) of Werner and Dyer's organisms may have no immediate application to secondary education. The approach is very abstract. Recent work on frog calls by Michael Ryan, and reported by Steven Jay Gould (Gould, 1991a; Ryan, 1990) and on moth antennae by Steven Vogel (Vogel, 1986) can be modeled relatively easily in The Evolutionary Tool Kit for secondary life science students.

The beautiful singing and exquisite plumage of birds or the nightly chorus of frogs are often seen as a hymn of praise to the earth, or to life itself. To the evolutionists' eye and ear, they are prime examples, in fact, of the great Darwinian struggle, a challenge to other males and an advertisement to females to ensure their reproductive success. In frogs the female choice model of sexual selection seems to apply. Michael Ryan noted that a particular Panamanian frog, *Physalaemus pustulosus*, has an unusually complex two part call. The call consists of a whine at about 400 Hz to 900 Hz, then a chuck with a base frequency of 220 Hz but with 90% of its energy in very high level harmonics starting at 1500 Hz, peaking at 2000 Hz. Direct anatomical examination of the inner ear of females reveals that it is most sensitive to about 500 Hz, but it also has other fibers that are maximally sensitive at about 2100 Hz. Ryan makes the hypothesis that the complex call evolved from an ancestral one, now including the additional chucks. These high frequency sounds take advantage of hereto unused properties of the ear. This phenomenon is called pre-existing sensor bias. Successive choices over thousands of generations of female *Physalaemus pustulosus*, is sufficient to cause an evolutionary pressure in favor of calls with high frequency chucks. As Gould states "the pre-existing bias in frogs is a basilar papilla tuned to high frequencies, not an irresistible urge to hear a chuck. Again this bias might have been exploited in many other ways. but *P. pustulosus*, evolved a chuck (Gould, 1991a)."

This tale of whines and chucks is beautifully adapted to modeling with cellular automata in The Evolutionary Tool Kit. Methods to do this will be explicitly explored in chapters three and four. Experiments with evolution of frog and bird vocalizations will call upon the abilities of students who may be dominant in the musical intelligence in Gardener's

Multiple Intelligence Schema. Students will set a sensory bias in females. The bias will consist of one or two maximal excitation levels for the "hearing organ" of the female automaton. Number of sensitive regions and which frequencies of greatest frequency will be chosen by students in a "design" phase of their frog call engineering. They will also set up a style preference: short bursts, long notes, octave jumps, fifths, or trills etc. Much as in the "Designer/selection" described previously with competition among Niklas' trees, another group of students (with no knowledge of the pre-existing bias) would design a "male frog call" would enter a natural selection competition with a species under an genetic algorithm. This could easily be done over a network. The question that may be asked is "Who can design a frog call that females find the most attractive?" The males of the species that produce the most sensory "excitement" would be chosen by females for mating. As the competition proceeds, and after the students' species starts to lose, they would be permitted to listen with a "microphone" to selected frog calls from the species undergoing "natural selection". Students could then go back to their design, and genetically re-engineer the calls of their male frogs, based on analyses of what they think works for this group of females. Can they design their frog "genes" good enough to take over the swamp?

As described above, the natural selection model is based on Mendelian patterns of inheritance. There is considerable evidence of a "cultural" or at least social component of animal calls (Csikszentmihalyi, 1988; Dawkins, 1983; Gould, 1988; Mayr, 1988). In the case of canary songs, there seems to be a genetic component of the song. Males raised in isolation will sing a certain series of notes; it is a greatly simplified version of the song of an adult canary. Much of the texture of the song, its swoops, trills, repetitions etc. seems to be learned from contact with other canaries. This Lamarkian form of inheritance seems especially important in higher animals and primates (Dawkins, 1983; Dawkins, 1986; Maynard Smith, 1978a; Maynard Smith, 1989). Learned behavior can be modeled with automata in The Evolutionary Tool Kit. Students can set up a competition between a fully genetically determined species, and another species whose males "learn" the stylistic component of the song from other males. The genetic component of the second species would still have to be engineered continuously by the student.

Another interesting set of experiments with automata that can appeal to students who think physio-kinetically is suggested by Steven Vogel's work in biomechanics (Vogel, 1986). The antennae of many moth species are very specialized structures. Males of many species are very short lived. Some are hatched without any mouth parts. They must find females and mate very quickly before the die. Their antennae are exceedingly sensitive to the pheromones of the females. Some are able to detect concentrations down to one in ten trillion parts. The sensors on the antennae may be only able to detect the presence of pheromone. The shape of many moth antennae is fern like, very similar to the fractal patterns generated by simple replacement operations.

Models for antennae as arrays of cylinders could be constructed in a computer and subjected evolution through a genetic algorithm. There would be both structural constraints, as with Niklas' trees, and a factor estimating aerodynamic drag of the structure. The problem would be to develop, or evolve through natural selection, a structure that provides the maximal surface area to trap particles of pheromone, while giving minimal weight and drag in flight. Calculation of drag coefficients is both computationally intensive and error ridden for anything but the simplest of shapes. The intermediate values that the computer generates could be tested against data drag coefficients could be gathered from student's own experiments with models of branched shapes placed in the air stream of fans.

In summary, the approach taken in The Evolutionary Tool Kit represents a new way of introducing and developing concepts in the life sciences. Building on the work of Werner and Dyer, students can investigate the patterns of inheritance of mating calls in both a genetic and memetic frame. Utilizing the work of Lindgren and Maynard-Smith, they can investigate effects of cooperative and non-cooperative strategies on populations. They can pose hypotheses on the structure and growth of trees and put themselves at the center of a Darwinian competition as modeled by Niklas. Students can explore at the level of the organism the effects such variables as breeding time, scarcity of food, metabolism of energy, have on predator prey relationships as modeled by Jefferson and Taylor.

New Ideas

As stated by Jefferson et al. (Jefferson, et al., 1991), "modern biologists have only a few ways to study macro-evolution: 1) mathematics of population genetics, 2) lab and field experiments, 3) examination of molecular relationships among modern species, and 3) examination of the fossil record." Each method poses unique problems, especially from the point of view of an educator attempting to give students an understanding of the beauty, and the claim to validity of evolutionary theory. The mathematics of population genetics is formidable, especially in non-equilibrium cases. Field studies, though close to ideal learning environments, are impractical in most school settings. The fossil record is notoriously incomplete, and generally inaccessible to students learning modern life science. Also, both the molecular and fossil records tell us about how evolution proceeded historically, not about the principles of evolution and how it might have been. Computer simulation provides a new tool. Jefferson (Jefferson, et al., 1991) further states that "We hope some day that biologists may use simulation to help resolve some of the outstanding foundational problems in evolution, including perhaps questions about modes of speciation, the evolution of cooperation, the unit(s) of selection, and the evolution of sex." Computer simulation will prove to be a valuable tool for research biologists in the coming years (Farmer, et al., 1991; Frenkel, 1991; Lander, et al., 1991; Langton, 1991). In addition to the pedagogic value, students will gain familiarity with the technology and techniques of computer simulations in the life science.

For science educators the newest and perhaps the most useful idea presented in The Evolutionary Tool Kit is ability to open up the global and local feedback loops of organisms and their environment for inspection and even manipulation by the learners themselves. Langton writes (Langton, 1991), that the important thing about life is "that the local dynamics of a set of interacting entities (molecules, cells, etc.) supports an emergent set of global dynamical structures which stabilize themselves by setting the boundary conditions within which the local dynamics operates. That is to say, these global structures can "reach down" to their own, physical bases of support and fine tune them in the furtherance of their own, global ends. Such LOCAL to GLOBAL, back to LOCAL, inter-level feedback loops are essential to life, and are the key to understanding its origin , evolution, and diversity."

The Evolutionary Tool Kit permits secondary students, without any knowledge of programming, a window, rather a multitude of micro-worlds to create and investigate the effects and relationships immanent in these global/local relationships. The ability of automata based simulations like The Evolutionary Tool Kit to "rewind" the history of its life and evolution, permits students to examine at close hand a model of evolution and natural selection based on that interplay between global and local (genotype and phenotype/environment) levels. Figure 2.11 attempts to graphically show the conceptual model. Individual 'genes' or local quantities collectively determine how each organism interacts with the environment and change it. The global variables, both the environment and the observable phenotypes, then interact through the non-random process of natural selection to influence the next generation of local variables, the new 'genes'. With software like The Evolutionary Tool Kit students can tally results after each generation, look at global parameters and evaluate them. They can even intervene at the level of the genes (or memes) in an attempt to change an outcome or modify a trend.

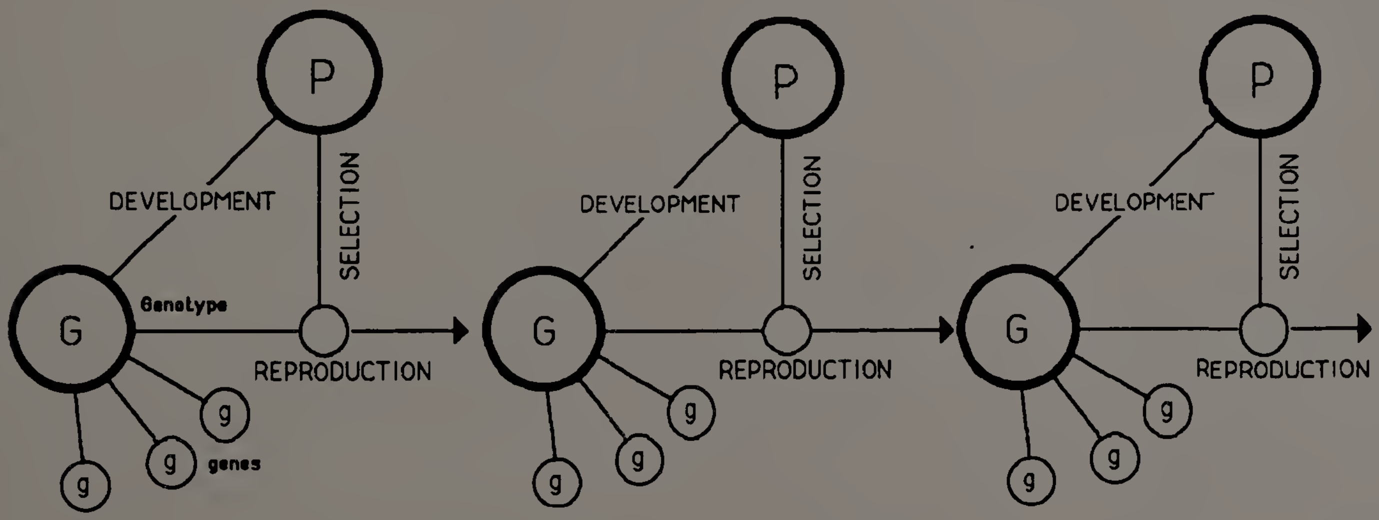


Figure 2.11 Model of the Evolutionary Process after Langton (1989)

A second 'new' idea, rather a new representation of an old one, is the emphasis of the modeling in The Evolutionary Tool Kit on change, and the dynamics of change. As Ornstein states (Ornstein, et al., 1989), "Since the world now changes more in a decade than it once did in millennia, the most important concept to get across in school is that of whatever is taught will soon probably become obsolete. That the rate of change is, if anything, increasing; therefore adapting to change must be the center of any new kind of teaching." The Evolutionary Tool Kit emphasizes heavily the curiosity, and self motivation of the learner; it is the 'life science hacker' ethic. The world in which our children will live will be very different than our own. It is most important for them, and for our human species, that they retain a life-long love of learning. We must provide an education that promotes a style of interacting with the world that encourages learning and growth from their experiences.

The third new idea is a challenge to the old ways of presenting materials in life science. For centuries the dominant mode of presenting knowledge has been text or lecture. Computational media provide a new, and potentially revolutionary way of reaching students at their own level, in terms that the students themselves define, an honest 'individualized' approach to learning. The Evolutionary Tool Kit takes a few faltering steps in that direction.

Adapting the three level distinction of knowledge from Andrea DiSessa (Disessa, 1988) of low level knowledge, middle level knowledge, and higher level knowledge, I wish to make a case for the general importance of the student centered, interactive approach taken by The Evolutionary Tool Kit in life science education. DiSessa defines low level knowledge as familiarity with facts, theories, language, terminology. Higher level knowledge brings with it an expertise in a particular field. DiSessa notes that one of the problems of "higher level knowledge" is that, the higher the order, the weaker the knowledge. It tends to be very powerful, but only in very limited domains of applicability. There is a case to be made for the importance of middle level knowledge.

According to DiSessa (Disessa, 1988) there are five characteristics of middle level knowledge. It is orienting: giving the student a broad view of what is going on in a field. It is strategic: saying more about what can and should be done with particular knowledge than is inherent in a presentation of the knowledge per se. It is synthetic: joining multiple points of view, providing ways of seeing them as the same. It is generative: easily extending to other ideas and genuinely new ideas the student might invent, not closing or limiting to particular ideas, sequences, or formats. And finally, it is sensitive to Relative Importance: providing a sense of relative importance, not just asserting truth or prescribing action.

The approach and design of The Evolutionary Tool Kit explores knowledge of life science along all of these dimensions. The development of a citizenry with sufficient middle level knowledge of problems and theories of life science is the socially overarching concern of our generation of educators. To serve our society's needs, each individual's needs, and the needs of the planet as a whole, we need citizens that can take responsibility for their own health, as well as support biologically sound decisions and policies, and object to biologically shortsighted ones (Clark, 1989). Approaches like that taken in The Evolutionary Tool Kit can aid educators to bring about future generations of such citizens.

As an example of the kind of "new" learning encouraged by this approach can be seen in the work of David Ackley and Michael Littman of the Cognitive Research Group in Morristown, New Jersey. Ackley and Littman's artificial life forms (called agents) live in a grid much like those of AntFarm or Genesys/Tracker (Ackley, & Littman, 1992). The simulation ran on workstation class machines. There are mountains that block them, food packets for nourishment, trees for shelter, carnivores that chase and eat them. In short, a world not unlike our own. For each object (rocks, wall, empty tree, occupied tree, carnivore, dead agent etc.) the agent has a genetically determined behavior. The agent, upon encountering these objects, would climb, turn, move, eat, avoid, depending on their particular code. They also had status variables for health and energy that could affect behavior with objects. The agents evolve by a genetic algorithm using crossover and point mutations as described previously for other programs. As with the other artificial life studies, Ackley and Littman seeded their world with random agents, usually 100 at a time. These would evolve behavior patterns that would succeed, to some degree, in this limited world. Ackley and Littman's agents were also permitted limited learning. The approach is called ERL (Evolutionary Reinforcement Learning). Agents could modify their own behavior tables based on its "experiences". Once relatively successful agents evolved, standard predator prey oscillations would appear; and the number of agents vs. carnivores would continue within a fixed range.

Of particular interest is that these relatively successful agents did not display optimal strategies. One rather successful agent showed no concern for its health status, and would exhibit avoidance behavior for the approach of a carnivore for all directions except south. If the carnivore came from the south, this agent turned and met it. The researchers analyzed its code, fixed a few of the errors to make it "better suited" to its environment and then tried the new agent in the grid. The result was not what was expected. The population of both agents and carnivores became very erratic. Instead of averaging in the forties or fifties with lows in the twenties, these populations averaged much lower, with some lows in the single digits. By replaying the simulation, the researchers were able to see what happened. Super agent was so efficient at stripping the environment of food and resources, it was out-competing itself. Plants and trees were eaten before they had time to regrow. Predators were deftly avoided, and many generations of young were spawned, only to die quickly in an environment continuously striped of its resources. The surprising conclusion drawn by Ackley and Littman was that there may be an advantage in the clumsiness of nature's Blind Watchmaker algorithm. Optimal solutions may not mean what we originally thought they did. This simulation may be more like real life than originally intended. Such a discovery would be a fine learning experience for any student or citizen of our world.

The educational challenge set out by software like SimEarth, SimAnt, and The Evolutionary Tool Kit is ambitious. But these are very special times. "More than any time in history we have the possibility to engage students' own goals and aesthetic senses in what is taught (Disessa, 1988)." There is nothing wrong with ambition especially in fields as important as education, and if the goals are within reach with consistent quality effort. Approaches like these show new ways to conceive of instruction beyond the printed page. Computers offer a new approach to knowledge through a new computational medium that can reach out and help to develop the individual talents of students in many new and different ways. The decision to change our "currency of representing knowledge" (Disessa, 1988) is not for one individual to make, but a highly social choice involving may constituencies, researchers, domain experts, textbook publishers, curriculum brokers, teachers, and the public. It is a decision that can be made after all parties have set educational goals in to build for the future of our species and our planet, and after we have summoned the will to pursue them.

A concluding note to this chapter is fittingly centered on the great biologist of the nineteenth century, Charles Darwin. Darwin is, according to Ornstein, above all others, the central scientist of the modern age (Ornstein, 1991). His work overturned much of the bases of Western philosophy. It showed that both humanity and the animals evolved to adapt to their world, with both a physical and a mental apparatus. This dissertation explores ways to adapt evolutionary thinking to an effective pedagogical form. Ornstein says, "Adaptation, which begins blind, organized around only one environmental niche, turns creative, and human organisms adapt the world to suit themselves (Ornstein, 1991). Evolution, once strictly biological, can become, in us, conscious."

With computational media like SimEarth, SimAnt, and the design set out in The Evolutionary Tool Kit educators can place students in an environment where they can explore, even invent, concepts like adaptability, selection, fitness, and other key constructs in the modern view of life. They can explore, among artificial life forms, and discover what is the meaning of a natural law. In their explorations, perhaps they can discover singly, or in groups the beauty and power of the processes that Darwin first saw and described. We can give them the platform on which they can experience for themselves what Darwin called "these laws acting all around us."

These laws, taken in the largest sense, being Growth and Reproduction; Inheritance which is almost implied by reproduction; Variability from the indirect and direct action of the conditions of life, and from use and disuse: a Ratio of Increase so high as to lead to a Struggle for Life, and as a consequence to Natural Selection entailing Divergence of Character and Extinction of less improved forms. Thus, from the war of nature, from famine and death, the most exalted object which we are capable of conceiving, namely the production of the higher animals, directly follows. There is a grandeur in this view of life, with its several powers, having been originally breathed by the Creator into a few forms or into one; and that, whilst this planet has gone cycling on according to the fixed law of gravity, from so simple a beginning endless forms most beautiful and most wonderful have been, and are being evolved (Darwin, 1859).

CHAPTER 3

STRUCTURE AND INSTRUCTIONAL DESIGN OF *THE EVOLUTIONARY TOOL KIT*

The micro-world of The Evolutionary Tool Kit (hereafter referred to as TETK) builds on some ideas from the world of sharks and fishes in WA-TOR game as popularized by Dewdney (Dewdney, 1984; Dewdney, 1988; Dewdney, 1989). Earlier accounts of similar simulations exist in the technical literature of biomathematical modeling (Barto, 1975; Burks, 1970; Burks, 1974; Conrad, & Pattee, 1970; Conrad, & Strizich, 1985; Stahl, 1967). TETK also incorporates some ideas from the descriptions of the RAM model described in the previous chapter (Jefferson, et al., 1991; Taylor, Jefferson, Turner, & Goldman, 1987).

As a concrete introduction to cellular automata modeling for readers unfamiliar with the technique, I shall briefly describe the ocean world of WA-TOR and the properties of the sharks and fishes that inhabit it. Cellular automata occupy 'grid worlds' defined as a specialized data structure. The topology of the world grid can be varied. The grids of SimEarth are spherical. Those of BIOSIM are rectangular with the vertical direction indicating the upper areas of the 'pond'. The ants in SimAnt live in a three dimensional cube. The ocean grid of the creatures in WA-TOR is toroidal. Figure 3.1 shows the analogical relationship of a cellular automata 'world' with a schematic drawing of a school of sharks feeding on fishes.

Following common convention, the two dimensional grid of the WA-TOR world is wrapped on both top and bottom edges to form a toroidal surface, hence the "TOR" in the name. It is possible to run the simulation without wrapping but effects due to the corners can produce anomalous results due to traping of organisms in the corners.

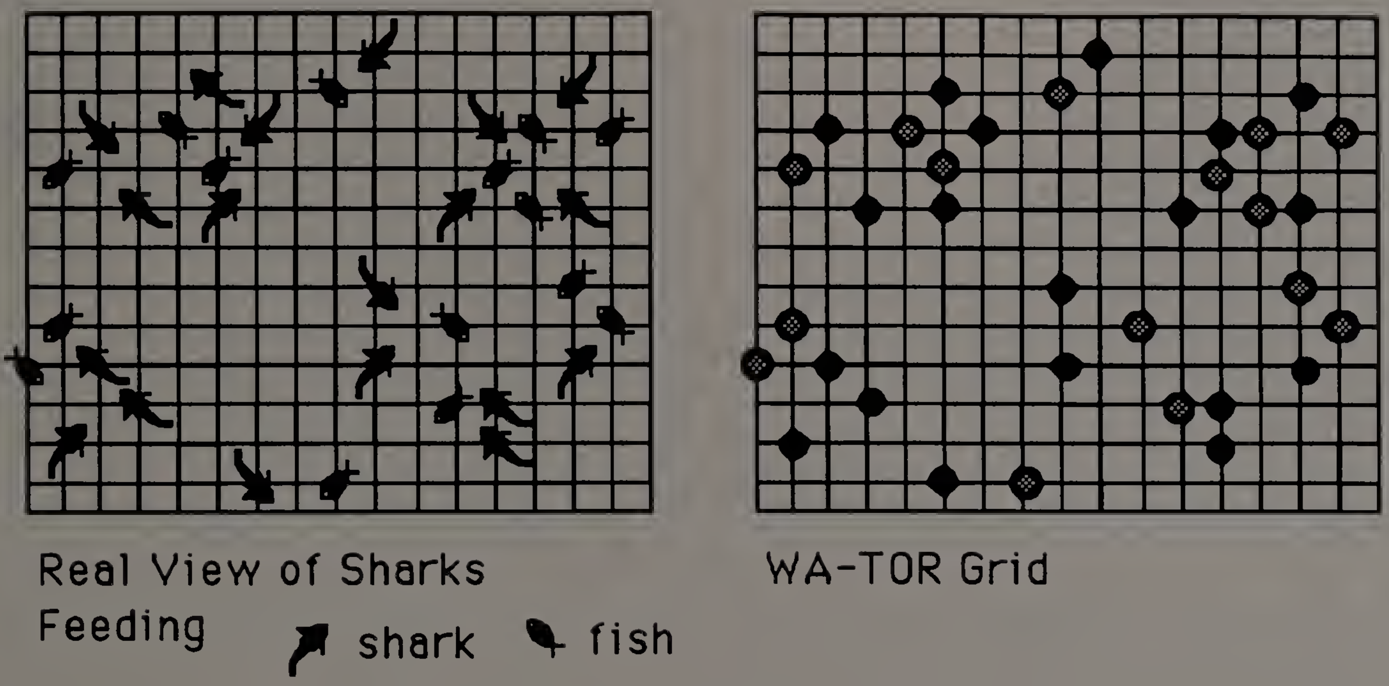


Figure 3.1 Grid world of WA-TOR

Figure 3.2 demonstrates the wrapping of the upper edges of the grid (A) into a cylindrical shape (B). The upper and lower edged are joined forming a cylinder. Importantly, the cell grid in WA-TOR is isotropic, there is no inherent directionality or global property to make any one cell different than any other. It is possible to generalize on the topology of this model, as the authors of SimEarth did, to include a spherical grid. Beyond the appeal of spherical worlds to students, this option permits the modeling of grids with different properties that depend on latitude, insolation for example. Future versions of TETK will include spherical grid models. SimEarth and TETK grids are not isotropic. Neighboring cells can have very different properties, which properties can affect the behavior of automata in them or moving onto them.

The cylindrical grid is then warped around an external center and joined at the date line to form a toroidal surface. Figure 3.3 demonstrates this warping. The right diagram in Figure 3.3 demonstrates the horizontal wrap of WA-TOR and the "real" world it represents - a toroidal ocean. A shark or fish on the left column of the grid moving left will appear on the rightmost column of the grid due to the "horizontal wrap around".

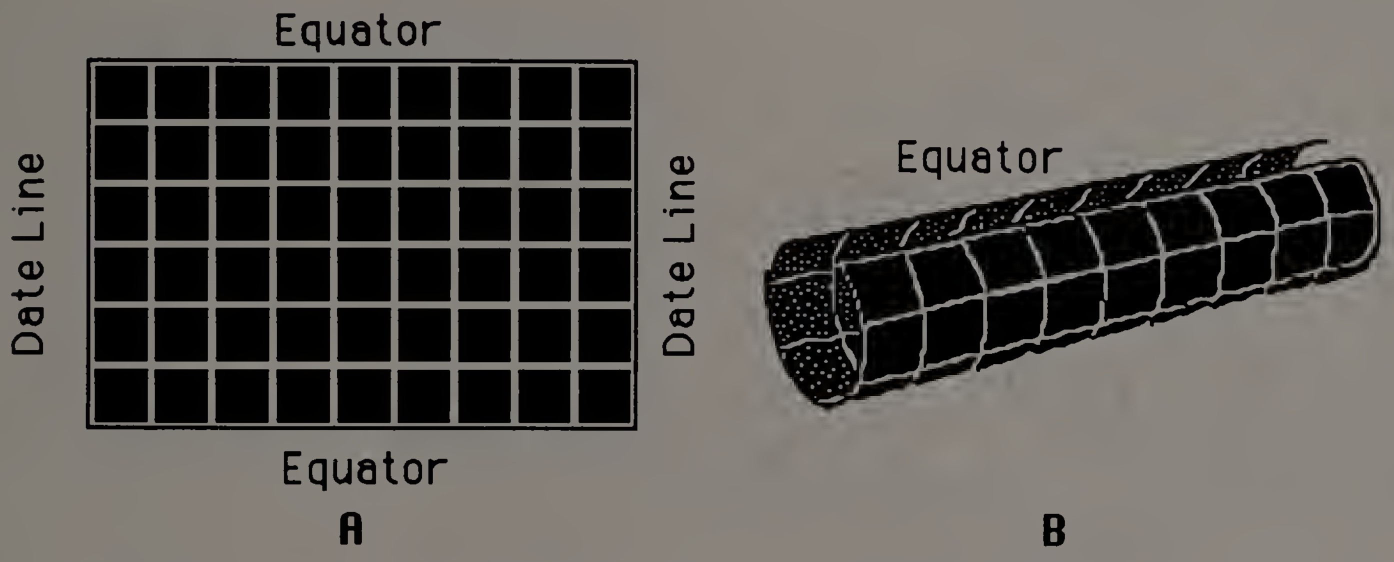


Figure 3.2 Vertical wrapping of the WA-TOR grid

Inspection of Figure 3.3 will show why these two wrapping conditions describe a toroidal surface.

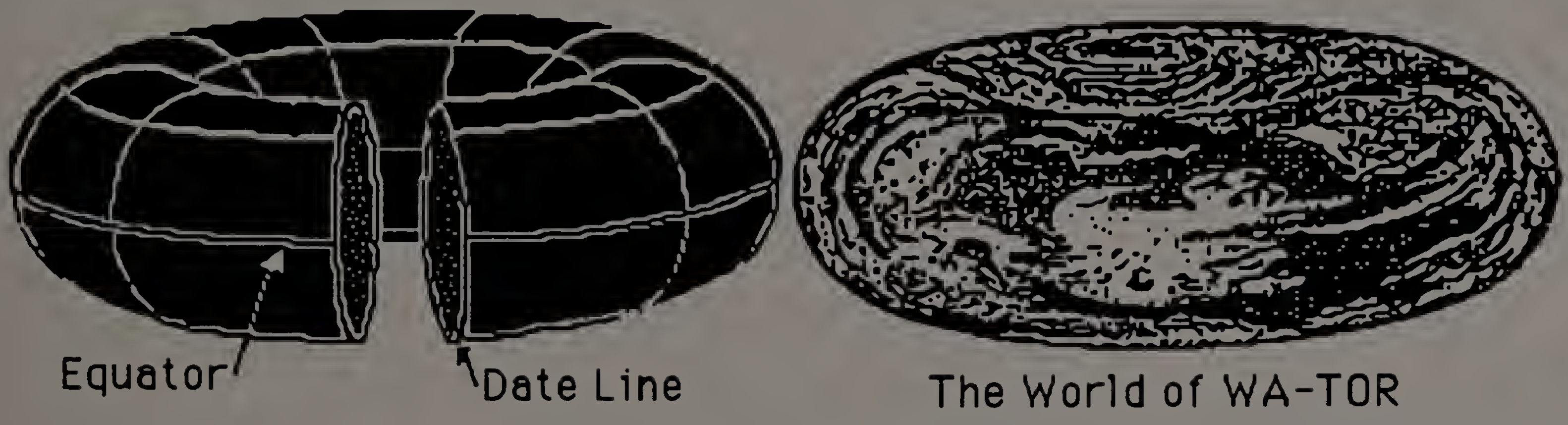


Figure 3.3 Toroidal world of WA-TOR

Please in Figure 3.3 note that a shark or fish on the top row moving up will appear on the bottom row of the grid due to the " vertical wrap around".

The rules governing life on Dewdney's WA-TOR are simple.

1. Only one occupant to a square.
2. Sharks can only eat fish. (Cannibalism can be permitted in more advanced versions, but it does not significantly alter the results.)
3. Fish eat plankton produced by the ocean.
4. Sharks and fish can breed only after they have reached their respective breeding ages.
5. Breeding is permitted only if there is an empty square adjacent to the parent fish or shark. The offspring occupies the square left by the parent.
6. The species are parthenogenic. (Single parents only on WA-TOR!)
7. During each time unit, each shark or fish must move (if there is a square available). Squares are selected randomly.
8. Hunting fish takes precedence over moving for sharks.
9. Each shark must find and eat a fish during the time given by the STARVE variable. Otherwise it dies and disappears from the screen.

To begin the simulation the player inputs five variables:

NFISH	the initial fish population
NSHARK	the initial shark population
FBREED	the age at which fish begin to breed.
SBREED	the age at which sharks begin to breed.

STARVE	the time during which a shark must catch a fish to avoid starvation.

The challenge to the student using WA-TOR is to find the most important variables and then combinations of values for these variables or regions of relative stability for the fish/shark population. Behavior can be chaotic; population crashes in either species can occur. An arbitrary definition will be made for stability of the population for creatures in the WA-TOR world. We will consider the population stable if it has cycled eight or more times. For those with time to spare watching simulations, or, alternatively very speedy CPU's, a stronger condition can be asserted. Populations have a tendency to crash as sharks surround the fish easily.

The WA-TOR simulation was very popular after its introduction. For a short time there was even a newsletter entitled *Running WA-TOR* published by an aficionado in Vermont. A few enthusiasts extended the range of properties of the inhabitants of WA-TOR. One derivative world, Palmitre's randomly evolving bugs, demonstrated some of the educational potential of this form of simulation.

Two serious pedagogical problems surface in attempting to extend Dewdney's WA-TOR. The first and most formidable is the technical skill demanded to perform any modifications on the world of WA-TOR or on the properties of its inhabitants. A secondary student needs direct knowledge of programing to attempt even the slightest modification beyond changing initial values of the fixed list of variables. The same difficulty arises with the bugs of Palmitre's world. The simulation can only be changed by attempting to alter the code directly.

The second problem is its lack of power to investigate the effect of change or mutation. The bugs of WA-TOR do not mutate. Palmitre's bugs do mutate but the analogy with natural organisms is only one dimensional. It is not easily extended to other properties and behaviors.

There is also a third problem that is more conceptual in nature; it is also at the heart of the difficulties students experience in attempting to study natural selection. The both the sharks and fish are treated typologically. Each shark or fish has the same properties as that of any other of its species. The organisms in WA-TOR do not form a population as evolutionary biologists would define it. The variables set by the user at the start of a run affect all sharks or all fish equally. Mutations would also affect the species as a whole. Palmitre's bugs are true populations, as each bug has its individual code determining its behavior. Descendants of successful bugs in Palmitre's world eventually comprise the total population. There no way is provided to watch the frequencies of the 'alleles' changes as Palmitre's bugs mutate into more successful hunting strategies.

An Overview of *The Evolutionary Tool Kit*

TETK attempts to address the first two problems by a design that permits students with little or no knowledge of programming to build their own micro-worlds to explore the dynamic interactions of automata and basic concepts of evolution and population genetics. The interface of TETK is very graphic oriented. Icons, instead of words, are used to represent the various life processes, traits (phenotypes) or characteristics assigned to the automata. The computer randomly constructs the genotypes for each individual, in a manner consistent with the choices of the user. Genotypes themselves are not visible to the student. It is possible to obtain, through reporting functions, tallies of allelic frequencies. They are 'represented' as unspecified patterns of 1's and 0's on linear structures called 'C-somes', the analog of chromosomes in this microworld. Mutations are permitted. Only point mutations are modeled. Textual information is kept to a minimum. The traits and reproductive strategies that can be given to the organisms and the environmental conditions that can be set up permit the user to perform hundreds of investigations.

The second and third problems are addressed by the data structure of the organisms in TETK. Each organism has its own 'genetic' code. Organisms are part of interbreeding populations that are the functional equivalent of species. The user can define the species either typologically (with all individuals identical) or populationally (with as much variation as he or she wishes). The rules governing the behavior of the cellular automata (organisms) are directly controlled by the student through their choice of traits, reproductive strategies, genetic systems, and environmental conditions.

The Evolutionary Tool Kit is intended as a support tool for introductory life science students. It is intended as a 'conceptual lab' in evolution and natural selection. Following the suggestions of Bishop, Clough, Halldén, Johnson, Ploger, and Slack (Bishop, & Anderson, 1990; Clough, & Wood-Robertson, 1985b; Halldén, 1988; Johnson, & Stewart, 1990; Ploger, 1991; Slack, 1990) cited in the previous chapter, the lab format of TETK starts with student conceptions (or misconceptions) of inheritance and evolution and encourages them to explore, to build models of how traits would, or could, be passed on to later generations. A model or investigation that a student builds based on a misconception, say 'blending of inherited characteristics', may not perform as he/she expects. The instructional use of the modeling strategy is similar to that described by Ploger (Ploger, 1991) which used DiSessa's Boxer program as a medium. TETK is a more specialized tool, permitting students to model evolutionary phenomena with populations of tens of thousands of individuals with many selectable traits and several different inheritance mechanisms.

Exercises or explorations in TETK are intended as platforms for students and teachers to explore thoughts on these areas in attempt to build a bridge between what Halldén calls "the students' questions and the school's explanations." The schools explanations, even the rationale behind what is being explained and the choice of language in which it is explained, makes very little sense to students as a response to their inquiries (Halldén, 1983; Halldén, 1988). Through a series of models within TETK cellular automata environment, each with progressive explanatory power, students can make what Gardner called a "Christoforian voyage" (Gardner, 1991) and build a rationale for new concepts and new types of explanations where others had failed.

The instructional model built into TETK is that of 'constructivism' as opposed to the a traditional 'transmission' model so commonly used (Mestre, 1991). A constructivist model recognizes that the students' knowledge of the world is the result of a process of mental construction over many years. The views they bring to class are tried and tested many times; from their perspective the views are consistent and provide meaningful interpretations of events. As Mestre states, "constructivism contends that students are not sponges ready to absorb and use transmitted knowledge; the knowledge already written in their mental slates affects how they interpret new observations and how they accommodate newly acquired knowledge." A scientist, however, may view these models as naive, incomplete, and self-contradictory. Some of the greatest advances in science have come from planned observations or experiments that refute these same mental models. Unfortunately talking to the students, or having them read or study materials does not sufficiently engage their mental apparatus to provide meaningful conceptual shifts. As Mestre states, "the transmission model does make a pivotal assumption about learning, namely that the message the student receives is the message the teacher intended." All of the educational research cited in the previous chapter attests to the folly of this assumption.

John Jungck and Nils Peterson have explored similar instructional strategies in genetics education (Jungck, & Calley, 1985; Peterson, & Jungck, 1988). Jungck's Genetics Construction Kit is designed much along these lines. In the visionary article, "Problem Posing, Problem Solving, and Persuasion in Biology Education", Jungck and Peterson describe a transmission based, algorithmic pedagogy, with cookbook labs and dry lectures that has "metastasized throughout biology courses." They propose an alterative approach that is fundamentally motivated by a respect for the learner, were students are treated as co-learners, not infantilized. The authors noted that phrases like "design of a hypothesis" or "construction of a meaning" may not seem appropriate to many science educators, but this is exactly what students must do in order to be involved personally in making their own science. They asserted the importance of "self-education through research" and noted that "a good deal of knowledge of biology involves experiencing first-hand the production and application of scientific knowledge. "If hidden assumptions are ignored during problem-posing, it is all too difficult to eradicate them at the problem-solving and persuasion stages of scientific practice."

Of special importance in the consideration of the topics explored by TETK are Jungck's and Peterson's remarks that "problems do not come pre-posed to scientists." There is often a historical thread woven in. Frequently, a problem's solution is much easier, if it were posed more clearly initially. Textbook problems pose a particular difficulty; "they could stand in the lab or field forever, and no text book stated problems would come to them out of thin air." Importantly, the authors state, "Students can only begin to appreciate the tremendous agenda-setting issues in problem posing if they are encouraged to pose problems themselves."

The third issue addressed by Peterson and Jungck, persuasion, is especially relevant for the explorations set out in TETK. The research by Bishop, Clough, Halldén, Jungwirth, and Greene (Bishop, et al., 1990; Clough, et al., 1985b; Greene Jr., 1990; Halldén, 1988; Jungwirth, 1986) has revealed a two-fold problem. Naturalistic and Lamarkian explanations dominate student thinking, even after several courses in evolutionary biology using conventional pedagogy. Second, students do not change their views on the validity of evolutionary explanations, even if they can demonstrate that they understand them (Bishop, et al., 1990; Greene Jr., 1990). TETK provides an educational platform on which students can pose problems and conjecture, then demonstrate their solutions, and attempt to persuade based on their investigations.

It is well known that Darwin's theory on evolution by natural selection was elaborated many years before any realistic mechanism was know for the transmission of inheritance. Unaware of the papers of Mendel, Darwin himself did not have any realistic explanation. I am convinced that this fact may be of considerable pedagogical as well as historical significance. Smith and Millman suggest exactly that in their use of Darwin's notebooks as instructional tools (Smith, & Millman, 1987). TETK permits students to design models and test hypotheses as if they were primary investigators during the times in which the early theories of evolution and natural selection, and particulate genetics were formulated. Students could create models that parallel arguments faced by Darwin, Huxley, and Weissman in the early years of the exposition of these theories. "Blending vs. particulate inheritance", which is the case? "Can there be change with blending inheritance?" "Won't dominant alleles eventually take over the whole population?"

With The Evolutionary Tool Kit students have in their hands a tool to do many of the thought experiments that fill his notebooks. Lab investigations could be designed by students as well as modeled after investigations or discussions from the history of biology. On a personal level students can explore the underlying issues, formulate questions about what the nature of the difficulty is, and, most importantly, discuss what kind of explanation would be satisfactory response to these questions.

The underlying assumption of TETK is that introductory life science, or any science for that matter, should be taught using a critical thinking model. One should examine an issue from all sides, including the naive concepts of biology that students bring to class. As the studies by Brumby, Clough, Stewart, Bishop, and Greene, cited previously show, these same students leave their classrooms at the elementary, secondary, and college level with these naive belief systems and misconceptions about inheritance and natural selection very much intact.

The approach taken by The Evolutionary Tool Kit is not intended as an introduction or a primer in genetics. As the studies of Halldén, Bishop, and Clough cited previously show, their difficulties in understanding natural selection are independent of their understanding of genetics. TETK is not a structured exploration of inheritance patterns as are the fine works of Judith Kinnear and John Jungck. Neither does it attempt to incorporate any advances in artificial intelligence or tutoring systems like the work of Streibel and Stewart on the computer program MENDEL (Streibel, Stewart, Koedinger, Collins, & Jungck, 1987). The students already have naive ideas about inheritance as well as instruction in modern theories of inheritance provided by their instructors. TETK attempts to provide a computational instructional medium which can give a context to explore the interaction of the naive ideas and the school's explanations. Every attempt has been made to keep the terminology used in TETK consistent with modern theory in genetics. Terminology has been limited to 'allele', 'gene', 'locus of the gene', 'trait', 'phenotype', 'genotype', 'dominant' and 'recessive'. Through interactions with their textbooks, other computer simulations designed to introduce genetics, and, above all, interaction with their peers and with their instructor in a community of inquiry, students build working definitions and knowledge of these terms and their relationships as seen by modern evolutionary biology.

There are several fine computer programs that can be used to introduce topics in genetics and inheritance quite well; perhaps in parallel with explorations in TETK. MacFly is an artificial laboratory that permits students to breed and investigate the common fruit fly, learning the rules of inheritance from an electronic image of the beast that gave humans their first look at genes themselves. Jungck's Genetics Construction Kit is designed primarily for college level students. Mendelbugs, Heredity Dog, and Judith Kinnear's delightful efforts, Catlab, CatGen, Birdbreed, and Kangasaurus are but a few other fine pieces of software usable at the secondary level. The Biology Explorer: Genetics is a very new package designed for use for upper level secondary classes. Heredity Dog can be used easily at lower level classes.

TETK also does not address the pedagogical problems of evolution at a molecular level. This topic is not appropriate for the population intended. There are a few programs, mostly tutorial in design, that explore molecular aspects of inheritance and evolution at a rudimentary level. Students could learn the technical terms and get a simplified understanding of the process of reproduction at the molecular level. None of these programs can be called 'simulations'.

Some recent theoretical work has been done on automata and artificial life in modeling the emergence of metabolic activity and self reproducing automata (Ackley, & Littman, 1992; Bagley, Farmer, & Fontana, 1992; Fontana, 1992; Schuster, 1992). This work is far beyond the level of current secondary pedagogy, though in the not too distant future it may be possible to permit students to make their own 'artificial soup' and watch the emergence of the analog of biological order from random elements.

Evolution via natural selection and evolutionary biology are very wide topics indeed. In fact, some authors state that all biology can be subsumed under the title 'evolutionary biology'. What specific topics does TETK address? There are three central pedagogical concerns addressed in TETK. The first is instruction in the concept of variation within a population and its importance in any discussion of natural selection. Studies by Bishop, Brumby, Clough, Greene, Hallén, Jungwirth, and Ploger (Bishop, et al., 1990; Brumby, 1984; Clough, et al., 1985b; Greene Jr., 1990; Halldén, 1988; Jungwirth, 1986; Ploger, 1990) have shown that concept has been shown to be very troublesome for life science instruction at both the secondary and college levels.

The second instructional concern is the development of a feeling for the random nature of mutation. Students very commonly associate the word 'mutation' with a complex of ideas from science fiction. Mutations are bad, deforming, lethal, and not-'natural'. The realization that mutation is the raw material that drives natural selection is far from their minds. Another problem arises when one considers students from different cultures or non-English speakers in our classes. In a study of native speakers of Catalan, Albaladejo & Lucas noted that in Catalan '*mutatio*' carries much different connotations than the cognate English word 'mutation' (Albaladejo, & Lucas, 1988). In English, the word 'mutation' has come to be almost completely associated with extensions of its scientific meaning. In Catalan, a scene change in a play, an insect's metamorphoses, puberty, and chemical phenomena like rusting can be properly called 'mutations'. If the constructionists arguments are correct the confusions that such a wide meaning of this word can cause are much in evidence in studies of students' interpretations of the terms 'mutation' and 'adaptation' when non-native speakers of English study evolutionary biology. TETK provides an environment in which students can refine and redefine the term in an evolutionary context.

Mutations in TETK are of two sorts: saltation and point mutations. To model saltation a student can stop a simulation at any point, introduce a new individual in the population with a specific characteristics, and then set the simulation in motion again. It is a "What if X happens?" In a second form, the computer, using output from a random number generator, can make point mutations on the genetic code of any species, or specific trait. The mutations can be either advantageous, non-advantageous, or neither. Which description obtains is not under control of either the computer or the user. Fitness, or advantage incurred by the change, is determined by the interaction of that genome with the population and the environment.

The third concern is the production of an environment in which the student can clearly explore the two fold nature of evolution via natural selection: the necessary variation of the population (which must be random) and the non-random action of the process of natural selection. The recognition of the two-fold nature of the explanation is the key to understanding Darwin's vision (Futuyma, 1983; Ghiselin, 1969; Mayr, 1988; Mayr, 1991). It is even possible to put two populations in competition for a single resource, one with different amounts of variation than another, in order to isolate the effects of both processes.

The student must first have a concept of population based on variation of individuals with a mechanism for the production of the variation that is random, and closed to external influences (will, goal, need, etc.). The second step, the process of natural selection, can then be demonstrated, both logically and functionally with organisms in the microworlds, as a directional, but not directed process by which some individuals with some characteristics die or produce fewer progeny than other individuals with other characteristics.

Certainly all of this is old hat. Any adequate instructional unit on evolution and natural selection will take these ideas as starting points and proceed with a logical exposition using a transmission instructional strategy. What is new is that the <u>TETK</u> permits a biology instructor to do is to create a learning environment, an evolution lab, that recognizes that the students' approach to the topic is not logical. The 'naive biology' they bring to the study of the discipline seriously distorts their understanding of the best logical,'crystal clear' presentations. With an instructional strategy modeled much after Pappert's microworlds described in Mindstorms a decade and half ago and the student centered investigations of Judah Schwartz and Michal Yerushalmi's Geometric Supposer , TETK attempts to put the student in the position of playing with building blocks, adding, combining, changing patterns, except that the blocks are now traits, inheritance patterns, reproductive strategies, and environmental conditions. The 'blocks' also are dynamic elements, changing in response to internal (genetic) and external (phenotypes interacting with the environment).

A basic question that a student might ask is "Assuming a random mutation takes place that is beneficial to the organism, how is it propagated through the population?" "What happens when a sexually reproducing population competes for resources with an asexual one?" "What is this 'natural selection' actually acting on? Who is struggling? Species or individuals or genes?" "Are some traits immune to natural selection?" "How does the pattern of distribution of properties change over time in a sexually reproducing population or in an asexual one?" "How does this change affect the species involved, as well as the substrate that supports them?" Students can explore this central feedback loop of information at the genetic level; how populations change, which effect the environment, which, in turn affect information at the genetic level, which effect the populations.

These questions are all fine, but what does the program do? TETK, in its pilot form, models specifically micro-evolution. It attempts to provide an environment in which students can see the crucial importance of variation in populations in any process of natural selection. It also attempts to provide an environment in which a student can directly experience the interaction of random changes and non-random natural selection which produces directional, but not directed, change.

Evolution by natural selection is a big topic. One cannot hope to model accurately the whole or even a small part of any living system in codes on silicon chips. Computer simulations cannot be mirrors of reality. Several important elements are missing. The program does concentrate on the temporal or 'vertical' aspect of evolution, the modeling of changes through time to the exclusion of other views of evolution. The second 'horizontal' aspect, a geographical, or ecological dimension, which includes competition for niches, geographic speciation, and many other very important topics are not currently modeled. Suggestions on how to modify the program to do this are presented. The current focus on competition, reproductive competition, and sexual selection is probably misleading in its narrow context. The program also does not attempt to model macro-evolution, nor any of the more modern interpretations of neutral evolution or punctuated equilibria. It attempts to deal with conceptual basics first. It is not usable in a classroom or for teacher training until many of the missing elements have been added.

Importantly, preliminary investigations with a concept simulator like TETK can provide a conceptual framework for introductory students for ideas and the various kinds of explanations and explorations attempted in later topics like inheritance, cell theory, metabolism, mitosis and meiosis, and classification.

The audience targeted by TETK are all secondary life science students, not just students talented enough to reach AP classes. Some may characterize any effort to introduce natural selection and populational reasoning and argumentation in evolutionary theory at such a level as being very ambitious indeed. I am firmly convinced that many of the experiments and concepts modeled in TETK are well within the scope of upper level middle school students. The popularity of games like SimEarth or SimAnt, both aimed at upper elementary and middle school children, as well as adults who have retained the capacity to learn as they play, demonstrate well that students and adults alike are very interested in complex ideas and relationships if presented in an accessible and entertaining manner.

SimAnt is particularly interesting case. If someone had told me a few years ago that they intended to present E. O. Wilson's views on sociobiology and their applications to individuals and to social behavior in insect societies to middle school students, I would have thought them crazed. I was wrong. It works, and quite efficiently too.

In Technology in Education: Looking Towards 2020 Raymond Nickerson comments on one author's remark lament of the passing in our age of even the potential for the Renaissance Man. The author claimed that the cruel truth is that it is impossible for one individual to gain competence across a wide area of domains. Nickerson responded:

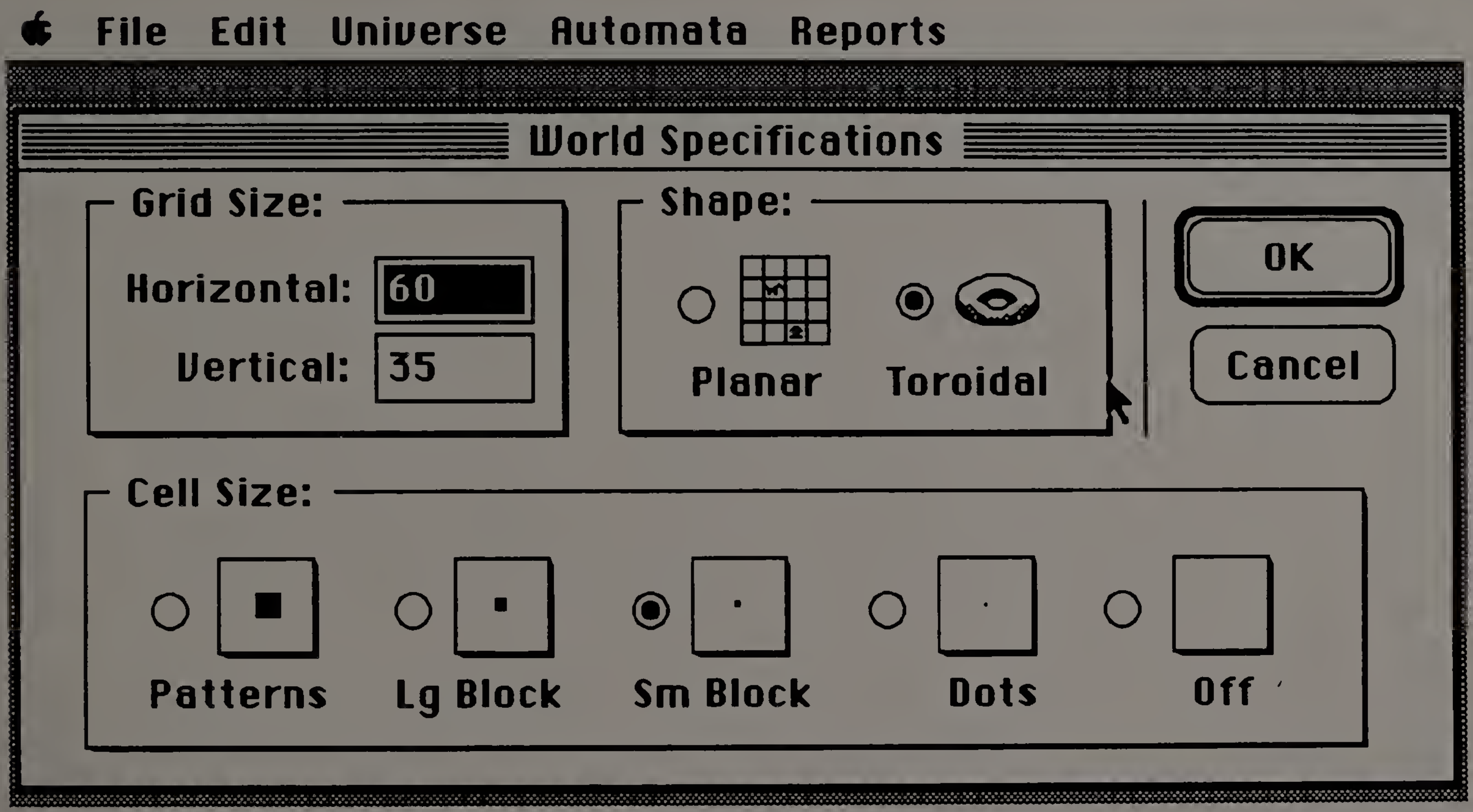
> "The cruelty may reside more in the limitations of our educational know-how and techniques than in the limitations of our minds. .... Our current primary means of knowledge acquisition - reading coupled with library access - is excruciatingly slow. We really do not know what we are capable of learning and cannot rule out the possibility that, with much more powerful

> techniques of storing, accessing, and representing information, for assessing what people know, and for combining instruction and exploration in mutually reinforcing ways, that capability might be very much greater than our experience to date would lead us to believe. Given the proper teaching and learning methods, might not individuals be able to acquire deep knowledge (at least by today's standards) in several areas? In the absence of compelling evidence to the contrary, I would argue that this assumption should motivate our efforts to exploit technology for educational benefit. It will be more important in the future than in the past, in my view for a significant fraction of the population to be well informed in a variety of domains both technical and nontechnical. The challenge to educational researcher is to develop the methods that will make this possible and it is not clear that this is a futile quest." (Nickerson, 1983)

I firmly believe that Dr. Nickerson's statements must be taken very seriously if educators are to make real changes in our schools. We must design curricula that respect the minds and capabilities of our students for what they really are and can become, and provide students with educational environments that permit them to develop the skills and talents that will be needed to approach properly and solve the problems that will face them as citizens in the coming century. The design of TETK is an attempt to apply this vision to the problem of instruction in the fundamental theories of life science for all secondary students.

Screens and Interface of *The Evolutionary Tool Kit*

The opening screen of TETK , "World Specifications", is shown in Figure 3.4. From this screen the student selects the type of world the automata will inhabit. Choices include planar, toroidal, and spherical (not yet implemented). Size of the grid is also selected. The size of the world is limited only by RAM. It may be advantageous to select a small grid, limiting populations, for some effects to appear more easily. The size of the representation is also selected. Several megabytes are needed even for relatively small simulations, as each organism has its own code, and some reporting functions keep track of all organisms that have lived and died during the simulation, a running paleontological record. Computational speed is roughly proportional to the number of automata present. Some analyses are very computation intensive and can take a great deal of time to complete.



Grid Size:
Horizontal: 60
Vertical: 35

Shape:
○ Planar
● Toroidal

Cell Size:
○ Patterns
○ Lg Block
● Sm Block
○ Dots
○ Off

Figure 3.4 World Specification Screen

Only two dimensional worlds are considered in TETK. The commercial program SimAnt by Maxis is unique in that the ant automata occupy a three dimensional space. Although the space modeled in SimAnt is limited to a small section of a suburban backyard, the visual and psychological effect of the dimensional modeling while playing the game is remarkable. With additional computational resources it may be worth attempting to extend TETK models to three dimensions to permit examination of trophic effects.

Layered worlds offer many possibilities but present heavy demands on the hardware platform. SimEarth does simulate layers of automata. It is possible for more than one automata to occupy a cell in SimEarth. The atmospheric, hydrologic, geologic, and tectonic 'layers' are sets of status registers which hold information at the bit level about conditions at each cell, such as climate, temperature, continental drift, atmospherics, etc. TETK holds information about the automata in parallel arrays. Besides the parallel arrays for the automata, TETK does provide a second layer, a set of status registers holding information about the substrate. These entries encode information about the local substrate and accumulations of metabolic byproducts. In future models the byproducts will be subject to diffusion processes. In the current version this array is used in a crude way. There is only one element of the substrate, very loosely labeled 'energy' on which the herbivores feed. Future versions, incorporating genes for metabolic reactions like those in Paul Deal's BIOSIM can be very useful pedagogic tools. There should be other elements of the substrate as in Deal's model.

The following sections attempt to describe the user interface for TETK. This is not an easy thing to do in words. Much of the interface based on mouse motions and placement of graphic icons in various parts of the screen. Described in words, it may seem unnecessarily complicated. The ease of its use will hopefully be made more clear after the discussion of some of the mechanisms of inheritance properties of the traits and some simple demonstrative examples.

Figure 3.5 The TRAIT PALLET

The core of <u>TETK</u>, and one of its major innovative features, is the TRAIT PALLET shown in Figure 3.5. The first of the eight boxes holds information about what kind of genetic system the organism is using. The next seven boxes represent the genome of the organism. In the current version there are only seven possible traits for each organism. The user 'creates' individuals or species at the phenotypic level. The 'TRAIT PALLET' is the set of boxes containing various icons that appears below the organism's 'Genetic System' and its 'Traits'. The icons that represent the organism's traits are selected from the trait pallet that can be viewed by clicking on any unfilled element of the seven possible traits.

The trait icons are divided into two sections, 'Genetic System' and 'Traits'. The user must first select the genetic system under which the automata he or she is creating will reproduce and pass on genetic information. This choice will determine the pattern of inheritance for that individual or group of individuals that the user is creating.

The first column of the trait pallet shows the four icons of the four different options for 'Genetic System' currently available in TETK. One of these first column icons must be in the first box for the user to make any further selections from the trait pallet. To assign a genetic system to an organism the user simply clicks on the open box in 'Genetic System' and then slides down to the system they wish to choose. That box will then appear in inverse, indicating that it has been selected. The user then drops that icon in the box representing genetic system. Likewise the user chooses other traits for the individual or group of individuals being created by just clicking on them and dropping them into the empty trait boxes.

The current version supports four 'Genetic Systems': ASEXUAL, SEXUAL , PAINT POT (mixing of characteristics), and GAME THEORETIC. These icons are in the first column of the pallet. The icons are respectively: 'a cell splitting', 'male female symbols', 'paint buckets mixing', and 'a pair of dice'.

The trait choices available for the organism's traits are in the boxes on the right side of the pallet. The traits depicted in the right side of the pallet are, in row order: AGE, HUNGER, MOVE, HUNT, HIDE, (row 2) FLEE, MALE TAG, FEMALE TAG, VISION TWINS, (row 3) BRANCHED TREE, AXIAL TREE, male FROG CALL, female FROG EAR, (row 4) butterfly WINGS, predator MEMORY, and STRATEGY. Each of these will be described in greater detail later. They are intended as demonstrations of investigations possible with a modeling structure provided by TETK.

Some of the traits will function only with specific genetic systems. For example, the STRATEGY trait is intended to model the Iterated Prisoner's Dilemma. It will function only with the GAME THEORY genetic system. If any other system is chosen (by being dropped in the first box), the STRATEGY icon becomes greyed, and cannot be placed in the trait description of an organism. In a parallel fashion, the MALE TAG and FEMALE TAG traits make sense only within a sexually reproducing population. If systems other than SEXUAL are chosen, these traits become greyed and cannot be placed among the organism's traits.

The mechanisms by which each of these traits affects the behavior of the organism and how they can be used by a student to investigate evolution and population genetics will be discussed in this chapter in a condensed format, their use in investigations or lab exercises will be discussed in chapter four, the draft of a teacher's manual for The Evolutionary Tool Kit.

A special note should be made on the use of concepts from genetics in this simulation. As stated previously it is not intended as a genetics primer. The interactions at the genetic level are hinted at. Students can even 'zoom' in on the analogs of chromosomes, the C-somes to see strings of 1's and 0's suggestively spiraling in helices. They cannot change or even interpret what is on these 'holders of information'. They cannot 'read' the information. This is very much like the position of Darwin himself and the first three generations of evolutionary biologists. One only needs a source of variation and a bit of knowledge about sexual and asexual inheritance. As Ernst Mayr states,

> "On the whole Darwin treated genetic variation as a 'black box'. As a naturalist and reader of the animal breeding literature, he knew that variation was always present and this is all he had to know. He was also convinced that the supply of variation was renewed in every generation and this was always abundantly available as raw material for natural selection. In other words, a correct theory of genetics was not a prerequisite for the theory of natural selection (Mayr, 1991)."

There is much pedagogical import in this paragraph. Darwin's position is not unlike the position of many students entering our secondary or post-secondary classrooms. They know very little about genetics. This should not stop them from learning the basic ideas of evolution by natural selection. With support from other software specifically designed to teach topics in modern genetics, the students themselves could come up with the arguments that built the evolutionary synthesis of the 1930's and 1940's.

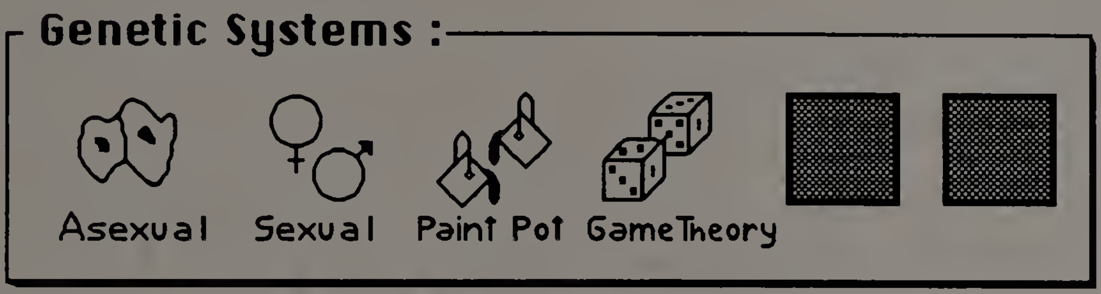


Figure 3.6 Genetic Systems

The ASEXUAL genetic system models the simplest mechanism of inheritance, that of cell splitting, or fission. Except for random mutations, mechanisms for which are described later, the genetic information of the parent organism reproducing asexually is identical to that of the daughter cells. The same genetic information is passed along, expressing the same traits as the parent. The transmission of traits is explicitly Weismannian.

The current version of TETK will not support the other mechanisms of inheritance employed by one cell creatures as outlined by Lynn Margulis (Margulis, 1986). The goal is to model for introduce students the simplest forms of inheritance and investigate their dynamic relationships entailed by this form of reproduction.

TETK also does not model symbiosis. The genes chosen for modeling do not make much sense within a context where a symbiotic event may occur and increase the symbiont's fitness with respect to either of the previous organisms. With the inclusion of metabolic properties, such as the five oxidative reactions and five reducing reactions described in Paul Deal's BioSim, modeling symbiotic events makes much more sense. It is possible to model such events a new genetic system would have to be added, ASEX-SYM. In this system, cells would divide and share information as standard asexual organisms, except at random times (set as a percent by the user) an adjacent organism, or a predator, would attempt to consume a neighbor as food, but the 'prey' would not be dissolved. It would share some of its genetic information with the predator.

The SEXUAL genetic system (its icon is the male and female symbols), demands two parents. Selection of this genetic system will cause half of the individuals of that species, both when populations are initialized, and at any reproductive event, to be male and the other half female. Each organisms holds a marker determining if it is male or female. The marker does not change during the organism's lifetime. Hermaphroditic organisms are not explicitly modeled. As genetic information is passed on only through the female line in this reproductive system, its effect can be modeled with the fission system. Organisms will breed only with other organisms of the same species. The genetic system is peculiar to each species. It is possible to have sexually reproducing organisms and asexual organisms competing for the same resources.

When sexual organisms breed, the offspring is randomly assigned a sex. In the current version, mating in a sexual population is assumed to be panmictic. All members of the population are assumed to be candidates for mating. Admittedly this is a rather unrealistic approximation to sexual breeding in general. Only sea urchins, oysters, clams, a few other aquatic invertebrates approximate this type of mating. In future versions females will be able to select mates from a region (specified by the user) around their current location. Because individuals can move, the amount of computer resources spent in creating look-up tables of potential mates is much too great. This option was omitted from the first version of <u>TETK</u>. This version also assumes a male/female sex ratio of 1:1 ; future versions will permit experimentation with skewed ratios.

All traits in <u>TETK</u> are naturally modeled by expression of genes with serial multiple allele systems. In the current version all traits sort independently. Each of these species can have several allelic forms giving each trait different expressions. In the case of the sexual species, the properties are potentially shared through the population. It is not possible to have subspecies of the same species of automata with different genetic systems. How all of this is modeled will be clearer when several sample populations of organism are constructed later in the text.

The PAINT POT genetic system, its icon is a pair of paint buckets mixing, is really not a genetic system at all viewed by modern biological standards. It is used as a pedagogic device intended to represent the common sense view of inheritance that dominated humanity's thinking for millennia. Some say it still does, through the 'naive' world views students both bring and carry away from their biology classes. It once was considered a viable explanation of inheritance, hence a scientific explanation in its day.

Paint pot inheritance is non-particulate and non-Mendelian; it is not unlike several of the unsuccessful inheritance mechanisms proposed by Darwin. Like the sexual case, individuals and offspring are assigned a sex. The traits of the offspring are simply the average of the traits of the parents. For example, if one parent has a 20% chance of fleeing, and the other parent is a non-fleeing individual, the offspring will have a 10% chance of fleeing. The question to be explored with Paint Pot genetics is: "Can there be any passing on of an advantageous trait at all, even if the trait is very advantageous?"

There is another, more sophisticated, use of the paint pot or blending system in evolutionary argumentation suggested by one of the reviewers, Dr. Wickender. Traits such as those represented in TETK are really expressed by gene complexes, phenotypically one would observe what amounts to a continuous variation, though the underlying system is particulate. This suggestion can be taken up in the modeling of mimicry in butterflies.

The GAME THEORY system is not really a natural biological system either by modern biological standards. Its icon is a pair of dice. It is used to model processes that are fundamentally stochastic, where populations compete and the fitness can be immediately reduced by computation to a single number. This fitness determines the representation of that individual's genes in the next population. All organisms die after each cycle. If the fitness of the individual, as measured by the computation falls in the lower quartile, that individual produces no progeny. Its space is taken up be descendants of other individuals with higher 'scores'. The genome of each offspring is a copy of its parent, except for those species which can mutate. The mutation rates are set by the user at the start of the simulation when they are building each automata. Consequently, in time, forms with favorable characteristics (achieving higher fitness measures) should be represented more frequently in the population.

GAME THEORY use is limited to a few specific traits from the pallet, such as STRATEGY, the tree growth simulation, and the frog call simulation. The game theory genetic system does not permit organisms to move. Depending on the trait chosen, a specific computational process defines a numerical value for the 'fitness' of the organism. There is no predation. The classic example is the STRATEGY gene which models the 'Prisoner's Dilemma'. If the results of the strategy chosen the individual is in the bottom quarter compared to ranking of the results of all other individuals, that individual is eliminated. Likewise, in the frog call simulation a fitness function measures 'attractiveness', and in the tree simulation the fitness function measures a combination of light gathering ability, structural strength, and reproductive potential.

The discussion has so far been rather abstract and a bit scattered. More understanding can be brought to this discussion by outlining, step by step, how the user would build an individual, a population, or a species. The 'New Automata' screen is the method by which a user creates or modifies organisms. The 'New Automata' screen is accessed by pulling down the 'Automata' menu.

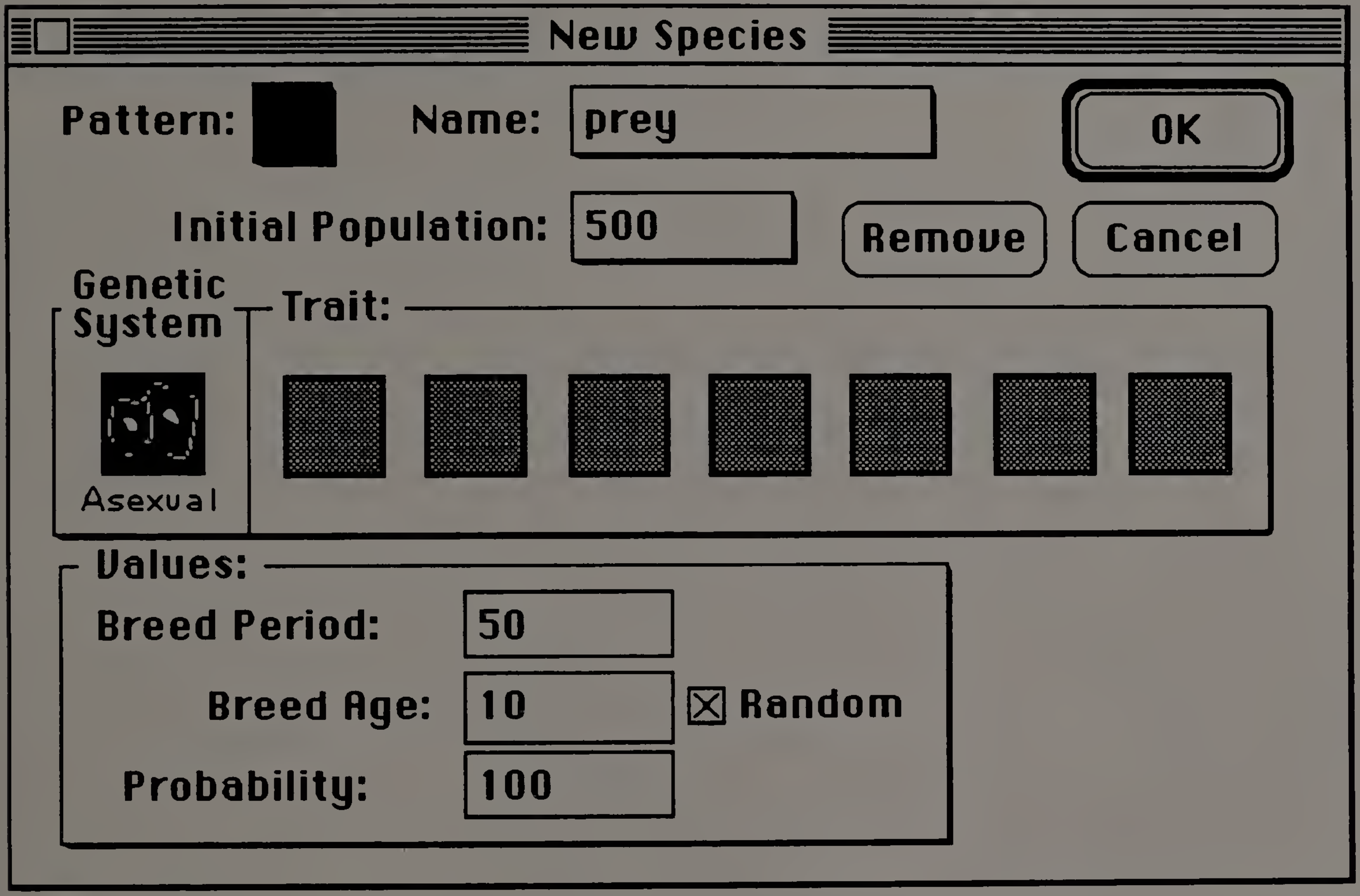
Figure 3.7 shows the first screen of the 'Automata' menu, 'New Automata' screen. It should be noted that considerable planning must be done before the user constructs organisms under the 'New Automata' screen. The following screens and discussion will show how a user can set up a simple predator/prey system using four simple traits, AGE, HUNGER, MOVE, and HUNT. The automata being designed here was given the SEXUAL genetic system by the user. The user simply clicked on the icon for fission from the trait pallet and dropped it in the first box. The trait pallet window then closed. The SEXUAL icon appeared in the

GENETIC SYETEM box, and the SEXUAL icon remaining on the trait pallet became greyed. It cannot be duplicated in the traits of that organism; it may be used for other automata, however. The sexual genetic system will govern the process of inheritance for all traits in individuals of this species of automata.

Once any icon has been placed in a trait list it becomes greyed in the trait pallet and cannot be duplicated in that organism's trait list by any further selection. A gene can be 'Cut' from the trait list by using the standard Macintosh 'Cut' function from the main menu.

Clicking on the ASEXUAL icon while it is in the GENETIC SYSTEM box, will open a special 'Values' window beneath the icon. The term 'values' is not truly appropriate for living systems, it is borrowed from models of artificial life. Another term, analogous to the function will be chosen in the next version, perhaps 'trait form' may be appropriate. This window is shown in Figure 3.7. The 'Values' window gives the user the opportunity to change some conditions or constraints on the reproductive processes of the organism.

Most traits have 'Values' windows that permit the user to modify their effects on the organism. In the 'Values' box for the ASEXUAL system, the user must specify "Breed Period"; "Breed Age"; and "Probability". The Breeding Period is a variable that determines the number of cycles that must elapse between breeding of the organism. If the value is set at 1, then the organism will breed on each turn, provided that it is able. Setting the Breed Period to 2, and selecting 'Random' will effectively divide the population into two different breeding groups, one that will breed on odd cycles, the other on even ones. The 'random' option means that when the population is initialized random breeding periods will be assigned. It is possible to make all individuals breed in the same cycle, with the other cycle/s used a food gathering periods, by using the non-random distribution property. The Breeding Probability is just what it says, it is the probability that the organism will successfully breed if it has the opportunity. If an organism breeds it divides its energy with its daughter cell (or male/female offspring if sexual reproduction is selected). There is no energy penalty if the organism does not breed.



New Species

Pattern: ■ Name: prey

Initial Population: 500

Genetic System: Asexual

Breed Period: 50

Breed Age: 10 ☒ Random

Probability: 100

Figure 3.7 Sample NEW AUTOMATA SCREEN

The possibility of multiple births is considered in the discussion of the TWINS trait, later in this text. Similar variables effecting breed periods and probabilities are set for the sexual and paint pot genetic systems. The game theoretic genetic system is treated as a special case, as it is fundamentally a statistical modeling process.

In Figure 3.7, the user named the species "prey", gave it an initial population of 500. The pattern that represents the organism on the world grid (as a black square) was also set. The 16 different alternative patterns for organisms. These are displayed by clicking on the 'Pattern' button. Moving the mouse and clicking on any of these patterns selects that one and assigns it to the organism. On a color monitor the patterns have different colors. Different cross hatchings are used on monochrome monitors.

Most importantly it is the 'Pattern' of the organism that determines whether one organism can breed with another. Patterns effectively define species of organisms in TETK. Organisms of the same pattern are considered to be part of the same gene pool, eligible for potential mating, if this is possible under constraints of the experiment, or the type of genetic system chosen. It was stated previously that it is natural for organisms in TETK to have genes with multiple alleles. It is through this menu that populations with varieties of traits and 'values' for these traits is constructed. One can set up the analog of multiple allelic forms expressing 'values' of a single trait of one species by choosing the 'New Automaton' menu repeatedly, retaining the same pattern, but choosing different values for the traits.

The current version assumes serial dominance with smaller values recessive to larger values. Future versions will permit users to change this order. The user can create true analogs of populations with variations in this manner. Up to eight different automata species (patterns) are permitted in this version of the program.

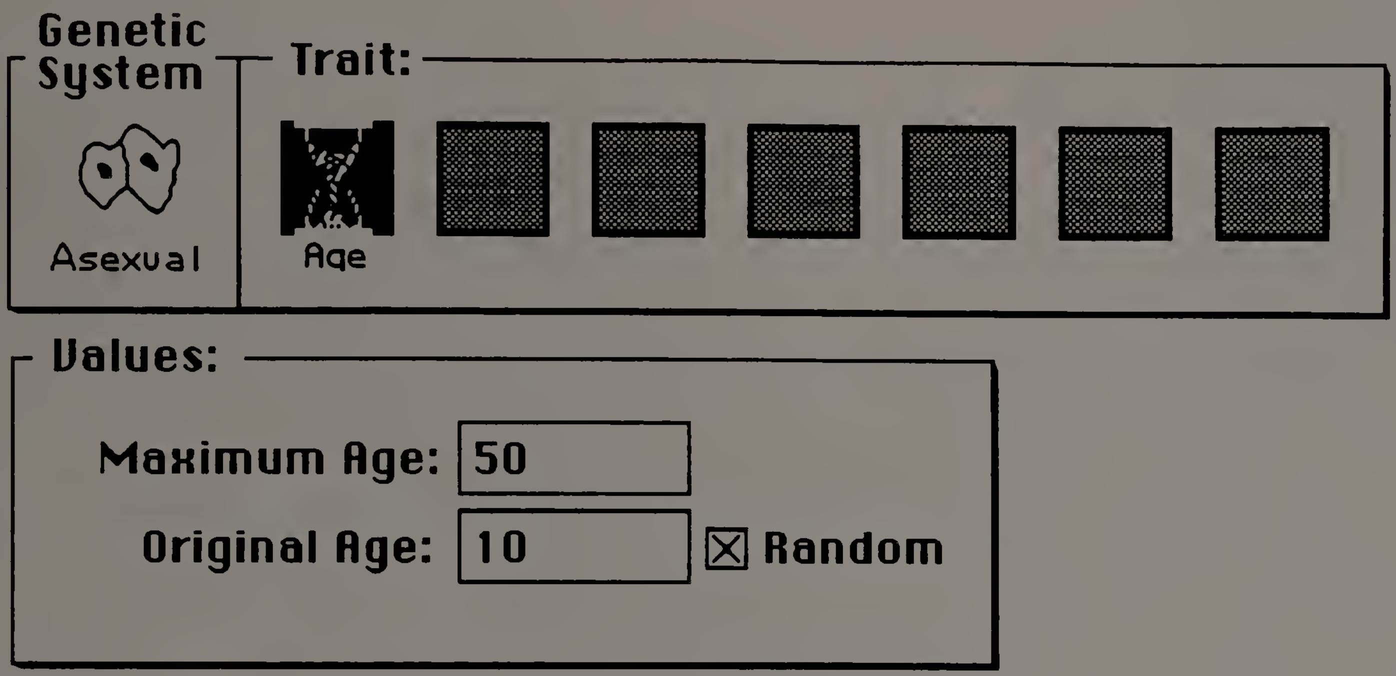
The user also sets the initial population of the automata in the run of the simulation. Here 500 individuals was selected. At the start of the run 500 individuals with that identical genotype will be randomly seeded on the world grid. Alternatively the user could have created five groups of 100 individuals (the population total still at 500) with breeding ages of 8, 9, 10, 11, and 12, respectively. The user could also have created 10 groups of 50 with breeding ages of 6, 7, 8, 9, 10, 11, 12, 13, 14, respectively. As an example of the power of this menu, it is also possible to create two populations (each with a different pattern, of course), with one defined typologically and the other defined as a population with variation, as with the last two examples. These populations can be put in competition with each other for the same resources provided by the substrate. All have the same average breeding age? Will any out compete the other? Why? It is possible to set just one individual with a different value for a trait, and see if that trait can propagate through the population. This discussion gives a glimpse of some of the conjectures and investigations that students can make. "What is the value of variation in a population?" "Are there processes that will limit natural variation?"

The SEXUAL genetic system could also have been selected. Selection of SEXUAL inheritance system changes the appearance of many of the submenus on other traits such as HIDE, FLEE, BAD TASTE, or VISION. If sexual inheritance is selected, an additional box will appear in the 'Values' menu below and to the right of variables used for the selected trait. This box will permit the user to determine, with buttons, whether the trait is to be inherited in a 'dominant' or 'recessive' pattern. The trait will be passed on to progeny in a Mendelian fashion according to ratios for these two cases. When the population is initialized genotypes will be assigned to the organisms randomly.

In the current version either 'Dominant' or 'Recessive' must be chosen. It is possible to extend the choices, but I am unsure of the pedagogic value, especially for the intended audience. The program is not intended to teach genetics. A second problem arises when considering the first simple extension. A seemingly natural extension would be to add 'Codominant'. Because both the traits and the genotypes are both digitally coded, the only way to express codominance would be to postulate an intermediate phenotype which expresses the 'average' of the parental alleles. This is misleading. Codominance is not averaging; both alleles are expressed not averaged. I have omitted this genetic interaction in the model. The interactions between the organisms through their phenotypes on the world grid would make interpreting results of more complex inheritance patterns exceedingly difficult.

It is possible to do simple investigations centered on the Hardy-Weinberg principle. Generally the model itself violates two of the Hardy-Weinberg conditions; there is mutation and natural selection. It is possible to turn the mutation generator off. Also the effects of natural selection can be removed by selecting traits like 'COLOR' (used with butterfly wings) that are selectively neutral, if not used in combination with 'BAD TASTE'. Mitchel Resnick at the Learning Laboratory at MIT reported a Logo model on a work station using multiple turtles which demonstrated a pattern that the researchers later found to be the Hardy-Weinberg equilibrium (Resnick, & Silverman, 1991). Using TETK there is no reason that beginning secondary students can't 'discover' this law themselves as well.

Pedagogically more important, I feel, is the program's ability to model the propagation of an advantageous or disadvantageous trait, or more basically, to inquire what is an advantageous trait and how would be passed on in a sexual or asexual population. Particulate inheritance will eventually fix such a trait in the population. The student can then see why mutation is so important as the engine that drives natural selection.

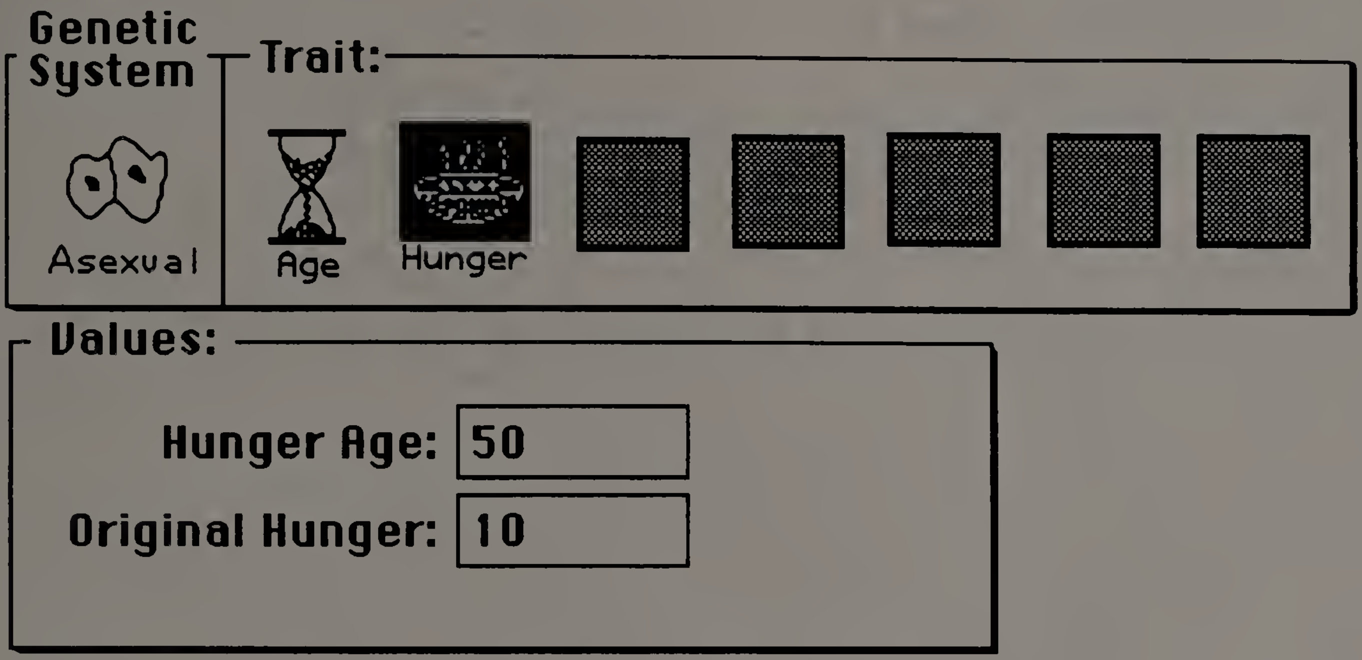


Maximum Age: 50
Original Age: 10
☒ Random

Figure 3.8 The AGE TRAIT

Continuing the explanation of constructing an organism from the trait pallet, Figure 3.8 shows the same asexual system with the AGE trait selected as the first trait. The AGE icon is now highlighted. Two variables must be set to initialize the population, 'Maximum Age', and 'Original Age'. The 'Maximum Age' is the age at which the organism will die. In the current version of the program, this is an absolute limit. The organism dies when it reaches the maximum age, and half of its 'energy' is added to the substrate at that location. The 'Original Age 'refers to the initial population. If 'Random' is selected, the ages of the initial population will be randomly selected from values between 'Original Age' and 'Maximum Age'. If 'Random' is not selected, all individuals will have the same age, the value of 'Original Age'. In this example, in which there are 500 prey organisms, the population will consist of individuals with randomly chosen ages from 10 to 50. Some experiments will require populations that age, reproduce, and die as a group. Such cases can be modeled by not selecting the 'Random' option.

Several very interesting inquiries into the evolutionary biology of aging are outlined after this introduction to modeling with The Evolutionary Tool Kit.



Hunger Age: 50

Original Hunger: 10

Figure 3.9 The HUNGER trait

Figure 3.9 shows the selection of the HUNGER trait. Its icon is a bowl of soup. This property determines whether the organism has eaten recently, and how the status of its nourishment determines its health. Each time the organism eats, the hunger trait is decremented by a quantity determined by the user in the ENVIRONMENT menu in the world set up. If the automata is a carnivore (this is indicated by another trait not yet discussed), this is the food value of one of its prey. Automata that are not carnivores obtain food from the substrate at a rate determined by the user.

The amount of food available in each individual cell is determined by the substrate matrix. This matrix holds values of four nutrients for each cell in the world grid; values are integers. The current version uses only one nutrient, the analog of an algae that everywhere pervades the world grid and feeds the herbivores. After each round the food supply in the cells is replenished by an amount set in the environment section, as poor, average, rich. In future versions it will be possible to set regions to have rich substrates, and other regions with substrates that are poor in nutrients. When an organism dies, a two thirds of the 'hunger' value of that organisms is added to the food level at the cell it occupies to represent the amount of nourishment returned to the substrate.

The interaction of the environment with the hunger trait is one of the weakest areas of the model. As stated previously there should be more than one substrate to feed organisms. There also should be a mechanism to isolate or restrict entry or egress from certain regions to permit inbreeding, or encourage an analog of allopatric speciation. With the current panmictic mating mechanism for sexually reproducing organisms none of these additions makes much sense. These points should be addressed in a future version.

The value of the hunger trait is also affected each time the organism gives birth since it must share the nourishment it has obtained with the daughter cells. The value of the hunger trait is also decremented each time the organism moves. The value of the hunger trait is the analogue of energy of the organism. The variable "Hunger Age" represents the value at which death from starvation would occur. "Original Hunger" is the setting of the hunger value for organisms at the start of the simulation. In future versions the behavior of carnivores will be affected by status of the hunger trait. "Eat only when hungry." should be an option.

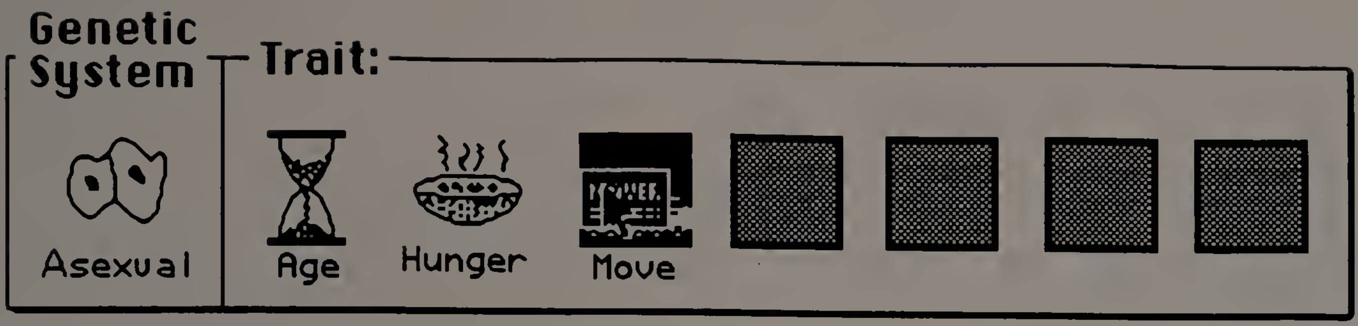
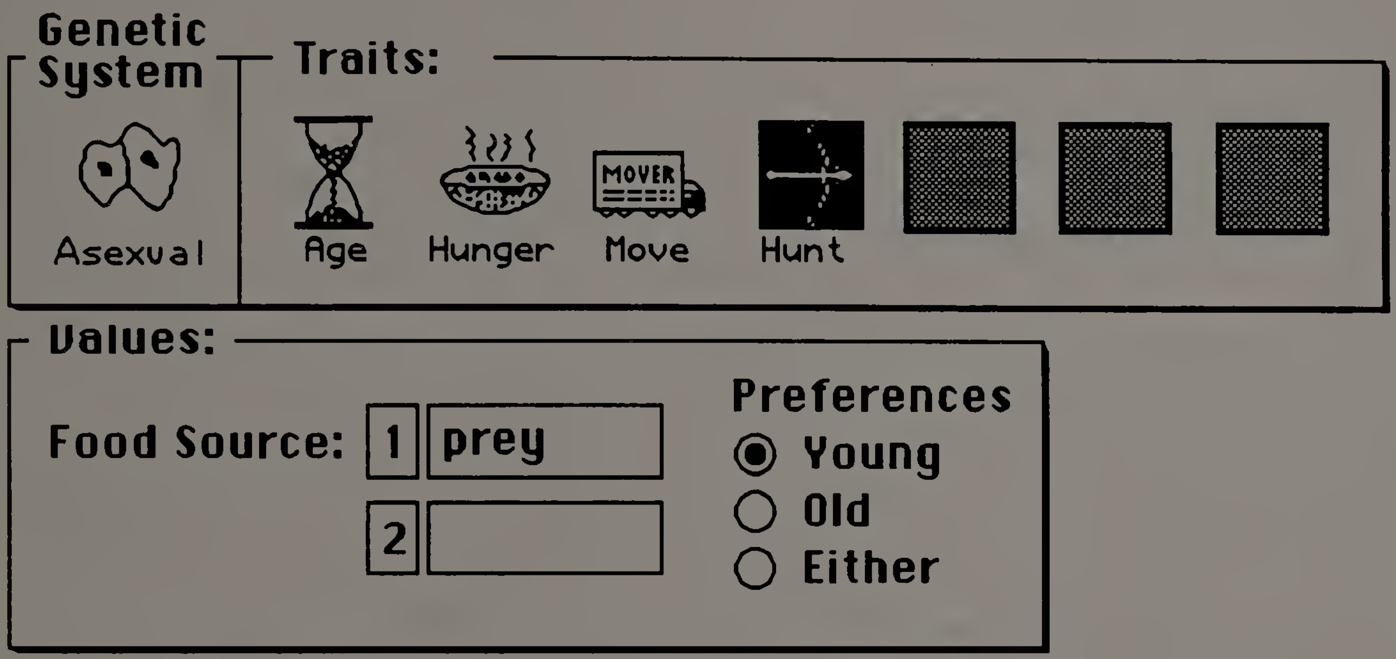


Figure 3.10 The MOVE trait

Organisms can move about the grid if they have the MOVE trait. Figure 3.9 shows the MOVE trait and its icon, a moving van. If the organism has the MOVE trait, it can move one square each cycle. Automata models of predator-prey cycles can be unstable. To partially alleviate this problem, the MOVE algorithm incorporates a 10% random function that permits herbivores, if there is a predator species, to move from three to five squares in any direction to land on an empty square. This additional possibility functions much like the 'refugium' in MacArthur modeling. Cellular automata predators have a tendency to form 'predation rings' that encircle prey and cause population crashes.

The MOVE trait is influenced by three other traits, the HIDE, VISION, and FLEE traits. These are described more fully below. There are no additional variables with the MOVE trait. Additional functions are handled through auxiliary traits like HIDE, VISION, and FLEE. A herbivore with only the MOVE trait performs a random walk on the screen. If a carnivore possesses the MOVE trait does give the organism a 'sensor' in the sense that it will prefer to move onto an adjacent square that contains a prey organism, rather than onto an empty square.

The traits and modeling strategies possible with The Evolutionary Tool Kit are very versatile. There may be investigations in which one does not want a carnivore to move about. If one wishes to study the effects of predation without introducing the often chaotic swings of Lotka-Volterra cycles, one can set up populations of non-moving carnivores with long lives and breeding ages just one year shorter. They will breed just once, replacing only themselves, keeping the number of carnivores constant. The hunting pattern of the carnivore can be set to be larger than simply the adjacent squares. This will simulate the behavior of a territorial hunter.



Food Source: 1 prey
2

Preferences
● Young
○ Old
○ Either

Figure 3.11 Trait list of a predator

The trait list of a simple predator is shown in Figure 3.11 above. The icon for predatory behavior (HUNT) is a bow and arrow. The user can specify which, of two species of automata, is the prey for this predator. Predation of a species on other members of the same species is permitted. In the current version of TETK, a predator can have only two species of prey. It is possible to have one predator prey on another, however. The user can also select a preference for the predator that depends on the age of the prey. Setting the preference makes the preferred prey 50% more likely to be taken than other organisms that do not share the preference attribute.

Normally the predator can eat a prey only by occupying a square adjacent to the prey, and on its turn to move, moving onto the square occupied by the prey organism. It is possible to change the hunting pattern of a predator to include a larger search area. The predator automata predates in a rather methodical way; it makes a list of adjacent squares that contain prey. If there are none it moves randomly. If there is a prey in its search area it makes a list of all such prey. The list is weighted according to any preferences set, and a random selection is made of which prey will be taken.

When a predator eats, an fixed amount of energy is decremented from the organism's hunger value. The order of preference of a predator, in the current version, is eat a prey, move, stay still (if no other move is available). Future versions of TETK will incorporate a trait for predation that eats only when hungry, an altruistic hunter. Is such a trait advantageous to the individual, to the population as a whole? If predators prefer older prey, natural selection predicts that individual prey that produce earlier in life and have multiple offspring will be favored. Students can make hypotheses about this relationship and try this out with organisms in TETK.

With the descriptions of traits so far it is possible to give a quick outline of some sample conjectures and investigations students can make with TETK. Given the simple trait lists as set out in Figure 3.10 for the prey and Figure 3.11 for the predator, it is possible for the user to pose many questions about evolutionary fitness and inheritance through time. A simple conjecture would be: "Is the ability to live longer advantageous to an organism?" The user would design a micro-world in which two asexual species of prey, each one with different preset life spans. Both would be preyed upon by a single predator. One run of the simulation would most likely be inconclusive. A whole class should pool their data. Runs will show that half of the time the short lived prey dominates, the other half it is the longer lived one. This should lead to a lively discussion about the meaning of 'advantageous' in an evolutionary context. This is a very useful and enlightening activity on the meaning of 'advantageous'. Do we mean 'advantageous' to the individual organism, to the group of organisms commonly bearing this trait, or advantageous to the propagation of the trait itself? Students themselves can become sources for arguments very much like those in Richard Dawkin's Selfish Gene. Questions are raised about natural selection and what it is actually operating on.

Are there other variables that can be changed so that long life is advantageous? The variables of 'Breeding Age' or 'Breeding Period' are possibilities. The user could also change the "Environment" section so that there are long periods of stress, or periods of abundance. Importantly, the "answers" to the experimental runs come as probabilities. TETK introduces students to probabilistic reasoning in a concrete natural setting. What is the meaning of the fact that equal numbers of the runs in the previous experiment ended up with long lived or short lived organisms winning? If breeding periods are changed, the results will be skewed, with perhaps 6 out of 10 times having the long lived organisms dominate (if they had a slightly shorter breeding period).

A whole series of experiments is suggested by the delightful article "On the Nature of Aging" by Steven Austad (Austad, 1992). Austad coins a term, "the one-hoss shay" mutation, after Oliver Wendell Holmes' poetic carriage that "was built in such a marvelous way,/ It ran a hundred years to a day." The AGE trait in Tool Kit organisms functions much like the design of this famous vehicle. Once the organism reaches the fixed age set in its AGE trait, it dies. Natural selection will act powerfully against 'one-hoss shay' genes that effect organisms in their youth. Austad claims that the power of natural selection wanes as organisms grow older. One-hoss shay mutations are not selected heavily against if they only affect older organisms. Experiments with TETK support this conclusion. Austad then applies this logic to give a possible explanation for the evolution of aging (Austad, 1992). "Since most new mutations are harmful and since mutations with effects late in life tend not to be weeded out, late-acting harmful mutations can accumulate over time. They are virtually immune to elimination by natural selection, which may be why certain diseases, like cancer, occur predominantly in old age."

In the above example, the student played the role of the Creator, designing organisms with various properties, and setting them in a world to compete against one another. There are obvious pedagogical advantages to this approach, especially for introductory lessons in the evolutionary process. The word 'design' has connotations of planing, of purpose. During the experiments, many unexpected and even counter-intuitive results emerge. The student's 'designs' often don't work. These unexpected results form the grounding of the insight, indeed Charles Darwin's insight, that what we view as design could possibly be the work of another process, one whose operation is random, but whose product can be finely tuned.

It is possible within the mechanisms of TETK to set up automatic mutations for specific traits to test conjectures in this fascinating area. If a more advanced student selects the mutation option from a special submenu on the 'Values' box, a random mutation will occur at each birth, effecting the value or values of the particular traits of the daughter cell. The mutation rate can be set as 2%, 5%, or 10%. These values represent the probability that the value of the 'Maximum Age' variable (in the case of the AGE trait) will increase, or decrease by one unit. The user could set up a micro-world where the genes expressing AGE trait are permitted to mutate in order to find out if there is a 'Maximum Age' that will dominate, or whether there will be an evolutionary pressure toward longer lives, or shorter ones, or perhaps neither. Is there an optimal age for a predator, or a prey to begin breeding? On what other variables may this depend?

The discussion of the genes controlling the age traits of the organism is particularly rich in raising novel questions and opening up many different avenues of inquiry well suited to a multi-media educational tool. I wish to extend the discussion of the modeling of aging to demonstrate the educational potential of investigations made possible by a combination of automata modeling and multi-media access. It is most important to note that the modeling permitted by TETK is not conceived as a substitute for experiment or inquiry into the beauty and wealth of complexity of the natural world. It is at best a schematic representation of natural events; but it is a representation in a form that can have great pedagogic impact for many students for whom many of these ideas remain inaccessible in the format we currently instruct.

I envision a program similar to TETK embedded in a CD-ROM format which can give students access to a host of other information, textual, audio, and visual. In such an investigation the students could search a database on the CD for information on thousands of animals with their habitats, maximum life spans, reproductive rates, and metabolic rates. By selecting groups of animals and plotting metabolic rate times age vs. age (clearly other plots could be attempted), students could discover for themselves the almost linear graph for mammals (excluding marsupials and monotremes). This plot historically gave rise to the "rate of living" theory of aging at the turn of the century. Theory was proposed by German biologist Max Rubner in 1908, and extended by American Raymond Pearl. It basically says small animals are, in some fashion, biochemically living more rapidly than larger ones. This follows directly from a constant slope of a (metabolic rate) x (life span) vs. (life span) graph. Rubner calculated that each mammal species expends approximately the same amount of energy per gram during its life time. A popularization states that all animals have the same number of heartbeats allotted; some use the supply up faster than others.

The modern version of this idea associates the accumulation of imperfect metabolic byproducts, defective proteins, and collision damaged molecules with the general deterioration we call aging. Austed asks whether this makes sense. Inclusion of other families such as marsupials, monotremes, and birds alters the data considerably. Birds and bats are relatively long lived creatures, even with their high metabolisms. Many marsupials live short lives with metabolic rates of only 70% to 80% of that of mammals. The linear relation is not linear at all. It may not reveal any fundamental connection. The explanation for the origin of aging lay, according to evolutionary biologists, in inquiries into the inheritance of "one-hoss shay" genes that effect young and old differentially. This process can be easily modeled with <u>TETK</u> as described above. Similar experiments can be performed on values of the HUNGER trait.

A thorough exploration of the meaning of the word 'advantageous' is most important for any student of evolutionary theory. <u>TETK</u> provides three traits designed to assist students in this exploration. These are illustrated in Figure 3.12.

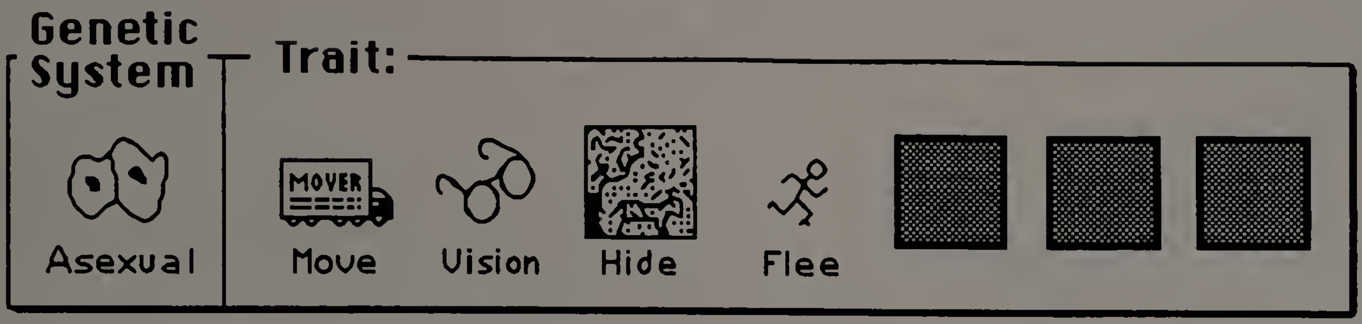


Figure 3.12 VISION, HIDE, and FLEE traits.

Three of the traits shown in Figure 3.12, VISION, HIDE, and FLEE, affect the function of the MOVE traits. The VISION trait is used only in predatory organisms. It permits the organism to 'look' two squares beyond its own position for the presence of prey organisms. An organism with the VISION trait will move in the direction that has the most prey. If there is no prey visible, the predator moves randomly.

The HIDE trait is possessed only by prey. If an organism has the HIDE trait it has 50% chance of escaping a predator. This is accomplished by modifying the predator's list of available meals. If a predator is nearby and hunting, any organism that has the HIDE trait has a 50% chance of not appearing on the predator's available to eat list.

The FLEE trait is also possessed only by prey. Possessors of the FLEE trait can move more than one square, if they sense a predator in an adjacent square. It really is two sequential executions of the MOVE algorithm. As the move algorithm is really a random walk for a herbivore, it is possible that the prey can move right back to the square from which it started. If this is modeling a squirrel crossing a road, perhaps the algorithm is rather accurate.

A probability is set by the user for the exercise of the FLEE trait. Setting the value at 25% means that one quarter of the time a prey will flee when approached by a predator. The direction in which it moves is random. If there are no empty squares in which to move, the prey will move only one square. There is an energy penalty for the extra movement. Naturally the energy cost to the fleeing prey is double that of a single square move.

The VISION, HIDE, and FLEE traits are used to explore the effects of mutations on predator/prey dynamics, as well as to observe how advantageous traits, or disadvantageous ones will propagate, or fail to do so, through populations. A user would presumably set up a predator/prey micro-world in which the predatory species has two allelic forms, one with the VISION trait, the other without it.

Sexual organisms have an additional variable associated with all traits. The pattern of inheritance of the trait can be set as 'dominant' or 'recessive'. Patterns must also be supplied for values expressing breeding such as percent of fertility, breed age, and breed period. The 'dominance' or 'recessiveness' will be interpreted by cellular automata's "reproductive machinery" in either of two manners. For mating with an organism of the same species with a trait to one without the genes that express that trait, the pattern will be as if the partner had an allele that did not express that trait. If there are multiple alleles for any trait, they will be interpreted as simple series dominance based on the value of the trait expressed by the allele. Higher numbers are dominant over lower ones. This, admittedly, is very primitive. In future versions the user will be able to select different patterns for the allele series such as 'lower values for dominance' or 'random assignment' in the series for dominance. In the latter case, as new alleles are generated, through mutation, or user intervention, they will be assigned a random position in the series.

For a sexual organism, the user would set initial populations of each form, and also determine if the trait is passed on in a dominant or recessive pattern. The VISION trait should be advantageous, permitting the predator to stalk its prey much better than its blind brethren. The sexual genetic system is particulate. One could set up a population with two alleles for such a trait. One allele with no vision, another with a limited amount. If no mutation is selected, these would be the only alleles in the gene pool for that trait. As noted in chapter one, the student will note a counter-intuitive result: the advantageous dominant trait will propagate through the population, but never reach 100%. A recessive advantageous trait will propagate slowly, but it will reach 100%. Similar experiments can be performed with the HIDE and FLEE traits.

In the case of asexual inheritance the process is one of competitive exclusion. If one trait is indeed more fit than another, individuals of that line will eventually overcome the descendents of other lines. Paint Pot inheritance proves an interesting pedagogic illustration. Even if given a very advantageous trait, such as the HIDE trait, there will be little or no change in the gene pool of the population. The effect washes out; unless there is continuous re-introduction of the same mutation. The idea of "tall father, short mother, average height kids" will not permit any evolutionary development. It is the particulate nature of Mendelian inheritance that preserves diversity.

<u>TETK</u> also includes some specialized traits used only in the sexual genetic system, the sex tag markers shown in Figure 3.13. Their icons are tags with the symbol for either male or female. They are not really 'traits',

rather they are markers placed on the component of the trait that determines sex. The markers can be read by the user and tallied for various reports. These tags are useful in studies of genetic drift or investigations of the analog of inheritance of mitochondrial DNA. When any of the tag traits are selected, the user must specify a numeric value to be set for each tag. For example a user can set up an initial population of 200 individuals, half of whom are male. Each of the 100 males could have an individual tag, each with a unique identifying number, 1 to 100. After 100 generations of breeding, the experimenter could make a report on the number and values of the tags on the remaining males. A similar experiment could be performed on the female tags. Daughter cells of tagged female organisms will have tag numbers identical to that of their female parent.

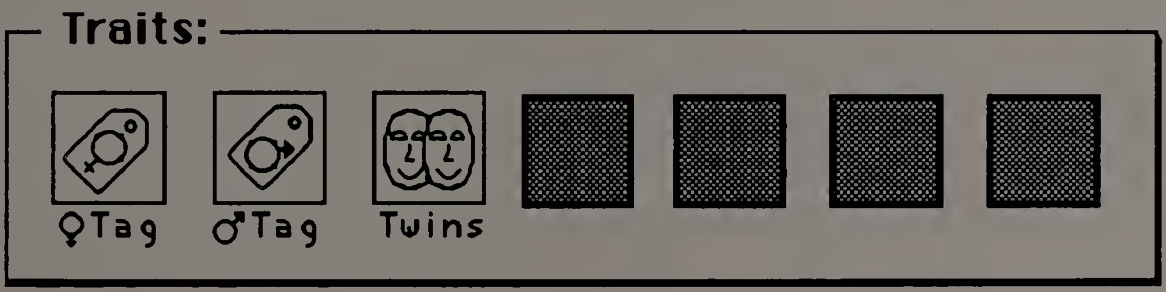


Figure 3.13 The TAG and TWINS traits

There are some counter-intuitive results even in such a simple reproductive patterns as inheritance of male or female genetic material. The least expected is the result that in an sexual reproductive scheme, eventually all individuals are descended from one individual. Which individual of the initial population, is not predicted by the theory. It is true that one of the originals is necessarily the progenitor of the whole population. The lines of all the other organisms will die out.

An analogy of this phenomenon can be found with inheritance of surnames through the male side according to English and Continental customs. As surnames are inherited through the male line, a surnames die out if there is a generation of only female progeny, as well as a generation with no progeny at all. This effect has been observed many times in isolated human populations. The descendants of the mutineers at Pitcairn are all surnamed Christian, from Fletcher Christian, the famous first mate of the *Bounty*. The 20 odd other names from the original crewmen died out in the century and a half of occupation on the island. Surnames on several Scottish and Irish remote isles also showed similar lack of variety in surnames before population shifts and ease of transit disturbed the patterns in the 19th century (Dewdney, 1988). The conclusion is that all males from Pitcairn have the same Y chromosome as Fletcher Christian, plus whatever mutations have occurred along the way.

A planned addition to the TAG genes for the next version of TETK is a 'genetic error'. Associated with the TAG genes will be a string of 1's and 0's that would be subject to mutation. The string would start out at all zero's. Any 1's would be introduced by mutations. The fertility of the organism would depend on the sum of the 1's and 0's in that string. The string would be used as a reservoir of 'defects', permitting the students to do their own investigations of Müller's ratchet and genetic drift. Students could easily model the genetic effects of population bottlenecks and their effect on fertility as seen in animals like the African cheetah (O'Brien, Wildt, & Bush, 1986; O'Brien, et al., 1987). It seems counter intuitive, but genetic defects, even those that can severely affect reproduction, do accumulate.

Two recent articles, usable as sources of explorations with TETK with secondary students show the extent of the problem. Craig Parker describes the difficulties faces by a group of lions that recently moved into the Ngorongoro Crater National Park in Tanzania (Parker, 1992). The 100 square mile Ngorongoro Crater Park occupies the floor of an extinct volcano. Its walls are sufficiently high to serve as a barrier to most immigration. A plague of flies in 1962 wiped out almost all of the lions in the park. There was one resident male remaining. Seven male lions entered the park in the mid 1960's. These were from three coalitions, probably siblings. These males deterred all other males attempting to enter the park since 1969, five generations of lions ago. Less competitive prides died out quickly. Only six prides remain. Measurements indicate that these lions have only half the genetic diverstity of Serengiti. Their level of sperm abnormality was twice that of the lion population outside the crater walls; all of this in five generations.

A study of the Florida panther reported by Jon Luoma paints a bleaker picture (Luoma, 1992). The Florida panther is a subspecies of the cougar that formerly roamed over Florida, Georgia, and Alabama. There are approximately 30 to 50 of the creatures left, mostly in the Big Cypress Reserve (1985 figures). In the early 1980's approximately 15% of the male cats had a genetic defect that gave them only one testicle. Now 70% have the trait. Sperm counts are dismal. Over 90% of the sperm are abnormal with serious defects like dual heads, thickened heads, or missing or cork-screw tails. Heart valve defects have begun showing up in kittens.

TETK can model this process rather easily. Figure 3.14, a diagram adapted from Maynard-Smith, Evolutionary Genetics, illustrates the concept. Starting with four male individuals, the entire gene pool eventually is occupied by descendants of organism A. On the next run of an automata simulation, it may be organism B whose descendents dominate the population. Probabilities of dominating the population will be equal assuming equal "fitness" of the four initial types. An analogous phenomenon occurs with asexual inheritance as well.

If the population is sufficiently small, after sufficiently long runs, all organisms carry the same number on their male tags. An extension can be made to human inheritance. If the planet survives long enough (and male surname inheritance prevails), all earth's inhabitants will probably be either Smiths or Changs, or perhaps Patels.

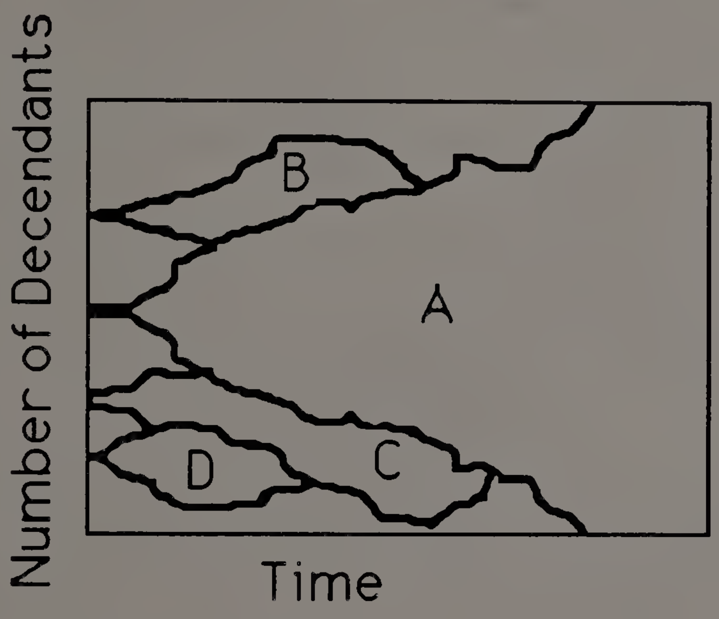


Figure 3.14 Surname Inheritance

There is an analogous phenomenon in the female line as well. This is the recent discovery of mitochondrial DNA which is passed only through the female line. Sperm have no mitochondria. The mitochondrial DNA in all modern humans is remarkably similar, so much so as to show that all humans are descended from the same woman. When the pattern and frequency of mutations of this DNA is overlaid on a map, the area showing the least isolation and inbreeding is Central Africa. This strongly points to an African origin of the species, an African 'Eve'. Explorations with TETK can show that, rather than providing support for the stories of *Genesis*, the phenomenon is at least partly statistical in nature. The African origin may be real; which woman was the real 'Eve' was not determined by which of them was first made from a rib, but by a genetic lottery.

The TWINS trait effects reproduction in sexual, asexual, and paint pot systems. If an organism has the TWINS trait, it has the potential to have two daughter cells upon fission or mating. This potential is set by the user in the form of a percentage. A TWINS variable of 50% means that half of the births for that organism will be double. The energy of the non-twinning parent is initially divided equally among the parent and the offspring. For organisms with the TWINS trait, it is possible to change the division of energy leaving fixed fractions for the parent. An interesting question is, "Is the TWINS trait advantageous?" The TWINS trait is very useful in investigating the effect of any changes on the 'Breeding Age' variable and its relation to predation.

Figure 3.15 Other traits available

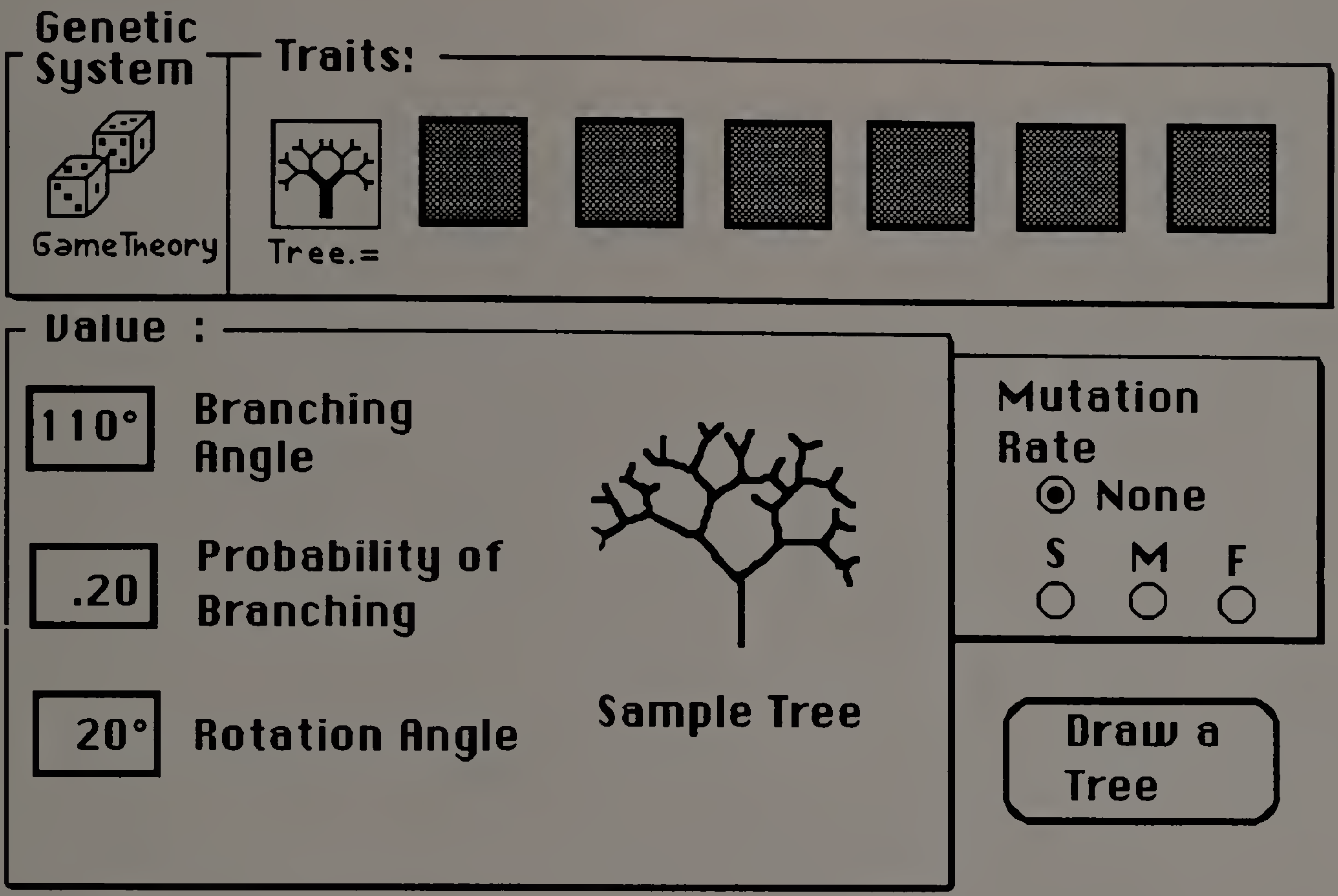
The experiments, instructional methods and traits discussed so far are similar to many text based approaches to the same material in that they predominantly address logico-mathematical, intrapersonal, interpersonal, and linguistic intelligences as defined in Gardner's model. Figure 3.15 gives eight other traits available for experimentation. These traits employ innovative pedagogical methods that address individuals who learn or approach the world through Spatial, Musical, and Physiokinetic intelligences. Some of the traits must be used in combination. Some function only with certain genetic systems.

The two tree growth traits model the growth of plants much like the work of Niklas described in chapter two. The simulation is intended to model the adaptations made by primitive land plants in the Silurian and Devonian, like *cooksonia*, in any attempt to take advantage of the new resources the land provided. Andrew Scott in a recent article in the Journal of Biological Education gives a careful examination of the problems faces by early vascular plants (Scott, 1984). The simulations permited by TETK give students an opportunity to explore this important but very often overlooked chapter of evolutionary history.

The word 'tree' is used very loosely in this context, as in the gaming, a time frame of many millenia is assumed. The early productions may not look like trees, but later ones bear considerable resemblance, as Nicklas remarks, to the odd fern palms and cycads of the great coal forming forests.

In the pilot version these tree routines are non-functional. They are very computation intensive. Models based on these traits are intended to appeal to the spatial and physiokinetic intelligences. The following description is rather mathematical, the mathematics involved in drawing the tree and computing its 'fitness' based on structural analysis, light gathering ability, and reproductive potential are invisible to the student. The actual interface used by the student is very graphic rather than. The

TREE.= and TREE.AXIS traits very generally model the two major forms of plant growth, sympodial and monopodial.



110° Branching Angle

.20 Probability of Branching

20° Rotation Angle

Mutation Rate
● None
S ○ M ○ F ○

Figure 3.16 Sample Sympodial Plant

Figure 3.16 shows a sample screen for a sympodial plant. To investigate the pattern of tree growth and how physical constraints effect the evolution of plant structure, students would select a type of plant growth. The sympodial growth rule was selected for the sample. In the values window the student sets the three parameters for that model and can "try out" the effect of these parameters on some plants. Importantly, the growth is in three dimensions; only a two dimensional representation is shown on the screen. In the current version, the user cannot rotate the tree around its axis to see what it looks like. Also, only lines are used to represent the branches; volume of the branches is not represented.

When the user has found some pleasing parameters, he or she could take the 'creation' to the micro-world of the Tool Kit and let it compete against other designs made by other students, or designs made randomly by the computer. The computer made trees undergo mutations at fixed rates. The student designed trees would, in this case, be competing against an opponent that is always changing. As the simulation proceeds, graphs of the population of different species of tree in the forest would show which species of tree is winning. If the student designed tree begins to lose, the student could halt the simulation and make changes in his or her design. The student needs to mutate the variables that determine the shape of his or her species of tree to keep pace with the adaptations of the computer generated one. The student and his or her 'tree' become the Alice in the race with the Red Queen. Judging what is wrong with a design is not at all easy. Very often it is a sense of balance or stability that is not easily quantifiable, but can be assessed from a drawing of a tree formed under the given parameters.

The TREE.= trait used in the sample models sympodial branching plants, like most bushes, some cactus, elms, or cauliflower. At each branch the plant divides symmetrically with the angle between the branches set by a variable within the trait. The TREE.AXIS trait models monopodial plants with axial symmetry, like conifers. For a tree growing with the TREE.AXIS trait, at each division one branch is designated as the central one, the trunk. It is the one closest to the normal to the plane. There are two different branching angles, one for the main trunk, the other for the branch. Sympodial plants have only one branching angle, all branches have equal angles from the parent branch. For a monopodial plant, the smallest branching angle is closest to the main trunk of the tree.

Both growth patterns have a 'Rotation Angle' variable. This variable determines the number of degrees the growing tip is rotated clockwise before setting off new shoots.

The 'Probability of Branching' variable determines the probability that the growing tip will branch after growing out a unit distance. Because the probability applies to each growing tip separately, the structure of sympodial trees, even with evenly divided branching angles, is not symmetric. The model also follows another convention used by Niklas. Another variable, dependent on the level of the branch, and the probability of branching, determines if the branch segment is terminal or not.

The representation of the tree in the first version is very primitive; lines represent branches. For purposes of computation of fitness of the structure, the branches do have volume. As each tree grows, the branches decrease in diameter. The cross sectional area of the branch is divided among the new branches by two different rules; one for sympodial growth, another for monpodial growth. If the plant is sympodial, the new branches have diameters equal to the parent branch divided by the root of two. This operation preserves the volume of the plant as it lengthens. This division gives the tree constant volume by level as it grows. If the tree is monopodial, the radii of the branches are unequally divided. The axial branch receives two thirds of the cross sectional area of the parent branch.

The user sets three variables for TREE.= : Probability of Branching, Branching Angle, and Angle of Rotation. Figure 3.15 shows how these variables are set up in the 'Values' box. For the TREE.AXIS trait, two Branching Angles are needed: Trunk angle, and Branch Angle. Both are measured from the previous branch axis. The user also sets the maximal angle of the sun to the plane. In a future version, students will be able to control the force of gravity. They could experiment to see what trees would look like on the Klingon planet with twice earth's gravity.

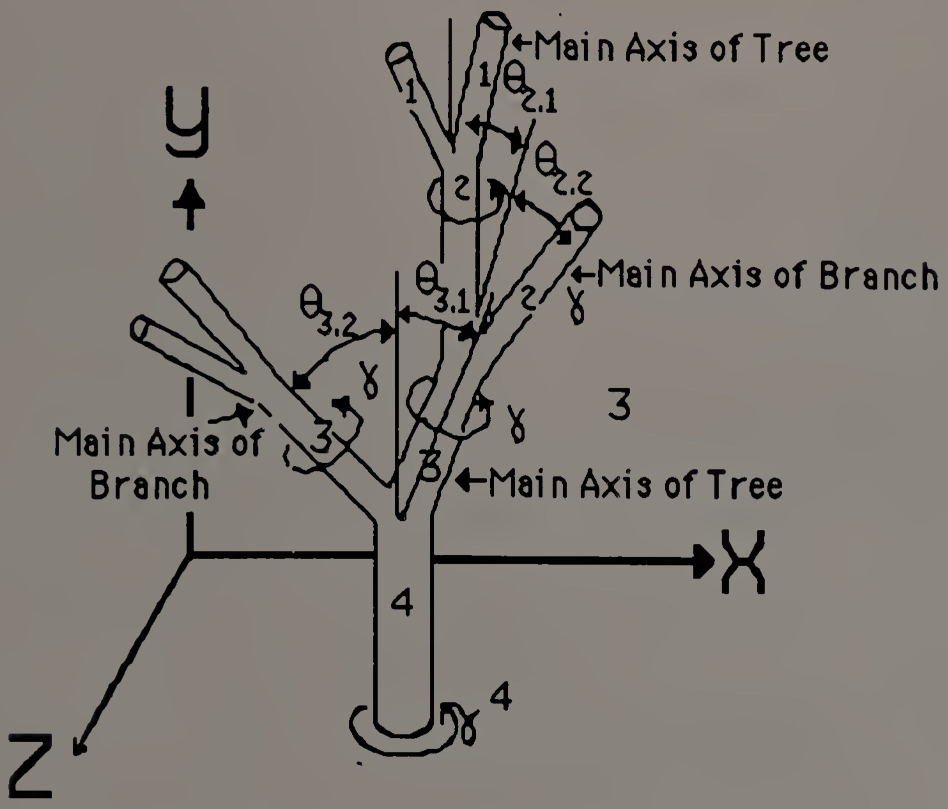


Figure 3.17 Monopodial plant growth

Figure 3.17 will clarify the geometry and notation for monopodial growth. A four level tree is show. Theta is the branching angle. Theta 3.1 is the smaller angle closer to the trunk in the branching at level three. It is approximately 20 degrees. Theta 3.2 is the larger angle, about 30 degrees. Students can experiment with drawing trees using these angles in an experimental mode before continuing with any investigations involving competition among species and any differences in relative fitness of the structures. Please note that the branch on the left side does not continue to the small branches at level one, as does the structure on the right. The left side of the tree stopped growing after level two as the termination probability for that branch determined that it could not continue.

The tree modeling traits must be used with the Game Theory genetic system. These traits do not function with a toroidal world. The fitness function determined by these traits is used by the game theory system to determine ratios of offspring for the succeeding generations. Fitness in the tree simulations is determined by the sum of the rank order according to three analyses. These analyses are based on those done by Niklas. First the computer calculates the ratio of the surface area exposed to the sun, divided by the total surface area. This calculation is done, in this simulation, under the assumption that the plant is growing near the equator. The machine calculates the ratio for morning (45 degrees insolation), noon (vertical insolation) and afternoon. The three are averaged. Plants are rank ordered. Second, the machine calculates the cumulative first moment of all branches as a measure of the integrity of the branching pattern. Plants are rank ordered. Third, the machine calculates the sum of the heights off the ground of the branch tips. It is assumed that the tips would bear flowers and hence higher placement would give better seed distribution and more aggressive shading of neighbors. Again plants are rank ordered. The ranks are added for each plant, and a cumulative rank order is made. The lowest quarter do not reproduce.

The modeling of trees is computationally intensive. To avoid bringing the simulation to a grinding halt while thousands of trig functions are calculated, several short cuts are employed. First, the arguments of the trigonometric functions are evaluated in increments of 2 degrees only. This means that 12.5 degrees will have the same trigonometric values as 13.9 degrees. With this short cut, trigonometric calculations can be reduced to a look up table for these values. Second, though thousands of trees could be shown on the world grid, the trees at each cell are not modeled for every cell in the grid. To reduce the burden of computation a square of one hundred trees is used as a sample. Trees are 'grown' in cells in that strip and and the rest of the grid is randomly filled from populations of that sample populations.

As described above fitness is determined. Some are eliminated. Randomly, one quarter of the remaining trees are selected for the spots held by these 'unfit' trees. Mutations, if they are permitted, occur only at breeding. The mutation rate is set by buttons shown in Figure 3.16. The mutation rate can be set at 'Slow' (2%), 'Average' (5%), 'Fast' (10%). The computer will randomly mutate any of the growth parameters when creating a new generation for species it controls. The mutation rate determines the chance that any one parameter will undergo change. A 'Slow' mutation rate means that each parameter has a 2% chance of going up or down between one and five units. The unit of the variables measured in degrees is 1°. The unit of probability is 1%. The current version will model only two species of trees competing.

A special feature of the game theory system is the control over mutations by the computer, or by the user. This control is set up at the start of an experiment. If a species is put under control of the computer, the machine will mutate the values of the parameters of the tree in a random fashion. Any change in the growth parameters for species controlled by the user will be done by the user by altering the species' trait list through the AUTOMATA screen.

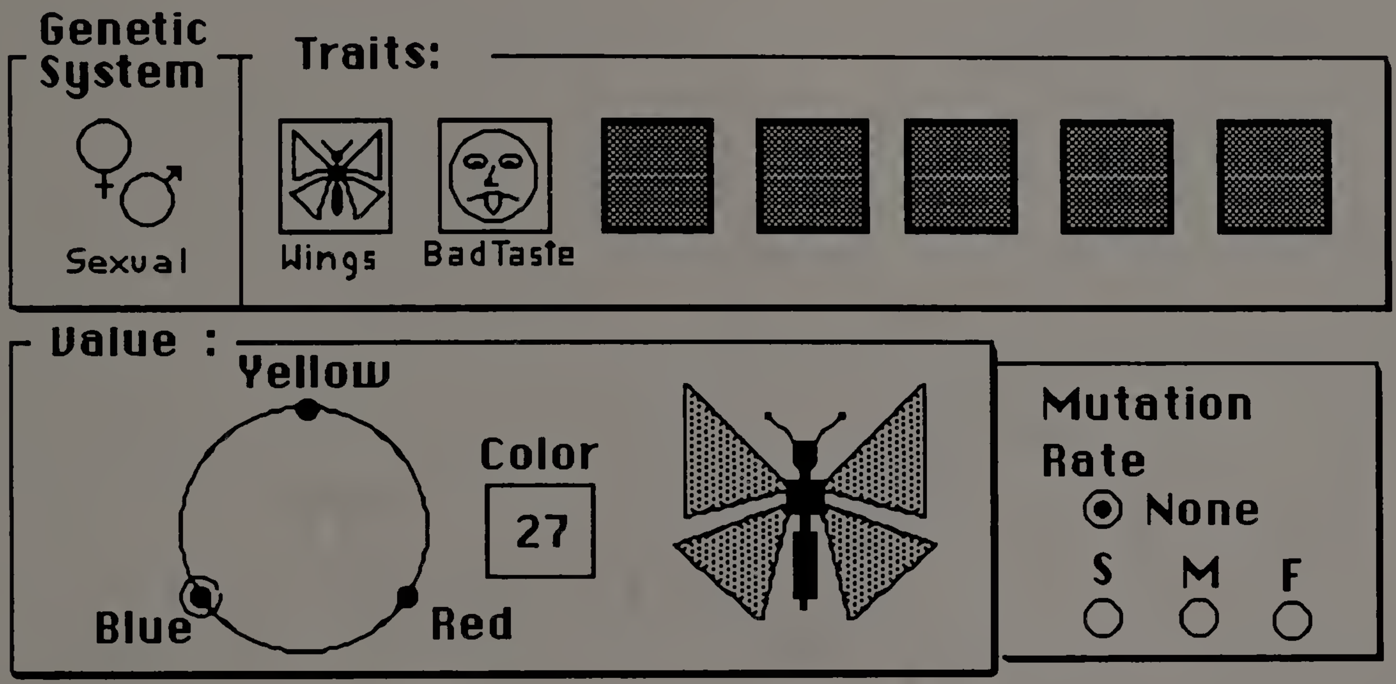
If one species is under control of the computer, and the other is controlled by the user, the effect of this structure is to put the user in competition with the computer running a genetic algorithm that determines the fitness of the trees. It is an evolutionary 'war game', as

Niklas remarks (Niklas, 1986). It is also possible to have the computer simulate two species of trees in competition for resources. The simulation can be stopped after any cycle and the shapes of the trees of either species examined.

On a spherical world (not yet implemented) the angle of insolation is dependent on the latitude of the cell. Snow loading can also be added. Cells on the equator will have the sun overhead most of the time, with little snow loading. Cells in the mid to upper latitudes will have increasingly acute insolation with increasing snow loading. The sample computational population on a spherical world will have to be larger so that it can be grouped in latitudinal strips. This structure will model competitive exclusion based on responses to light gathering ability and morphological constraints. Most tropical trees are sympodial, to gather the maximum light with little stress from weather factors. Temperate and north latitude trees are generally conifers which have monopodial growth patterns. Their morphology is a response to the mechanical stress of heavy winter snows.

The MEMORY, WINGS, and BAD TASTE are all associated with the butterfly simulation. These are functional in the pilot version. This simulation is intended to appeal to students whose dominant intelligence is spatial; it is also very appealing aesthetically. The butterfly simulation models the evolution of Müllerian and Batesian mimicry among tropical butterflies.

Figure 3.18 shows the windows associated with the butterfly trait, WINGS. This simulation works only with sexual inheritance. In this simulation the WINGS trait is given to all prey. In the setup windows of the WINGS trait the user determines the color of the wing for each species of organism. It can be any of 128 different colors. It is also interpreted as cyclic (both 127 and 2 are the same 'distance' from 0). The circle is a color wheel; on a color monitor it appears as a circular rainbow. The color is determined by placing a circle tool on any part of the color wheel. The corresponding number of that color appears in the color box. Here a primary blue was chosen; it is number 27. The butterfly appears in the same color as that chosen by the user.



Color 27

Mutation Rate
● None
S ○ M ○ F ○

Figure 3.18 Choosing a Butterfly Color

The color of the wing may be subject to mutation, if the mutation button is activated. With the mutation option selected, the number specifying the color of the wing can change with each generation. The rates are the same as in the tree growth option option: 'Slow' (2%), 'Average' (5%), 'Fast' (10%). The number specifying the color can increase or decrease.

A feature not yet incorporated into TETK is an examine pointer that will let the user examine how any organism 'looks' by just pointing at it on the world grid. The examine pointer will not interrupt the game simulation.

The BAD TASTE trait (its icon is a grimacing face) is given only to prey. It can be set as either 'Recessive' or 'Dominant'. The BAD TASTE trait in a prey alters the method by which a predator prepares its potential meals list from organisms adjacent to it. If an organism has the BAD taste trait it has a chance at being rejected as a meal by a predator with a memory of a meal that tasted bad with a color similar to that of the prey.

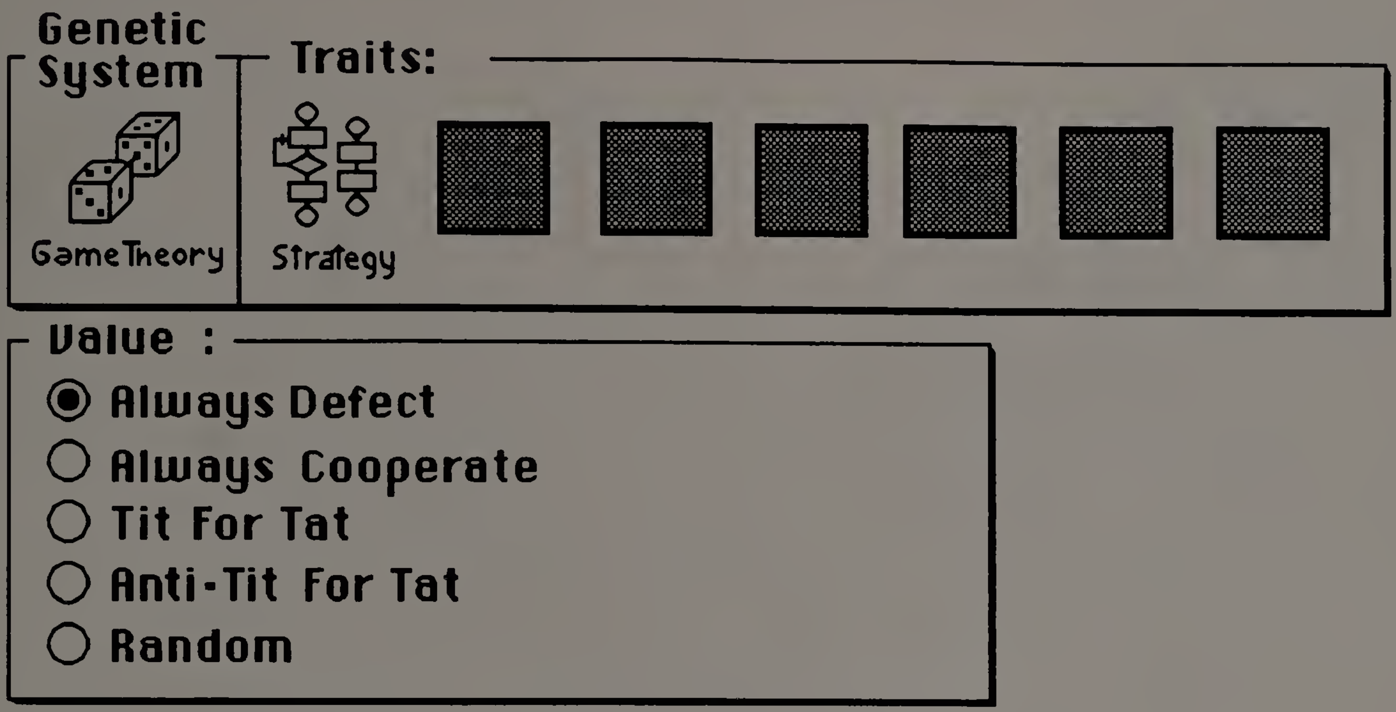
The MEMORY trait is given only to a predator. Its icon is the head of an elephant. In the current version it is functional only as part of the butterfly simulation. All predators in the butterfly simulation should have the MEMORY trait. A predator with the MEMORY trait remembers the color of its last five distasteful meals. If the meal was distasteful, it has a special mark in its memory. After each new meal the predator forgets the oldest one. The selection rule used by the predator is simple: the closer a color is to any of the distasteful memories, the better the chances the prey can escape being eaten.

If the predator encounters a potential meal, it checks its memory for marks of distasteful memories associated with that color. The code governing the predator's selection process is quantizes as follows. If the color number exactly matches, the prey has a 50% chance of being taken off the potential meals list. Distasteful butterflies are not free from predation, they just have a higher chance of escaping. For every five units difference from a 'distasteful' color, the chance of the prey escaping the potential meal list decreases by 10%. Roughly this means "the closer the color of a butterfly is to a distasteful meal, the greater the chance of escaping."

The structure of the WINGS, BAD TASTE, and MEMORY traits permit TETK to model Müllerian and Batesian mimicry in tropical butterflies. Both Müllerian and Batesian mimicry are dependent on predators having memories of which meals tasted bad. In Müllerian mimicry several unpalatable butterflies share similar color patterns (aposematic colors). These Müllerian rings, as tropical ecologists call them, are named after the nineteenth century German naturalist Fritz Müller. Müller reasoned that if distasteful butterflies shared common patterns, the young, inexperienced birds would kill many fewer butterflies before learning which ones to avoid, than if each species had different markings. A detailed method of setting up a model of the evolution of Müllerian mimicry is described in chapter four.

Named after nineteenth century British naturalist, Henry Bates, Batesian mimics are palatable butterflies that take advantage of the avoidance predators show for some patterns. These mimics share wing patterns with unpalatable species. To experiment with Batesian mimicry the user would design a species of distasteful butterfly with a color on one side of the color pallet. A tasty species that can mutate would be placed on the other part of the color wheel not too far from the color of the distasteful butterfly. It helps to speed the simulation up if the tasty species breeds frequently. The unpalatable organisms are non-mutating. After a few hundred generations both the palatable and unpalatable organisms will share the same color. Natural selection will favor tasty butterflies that have similar colors to the distasteful one.

A similar experiment with two unpalatable species, one mutating, the other not, will demonstrate the evolution of the analogue of Müllerian mimicry in cellular automata. There will be an evolutionary pressure on the mutating species to have the same color as the fixed color species.



Value :
● Always Defect
○ Always Cooperate
○ Tit For Tat
○ Anti-Tit For Tat
○ Random

Figure 3.19 Prisoner's Dilemma Strategies

The STRATEGY trait, whose icon is a flow chart, can only be used with the game theoretic genetic system. It models relative fitness of behavior in the form of the Prisoner's Dilemma. Figure 3.19 shows the menu of the STRATEGY trait. This should be the only trait in the trait list for modeling this simulation. Only strategies with one unit memory are modeled. In this version also only pure strategies are permitted. One cannot play 'Tit for Tat' 50% of the time and 'Always Defect' for the rest. Future versions of TETK will include the option of employing mixed strategies.

Under the GAME THEORY system for this trait, every organism plays every other one 100 times. All squares must be occupied. A user would set up a world with two or more species, each playing only one strategy. Population is held constant. The pay-off matrix is set as in

Axelrod's simulation discussed in chapter two (both cooperate = 3, both defect =1, cooperate/defect = (0,5), and defect/cooperate = (5,0)). Only single memory strategies and pure strategies are modeled in the first version of TETK.

Fitness of the strategies is determined by a statistical process. After each round scores for each strategy are summed and averaged for each strategy (species), as well as for the population as a whole. Individuals whose scores fell in the bottom quarter are killed off. The remaining individuals are permitted to duplicate with a probability of .25 in order to fill the squares vacated by the poor performers. A graph displays the average score for all individuals, as well as average scores of the species. There are several questions that a student can explore. "Which is the best strategy for an individual to play?" "Can one strategy displace another through the whole population?" "Which strategy is stable against challenges from others?" The counter-intuitive result is, only "Tit for Tat".

The FROG CALL and FROG EAR traits are used only with the game theory system. These model the effects of female selection analogous to that shown in the work of Michael Ryan on the tungara frog (Ryan, 1990). This simulation is designed to appeal to individuals for whom Gardner's musical intelligence is dominant. It models female selection as with a basis in sensory bias. In this simulation female frogs are given a sensory bias in the form of sensitivity to two bands of frequency, and a predisposition for certain modulations of sound, such as trills, beats, pulses, or throbs. The frog call for this species consists of four notes that is repeated three times. The male frogs make sounds to attract the females. Males that make the sounds that are most attractive to the females are those chosen for breeding. The cycle repeats with the least attractive songs (to the ears of the female frogs) eventually dying out.

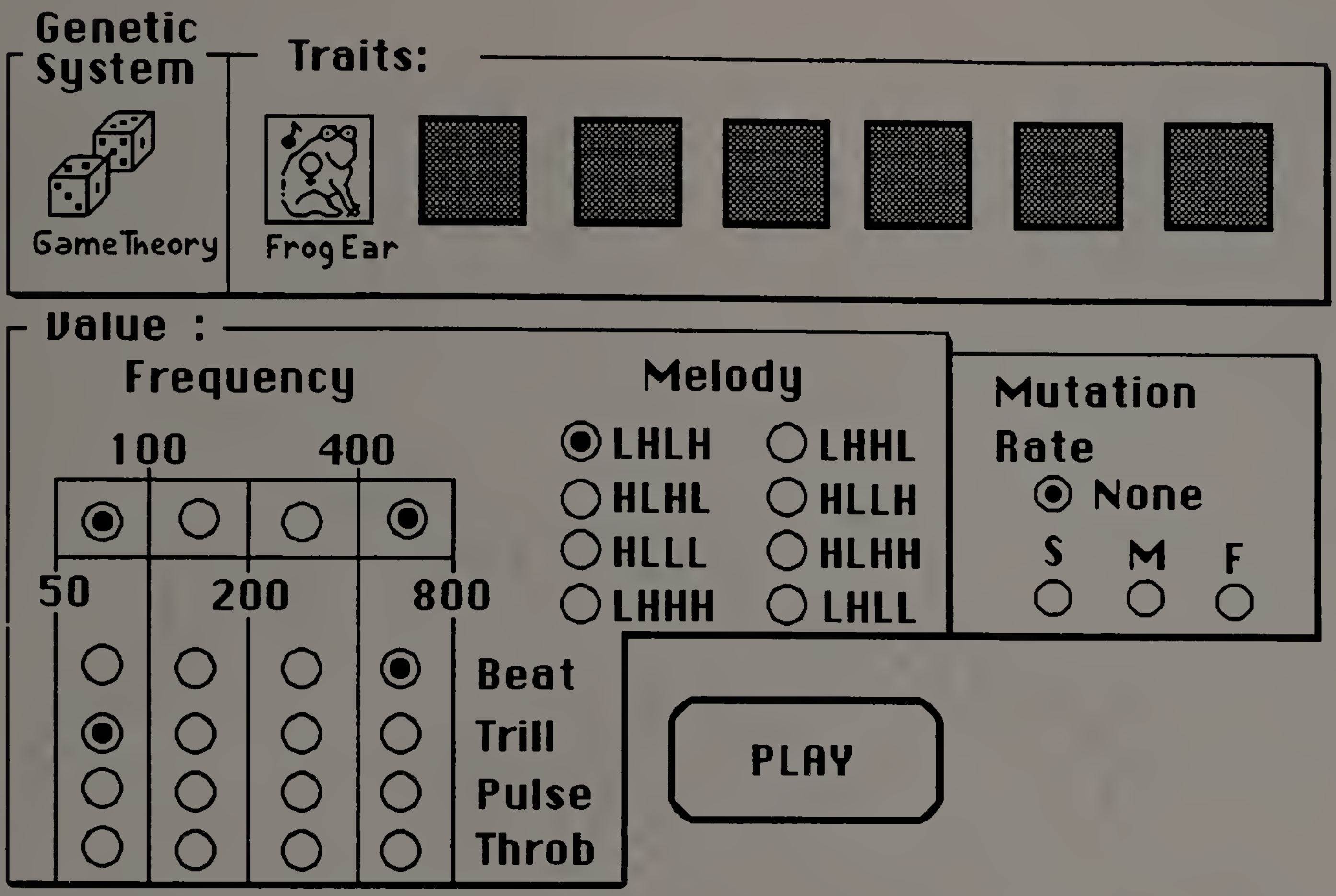


Figure 3.20 FROG CALL screen

The voices of the male frogs are either under the control of students or under random mutation by the computer. The student designed male frogs can be in competition with the randomly mutating male frogs. A pointer will let the user hear what any frog sounds like.

Automata that are given the FROG EAR trait act as females. FROG EAR trait sets the sensory bias of the female. Figure 3.20 shows a how the user would select the frequency of sensitivity of the female, the "melody" that she likes, and the kind of inflection that gives the greatest stimulus.

The ear of the female frog in Figure 3.20 has been designed to be sensitive to two regions, 50 Hz to 100 Hz and 400 Hz to 800 Hz. She also likes the pattern, Low, High, Low, High. The inflection which is most stimulating is beats on the high note and trills on the low note. The user can "PLAY" the sound to see what sounds such sensory bias would find stimulating. Another user or group of users would then attempt to design the male frog that would make sounds that would maximally attract such a female. The user would compete against other male frogs that are randomly mutating. In the current version female frogs cannot mutate.

All variables from the 'Value' box are encoded in binary form. Mutations in this simulation are simply changes of 0's to 1's. These take place at each element of the genes that express the traits at the same rates specified previously, 2%, 5%, and 10%. The attractiveness of a male frog is simply the number of matches with the sensory bias of the female. The lowest scoring quarter of the male frogs do not breed; their traits are not represented in the next generation.

The set up for the MALE FROG CALL trait is very similar. There are 768 different possible calls or sensory bias combinations. Mathematically the problem is one of finding an optimal fit in a finite field of possibilities. The problem is solved, in this case, by a genetic algorithm. It is surprisingly effective. Just as with the growth pattern of trees, and the color patterns of butterflies, students can be put in competition with the computer in an 'evolutionary war' with the computer running a randomly mutating process. From graphs or rough pictures of the world grid students would be able to assess if their frogs were losing . The problem is finding what is wrong with their design. They would not be able to look at its genotype. They can use the 'Examine Tool' to 'listen' to any of the mutating frogs made by the computer in order to see what kinds of sounds it is making. They could then redesign the song of their frog in an effort to make it more successful in breeding.

Future versions of TETK will permit mutation of the genes which express the traits of the ear of the female frog. With such mutations, and a large enough grid it is possible to model allotropic speciation. By placing semi-permeable natural barriers in the environment and permitting mutating females to breed with only the most stimulating 'local' frogs, it is possible to evolve 'dialects' that enforce separate gene pools (Werner, 1992).

The 'REPORT' menu is greatly simplified in the first version of TETK. It is by far the weakest part of the program. Currently it permits the user only to write an external file with populations of the automata species in the simulation that is running. A simple graph of the population of each species through time can be presented simultaneously with a view of the world grid from within the 'REPORT' menu. It does not currently permit the user to make reports on frequencies of allelic forms, or average values of variables in 'Values' boxes.

Improvements like these are planned for future versions of TETK. Operating under systems with dynamic data exchange it is possible to have elegant graphing or spreadsheet programs such as Wingz or Excel display the file generated by the report writer in any manner the user wishes. For the butterfly simulation, for example, it would be possible to produce a 'live' three dimensional plot of time vs. 'value of the color' vs. number of organisms that have that color. This would demonstrate 'time slices' of the evolutionary process as, at each graph there are equal numbers of butterflies around a central value (showing the randomness of any mutations at any one time), but the central value is in motion. It is a directional evolution towards the color of the distasteful butterfly.

A second very useful feature that is only partially implemented in this version is what I have called the 'MORGUE'. It is an external file that the computer writes that holds information (traits and values, age, species, reason for death) of every organism as it died. The morgue file could also be read into a database for quick and graphic analysis. Obviously the morgue file gets big very quickly. This is the current problem. Some sampling techniques must be employed. The sampling could either be random, or biased geographically (information from one region only). A regional sampling system can give the student an insight into the 'horizontal' aspect of evolutionary theory discussed by Mayer. If an advantageous mutation is introduced, and one sets up several 'observation' sites, one can see the trait propagate through the population both temporally and spatially by viewing the morgue files from each of the regions.

Another feature I would like to incorporate in TETK is the use of 'agents' to gather information about the population. An agent would be a cellular automata 'observer' who would go and observe and collect data about inhabitants in regions the user would specify. The agents would furnish random samples of portions of the population. The agent strategy may prove more useful than the morgue file, or perhaps a good supplement to it.

When using the simulation at this level, the user would be introduced to problems created by sampling. It is possible for the machine to make global tallies of populations and compare them with the tallies and estimates made by the student's agents. A cost would be associated with the use of an agent, $x.xx dollars per observation of an automaton and $y.yy for each cycle each agent spends in field work. The task given the student would then be to design an experiment to verify a certain conjecture to a specific measure of certainty, all within the constraints of a fixed budget. Besides adding some realism to their research, placing a cost limit on their activities can force students to invent novel sampling and investigation strategies, as well as verify that they are accurate to the limits that they claim.

CHAPTER 4

DRAFT FOR A TEACHER'S MANUAL FOR *THE EVOLUTIONARY TOOL KIT*

The task of writing a complete teacher's manual for this software is well beyond the scope of this dissertation. This chapter provides a document intended to serve as the core of a user's manual for a commercial product based on the ideas of The Evolutionary Tool Kit. It will focus on the projected use of the program, the change needed in curricular sequence, and the classroom strategy that the approach taken by The Evolutionary Tool Kit will require. The exposition of the manual follows the three themes set out in the rationale for the dissertation:

Accurate and Efficient Pedagogy: restructuring the order of topics, integrating the 'big ideas' of modern biological thought in an active, guiding fashion at the outset of studies, actively making connections between different parts of the subject matter.

Student Centered Learning: students experience ideas, rather than passively receives information; instruction addresses the 'Multiple Intelligences' and develops the critical thinking skills of students.

New Ideas: the role of information in living systems must be a central concern; use of technology to extend their senses and perceptions to previously unseen and unperceived mechanisms of dynamic change.

Introduction

In 1868 Darwin published The Origin of Species. The dust has not yet settled. It was not till 1968 that the Tennessee legislature saw fit to repeal the anti-evolution law and Man was permitted to be classified as a mammal in the curricula of that state. Some see here a victory for enlightened educators and a vindication of the modern scientific view. There are other lessons to be learned. Why did it take over one hundred years, more than five generations of students and teachers, for these ideas to gain even a minimal standing in a state curriculum? There is nothing dynamic, no mention of the possibility of mutability, in this classification of man as a mammal. The challenge set to science education is a very difficult in the light of historical precedents like this one.

In any attempt to rise to this challenge it may be helpful for science educators to ponder the following quotations from two great scientists of our time.

> The theory of evolution by natural selection was certainly the most important single scientific innovation in the nineteenth century. When all the foolish wind and wit that it raised had blown away, the living world was different because it was seen to be a world in movement.
> Jacob Bronowski (1973)

> Nothing in biology makes sense except in the light of evolution.
> Theodosius Dobzhansky (1951)

The problem is indeed a large one; it is also two fold. There is a unifying principle to modern life science, but it is a principle that is based on change. In Kuhnian terms Darwin's thoughts and the evolutionary synthesis brought about by paleobiologists, geneticists, naturalists, and molecular biologists in the 30's to the 50's brought a new dynamic vision of the living world around us. For many it is not a comforting one, it is a view of life in constant motion. The whirlwind of change in not at all over. Discoveries in the life sciences over the next several decades promise to advance our knowledge of living systems far beyond all that has been discovered previously. As science educators this means that acquisition by our students of information, or even systems of information is not enough. We must go far beyond the level of information and learn to teach for understanding and to find ways to develop the synthetic and analytic skills students will need in the world in which they will learn and live. Classroom teachers must feel comfortable and be able to learn and to teach with new methods, new ideas they have never seen in a classroom themselves. All of this presents a considerable challenge on many levels.

The pedagogical design of The Evolutionary Tool Kit represents an effort to address this difficulty in two ways. First it provides a practical model in life science education of the new constructivist epistemology (Gardner, 1989; Gardner, 1991; Howard, 1990; Perkins, 1987; Perkins, Lochhead, & Bishop, 1987; Posner, 1983; Resnick, 1987). It provides a modeling environment in which students at the beginning of their secondary studies in life sciences can experiment in an open ended manner to investigate and, indeed, discover for themselves some of the key ideas and relationships of evolutionary biology. Secondly it demonstrates the impact of new ideas springing from the information sciences on modern biological thought. Central to the development of these ideas, and the pedagogical vehicle that presents them, is the use of the computer as a tool for reasoning in the science curriculum. The Evolutionary Tool Kit attempts to model at the secondary level in a qualitative manner some of the spirited pedagogy pioneered at the college level by Jungck, Kinnear, and Streibel (Jungck, & Calley, 1985; Kinnear, 1986; Peterson, & Jungck, 1988; Streibel, Stewart, Koedinger, Collins, & Jungck, 1987; Watkins, 1992).

Rationale for the Design

The core of the instructional design of The Evolutionary Tool Kit is a radical reworking of the approach to teaching evolution to secondary students, with suggestions of extensions of materials to the middle school grades. Importantly the target audience is secondary students beginning their studies of life science at the general level, not just advanced sections or AP students.

Traditional methods of instruction in life science has always relied on "a firm grounding in the basics". This conservative approach has not doubt considerable merit, but there is a negative side as well. In the past the development of a 'sound knowledge base' meant a concentration of arbitrary, or at best conventional, distinctions such as classification, terminology, and not on the large unifying ideas of the discipline. Lectures, demonstrations, 'hands-on' labs, texts were the standard medium of transmission of this knowledge. The emphasis on sequential topics without a unifying conceptual thread left the curriculum was fragmented (Cho, Butler, & Nordland, 1985; Hill, 1986; Jungwirth, 1986; Nussbaum, 1983). Also the concentration on development of a knowledge base made the student essentially a passive recipient of information. The underlying assumption of transmission pedagogy is that if the topic is presented clearly or persistently enough, in small enough units, or at an acceptable pace, then the student will learn. Recent research on misconceptions in both physical and biological sciences (Brown, 1990; Browning, & Lehman, 1988; Brumby, 1984; Clement, 1982a; Faucher, 1983; Greene Jr., 1990; Halldén, 1983; Kargbo, 1980; Mestre, 1991; Novak, 1987; Scharmann, 1990; Simmons, 1987; Stewart, 1983), as well as first hand evidence from classrooms shows that this is neither a necessary or sufficient condition for learning.

The constructivist view, which has emerged over the last decade, provides a new model of instruction based on a view that all of our knowledge is constructed. Meaningful learning requires significant engagement by the learner with the material if any conceptual change, or 're-construction' of the students' views is to take place. Constructivists claim that the student's mind is not a blank slate on which the instructor can imprint the latest scientific theories. The student very often brings to their learning some naive world views or misconceptions that serve as filters for their experience. These naive world views can be very resistant to change indeed.

Recent research on the robustness of misconceptions and naive world views that students bring to life science classes has cast serious doubt on the effectiveness of standard instructional techniques even for some of our most able students. Margaret Brumby studied the understanding of evolution and natural selection of Australian second year medical students (Brumby, 1984). She found that over 80% used Lamarkian or naturalistic (adaptation because of 'need') explanations to evolutionary problems posed to them. College level biology students show a strong preference for invoking teleological explanations (Bishop, & Anderson, 1990). One startling result was that "the amount of previous biology instruction had little or no effect on student conceptions" and their understanding of evolutionary processes (Bishop, et al., 1990; Greene Jr., 1990). Even after a course specifically designed to produce conceptual change fewer than one quarter understood the underpinnings of the theory . Half of those who demonstrated understanding also stated that they did not believe it (Bishop, 1990). Students have a great difficulty understanding the undirected nature of evolution, "preferring to see later-evolving species as in some way better, more closely approximating an ideal of perfection (Gardner, 1991)."

Remarkably similar results were obtained by several other researchers in evolutionary theory as well as in genetics at both secondary and college levels (Brown, 1990; Browning, et al., 1988; Halldén, 1983; Halldén, 1988; Johnson, & Peebles, 1987; Jungwirth, 1975; Longden, 1982; Martin, 1983; Simmons, 1987; Slack, 1990; Stewart, Hafner, & Dale, 1990). In all of these studies the number of students demonstrating understanding at the conceptual level of either of the topics was under 25%, sometimes considerably so. Among secondary students of genetics who could solve Dihybrid and Trihybrid crosses as well as those who could not, there was the "almost total lack of student perceptions to how meiosis and Mendelian genetics are related (Stewart, 1983)." Students of genetics Students' own preconceptions strongly influence the way they view the world as well as the kinds of misconceptions that they have of scientific concepts (Hatano, & Inagaki, 1987; Rowe, 1990). Many succeed, much the same way they do in mathematics, by following algorithms with out understanding the conceptual knowledge underlying them (Rowe, 1990; Stewart, 1983).

The importance of placing such emphasis on developing students' perception and the importance of cognitive research to teachers is the central theme of Howard Gardner's book, The Unschooled Mind (Gardner, 1991). Gardner asserts that the raft of books and reports lamenting failing of the schools does not go far enough. "Even when school appears to be successful, even when it elicits the performances for which it has apparently been designed, it typically fails to achieve its most important missions." The "smoking gun", Gardner claims can be seen in the studies of researchers in physics education in the early 1980's at M.I.T., Johns Hopkins, and the University of Massachusetts. The gaps in comprehension of even highly educated technical students can be stunning.

Large percentages of undergraduate, even graduate students at highly respected institutions, were found to use non-Newtonian paradigms in problems just slightly out of 'text book form' (Clement, 1982a; Clement, 1982b; DiSessa, 1983; Faucher, 1983; McCloskey, 1983; Mestre, 1991). John Clement of the University of Massachusetts reported that over 70% of mechanics students, after one year of college physics, gave incorrect answers to inquiries about forces on a tossed coin at the top of its arc (Clement, 1982b; Clement, 1983). Their answers were the same as those of untrained non-science majors. Questions about tides, phases of the moon, and other phenomena revealed the persistence of a naive view of the world even among 'scientifically' sophisticated audiences (Novak, 1987).

Andrea DiSessa's work with a computer model of dynamics is particularly instructive (DiSessa, 1982). DiSessa studied the dynamical conceptions of middle and secondary school students, and also those of freshman physics students at M.I.T. DiSessa built a simple computer game in a Logo-like environment. The game was called 'Target'. Target was really a game with a few very simple rules, and a few hidden variables. The goal of the game was to get an object called the 'Dynaturtle' into the circle at the upper right of the screen. The Dynaturtle moved like a Newtonian point mass; it had inertia and obeyed Newtons laws. The M.I.T. physics students were perfectly knowledgeable about vector addition and the mathematics it entails. They also tested very well in their knowledge of Newtonian motion; yet they had a great difficulty understanding how to control the Dynaturtle. This technical information was simply not part of their problem solving strategy outside the very specific context of textbook examples. The naive Aristotelian world view was surprisingly persistent. Most high school students and almost all younger students insisted quite vocally that 'the turtle was broken'.

The naive understanding of biology is much less researched but Howard Gardner suggests that "once one probes more thoroughly into the subject matter of biology, one finds primitives and misconceptions that align quite closely to those encountered in physics. The understanding of evolution seems to harbor as many land mines as the understanding of Newton's laws of motion (Gardner, 1991)". The studies cited above demonstrate but a few of these problems .

Unfortunately, even accurate understanding of science concepts does not at all mean that these ideas are part of a students' repertoire of problem solving strategies in real world situations (Gabel, 1989; Rowe, 1990). Bishop and Anderson concluded that "the concepts of evolution by natural selection are far more difficult for students to grasp than most biologists imagine." "Over half of the well educated population possess naive conceptions about evolution." They also concluded that "many students can change their naive conceptions on the subject if instructors are aware of them and are prepared to confront them (Bishop, et al., 1990)."

How can educators confront students' naive conceptions or misconceptions and put the insights of this research into a classroom environment? Gardner proposes a possible way: the inclusion of 'Christopherian' encounters (after the navigator, Colombus). Christopherian encounters are "situations where students' earlier models or misconceptions are brought into sharp focus because of an experience that directly challenges the viability of the model they have been favoring (Gardner, 1991)." The The Evolutionary Tool Kit is such a focussing tool. It attempts to provide secondary students with an active computer modeling environment, a tool for exploration of Christopherian voyages in the life sciences. It permits students to model and manipulate micro-worlds where organisms share and pass on information dynamically, worlds which present direct evidence that contradicts their intuitive theories.

Let us consider what the traditional, 'transmission' approach to instruction in evolution and natural selection has been at the secondary level. First, evolution labs were non-existant, especially for students not in the accelerated tracks. In lower level classes a discussion of evolution was accompanied by the standard photos of dull British moths that became dark gray in the 1800's in coal mining and smelting regions, dull gray finches from Galapagos, and some black and white photos of long dead, two and three toed horses. It is small wonder that students leave such experiences with their naive views of biology and inheritance and alternative explanations for natural variation so intact. The central idea of modern life science, the theory of evolution via natural selection, generally got short shrift.

For upper level students similar demonstrations and readings were given, including a dose of genetics presented within a context of an algebraic formalism. Those students who remained in life science classes long enough would be introduced to the theory that ties together the treads of modern biological thought. This sequence is simply not adequate and the connections or understandings occur much too late in a student's career.

This swift caricature may seem very unfair to the efforts of some earnest publishers, and most certainly to that of many energetic and talented teachers. Despite heroic efforts by some members of the teaching profession to create understanding and give meaning and unity to the life sciences for their students, there is something missing from the traditional instructional design in life science - an interaction of the students' minds with the materials. If the constructivists are correct, as recent studies of students understanding of genetics and evolutionary theory reveal the ineffectiveness of much of this effort, a way must be found to bring these ideas alive for students' minds to experience first hand. The Evolutionary Tool Kit attempts to proved students with an evolutionary lab using artificial organisms whose genotypes and phenotypes, as well as the mechanisms of inheritance, are directly manipulated by the student.

Computer modeling of genetics has had a long and rather distinguished history. Several commercial packages, inspired by the work of research geneticists, have enjoyed considerable classroom success with this topic both at the secondary and college levels (Jungck, et al., 1985; Kinnear, 1986; Simmons, 1987; Streibel, et al., 1987; Watkins, 1992). The Evolutionary Tool Kit attempts parallel these efforts to bring students in contact with the basic ideas and explorations of the founders of modern evolutionary biology within the confines of a computer simulation using artificial organisms derived from techniques of research on the new discipline of Artificial Life. With software like The Evolutionary Tool Kit it is possible to bring about three important changes.

First, the concept of dynamic change and the importance of variation in living systems should be actively introduced very early in a student's study, as a central, guiding theme. Some programs succeed at this effort within a context limited by textual presentation and school lab facilities; but even if the student understands the importance of dynamic change and variation, a most important hurdle remains. Does this new 'understanding' change the way the students view the world? Research says "No." (Bishop, et al., 1990; Carey, 1985; Gabel, 1989; Gardner, 1991; Hatano, et al., 1987; Kinnear, 1983; Rowe, 1990). Naive views of biological phenomena, much like the Aristotelian views described by DiSessa (DiSessa, 1983), dominate their every day reasoning (Brown, 1990; Carey, 1985; Halldén, 1988; Kargbo, 1980; Novak, 1987; Simmons, 1987; Stewart, et al., 1990; Thomson, & Stewart, 1985; Wandersee, & Mintzes, 1987).

Students must be given an environment in which they can actively investigate the nature of inheritance, the nature of variations in the gene pool and its effects on a population, and the nature evolutionary change and its mechanisms. Students must have an environment in which they can 'do' evolution. The micro-worlds of The Evolutionary Tool Kit populated by species of artificial organisms can provide that environment.

Second, the student must be at the center of the learning. Each class discussion should approach the discipline through the core questions that define it in a manner that actively engages the mind of the student and fosters a Community of Inquiry that is critical, reflective, and self-correcting. Students must become the active focus of his or her own inquiry. This is the goal of the critical thinking movement, to which I firmly subscribe. We have new methods and new technologies that can deeply change the environments in which students learn and teachers teach. As Richard Paul states that we must "re-design instruction so that students in biology courses do more than simply rotely memorize random biological facts and principles, so that students themselves engage in disciplined biological thinking, over the course of a semester or more, leading to a deep and long term internalization of biological concepts (Paul, 1992)."

John Jungck has designed and piloted a genetics package called The Genetics Construction Kit in which he advocates a new approach to computer use in biology classrooms. He calls it the 'strategic simulation'. The program 'creates an experimental universe in which most of the professional tools are available to perform open ended experiments" in genetics (Jungck, et al., 1985). Jungck gives several criteria for such strategic simulations which include: novelty each time it is run, realistic outcomes, unlimited opportunity to perform experiments, facilitating hypothesizing and several others (Jungck, et al., 1985; Peterson, et al., 1988; Watkins, 1992).

Jungck states that strategic simulations "allow a major revision, if not a revolution, in science laboratory education." The teacher and student are put on similar footing; neither knows the answer before hand. Also the processes and tools available to solve the problem are very much like the professional tools of the discipline. Jungck claims that these simulations transform the student teacher relationship as he or she is a co-participant in solving a problem. The teacher becomes a facilitator rather than a disseminator. Their authority then comes from their facility or problem solving expertise, rather than as a dispenser of facts. The Evolutionary Tool Kit is designed in this tradition of "post Socratic pedagogy."

Third, the instructional environment in the life science class must also take into account individual learning styles and modes of learning. Howard Gardner's 'Multiple Intelligence' framework provides a guideline for planning and constructing instructional sequences that are accessible and intelligible to a wide range of student interest. An innovation piloted in

The Evolutionary Tool Kit permits students to use the computer to generate arguments. Its approach is novel in that it provides a visual representation of a line of argument. The design also provides visual (and sometimes spatial and aural) illustrations of theoretical outcomes, permitting students to experience and express complex ideas in a non-verbal way.

The Evolutionary Tool Kit uses a new instructional design based on recent technical work in artificial life and cellular automata in an attempt to accomplish these goals.

What are Cellular Automata?

Cellular automata were invented by the great mathematician John von Neumann in the late 1950's. They are 'creatures' that occupy cells in a grid that is modeled in the memory of a computer. Rules govern the manner in which each automata changes through time. The rules can depend on conditions of neighboring automata, or on global conditions for the whole grid, or on internal conditions specific to that automata. Initially automata modeling was used on physical systems such as fluid flow, annealing of metals, or atmospheric modeling. The mathematics of each of these applications is notoriously very difficult. If conditions are changed even slightly, the new phenomenon is totally different than that which preceded it. Recent studies have shown that many systems studied in these fields are chaotic in behavior; it is theoretically impossible to obtain general models for phenomena in fluid flow, metallurgy, and atmospherics for other than very simple cases (Briggs, & Peat, 1989; Gleick, 1987; Langton, 1991; Morrison, 1991; Stewart, 1989).

Von Neumann attempted to bypass the problems presented in finding differential equations that would predict global properties of these dynamical systems from initial conditions by attempting to model them locally. The cells would represent regions of a flowing liquid, a cooling metal, or a small region of the atmosphere. Based on these local 'events', and known physical laws, each cell would interact with neighbors, and the global pattern of interaction could be extracted by massive computation at the cellular level. In general the effort was successful. Much climatic modeling is based on von Neumann's insights. Automata modeling also is subject to chaotic behavior under certain conditions, but it is more easily understood and modeled than current alternatives.

In the early to mid 1980's research in cellular automata took a turn that even von Neumann had not predicted. Scientists began to use automata to model natural systems (Barlow, 1991; Barto, 1975; Burks, 1975; Hogeweg, 1988; Langton, 1986; Margolus, 1984; Preston, & Duff, 1984; Wolfram, 1983; Wolfram, 1986). Cellular automata had properties, or could be defined to have properties, much like natural organisms. Each automata could be set up with a 'genetic code', a packet of data, analogous to a genome. The information in the code determines the physiological or social behavior or physical properties of the automata, its 'phenotype'. Each automata would interact with other automata, or its environment according to the rules set up by the programmer. The modes of inheritance of information from one 'generation' to another can be modeled by rules governing the cellular automata. Mutations in the pseudo-genetic code can be provided by a random number generator.

Based on research in this new area, a new discipline sprang up called "Artificial Life" (Brockman, 1988; Langton, 1986; Langton, 1991; Packard, 1987; Pattee, 1987). With the new discipline also came more questions (Augros, & Stanciu, 1987; Barlow, 1991; Margulis, 1988), "Is this life at all?" "Is this biology or computation?" For an educator the question is a side issue. If these artificial organisms have properties and behaviors analogous to living organisms, they can be very useful indeed. With microworlds based on these models students can have complete control over environment, inheritance mechanisms, mutations, agents and effects of natural selection, long range studies of effects of mutations, and many more key constructs of modern evolutionary theory.

A most important difference between modeling natural systems with cellular automata and modeling with other systems like spread sheets, specialized languages like Stella, or methods based on probabilities or differential equations. Cellular automata are fundamentally local phenomena, locally determined. Each occupies a 'space', from which it may move. It carries its own unique information, its 'genome'. The genome can carry information about a great many 'life-like' properties like type of heredity, number of offspring and breeding period, life span, predatory behavior, ability to camouflage and many others. Mutations also are localized to individuals; they are not expresses as 'Let 1% of the population mutate." The fundamental unit of analysis and interaction is the individual, not a global variable holding information about the group as a whole.

In a remark that may prove most helpful to educators attempting to use these newest techniques Christopher Langton comments (Langton, 1991) that the signal feature of life is not the carbon-based substrate that supports the naturally occurring forms but a system of local dynamics of interacting entities (molecules, cells, etc.) which supports the emergence of global dynamic features (populations, resource use, substrate degradation or enhancement, etc.) that can 'reach down' to the physical basis of support and 'fine tune' the local entities to further global ends. It is the inter-level feedback loops, LOCAL (genes) to GLOBAL (phenotypes/environment) then back to LOCAL (genes) that "are essential to life, and are the key to understanding its origin, evolution, and diversity."

The instructional design of The Evolutionary Tool Kit permits students explicitly to see this LOCAL to GLOBAL, back to LOCAL interaction, as well as to explore personally the features of the interaction and modify any parts or variables that can effect its processes. The elegance that first attracted mathematical modelers to cellular automata also provides educators with a new way to present complex, dynamic relationships. Examples of new teaching strategies, emphasizing the potential for modeling with cellular automata, are discussed in the section on sample projects.

Gardner's Theory of Multiple Intelligences and its Application to Pedagogy

The second theme in the instructional design of The Evolutionary Tool Kit is the use of technology to accommodate student's learning styles. A key element is the incorporation of ideas from Harvard psychologist Howard Gardner's 'Theory of Multiple Intelligences'.

Gardner's theory provides a framework for restructuring curricula for individual learning (Nickerson, 1983). He sets out seven 'intelligences' by which humans learn and interact with their surroundings: Linguistic, Logico-Mathematical, Intrapersonal, Spatial, Musical, Interpersonal, and Kinesthetic. Gardner believes that all of us have a dominant mode with capabilities in the other six. He calls them 'intelligences' rather than modes or abilities because there is a 'stand alone' quality to many of the mind's systems, including cognitive ones. This quality probably reflects the evolutionary processes that formed its structures (Ornstein, 1991).

Unfortunately most classrooms and instructional techniques rarely go beyond the first three (Linguistic, Logico-Mathematical, and Intrapersonal-mentation), with much science instruction assuming a Logico-Mathematical mode continually. There are many students who understand and interpret information spatially, or through interactions with people or surroundings, by sensitivity to sounds, or through active physical involvement. It is no accident that the first three intelligences fit well with educational practice; one can put these kinds of activities very easily on a worksheet. Pedagogy of this sort creates what one educator described as "the worksheet disabled student (Thornberg, 1991)."

Limiting educational practice to these modes fails students in two ways. First, it ignores the needs and abilities of students whose dominant intelligence is not one of these three. Secondly, it fails other children in the class whose intelligence and experience are not validated in these modes. Computers offer educators an invaluable tool in opening up their classrooms to multiple paths to learning. In the pilot version of The Evolutionary Tool Kit I have specifically designed model experiments that address spatial, musical, interpersonal, and physio-kinetic intelligences. In these experiments students must evaluate both the process and the outcomes based on non-verbal, non-mathematical representations of change. The object undergoing mutation, and natural selection, is sometimes a shape, a pattern, or a sound.

A novel feature of the instructional design of The Evolutionary Tool Kit is that uses computers to generate arguments in which the computer provides a visual representation of the line of argument. The Evolutionary Tool Kit also provides visual (and sometimes spatial and aural) illustrations of theoretical outcomes. It permits students to experience an exposition of complex ideas in a non-verbal way. One of the new pedagogical techniques that permits this experience is what I have called 'the Designer/Selection' strategy. Using an experiment conceived by the student, several species are set in competition in a micro-world. One of the species is under control of the student. All changes in its genome must be made by conscious decision of the operator of the simulation. The genome of one or more of the other species is mutated randomly by the computer. The effect is to put the student in competition in an evolutionary 'war game' with a randomly mutating process with both judged by the same fitness function. The fitness function may evaluate a sequence of sounds, the functional morphology of a shape, or the effects of a pattern on predation. The student is free to change any design depend on finding a better sequence of notes, a more functional shape or pattern. It is remarkable how effective the computer's random mutations can achieve the same effect. With interactive designs like the 'evolutionary war' game the student is able to 'experience' personally the power of natural selection based on random variations in way not possible through verbal discourse.

Instructional designs like the "Designer/Selection" strategy also empower students whose dominant intelligence is neither Linguistic or Logico-mathematical. Words can only hold and get across a limited amount of information before they fail in both quality and quantity. The key concepts of both evolutionary theory and population genetics are dynamic. The computer is able to capture the quantity of information necessary for understanding the concept, to telescope parts of history onto the screen, and to display dynamic relationships within the disciplines. The "Designer/Selection" approach is unique in life science education in that it takes advantage of the computing power of the computer simultaneously with student interaction with students exploring the subject area.

New Ways of Thinking

The problems that the current generation of students will face in the 21st century threaten our species as well as the planet itself. The Biological and Health Sciences Panel of *Project 2061* states that "The socially overarching need is for citizens in a democracy to take responsibility for their own biological health and support biologically sound social decisions - as well as to object to biologically shortsighted decisions. This practical goal presupposes a general understanding of Nature and of humankind's place in it, which is the primary and greater goal of teaching biology (Clark, 1989)."

A central problem for educators in bringing our youth to this general understanding is that many of the processes that have formed the patterns of the living world are completely invisible. Many of the root causes of the dangers the youth will face are not perceived as problems at all. Our minds and sensory apparatus cannot sense toxic chemicals, nuclear waste, ozone depletion, green house gases, or urbanization. Inhabitants of smog filled cities do not notice the irritating pale that covers their homes. Their lacrimal tissues have become accustomed to the pollutants. Third world farmers, and some politicians, look on the hardwoods of the rainforests as cash crops to be harvested rather than the source of much of the oxygen and atmospheric humidity for themselves and the rest of the world. The list is virtually endless. Our mental apparatus, our habitual ways of thought, does not perceive long term change. Ornstein has called this the 'boiled frog' syndrome. Frogs can only sense differences in temperatures over short periods of time. If a frog is dropped in boiling water, it will immediately hop out. If a frog is left in a pan and heat is gently applied, it will not jump out even when the water becomes too hot for the animal to live. The frog just remains placidly in the pan until it is boiled.

The disciplines of evolutionary biology and population genetics fundamentally deal with dynamic, long-term processes, all but invisible to the eye. As such they are particularly well suited to demonstrate the cumulative effects of very long term, seemingly minute changes. The myriad of variations in living system surrounding us is the mark of these evolutionary processes, but our perceptual and conceptual frameworks are not well equipped to observe the changes.

Psychologist Robert Ornstein attributes this difficulty to "old mind" mental mechanisms that have dominated our thought patterns since our Hominid ancestors found them so useful on the African plains that first supported them (Ornstein, 1989). One such mechanism is "fight or flight"; others tend to concentrate our attention to perceived immediate causes, the snapping twig, the unseen sound. As advantageous as these mechanisms were in our past they pose mortal peril for us in the modern world. The world is changing in a decade more than it changed in a millennium; the rate of change is ever increasing. "Adapting to change must be the center of any new kind of teaching (Ornstein 1991)." Disciplines like Evolutionary Biology and Population Genetics, where dynamic change is a central element, are most important in forming perceptions that will aid a student in understanding the world in which they must live. Students investigating with computers through cellular automata modeling can gain precious insights that can help mankind solve the problems in the next century. Models like this can extend encourage the development of 'new mind' mechanisms that can give them a way to see the effects of constant change.

Central to this pedagogical problem of developing new ways to look at the world providing a metaphor, a new a *gestalt*,, that not only demonstrates to the student but also permits them to experience how the forces of natural selection, operating on random variations, can produce ordered structures. Students need an environment in which they can actively participate, or even compete, while Richard Dawkins' 'Blind Watchmaker' using random processes under natural selection makes a watch. <u>The Evolutionary Tool Kit</u> attempts provide such a learning environment by modeling, in a schematic format, the long term dynamics that shaped the natural world. It provides a 'micro-world' in which the student can explore, without reliance on complex verbal arguments or mathematical formalism, the central ideas of evolutionary theory and gain some grounding to consider at least the plausibility of its central tenets. It provides a platform which challenges 'naive' conceptions and supports an environment in which students can build for themselves a knowledge of the interaction of organisms, genetic information, and their surroundings.

Mark Ridley in *The Problems of Evolution* (Ridley, 1983), masterfully frames, for the general reader, the main lines of inquiry of evolutionary biology in the form of ten 'Great Questions'. The first four are: "Is evolution true?", "What is the nature of heredity?", "What is the mechanism of evolution?", and "How does natural selection work in nature?" Why can't students ask the same questions and explore them within an environment that will support their active involvement in the inquiry? The exploration of these questions can provide the themes for many Christopherian experiences.

Ridley gives other questions that explore the nature of molecular evolution, principles of classification, 'What is a species?', 'What are forces that drive speciation?', rates of evolution, and problems of macro-evolution. Professor Ridley asserts that almost all biologists are firm in their belief that the answers to the first four questions are settled. The answers to the last six are less certain; some lend themselves, even in professional circles, to heated discussion and very diverse opinions. Why not give students similar opportunities and experiences?

The model for student interaction with the models in The Evolutionary Tool Kit is the conjecturing strategy of Michael Yerushalmi and Judah Schwartz in The Geometric Supposer. There is a key difference in the approach, however. With The Geometric Supposer students are given a figure, or a description of that figure, with some specific relationships among the elements. They are asked to explore the mathematical environment with the computer as a tool and arrive at some conjectures they believe are true. Other elements of the environment can be changed to see if the conjecture can be extended. If they find their conjecture true for as many cases as they have tried, the students then seek a 'proof' of the conjecture in other ways. One way could be the traditional 'two-column' format. The Geometric Supposer turns geometry into an inductive science. The intellectual investment the students have put in the problem gives them a reason to find out why it is true in the general case through a deductive method.

Science is not mathematics. There is little need to spend a great deal of time in convincing the student for the need for either the deductive or inductive method. The model of interaction and understanding through personal experience of the nature of the key ides is similar. The Geometric

Supposer values the insight and experience of the student and allows students to 'do' mathematics themselves. In parallel with this approach, The Evolutionary Tool Kit permits students to work as biologists, not just become biology students. It parallels at the early secondary level the efforts of John Jungck and the BioQuest program at the college level (Peterson, et al., 1988; Watkins, 1992).

Contrary to common belief, in science the majority of student's errors and misconceptions lay not in any misapplication or misunderstanding of induction and deduction (Carey, 1985; Lockhead, & Mestre, 1990). Analogical thinking lies at the core of the discipline. The basis of many students' problems with understanding many concepts were based in use of faulty or inappropriate analogies (Gabel, 1989; Hatano, et al., 1987; Rowe, 1990). It is in this direction, methods of clarifying analogous concepts and patterns, that the efforts of science educators should be directed (Novak, 1987).

In Evolutionary Tool Kit models students can explore interactions of micro-worlds of artificial organisms, operating under rules that are closely analogous to those constraining living organisms. Students are encouraged to explore possible mechanisms by which inheritance can be transmitted from one generation to another. The design of The Evolutionary Tool Kit permits students to explore counterfactual situations. It is possible to design experiments using organisms with non-Mendelian inheritance to see what the result of competition between species would be in this case. Future versions of the program should permit students to set their own rules for the inheritance of characteristics. They can then modify the rules, make hypotheses, and falsify or verify them. In the course of their investigations seminal terms like, mutation, population sample, natural selection, evolutionary pressure, gene pool, and gene frequency will appear in a natural context, as descriptions of phenomena they encounter. Students can experience the need to use abstract terms like "evolutionary pressure". How can a student experience or become convinced of the validity of the "forces" of evolution, or unless he or she can actually see these forces drive changes in organisms before their eyes?

Another powerful pedagogical advantage of modeling with cellular automata is the personal interaction with the subject matter associated with investigations of their own 'micro-worlds'. Students need "hands-on", also "eyes on" and "ears on" time to manipulate and work with complex ideas before they can really be said to have any deep understanding of them. The conjecture format actively actively involves the student from inception of the conjecture to the design of the experiment, to the interpretation of the results.

Classroom Strategies

It is most important to note that The Evolutionary Tool Kit is not intended as an introduction or a primer in genetics. The student should already be familiar with the basic laws of inheritance from other sources, if only on an introductory level. There are several fine programs that introduce these topics quite well. MacFly is an artificial laboratory that permits students to breed and investigate the common fruit fly, learning the rules of inheritance from an electronic image of the beast that gave humans their first look at genes themselves. Mendelbugs, Heredity Dog, and Judith Kinnear's delightful efforts, Catlab, Birdbreed, and Kangasaurus are but a few other fine pieces of software. The new simulation entitled Biology Explorer-Genetics marketed by *Wings for Learning* also provides a excellent introduction to elementary concepts in genetics. The Evolutionary Tool Kit is a complement to the approach taken by these programs. Though excellent in their own context none of these programs addresses the question of fitness of an organism, nor the changing proportions of any gene or set of genes in a population undergoing natural selective processes.

The Evolutionary Tool Kit does not, however, address the pedagogical problems of evolution at a molecular level. There are a few programs, mostly tutorial in design, that explore inheritance and evolution at a rudimentary level. Students can learn the technical terms and get a simplified understanding of the process of reproduction at the molecular level. None can be called 'simulations'; none provide an interactive experience of the ideas. Some recent theoretical work has been done on automata and artificial life in modeling the emergence of metabolic activity and self reproducing automata (Ackley, & Littman, 1992; Bagley, Farmer, & Fontana, 1992; Fontana, 1992; Schuster, 1992). This work is far beyond the level of current secondary pedagogy, though in the not too distant future it may be possible to permit students to make their own 'artificial soup' and watch the emergence of the analog of biological order from random elements.

The question addressed in TETK is the dynamic nature of inheritance. Why is variation needed for natural selection to operate? Assuming a random mutation takes place that is beneficial to the organism, how is it propagated through the population? Can harmful mutations propagate through a population? Are some traits immune to natural selection? How does the pattern of distribution of properties change? How does this change effect the species involved, as well as the substrate that supports them? Students can explore this central feedback loop of information at the genetic level; how populations change, which effect the environment, which, in turn affect information at the genetic level, which effect the populations. TETK addresses directly the central pedagogical issue of the importance of the role and flow of information in biological systems as set out by the Panel "Education for the 21st Century", cited in the previous chapter.

The audience targeted by TETK is all secondary life science students. Some characterize any effort to introduce population genetics and argumentation in evolutionary theory at such a level as very ambitious indeed. Many of the experiments and concepts modeled in TETK are not generally taught at the secondary level, but, with sufficient support and careful introduction are well within the scope of secondary students and even many middle school students. Support for this claim can be found in the popularity of games like SimEarth or SimAnt, both aimed at upper elementary and middle school children, as well as adults who have retained the capacity to learn as they play. These commercially successful programs demonstrate well that students and adults alike are very interested in complex ideas and relationships if presented in an accessible and entertaining manner.

SimAnt is a particularly interesting case. If someone had claimed a few years ago that they intended to present to middle school students E. O. Wilson's views on sociobiology and their applications to individuals and to social behavior in insect societies, most educators would have thought them crazed. They would have been quite wrong. SimAnt and its layers of behavioral modeling is captivating, accurate, and quite efficient at imparting subject area knowledge as well. In Technology in Education: Looking Towards 2020 Raymond Nickerson comments on one author's remark lamenting the passing in our age of even the potential for the Renaissance Man. The author claimed that the cruel truth is that it is impossible for one individual to gain competence across a wide area of domains.

> "The cruelty may reside more in the limitations of our educational know-how and techniques than in the limitations of our minds. .... Our current primary means of knowledge acquisition - reading coupled with library access - is excruciatingly slow. We really do not know what we are capable of learning and cannot rule out the possibility that, with much more powerful techniques of storing, accessing, and representing information, for assessing what people know, and for combining instruction and exploration in mutually reinforcing ways, that capability might be very much greater than our experience to date would lead us to believe. Given the proper teaching and learning methods, might not individuals be able to acquire deep knowledge (at least by today's standards) in several areas? In the absence of compelling evidence to the contrary, I would argue that this assumption should motivate our efforts to exploit technology for educational benefit. It will be more important in the future than in the past, in my view for a significant fraction of the population to be well informed in a variety of domains both technical and nontechnical. The challenge to educational researcher is to develop the methods that will make this possible and it is not clear that this is a futile quest." (Nickerson, 1983)

All educators should take Dr. Nickerson's statements very seriously, if they are to make real changes in our schools. We must recognize the inefficiency of our current methods, and learn to respect the minds and capabilities of our students for what they really are and can become, to provide them with educational environments that permit them to develop the skills and talents that will be needed to approach properly and solve the problems that will face them as citizens in the coming century. The design of TETK is an attempt to apply this vision to the problem of instruction in the fundamental theories of life science for all students.

The questions posed for exploration in TETK should be fundamental and bold. Questions like those posed by Mark Ridley are a good start. Much like the conjectures used in The Geometric Supposer, there should not be just one answer for any of them. It is important to understand that the investigations students make in TETK are generative, not diagnostic, prescriptive, and certainly never closed in conclusion or format. The results of any investigation in TETK should be seen as only part of any investigation or argument either for, or against, any conjecture or theory about biological systems. The following pages give some sample conjectures and suggestions for including them in a life science instruction. Only a few sample explorations are given. The spirit of inquiry required by The Evolutionary Tool Kit demands that students come up with their own conjectures or hypotheses to investigate with automata micro-worlds.

Clearly any teacher's manual would have a description of the interface used in the program as well as a description of the genetic systems modeled and the use and function of the genes in the gene pallet. This description is omitted here as it has already been given in chapter three.

It must also be noted that The Evolutionary Tool Kit is generative in its approach. It is not intended as a review, nor a form of computer aided instruction. Ideally beyond a description of the interface and short descriptions of the genetic systems and each gene and its effect on the organism, no student manual should be needed. Questions to be investigated with The Evolutionary Tool Kit should arise from class discussion or interpretation or exploration of ides from the textbook used in the class.

The sample explorations given below are organized to demonstrate the ability of The Evolutionary Tool Kit to support student explorations in three different areas: Misconceptions involving populational thinking, randomness, and directed evolution; Misconceptions involving inheritance and change; and Specific examples of types of evolutionary change.

Populational thinking, randomness, and directed evolution: The studies by Brumby, Bishop and Anderson, and Greene show that the development of a populational view of organisms is a major stumbling block for students of evolutionary theory. Students need an environment that they can control, that can demonstrate to them the value of variation in a population and the necessity of variation for any evolution to take place. They can construct worlds that model the changing proportions of individuals with discrete traits. The origin of new traits in the worlds in TETK is random, yet the population may show a trend in one direction as some traits are favored over others. The randomness of the source of the origin, and the non-random nature of the process of natural selection can be directly modeled. Random processes account for the appearance of the traits. Natural selection accounts for their survival or disappearance.

Preconceptions about inheritance and change: TETK is unique in that it is specifically designed to model counterfactual cases. It is intended as a concept simulator so that students can try out ideas about inheritance and see what the results would be of such genetic systems. "What if blending of characteristics were the basis of inheritance?" "Could a favorable trait be passed on?" Students can actually set up competitions between organisms with blending inheritance and particulate inheritance.

Teleological views can be directly challenged by the Designer/Selection mechanism in which organisms 'piloted' by the student directly compete with organisms undergoing random mutations controled by the computer. This mechanism functionally puts the argument by design in competition with evolution by natural selection. Adaptation without any teleological mechanisms can be demonstrated to be a rather effective process.

Exploration of specific areas or particular cases of evolutionary change: TETK permits students to explore models of Müllerian and Batesian mimicry, selection by female choice, genetic peril, and evolution of cooperative or altruistic behavior.

Sample Explorations

The following conjectures illustrate explorations of each of these three main topics. General teacher's notes are given to provide alternative ways to explore the ideas, as well as suggestions on methods to encourage student interaction with the ideas.

Exploration One: A visit with Malthus - Darwin's Study, September 28, 1838 at Downs Cottage in Surrey, England. Focus: Developing Populational Thought.

Ernst Mayr cites those three days starting September 28, 1838 as a turning point in Darwin's thought. "The one sentence of Malthus" acted like a crystal dropped into a supercooled fluid (Mayr, 1991). Darwin had read previously about the prolific reproductive abilities of bacteria, with their populations increasing exponentially. "He did not appreciate the fierceness of this struggle before reading Malthus." Malthus described the outcome as a continuous struggle, a maintenance of an equilibrium in conflict. Darwin recognized another dynamic element: if it is the individuals who are struggling, rather than the species, any minute variation in the individual may give that organism some advantage. The key element is the view of the population as composed of individuals with differing characteristics. It is these differences that give rise to adaptation through natural selection. The point is a very subtle one. Mayr notes that "Even a small deficiency, like defining the word 'variety' typologically instead of populationally, might be sufficient to prevent the correct piecing together of the components."

Using the 'NEW AUTOMATA' menu the student can create species of organisms defined typologically (all with the same properties) and set two or more in competition for the same resources. Particulate (Mendelian) inheritance should be selected, specifically 'asexual' reproduction. If the grid is small, random effects will cause one or the other to dominate after a relatively short amount of time, particularly if the substrate is not fertile. As a variation on this model, the student can make just one organism of one of the species different in one of the variables governing reproduction. Descendants of that organism will prevail in any competition. The scene can be changed to set species of different degrees of variation in competion. Each could have the same average reproductive rate, but different distributions of values. The species with the greater variation will be more successful in the competition.

<u>TETK</u> permits students to separate the two parts of evolution by natural selection. Here the selective process itself is modeled. The source of the variation is totally in the hands of the student. The student can be challenged to answer "What is competing? The individual, the species, or the trait, or the gene?" What is the 'natural selective' process operating here? Is it random? Is the result of the competion the fixation of one of the traits, if there is no mutation permitted? The digital nature of the creatures

is a pedagogical advantage. "Is there a way for the automata to 'know' that some traits are advantageous and others are not?"

Exploration Two: Origin and survival of new traits. Focus: Developing Populational Thought. The previously cited study of Bishop and Anderson highlighted one of the major misconceptions that students held concerned the origin and survival of new traits in populations. Biologists recognize that there are two distinct processes at work. They are different in both cause and effect. The first process is the origin of the changes in a random manner over time or through sexual recombination. The second process determines the survival or disappearance of the mutation due to environmental factors. Students do not recognize the distinctness of the two processes. "Rather they think that there is a single process in which the characteristics of the species gradually changes (Bishop, et al., 1990)." Students also believe "that the environment, (rather than random processes and natural selection) causes the traits to change over time (Bishop, et al., 1990)." The inability to see how change "can result from the combined effects of random mutation and non-random selection is an especially persistent problem."

Consider two asexually reproducing species. One has several hundred members. Another is a mutation of the first; they do not interbreed. Both have the same reproductive potential. The second permits the organism to persist on the average about 10% longer in a hungry state than the first organism. Can you predict what would happen in a world populated by these creatures? Model the interaction and see what happens. Try changing the environment from very supportive to average, to poor. What happens if mutations are permitted on this trait?

The Evolutionary Tool Kit has a special option under the REPORT menu called 'The MORGUE'. This is a file that holds information on all organisms that died by natural causes, or were killed and eaten. The entries in the Morgue can be exported to a database for examination and hypothesis testing. It functions much like a complete fossil record for the automata world. The Morgue file is subject to sorting, grouping, and totaling by a database for use in supporting or falsifying conjectures. "Using the MORGUE can you make a graph through time of the numbers of individuals with specific traits in each population?"

In this experiment, in a very supportive environment, there is little or no advantage to efficiency in food usage. The mutant will stay a small percentage of the population or it may be eliminated. If the environment is poor, the mutant form will gradually take over the whole grid. If the populational variation is defined with one organism with a very large spread of values, it can dominate, even though its 'species hunger tolerance' is on the average lower. Students, themselves, can work out the language needed to describe these events, in Mayr's terms 'selection of' and 'selection for'.

Questions to explore and present answers before the class are: "What is the origin of the mutation?" "What role does the environment play in any population change?" "What does natural selection mean in this case? Can you support your argument with data from organisms in the morgue?" "Are there any trends?" "Are the 'pattern' in the morgue data random or non-random?" "What changed over time in this study?"

Exploration Three: The Role of Mutation - Focus: Developing Populational Thinking. The two part nature of the process of natural selection demands that there be an inexhaustible source of variation within the population. Historically this demand caused considerable conceptual difficulty. Lacking an infinite source of variation, natural selection will bring about the fixation in the population of a favorable gene.

Consider mutating species with little variation in competition with a non-mutating one with considerable variation. What can be said about the result? Is the result the same with sexually reproducing organisms?

The morgue file is very useful in this case. Consider the HUNGER gene as the subject of the mutation. The number of increased hunger values will be just the same as the number of decreased number values. The mutation is random. But more of the decreased hunger values will be in the morgue. The effect will be a non-random direction, an 'evolutionary pressure' to increase the value of the HUNGER gene.

Exploration Four: Meaning of evolutionary terms - Focus: Preconceptions about inheritance and change. The meaning of 'advantageous' is well worth considerable discussion. It can lead to a fuller understanding of the evolutionary meaning of the 'fitness' of an organism. As Bishop and Anderson note, 'fitness' is used to denote health, and well-being, strength and intelligence in common parlance. An evolutionary biologist uses the term much differently. It denotes, in this technical sense, "the relative capacity of individuals (or genes) to produce surviving offspring." Bishop and Anderson note that "students often recognize only 'desirable' traits such as health, strength, and intelligence as contributing to fitness (Bishop, et al., 1990)." This exercise challenges students to come up with their own definition of 'fitness' in an evolutionary sense.

A sample investigation in this area is: "Is the TWINS gene advantageous? Does it make any organism more fit to survive?"

There are many contexts in which this conjecture can be explored. Clearly the answer depends on many factors such as nature of the genetic system, environmental factors, values of other genes like HUNGER or BREED PERIOD. The student would be expected to find evidence to support his or her conclusion, or general theory of fitness.

In chapter three, some very interesting conjectures relating to the evolutionary theory of aging were discussed. "Is long life advantageous (in the evolutionary sense of the word)?" The answer, oddly enough, is no. It is possible to accumulate many factors that limit the life of an individual, yet do not significantly affect its ability to pass on its genetic information to the following generations.

Exploration Five: Teleological views vs. random processes under natural selection - Focus: Preconceptions about inheritance and change. The origin of life is always a fascinating topic. A very interesting question is "How many times did it originate?" The question is not life on other planets, but life here on earth. The evidence from DNA shows a surprising similarity of coding for all animals and plants. Could there have been other coding systems in the past, quite different from the triple codons of modern DNA? This investigation was suggested by some comments in David Jefferson's article in Artificial Life II (Jefferson, et al., 1991).

"How many times could life have originated on earth?" The natural response is once. Some may respond "A great many times." Both answers are incorrect, in that they are incomplete. By setting up several asexual species in competition for the same resources, the stochastic processes driving their interaction will bring about a condition much like the following diagram.

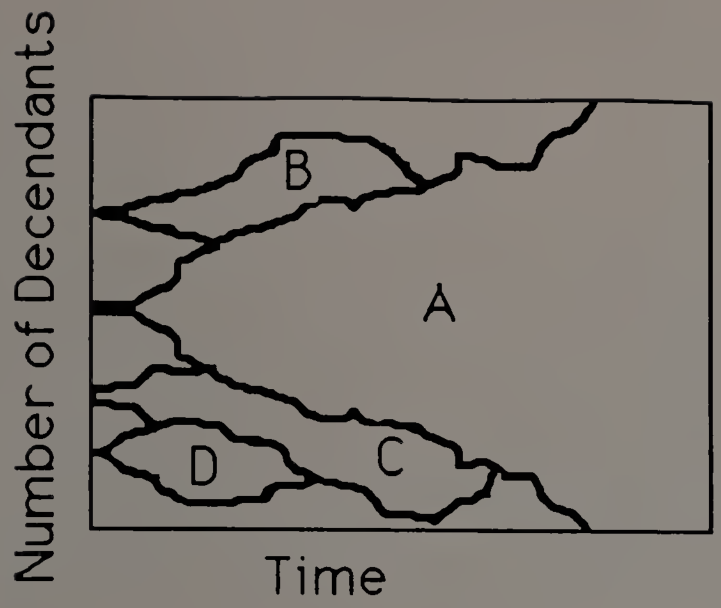


Figure 4.1 Multiple Origins of Life

The result is not intuitive. If the grid is chosen to be sufficiently small, and the substrate is poor, random fluctuations in populations will eventually cause the descendants of one organism to eventually dominate the whole grid in a relatively short amount of time. Which organism is the progenitor is not predicted. There is no advantage given to any one organism. The probability of organism 'A' winning is .25, as is that of any other one. Interestingly enough the argument has nothing to do with fitness. There is only one form of life on this planet, if one considers the commonality of the DNA code in all earthly organisms. There may have been other, alternative formulations that did not make it into the Cambrian. Darwin's theory of common descent may have a statistical basis, as well as a physiological and cytological one.

Students can try a similar setup with a very slight advantage in reproductive success for one of the species. Is the result determined by this advantage? Not in every case.

This exploration provides a fine introduction to some recent work on the explosion of life during the late Pre-Cambrian, and early Cambrian eras. Steven Jay Gould's popular book, Its a Wonderful Life gives a fascinating laymen's account of the unraveling of the mysteries of the fauna of the Burgess shale (Gould, 1989). The common belief is that life, once it began, started on a long road of divergence giving rise to the many species of the past, and those of today. Evolutionary forces caused species branched off 'the evolutionary tree' making it wider and wider as time passed. That belief is false. The fauna of the Burgess shale show more diversity, over 24 phyla, in that one lens of soldidified clay than in all other deposits over the world combined. Instead of a branching of the 'tree', there has been a process of severe pruning. This newer view deserves careful explanation and discussion.

Exploration Six: Alternative genetic systems - Focus: Preconceptions about inheritance and change. A major pedagogical difficulty surfaces when attempting to support evolutionary theory with demonstrations based on Mendelian inheritance. Demonstrations of the underlying algebra of Baysian probabilities by drawing colored marbles from jars are insufficient. The natural process is dynamic, not algebraic. Under Mendelian inheritance there is no directing process that could bring about evolution. Students sense this problem immediately: how can randomness bring about any change other than some organic smearing? The relationship is not obvious; but it is exactly this random change, random mutation that is required by natural selection to bring about adaptive states.

The randomness of heredity provides only the raw material. The particulate nature of Mendelian inheritance actually conserves variation while natural selection operates on it. Mendelian particulate heredity is an all or nothing affair, the traits produced by the genes do not blend. It is very easy to hold the idea that, in a large population, one mutation, advantageous or not, will naturally "wash out"; this idea is also quite wrong. Conjecturing with cellular automata can be a strong first step in providing a student with hands-on experience that particular inheritance will actually preserve variation. Using automata operating under alternative models of heredity, for example, "paint-pot" genetics, students can explore the counterfactual environments. As an example, students can explore the conjecture that under "paint-pot" genetics where the offspring are a blend of the characteristics of their parents. Such an inheritance system does not preserve diversity. It will function to remove variation from the population so that no evolution, even of highly advantageous traits, can take place.

So often we think of inheritance as a blending of traits. "Tall father, short mother means average size kids" Or, "Light colored hair mated with dark colored hair should give an intermediate result for the offspring." If inheritance were a blending, a "Paint Pot", could a highly advantageous trait be passed on to the following generations?

There are many ways to model this in The Evolutionary Tool Kit. One method is to choose a gene that should be advantageous in a poor environment, a high value for the HUNGER gene. Either a sexually reproducing population should be chosen. It is even possible to put a sexually reproducing population in competition for resources with a species with Paint-Pot inheritance. The beneficial effect of the mutation is washed out very quickly in a Paint-Pot system.

It is also instructive to place an asexual population in competition with a sexually reproducing one. If there is no environmental change during the time span of the simulation, the asexual population will dominate. Why aren't there more hermaphroditic species? In the next version of TETK there will be a way to change the environment so that different colorations of the HIDE trait can operate. The sexually reproducing populations can hold a reservoir of different traits and exhange genetic information between individuals to share that information. This reproductive strategy, though half of the population cannot produce young, is very plastic in response to change.

Exploration Seven: Meaning of 'advantageous', Focus: Preconceptions about inheritance and change. This exploration was already discussed in chapter three. That longer life should be advantageous to the organism seems intuitive; it is not advantageous in an evolutionary sense. As discussed previously, the investigation gives perplexing results. It is not predictable which organism will win. The result is much like figure 4.1. Long life is neither advantageous or disadvantageous. Why?

Exploration Eight: Predation and Predator/Prey Cycles. Focus: Meaning of evolutionary terms. Predation is clearly an important aspect of natural selection. There is a very delicate balance maintained between the life cycles of the predator and prey. This exercise permits students to explore this relation. It also permits students to explore some of the ideas in Dawkin's Extended Phenotype at an introductory level. Do some genes of the prey have an effect on the genes of the predator?

Can you find values of the AGE, HUNGER and BREED variables that will give a stable cycling of predator/prey for five or six generations? Can you 'fine tune' the values to get more cycles?

Additional Notes: Modeling with automata is much different than modeling with continuous variables or with Systems Dynamics tools like Stella. With these systems it is relatively easy to make systems that oscillate in very un-biological ways. Negative populations, unbounded growth, or neat cyclic patterns are all possible with these approaches. Automata models are stochastic, they will not repeat their pattern. They are also subject to random fluctuations that can cause population crashes. There is a region of relative stability for choice of variables in predator/prey models. This region should be mapped out by the class. It will be used extensively in later modeling.

Exploration Eight: A Glimpse at Hardy-Weinberg, Focus: Examples of Natural Selection. One of the landmarks of modern life science was the development of the foundation of population genetics in the early part of this century. A very interesting and counter-intuitive result can be demonstrated with organisms in TETK. If a trait is expressed by a recessive allele possessed by 10% of the population, and if the trait is neither advantageous or disadvantageous for the survival of the individual in heterozygous or homozygous forms, will it be bred out of the population and replaced by the dominant allele?

Exploration Nine: Genetic Peril, Focus: Examples of Natural Selection. It is also true that an analog of asexual inheritance occurs in sexual populations. Some genetic material is passed on by one parent only. This is clearly true of the Y chromosome in mammals. The line for any particular Y chromosome can die out for the same reason that all other names besides Christian died out on Pitcairn. A generation of female children effectively removes a Y chromosome from the gene pool. Very serious problems can develop from dilution of the Y chromosome pool.

Because the pool has a tendency to shrink, yet it is still subject to random mutations at the molecular level, as are all other chromosomes, deleterious or even potentially lethal mutations tend to collect in haploid genetic material (Eldredge, & Gould, 1972; Maynard Smith, 1986; Maynard Smith, 1989).

It is possible that the African cheetah is a victim of just this kind of genetic garbage collection (O'Brien, Wildt, & Bush, 1986; O'Brien, et al., 1987). It was known for quite a while that cheetahs were not very fertile. Infant mortality was very high, even for large cats. Examination of sperm revealed that over 80% were non-motile. Of those that could move 60% had serious abnormalities: doubled, twisted, or right angled tails, misshaped or thickened heads. Any of these abnormalities would make the sperm incapable of fertilizing an egg.

A further shock came when sample skin grafts were made between cheetahs in the early 1980's. Skin from any cheetah could be grafted onto any other cheetah without rejection. Animal trainers had long remarked that the temperaments of all cheetahs was remarkably similar. Genetic studies revealed that all cheetahs were effectively fraternal twins. The dangers of such a small gene pool are very great indeed. Besides decreased fertility, reduced immune response is quite common. A single virus, not lethal to other cats, could wipe out all of them. Data is not yet in, but the great whales, because of severe hunting at the turn of the century, could be in similar genetic peril. The northern elephant seal and the Florida panther are also in peril. In 1864 there were only 24 northern elephant seals left. Its breeding habits, with huge alpha bulls dominating the mating sites and all females for a whole season, may cause dilution of whatever diversity is left in the population. The population of Florida panthers went as low as 14 in the 1970's. Now over 70% of the male cats have only one testicle. Sperm counts are very low.

What could cause such a drastic shrinking of the gene pool in cheetahs? There is evidence that cheetahs underwent at least one, and probably two 'bottle necks' (O'Brien, et al., 1987). This is an evolutionary biologists' term for a period of extreme population pressure wherein the population was reduced to fewer than a dozen individuals world wide.

Using the Male TAG genes, this exploration models one mechanism of dilution of the gene pool. Conjecture: The Y chromosome is carried only by males of the species in mammals. Can you investigate the inheritance pattern of this chromosome in non-predated organisms, in prey, in predators?

The result of many generations will be much like the diagram in Figure 4.1. Most of the male organisms will be descended from one individual or at most just a few individuals. Populations with such limited gene pools are very vulnerable to diseases. Feline viruses from domestic cats almost wiped out several captive cheetah breeding programs in the mid 1980's. The current version of The Evolutionary Tool Kit does not permit either the modeling of effects of inbreeding, or the effects of viruses or other diseases on populations. The next version will contain these additions.

Exploration Nine: Competition between genetic systems, Focus: Meaning of evolutionary terms. Grasping the meaning of 'dominant' and 'recessive' is very difficult for students. As Stewart's study suggests, even successful genetics students do not understand the mechanisms underlying meiosis and the variations permitted by sexual recombination (Stewart, 1983). This exercise attempts to build a micro-world which challenges the naive interpretation of 'dominant' as 'overpowering' or 'stronger'. There are many genes available for this kind of investigation. For non-predatory models, birth rates can be changed, the HUNGER gene can be given favorable values in relation to an environment. For predator/prey models, students can use the FLEE or HIDE genes for prey, or the VISION gene for predator.

Conjecture 1: Descendants of a mutation that gives rise to a dominant advantageous trait will out compete a non-mutant competitor species. Eventually, all organisms will carry the dominant trait.

Conjecture 2: Descendants of a mutation that gives rise to a recessive advantageous trait will out compete a non-mutant competitor species. Eventually, all organisms will carry the recessive trait.

Conjecture 3: In a single species experiment descendents of a mutation that gives rise to a dominant advantageous trait will take over a population. Eventually, all organisms will carry the dominant trait.

Conjecture 4: In a single species experiment descendents of a mutation that gives rise to a recessive advantageous trait will NOT take over a population. Eventually, NO organisms will carry the recessive trait.

Carrying the trait is very different from displaying the phenotype that permits the organism with that trait to interact with its environment with the functions a trait enables. Conjecture #1 is true, but all individuals will not have the phenotype associated with the function. Homozygous recessives will remain in the population. The current version of the software does not allow the user to color the homozygous recessives differently from others of its species. Data can be obtained from the "Report" menu, or the "Morgue" file.

Conjecture #2 is also true. Counterintuitively, every member of the population will be homozygous recessive, as the advantageous phenotype will be expressed only with a homozygous recessive genome.

Conjecture #3 is false. Homozygous recessive individuals will constantly appear in the population.

Conjecture #4 is false. A recessive advantageous gene will take over a population. In fact 100% of the individuals will eventually have the gene. It takes much longer for this kind of mutation to propagate, however.

Exploration 11: Selection by female choice, Focus, Examples of natural selection. Female choice was recognized by Darwin and other early evolutionists as a very powerful force in natural selection. The FROG CALL genes model both female choice and sensory bias as factors in selection. A fuller description of the FROG CALL genes is given in chapter three. A possible classroom strategy is to have one group of students set the sensory bias of the female frog, while another group is not present. The second group of students would now compete with an initial group of male frogs randomly generated by the computer and subject to random mutations as the simulation progresses. Because the GAME THEORY genetic system is functioning, one quarter of the frogs are not permitted to reproduce each turn. A favorable mutation will gain any individual a higher score as judged by its match with the female preferences. This mutation will be in the group that is permitted to breed next round. The students or group of students playing against the mutating species is permitted a finite amount of time to listen to the songs of the other male frogs and then 'program' the genome of their species with what they believe is a more pleasing song. The optimizing power of the random mutation is considerable.

Conjecture: Can you find a song that the female frogs like before a random mutation in the genome of the computer frogs stumbles on a most pleasing 'frog love song'.

Feedback on what songs the female likes can only be obtained by the observation tool, listening to songs of successful frogs. Students with discriminating ears are at an advantage in when deciding what elements of the songs of other frogs are 'in common' and probably close to the patterns that the female finds most pleasing. The digital coding of the song is rather crude in the pilot edition. In future versions I would like to have students draw wave forms or place icons for kinds and pitches of notes that would be "played" by the frogs. A Fast Fourier Transform (FFT) could reduce the song to a digital form that can be stored and used as a basis for comparison as well as a source for mutation.

Exploration Twelve: Mimicry, Focus, Examples of Natural Selection. The evolution of mimicry in tropical butterflies is powerful evidence of the validity of the theory of evolution. The function of the butterfly genes is described in chapter three. The simulation is particularly rich in that it obviously presents students with organisms that have no existence outside the computer. The 'organisms' are only binary strings within a program that assigns shape and color to certain numbers. There is no sense of 'will' or 'need' in any of these creatures. This 'semi-reality' of the organisms can be used to set up a dissonance with a common misconception, according to Bishop and Anderson, that students see traits developing as organisms 'need' them to survive. For example: "Because they (cheetahs) needed to run fast for food, so nature allowed them to develop faster running skills (Bishop, et al., 1990)." The butterflies in the computer do evolve under a selective pressure without any 'need' on the part of the organism. One can keep predation constant by defining the predators as asexual reproducers with breeding periods just one unit short of their maximum life span. With this condition, they need not move. One can define their hunting zone as being three squares in any direction.

A helpful addition to the program to enforce the randomness of the mutations would be a "Mutation log". The mutation log would keep track of each mutation in each cycle. It would also automatically beep when a mutation appeared, displaying that organism and its phenotype in a special window. This log, and the individual display would enforce the idea that mutations occur only at breeding and that natural selection operates on a population composed of individuals, not on the species as a whole.

Conjecture #1: Can you model the process in which one species of butterfly would be a Batesian mimic of another? What happens if more tasty species are added?

Conjecture #2: Can you model the process in which two species of butterfly would form a two species Müllerian ring. What happens if more than two species is in the system?

Exploration Thirteen: Teleological vs. random processes under natural selection, Focus: Examples on Natural Selection. The description of the TREE genes is fully set out in chapter three. It is intended to appeal to students with Gardner's physio-kinetic and spatial intelligence. The evaluative procedure used by the student to determine what morphology is better involves both spatial and physical evaluation. The light gathering ability of the plant, as well as its strength must be evaluated from an image of a sample plant that 'grew' under parameters set by the students. The current program only shows the structure as a stick drawing, the branches do not have volume. It also does not render the image to show how light would fall on it at various times of the day. Algorithms calculate its phototaxic ability internally. Also the student cannot rotate the tree around an axis to see what it really looks like.

With all of these limitations, the simulation is quite interesting. Students design a 'primitive' plant, much like a fungus with random branching angles. The computer starts with a similar design. Under selection rules that kill off one quarter of the population each round, the trees compete and evolve. As Niklas work shows, some of the plants in the evolutionary path followed by these artificial organisms are startlingly similar to that found in the fossil record. Andrew Scott's 1982 Darwin Lecture at the Royale Society gives some good material suitable for inquiry by students (Scott, 1984).

The simulation is also unique in that it depends on 'real time' computation by the machine in the 'evolutionary war game with the students' species.

Conjecture: Is there a fixed path that the evolution of plant forms follows? Is there an optimal form? What would 'optimal' mean? The Klingon home world has gravity 2.5 times that of earth. Can you model what some of the vegetation would look like on that world?

Exploration Thirteen: Evolution of Cooperative or Altruistic Behavior, Focus: Examples of Natural Selection. In the 1980's the theory of games was applied to natural phenomena in an attempt to explain some perplexing biological behavior. How could altruistic behavior that brings harm, even death, to an individual (thereby destroying any possibility to pass on genetic information) but beneficial to a community have evolved? The evolution of cooperative behavior is also puzzling. If hunters can hunt better in teams, why doesn't one hunter, once the kill is made, claim the kill for itself and frighten off its hunting companions? This behavior certainly would be advantageous to the hunter which would now not have to share its meal with others. The STRATEGY gene permits students to explore game theoretic modeling at an elementary level. Poundstone (Poundstone, 1992) gives a fine account of the history of game theoretic modeling in biology and social science for the general reader.

Conjecture: A crocodile lies on a mud bank, its jaws gaping wide. A bird enters its mouth to feed on parasites. The crocodile does not eat the bird.

A large grouper swims into a special spot on a reef. Several brightly colored blennies come from the rocks and begin to groom the much larger fish. They enter its mouth, its gills, and comb its body, eating parasites and dead tissue. Why doesn't the grouper eat the blennie? Its natural food is quite similar in size?

Can you explain how such behavior could evolve using the STRATEGY gene and the game theoretic modeling system?

CHAPTER 5

VALIDATION OF *THE EVOLUTIONARY TOOL KIT*

The design of the validation procedure for The Evolutionary Tool Kit follows directly from the three areas of inquiry set out in Chapter Two: accuracy of concepts presented; efficient and innovative use of new pedagogy; and new ideas extended to include classroom applications of recent developments in computers and instructional strategies. The format of the design is a two level review procedure through experts in evolutionary science, science pedagogy, and curriculum development and staff training. Two interviews were conducted separately with each of the reviewers. Interviews were each approximately two hours long. At the first interview each reviewer was provided with a packet describing the goals, instructional strategies, and draft of a teacher's and students' manual for the program. The curricular goals and general strategies to bring them about were discussed and sections of the manuals for The Evolutionary Tool Kit that addresses these issues were pointed out. The reviewers were asked to comment freely on The Evolutionary Tool Kit from the perspective of their areas of expertise. Each was also requested to respond in writing to a series of questions about specific aspects of the instructional design and curricular content. Suggestions from the reviewers remarks and comments were incorporated into a revision of the code of The Evolutionary Tool Kit. The revised version was taken to the local reviewers for a demonstration and further comments at a second interview. Phone interviews were held with the out of state reviewer. In response to suggestions, revisions were made to the program. The code is still rather finicky and crashes often. The review version was designed to run on a

Mac II with a minimum of 8 megabytes of memory. This is still insufficient for some experiments, as populations of organisms must be in the tens of thousands to exhibit adequate stability. All Traits except the Tree, Frog Call, and Strategy are functional. It still crashes frequently. Considerable work on the coding must be done before the program is suitable for use in a beta test site, or as a tool for research in science education.

Dr. Richard Wickender, an evolutionary paleobiologist trained at the University of Massachusetts, and Paul Deal, research microbiologist for NASA and author of the only other cellular automata simulation BIOSIM, reviewed the program for accuracy of content. Dr. Seymour Itzkoff of Smith College reviewed the program for its use of new pedagogy and potential for innovation in science education. Dr. Neil Davidson, Sci-Net Coordinator for the State of Massachusetts and Science Curriculum Resource person at the State Department of Education, reviewed the program for its potential as a curriculum development tool and as teacher training vehicle.

Accuracy of the Content

The reviews from Dr. Wickender and Paul Deal were both positive. Dr. Wickender graciously pointed out several points of terminology that were either incorrect or misleading. The original version was intended to permit students to model investigations or carry out thought experiments that Darwin himself may have made or envisioned. The students could try different interpretations of 'evolution' or 'inheritance' and the meanings in each of 'selection'. The initial design of the interface of The Evolutionary Tool Kit was sufficiently vague to permit students to supply their own theories how traits are passed on. Students have very little knowledge of the scientific basis of inheritance (Clough, & Wood-Robertson, 1985; Deadman, & Kelly, 1978); yet the naive concepts they do have show remarkable robustness. The specific intention was to provide an environment in which students could attempt to formulate more precisely their own naive theories and 'try them out' to see how organisms would interact under these hypothetical rules.

One must remember that Darwin had no cytological basis on which to draw to explain inheritance. His own theory or, rather, theories of inheritance were wrong (Mayr, 1991; Smith, & Millman, 1987); yet he did arrive at a precise definition of the mechanisms of evolution through the process of natural selection. In retrospect the first implementation of this pedagogical strategy was laudable in that it tried to provide a conceptual environment much like that at the turn of the century, but it was much too vague. This approach could not lead, without considerable teacher intervention, to experiences in which students could sufficiently distinguish between the concepts of traits and the structures within the cells like chromosomes, and the concepts of genes, alleles, and loci of the genes. The language of modern genetics, in a very limited form, was made much more explicit in the revised version. This approach makes the program much more consonant with common practice in life science instruction. The language of evolutionary biology was left more open. Students must construct and explore for themselves the ideas and consequences of traits passing from generation to generation under several genetic systems.

The pallet in the revised version is expressed as a 'trait' pallet instead of a 'gene' pallet. In general the student interface was moved to a phenotypic level from a genotypic one.

The student generates populations of organisms with specific traits. These traits are then associated with patterns at positions on structures called 'C-somes'. The C-somes are to be conceived as physical entities that carry 'genes' that express the traits. The new term 'C-somes' was chosen rather than 'chromosomes' to reflect the artificial nature of the inhabitants of these micro-worlds. The 'C-some' is a physical entity that carries information. It is through the 'some' that information is passed on to the next generation - Weismannian inheritance. There are different mechanisms by which the inheritance can be passed. In the next version of The Evolutionary Tool Kit the user will be able to request to see the 'C-somes' of an organism. The display of the C-somes will show the locus of the genes schematically. This is a most important feature needed to prevent a common misconception. There must be a way for the student to see that natural selection can bring about a strengthening of the trait at a phenotypic level, but the gene does not get 'stronger'. Computer simulations necessitate the use of numeric values. The numeric values are associated with the trait, not the gene. To enforce the distinction between the 'genotype' of the micro-world organisms and their 'phenotype', in the next version the user should be able to get a list of an organism's phenotypic properties/behaviors. It is available now only through the trait pallet, individually by trait.

The reviewers noted other some problems with the presentation most of which have been addressed in the revision. In the SEXUAL genetic system only diploid organisms are modeled; this was seen as a minor problem. In the Mendelian model only simple dominance and multiple allele inheritance is modeled; again this was seen as a minor problem. A more serious difficulty is that the current version can leave the impression that traits are carried by entities (genes) which each lie on separate structures (chromosomes) and sort independently. A graphic mechanism to suggest that a trait may be the result of the action of a combination of genes on separate chromosomes, gene complexes (Deal, 1992), should be incorporated in the next version.

Dr. Wickender remarked favorably on the instructional sequence made possible by The Evolutionary Tool Kit. Using an environment like that provided by The Evolutionary Tool Kit, students at the beginning of their studies can explore and integrate ideas in life science much in the same order as the actual historical sequence. Evolution through natural selection preceded the development of the theory of Mendelian particulate inheritance by more than half a century. Standard pedagogy places classification, metabolic studies, cell function, cell division and reproduction, anatomy, and genetics as part of a long 'inductive' sequence at the end of which evolutionary theory allegedly synthesizes and unifies these topics into a grand picture. The end is the just the wrong place to provide the unifying threads; besides being too late, too few make it to the end. Evolutionary theory should be immanent all along, much like the exposition of natural selection and modern biological thought in Ernst Mayr's One Long Argument, (Mayr, 1991).

Another difficulty in the teaching of evolutionary biology noted by Wickender relates to its dynamic nature. "Paleontology, as a static, descriptive discipline, and genetics as applied to individuals and populations, were combined after decades of mutual antagonism only in the early 1950's (Wickender, 1992)." Developments in the 70's and 80's have brought even greater changes. Textbooks, especially those at the secondary level, have retained a 'frozen' inductive sequence of topics with little or no evidence of the dynamism of the field. Educational opportunities are missed, perhaps even misleading the students, if the field is presented as known and well surveyed.

The 'great questions' set out by Mark Ridley are more problematic than it seems. Wickender noted that there has been some quite recent evidence that a form of Lamarkian inheritance may operate in some spheres. I intended to have a mode in future versions of the program in which the artificial organisms could 'learn' from neighbors, much like juvenile male canaries take what seems to be a genetic imprint of a simple tune and learn to embellish it by listening to other mature males sing complicated songs. The capacity to learn these embellishments, and the complex songs themselves are both passed on from generation to generation. The addition of a somatic form of inheritance (Mayr, 1991) to the range of models provided would certainly be pedagogically advantageous.

Wickender pointed out a major weakness in the ENVIRONMENT section. In the current version there is only one substrate provided for nourishment for herbivores. This severe artificial limit makes all herbivores competitors for the same resource, only one will prove the fittest, with others becoming extinct. The model focuses on direct competition. Effects of mutualism, commensualism, or symbiosis cannot be modeled with this constraint. A richer environmental substrate should be incorporated in the next version. Also this exclusive formulation based on competition may be misleading.

There is a duality to evolutionary thought (Mayr, 1991). A vertical evolutionism "deals with adaptive changes in the time dimension"; this has been studied by paleontologists and geneticists. "Horizontal evolutionism deals with the origin of new diversity in the space dimension"; this has been studied by naturalists. The model presented deals almost exclusively with change through time. Environmental tracking plays a very significant evolutionary role. The environment is static in the current model, the substrate is replenished at a constant rate at each grid location at each cycle; this is an undesirable feature. An option to modify features of the substrate through time should be included. Wickender noted that because there is only one substrate, there is a very limited ability to model niches. If barriers could be set up, with grid sections that provided different substrates that could vary replenishment rates with time, much richness could be added to the model.

Wickender made several suggestions that would modify the MOVE, and HUNT traits. The MOVE behavior in herbivores should at least be partly associated with the HUNGER trait. Also the HUNT trait is much too indiscriminate. This trait was modified in the revised version to permit predators to show a preference for prey in terms of AGE. Later versions could perhaps add 'health' of the prey as measured by the analog of energy in the HUNGER trait as a variable affecting interaction with predators. I will try to incorporate these modifications in the next version.

For both Deal and Wickender the PAINT POT and GAME THEORY genetic systems demanded comment, both favorable and adverse. The mechanism for determining fitness in the GAME THEORY genetic system was unclear. The sections describing it in chapters three and four have been completely rewritten. The intention of the GAME THEORY system was to provide a generalized model in which students could explore competition and interaction in a population that did not involve motion of individuals. Individuals, under constraints of the traits given them initially, interacted with all others in the population and achieved a single relative 'score' based on their performance against the mean for the population. The method of computing the single score varied with the traits chosen; the text was unclear on this point. Individuals in the lowest quartile were removed from the population and replaced randomly by descendants from more 'successful' organisms.

The representation of the game theoretic model was a highly graphic adaptation of the mathematical work by Axelrod and Maynard Smith. The classic study in this area, 'The Prisoner's Dilemma', was included as the first example. The intention was to provide a graphic, non-mathematical way to explore topics like the evolution of altruism, or the advantages or disadvantages of cooperative or exploitive behavior. Students do come to the study of evolution with some culturally accrued images of evolution by natural selection as 'nature, red in tooth and claw'. I had hoped to use this simple mechanism to help them explore and dispel this myth. I hope to extend the model to more realistic situations in a future version.

The PAINT POT system brought the most comment. Wickender noted that the phenotypic expression of the genotype frequently approximates what can be called a "paint pot". "Inheritance is particulate, but phenotype expression isn't (Wickender, 1992)." In later discussions with him, we realized a further richness in this paint pot option. I had intended the paint pot strategy as a schematic representation of a naive view of inheritance, a blending of characteristics - the classic 'wrong way'. The initial instructional strategy was to show that species with paint pot systems (e.g. with an average fertility of 50%), when set in competition with species with particulate inheritance systems (e.g. with an average fertility of 50%), given the same initial amount of variability, always lose.

Descendants of individuals with more fertility will crowd out the others. The experiment can be repeated with other traits as well.

Any point mutation, or even a mutation of a group of individuals, in a paint pot system gradually gets diluted until there is no net effect on the population of even a highly advantageous change. Experiments with the paint pot systems were intended to show the inherent problems with typological thinking, as paint pot is an averaging process. It averages towards a 'typology' of the species. Specific discussions of exactly this process are found in Darwin's work as well as in analyses by historians of biology (Mayr, 1988; Mayr, 1991; Smith, et al., 1987). Variation is eliminated; natural selection is brought to a halt. Certainly it is a valuable experience for students to see such a counterfactual inheritance schema play itself out before their eyes.

Wickender's discussion put a new and very positive light on this process. In initial experiments such investigations can and should be made. Once a student is comfortable with the particulate nature of inheritance, he or she can begin to propose investigations conceiving the traits as expressions of 'gene complexes' resident at multiple loci at several C-somal sites. The trait expressions can produce a continuous 'blend' of the traits considered with this model. If random mutations are introduced, for example in the Batesean mimicry simulation, values of the color trait closer to the color values of distasteful butterflies will prove advantageous. Values further from these colors will suffer more predation. The average value of the color trait will change in time in the direction of the color of the distasteful butterfly. This is a rather realistic example of a gene complex undergoing directional evolution. It should be noted that it is not directed evolution; mutation both towards and away from the more advantageous color are happening all the time.

The MORGUE feature is very useful in this example. It can be seen from the MORGUE files in a database (listings of all dead organisms along with their phenotypes, through predation or otherwise, along with the cycle in which they died and the traits and values they carried) that at all times the mutations were random. Examination of the list reveals that an equal number of mutations occurred in a direction away from the value of the distasteful species. It is clear that natural selection is composed of two separate processes: a production of a large amount of variation through random genetic recombinations and mutations, and second, a non-random retention (survival) of new variants.

In speaking to both Deal and Wickender about their reviews of the program, it is in the active modeling of typological world views and populational world views that The Evolutionary Tool Kit shows its greatest potential. Ernst Mayr takes great pains to point out that the first step toward understanding natural selection must be the abandonment of typological thought based on essentialism and commonality of characteristics and the acceptance of populational thinking where the uniqueness of the individual is critically important. Through Darwin's vision, 'variation, which had been irrelevant and accidental for the essentialist, now became one of the crucial phenomena of living nature (Mayr, 1991)." Before any student can be said to assert a belief in the validity of evolution through natural selection, they certainly must understand its two step nature, and be convinced of its plausibility. In setting out to clarify the mechanisms of necessary variation (population thinking) and non-random selection, both agree that the approach shows much educational potential. In this assessment I am greatly pleased; it was the main goal of the design of the program.

The program does not address deeper aspects of heredity, mutation, molecular evolution, variability of rates of evolution, systematics, species and speciation (sympatric or allopatric), and levels of evolution (e.g. species selection) (Wickender, 1992). The important issue of completeness must be dealt with with other resources besides The Evolutionary Tool Kit, As presented the program is highly schematic. "It models inheritance as one component of the complex we call evolution via natural selection (Wickender, 1992). Inheritance is only one aspect of evolution." Organisms exist as parts of communities, of dynamic ecological systems. More materials are needed to provide an adequate and accurate introduction to this topic.

Deal raised some serious questions about the 'genetic systems' especially the 'paint pot' mechanism. His concerns centered around the perception of the relative explanatory power of all four of the systems to a naive user. "Is it possible all four will be though to be legitimate alternatives? What chance might there be for a biased teacher (unconsciously) to use this system to lend credence to the notion of inheritance of acquired characteristics?" The concerns, I feel, are very real.

The core of the instructional strategy of The Evolutionary Tool Kit is very much a generative exercise, much like the approach taken by Schwartz and Yershalmi's The Geometric Supposer. Students are encouraged to discover their own mathematics. The program permits geometry instruction to treat the student as a serious inquirer in the discipline. Paralleling the reliance on inductive inquiry in geometry, The

Evolutionary Tool Kit relies on inquiry into a problem by formulating conjectures based on different analogies. It is a concept simulator. The student is encouraged to make conjectures like: "What if a trait were inherited this way? It will/ will not propagate through a population." "Over time, with inheritance and environmental conditions of such and such a trait will do X through the population." "Disadvantageous mutations will/will not be eliminated from a population over time in a particulate inheritance system." It can provide a framework where a student can observe and hopefully reinvent, explore, and resolve the problems and solutions that led to the synthesis of evolutionary thought in the '40's and 50's.

This pedagogical approach is certainly not without its perils. How does a teacher assist a student in conjecturing and designing experiments to test the conjecture out? How does one know if a conjecture is refuted or supported by an experiment or series of experiments? These are questions whose answers are not found in textbooks. These are also the same questions that are faced when students are put at the center of their own learning. The Evolutionary Tool Kit does provide students an alternative way to textual exposition to explore and learn this fascinating discipline.

Following the path set out in mathematics by Judah Schwartz and Michal Yerushalmi (Schwartz, & Yerushalmy, 1987), and by Judith Kinnear (Kinnear, 1983; Kinnear, 1986) and John Jungck in genetics (Jungck, & Calley, 1985), The Evolutionary Tool Kit places the student and teacher on more equal footing. It is intended that topics be explored using the program as they arise in discussion. The teacher is a facilitator, a collaborator with the student in investigating a conjecture. The greatest source of difficulty with this approach is the level of understanding of the instructor. Instructors must be knowledgeable and confident in their own discipline to work with this 'think on your feet' approach. Several studies confirm that many university students, including those about to enter the teaching professions harbor serious misconceptions about some basic processes in life science, including genetics and evolutionary theory (Bishop, & Anderson, 1990; Brown, 1990; Brumby, 1979; Brumby, 1984; Greene Jr., 1990; Jimenez Aleixandre, & Fernandez Perez, 1987; Jungwirth, 1975; Jungwirth, 1986; Kinnear, 1986; Martin, 1983; Simmons, 1987; Stewart, Hafner, & Dale, 1990). Brumby's study shows over three quarters of first year medical students using Lamarkian explanations of adaptation. The case in life science is not at all unlike the 'smoking gun' in physics education cited by Howard Gardner in *The Unschooled Mind* (Gardner, 1991). The students can perform well, even in a superior fashion, algorithmically, but their understanding of fundamental ideas can be weak indeed. The cited studies by Bishop, Brumby ('79), Jimenez-Aleixandre, Jungwirth, and Greene show that a large majority of those who are very probably the secondary science teachers of the future hold serious misconceptions about natural selection.

The situation is not as difficult as it seems; despite its unorthodox approach and strong demands on the teacher, The Geometric Supposer and, to a lesser degree, the two genetics simulations mentioned have made a positive impact on secondary education. Teachers are not immutable species; they can learn too. Further comments on this topic will be made in the discussion of curriculum development and staff training.

A second, perhaps more daunting, problem was raised by Deal relating to the perceived role of natural selection in the creation of successful (surviving) genomes. He writes, "I know it is the main thrust of the work, but in so many cases the user is involved in designing genomes (there is an element of that in BIOSIM too, so I don't deny its utility) and then the testing of their survivability (evolutionary war-gaming) that the impression might be gained, especially by naive or unconsciously biased users, that genomes must be designed if they are to have any chance of making it (Deal, 1992). I offer these comments only as a cautionary note and not to suggest any serious flaws in the approach."

The point is an excellent one; for micro-world builders, where does teleology stop and natural selection begin? It is most important to note that programs like The Evolutionary Tool Kit and BIOSIM are not intended to be run by students unassisted and in isolation. The teacher is very much a part of the investigation, as a collaborator, as a resource, as a facilitator. As such the teacher must be be both free, and knowledgeable enough to intervene and assist students in formulating and interpreting the design and results of their investigations. What is being investigated is the process of change, students are seeking a metaphor, an explanation for the processes that are appearing in their micro-world organisms. Labeling some processes 'natural selection', 'adaptation', 'typological or populational' thinking, or 'teleological explanation' is just not enough. They must internalize the meanings of these terms.

The Evolutionary Tool Kit is constructed so that students can sharpen their own naive theories and even contrast them against other more scientific ones. Questions like "Where is this mutation coming from?" "How did the organism (or the user) 'know' to make that change?" should be encouraged. The fact that all of these organisms are fabrications is a pedagogical advantage not to be squandered. All the traits, the 'genes' that express them, and the 'C-somes' that hold the genes are just strings of bits inside a core memory. One 'gene' does not 'know' anything about the contents of another gene in the same organism, or in any other organism. Christopher Langton's perceptive description of the strength of cellular automata modeling, in that they automata at a 'local' level (here 'C-somes' and 'genes') interact with 'global' properties (here phenotypes, environments, populations, substrates) that, in turn, influence the 'local' quantities, is most appropriate.

The instructional strategies in which species controlled by the user compete with species controlled by the computer under a random mutation with both under natural selection can effectively point out the parallels and important differences between the two models, random mutation with selection vs. direction with 'teleology'. Any further inquiries into the effectiveness of this approach must wait for field tests of the software. Deal's cautionary notes on this point must be well considered. The computer is a co-investigator with the student in this model; the novelty of this approach must be made clear to students using it.

Both Deal and Wickender found suggested investigations in the draft of the teacher's notes about "Why sex at all?" to be, though of compelling interest, of fairly narrow scope and somewhat technical in nature. "I can see some dangers in designing a simulation to address the question if that simulation incorporates too many assumptions that are poorly substantiated. One could end up inadvertently provide an erroneous 'answer' where it is only intended to provide a conjecture. Simulations are limited to the logic that is build into them and cannot be expected to embody all the factors that exist in the real world. They might lead us to astonishing and wonderful insights, but also to bizarre and misleading conclusions as well. It may not always be possible to distinguish these, even by the experts! The notion that sex might have evolved as a response to parasitism is thought provoking to say the least, but I doubt it should be considered proved at this point. ... I'm not sure that questions of such an advanced level are useful at the secondary level (Deal, 1992)." Viewed in this light I totally agree. One can set sexually reproducing species in competition with asexually reproducing ones, and perhaps vary the environment or add parasites but any conclusions would be worthless from such investigations. The student and teacher's draft manuals were rewritten to reflect these concerns.

The series of investigations centering around the AGE trait provided in the draft teacher's manual was lauded by both reviewers. "I was especially, and very favorably, impressed by the wonderful experiments that were outlined around aging and the use of the AGE trait. The notion of the 'selfish gene' and what it means to how some of the seemingly disadvantageous characteristics of organisms have come about is, in my opinion, extremely important. You have shown here a convincing, relatively simple, and easily manipulated tool for exploring some of these questions. It would be exciting to see how well some of these concepts are garnered by students in an actual teaching setting using The Evolutionary Tool Kit (Deal, 1992)." He continues, "For the average students, who will not be making a career of biology, I think the greatest advantage to the simulation will be in giving them a change to grapple with the basic concepts of modern evolutionary biology. They should learn what is meant by evolution, how it is possible for simple systems to give rise to complex ones through natural processes, and why understanding such processes increases mankind's ability to deal with some of its problems."

Pedagogical Considerations

In their general comments about the approach both Deal and Wickender noted that The Evolutionary Tool Kit should not be construed as a genetics simulator or primer; both agreed that this point should be stressed to potential users. Deal called the approach a 'concept simulator' much like his program BIOSIM. Concept simulators like these represent in an schematic way the "sophisticated notions surrounding theories of population dynamics and evolution (Deal, 1992)." Deal noted that is true that the 'genes' in these systems are rather remote from what a biologist recognizes as genes but 'this is an inevitable consequence of the simulation process." The micro-world genes of cellular automata are not real 'things', nor can they ever be.

Neither Deal nor Wickender thought that the generalizations or simplifications of 'pseudo-genes' obviated their utility in an educational package such as The Evolutionary Tool Kit. A similar conceptual hurdle exists with the concept of phenotype for organisms in computer micro-worlds. Certainly researchers in Artificial Life grappled at length with the question as noted in chapter one. If 'phenotype' is understood as 'an aggregate of properties and/or behaviors', then organisms in micro-worlds can have phenotypes. These phenotypes can then be the objects of evolution through an analog of natural selection.

Seymour Itzkoff was pleased with the "novel and imaginative concept" of The Evolutionary Tool Kit. He stated that "The Evolutionary Tool Kit addresses an area of curricular ignorance that has long been a scandal in science education. Any innovative work in this area must be welcomed. Collison's contribution, when perfected and in place in the schools is imaginative - if not superior. I don't know that it will work - I hope so - the learning possibilities for our secondary students is enormous (Itzkoff, 1992)."

Itzkoff was also pleased by the variety of approach to topics enabled by the design of the simulation. "The visual relationships that could be generated probably could not be duplicated in verbal form or in books. I concur that many abstract relationships will here be underlined that developed in words could remain blurred and indistinct." He agreed that the approach piloted by The Evolutionary Tool Kit using "non-verbal narratives" has considerable pedagogic potential. "I can agree with Collison's stipulation as a general principle. Such dynamic relationships set forth in concrete visual form would be worth much verbal discourse." The novel use of the computer has great potential for critical thinking in science education.

In a gloss requested about the potential of The Evolutionary Tool Kit for teacher education Itzkoff writes, "Teacher preparation is a more difficult issue. I believe that a whole integrative domain of studies using computer simulations would have to be available to make this a practical teacher education pathway. On the other hand, here is no reason why such a program could not be learned as part of our in-service within the district effort."

Teacher Education and Staff Development

Issues relating to Teacher Education and Staff Development were addressed by Neil Davidson, Staff Developer and Sci-Net Coordinator for the Massachusetts Department of Education. Davidson was generally very please with the design of The Evolutionary Tool Kit. He had many concerns relating to the elliptic exposition in both the student and teacher draft manuals. His concerns were certainly well grounded, I feel. A great deal of work needs to be done to make the goals and mechanisms of the program accessible to secondary classroom teachers. The draft manuals need radical restructuring. The mechanisms of the genetic systems and the actions of the traits are discussed much too early. The general instructional design of the program, its novel approach to use of the computer, and modeling of concepts needs more careful elaboration (Davidson, 1992).

On encountering the program for the first time one asks, "Is it a learning tool, a reviewing tool?" The place that such a program would occupy in a curriculum and the needs it attempts to fill must be made much clearer. There will probably be a strong initial reaction to the complexity of the simulation. It is not at all like the common tutorials in life science education that most educators are familiar with. A related question an instructor may ask is "Has the student at the ability level necessary to work this program already considered the questions posed by it?" Exactly what is being modeled, especially the conceptual orientation, should be more clearly set out.

The program shows several strengths. First is its unique ability to model historical evolutionary sequences. "I am familiar with other programs in life science like Birdbreed, Catlab, and Heredity Dog. The Evolutionary Tool Kit picks up on the dynamic nature of inheritance and moves the student to a higher level of understanding." A second strength is the use of the computer as a 'partner' in the simulation. "Many, many of our computer 'educational environments' miss the ability of a computer to compute and pass along to the student the benefit of such computations. In this area of study, were genetic patterns and mutations can be vast, the computer is a perfect choice for bringing concepts to the desktop. Having these simple beings evolve at the student learning station is best done through simulation and most interesting to the student when they can impact on such evolution (Davidson, 1992)." He also noted the potential for use of The Evolutionary Tool Kit in computational environments like System 7 where machines can exchange data packets transparently. Networked machines could evolve micro-worlds in parallel.

Davidson also noted that he thought the goals of the program were very ambitious, a sentiment echoed by other reviewers. The richness offered does have some drawbacks; it can be overwhelming to a student just sitting down and beginning to 'try out' the experiments. The environment seems well designed to illicit 'what if' inquiries from students if sufficient background material and introductory material are provided in other contexts, perhaps through other media. Considerable staff development or inservice training would be needed to use the program effectively as the 'live' quality of the conjecturing strategy puts students and teachers in challenging, but unaccustomed roles. He also noted that, as it stands, the program in not user friendly. He had reservations about using the design with middle school students; but a decision on this would have to wait until a more complete, polished version is available for field testing.

He concludes, saying "I think that this program offers an exceptionally good learning environment for high school students, given adequate preparation in the subject area. They will be challenged with the concepts presented here and they will be capable of making "attacks" on the assumptions. Teachers will be asking their students to react to the subject of natural selection in a way that is dynamic and realistic. The computer will play a key role as the tool which gives the student the capability of simulation evolutionary activities and gives the teachers the freedom to pose higher order questions."

Further Developments

Clearly more work must be done on both the coding and manuals. More review by biology educators and curriculum developers is needed. Field tests of the software are also in order. I initially designed the program as an instructional tool; two of the reviewers remarked at its usefullness as a research instrument. This area should also be explored.

Beyond this developmental effort of software of this type, there also must be a change in attitude toward the way science, including the life sciences, are taught. We must work hard towards what Howard Gardner has called 'teaching for understanding' with the technological tools now available to us. An annecdote may be helpful in exploring this idea.

Several years ago in other corners of the world there was much rejoicing at the announcements of the Nobel Prize Award in physics. The Pakistani researcher Abdus Salaam shared the physics prize with Steven Weinberg for their work on fundamental particles. Awards of this sort had been a long time in coming for Muslim peoples. The Twelfth Century had seen scientists from Spain to Eastern Asia erect the first modern universities, precisely map the heavens, build the first hospitals, establish the first clinical practices, explain the mysteries of light and optics, and invent the field of algebra and the theory of equations. In less than two centuries the centers of learning had moved elsewhere. The ceremony in 1980 in Stockholm was a wonderful moment for Muslim science. After seven centuries a Muslim scientist again stood at the pinnacle of scientific achievement. At the presentation ceremony recipients can wear any clothing they feel appropriate. Dr. Salaam chose 13th century North Indian courtly dress. A stately, bearded figure clad in a white turban and elegant white silk brocade, complete with silken upturned slippers, stepped forward to receive the award. In an interview after the ceremony he was asked many questions about his feelings at the moment, and about his choice of dress. He was also asked tellingly, "What happened to the society and culture that had developed excellence in science and learning so long ago that it took this many centuries to rebuild?" He responded simply. "The mullas."

Though the analogy may not be appreciated by some, but we, the science educators of our society, are 'mullas' of a sort as well. The national committees and reform efforts, local committees (often with very different goals and visions from their national counterparts), the text book publishers, the curriculum and assessment specialists at national and local levels (including the media reporting the 'results') all combine with the efforts of individual schools and classroom teachers as well as with the perceptions and potential of our students to present a very complex picture. It is a picture that, much like the world views students bring to classes, may prove resistant to change. Yet, I feel, there is much room for optimism. The constraints built into this system can serve as a guide for the development of understanding. Sets of these constraints define our goals, our disciplines, our theories of life and matter. The existance of these patterns makes it possible to recognize the 'mullas' in all of us. It is by recognizing, appreciating, and perhaps removing, or redefining these constraints that we can overcome entrenched thinking and achieve a new level of understanding. It is my hope that the conceptual simulating environment provided by The Evolutionary Tool Kit can be of some use in this most important effort.

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