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Title: Disaggregative and Individual-Tree Growth Models in Theory and Application

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Disaggregative and individual-tree/distance-independent modeling methods are compared and contrasted. Differences between the two are related to differences in functional and apparent resolution and may be illustrated using aggregation theory. When considering models of different levels of resolution describing a given phenomenon, invariance with respect to the aggregation implied (symmetry) may be important to both the modeler and the user alike. In the absence of invariance between stand and tree-level predictions, conflicting predictions arise.

Some limitations of whole-stand models are also present in disaggregative models, however one way to bridge the gap between traditional individual-tree/distance-independent and whole stand models may be to use the individual-tree growth function in concert with the whole stand projection model as a disaggregator of growth. While the use of individual-tree models in this way is intuitively appealing, findings in this paper indicate that the more traditional, unconstrained tree growth functions may better predict growth of individual-trees.

Five-year growth data from 105 Douglas-fir stands in western Oregon were used to compare various individual-tree, disaggregative and whole stand models at both the stand

and tree level. Traditional approaches to disaggregation were unable to match the individual-tree growth rate functions for predicting five-year growth rate of individual-trees. Both suffered due to a lack of any index of tree position, lack of a crown ratio component, and reliance on linearity between growth and tree dimension. The very simple proportional allocation approach based on tree dimension was most unsatisfactory. It remains to be seen if these trends will also hold for longer term projections of growth.

At the stand level, the symmetric disaggregative model reduces to a simple whole stand approach to modeling. With respect to whole stand predictions, the individual-tree gross basal area growth model resulted in lower mean squared error than the aggregate (whole stand) model. There is a loss of information associated with the aggregation of tree data to predict growth. This loss of information may be responsible for the differences in mean squared error. Some of this difference may also be attributed to the inclusion of crown ratio in individual-tree predictions of growth.

Disaggregative and Individual-Tree Growth Models in Theory and Application

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Disaggregative and Individual-Tree Growth Models in Theory and Application

Chapter 1

Introduction

1.1. Existing Tree-Based Distance-Independent Architecture

Research in the field of growth and yield has provided two related methodologies for modeling the dynamics of forest stands. These are individual-tree/distance-independent models and disaggregative models. While the individual-tree/distance-independent models have gained wide acceptance and application (Stage 1973, Belcher et al. 1982, Wensel et al. 1986, Hann et al. 1992), examples of disaggregative models are fewer, and less well known. Some examples of the disaggregative models include Opie (1972), Dahms (1983), and Harrison and Daniels (1987).

Individual-tree/distance-independent models maintain functions for individual-tree growth as a function of tree and stand variables. A sample tree list with measured diameters, heights, and often crown ratio is required to operate such a model. The trees are "grown" by functions which will predict each element of tree dimension used from the tree list. The functions work together to simulate the development of stands over time. Stand dynamics are inferred from aggregating the individual-tree predictions over the sample of trees for the given stand. Competitive stress on any given tree is reflected in distance-independent measures of tree position in the stand and or stand density measures. By distance-independent is meant that tree coordinate locations in the stand are not employed.

The disaggregative model works by first aggregating tree-level information to drive a whole-stand model for growth of some feature(s) of the stand. This growth is then effectively disaggregated, or divided up amongst trees in a sample tree list by means of some simple allocation relating tree growth and tree size in such a way that larger trees are allocated greater growth than small trees in the sample. The key feature of this methodology is that the whole-stand component drives the model. The disaggregation function is subservient to the stand-level prediction.

Either modeling method is capable of maintaining tree-level information in growth projections. They are related because both are, to some extent, dependent on individual-tree information and both have the capacity to provide output of similar resolution. Because of the apparent interchangeability of these two modeling strategies from a standpoint of utility and dimensionality, either may be considered as a viable option for any modeling application where the within-stand variability reflected in a tree list is of interest, yet inter-tree distances are not to be maintained or considered in the system.

Both are capable of incorporating some information from individual sampled trees into any given projection of growth over time. While the development and application of traditional individual-tree models is well documented and understood, the disaggregation method is less so. In order for modelers and users to make informed decisions on the applicability of both of these methodologies it is important to more fully understand the advantages and disadvantages of each.

The modeling methods discussed here have a decidedly practical goal; they are intended to predict, for actual sampled stands, growth and yield, over a period of interest to forest managers. Often managers may need to predict growth to some rotation, or simply to update inventory records for a more limited time horizon. Because of this, the key factor of interest to both modeler and user alike, is the ability for a given modeling methodology to match closely the actual growth to be achieved by the stand of interest.

The purpose of this paper is to investigate the comparability of both methodologies in two ways. The first area of discussion addresses the theoretical or philosophical differences. The second phase of this discussion is based on an empirical evaluation, both at the stand- and tree-level, of the differences between several applications of the general methodologies.

1.2. Theory

Chapter 2 presents a discussion of the differences, and similarities, between disaggregative and individual-tree/distance-independent models. At first glance, it may appear that the two "different" modeling approaches are really one and the same. Some modelers may yet hold to that opinion. One difference, however, is that individual-tree/distance-independent models make use of a passive aggregation scheme while disaggregative models employ a dynamic aggregation scheme. A second difference is that disaggregative models tend to be simpler. This simplicity is not a necessity, but rather by tradition, reflecting a philosophical preference toward less complex structures.

It is important to note that, within any given general modeling construct, there are any number of different specific expressions of that construct. Models such as Prognosis, CACTOS, STEMS and ORGANON all differ to varying degrees in such things as specification of model forms, selection of driving variables, as well as selection of primary and secondary components of the dynamic representation. Since the early versions of Prognosis (Stage 1973), the number of individual-tree models has increased, as have the number of variations of this modeling theme. It is not the intent of this study however, to address questions pertaining to which specific approach to individual-tree growth and yield modeling is best.

Rather the emphasis of this study is to focus on the examples of disaggregative models which have been published, and how they relate to passive aggregation. As with individual-tree/distance-independent models, there are striking differences among the various disaggregative modeling efforts which have been presented in the literature. The traditional disaggregative model is very simple, often being dependent on only one tree dimension, such as basal area, or diameter. The relative simplicity of the traditional disaggregative simulators does allow for some generalizations to be made about the degree to which any particular function may be appropriate.

1.3. Application

In Chapter 3 both individual-tree and disaggregative modeling techniques are compared empirically for predicting basal area growth at breast height. The analysis is based on 105 Douglas-fir stands in western Oregon. The methods presented include individual-tree/distance-independent growth models, both constrained and unconstrained for predicted stand growth. Disaggregation functions include both additive and proportional allocation disaggregators. These are evaluated at both the stand and tree level.

The analysis does provide a first glimpse at the type of predictions one can expect to generate for various modeling methodologies. The analysis is limited by the scope of the data. These are generally even-aged single species stands. Furthermore, since these are evaluated for one 5-year projection period, it is not possible with this analysis to determine, with any certainty, the long term implications of the various modeling methods. Long term analyses are complicated by additional model components necessary for completeness of a model. The findings here may help direct further study of this topic and provide a basis for decisions on model structure for future modeling efforts.

Chapter 2

Symmetry and Aggregation: Implications in Disaggregative and Individual-Tree Modeling

2.1 Abstract

Two fundamentally different, yet logically linked, simulator types are individual-tree/distance-independent and the whole-stand/disaggregative. This paper addresses some of the similarities and differences between these two methodologies. A discussion of assumptions underlying various applications of these techniques for simulating stand dynamics is presented in order to foster a better understanding of the proper application of these models.

The concepts of symmetry and aggregation are introduced as central themes in the differences between these two approaches to modeling. The implications of the use of either of these two types of simulators in predicting growth and yield need to be considered in comparisons of these two philosophically different modeling approaches.

Disaggregative models may be lacking in the ability to predict growth of structurally diverse stands or stands of advanced age. These models rely on an assumption that individual-tree information is irrelevant to the prediction of stand growth. Typically these models allocate predicted stand growth based on tree dimension, ignoring tree position variables or crown ratio.

2.2 Introduction

Growth and yield research efforts have provided forest managers with an expanding selection of tools for predicting stand dynamics and anticipating response to various management alternatives. The emergence of personal computers has provided increased access to computer based management tools such as growth and yield models. Existing models used to simulate stand growth may employ any one of a number of accepted modeling methodologies. Munro (1973) provided a classification scheme for some of these. In the years since, others have been invented which do not readily fit into Munro's classification. While Munro's system of classification may be, in retrospect, somewhat limited in application, it has provided a basis for differentiating between models and understanding how they relate to one another.

Two closely related methodologies are those used in individual-tree/distance-independent models and disaggregative models, although some characteristics of disaggregative models are borrowed from whole-stand models. Comparisons between the individual-tree and disaggregative models are natural since they both work with tree-level data. While some similarities are obvious, the characteristics which differentiate these two paradigms and their implications are less so. The objective of this discussion is to establish a basis for understanding these similarities and differences. This is necessary in order to properly judge the applicability of different methodologies. Concepts of aggregation theory, resolution, and symmetry are introduced in order to facilitate this discussion.

Aggregation theory provides a foundation for a discussion of modeling methods used in many fields of study. The concepts of consistency or, more generally, symmetry are at the heart of this discussion. Four types of symmetry (perfect symmetry, filtered symmetry, constrained symmetry, and characteristic symmetry) are discussed here in the context of growth and yield modeling.

These concepts are useful in establishing a better understanding of the functioning of forest growth and yield models, and the design effects on predictions both at the stand level and the tree level. Resolution is a key element of simulator design. It is argued here that the disaggregative approach is, in some respects, a whole-stand approach and functionally very distinct from the traditional individual-tree methodology.

Evaluation of either of these models may take place at either the stand (aggregate) level, or at the tree level. It may be argued that the proper modeling methodology depends on level of detail needed of output. That is, the best approach may depend on the intended use of the simulator in question. This reflects a utilitarian perspective of models which may well be justified given their very practical objectives. Users generally are not interested in the more theoretical aspects of model design, but rather the more practical aspects of anticipating how any particular stand is likely to develop over time. It may also be true, however, that the very nature of the process and the assumptions driving any particular methodology are critical in determining model applicability.

2.3 Common Modeling Constructs

Three common model constructs for forest stands are individual-tree/distance-independent, disaggregative and whole stand models. Whole stand models are relevant to this discussion because disaggregative models are derived from these. The philosophy reflected in any given model may be instructive in understanding applicability.

The factors or variables used in stand and tree growth models can generally be categorized in one of several classes: tree dimension (w), tree rank (p), tree unit area expansion factor (n), site quality (S), stand age (A), and stand density (D). Tree level variables are represented here by lower-case letters, and stand-level or aggregate variables are represented by upper-case letters. Tree-level variables may be aggregated to obtain stand-level expressions for density. For example, individual-tree expansion factors may be aggregated to obtain the number of individuals per unit of area.

We will consider various model constructs in terms of these types of variables. Tree dimension, w, may include diameter, height, crown length, or all of these. Tree rank relates the size of the subject tree to the size of the other trees in the stand. This relationship can be relative, such as the height of the subject tree divided by the top height of the stand (Ritchie and Hann 1986), or the diameter of the subject tree divided by the quadratic mean diameter of the stand (Cole and Stage 1972), or the relationship may be expressed in absolute terms such as the basal area per acre in trees with diameters larger than the subject tree's diameter (Wykoff et al. 1982, Hann and Larsen 1981) or crown closure at some percentage of the subject tree's height (Wensel et al. 1987, Hann and Ritchie 1988).

The unit area expansion factor determines the number of trees per unit area each individual represents in the sample. Site quality can be expressed as site index (Wensel et al. 1987, Hann and Larsen 1991) or in terms of variables such as habitat classification , slope and aspect (Wykoff et al. 1982). Stand density may be expressed any number of ways, and many of the more common density measures are closely related (Curtis 1970). In ORGANON, density is expressed simply as stand basal area (Hann and Larsen 1991), in Prognosis, crown competition factor (Krajicek et al. 1961) is employed as measure of stand density (Wykoff et al. 1982) and both of these are based on an aggregated transformation of tree diameter. Density in DFSIM (Curtis et al. 1981) is expressed by a relative density index,

$$\mathrm{RD} = \frac{\text{stand basal area}}{(\text{quadratic mean diameter})^{1/2}} .$$

For the purpose of illustration, the following discussion will consider a very simple modeling objective, that of predicting gross basal area growth. In this context it is possible to construct either an individual-tree model, a whole-stand model, or a disaggregative model.

2.3.1 Individual-Tree/Distance-Independent Models

Operationally, individual-tree models have been widely applied, particularly in the western United States. Examples include Prognosis (Stage 1973, Wykoff et al. 1982) and it's numerous variants, STEMS (Belcher et al. 1982), CRYPTOS (Krumland 1982), CACTOS (Wensel et al. 1986), ORGANON (Hann et al. 1992). These simulators are representative of a modeling technique as well as a philosophical view of the system in question. This is a reductionist approach in which the heterogeneity inherent in the dynamics of any aggregation of trees is accounted for by modeling trees individually and then aggregating these individual projections to realize the dynamics of the aggregate (or stand). One primary justification for this tactic is that the behavior of some aggregates of trees, particularly those representing uneven-aged conditions and/or mixed species, may be too complex to have well defined functional relationships at the aggregate level.

In some modeling constructs, the problem may be addressed by partial aggregation. As with the individual-tree methods, partial aggregation is also a reductionist approach, differing primarily in the degree to which the reduction is taken. For example, Lynch and Moser (1986) opted to use the species cohorts as the modeling unit. In theory, individual species cohorts should behave in a more predictable fashion than would some aggregation of the cohorts. In any reductionist approach, the opportunity for output at higher levels of resolution is maintained.

Output may be fully aggregated or partially aggregated (to diameter class level or to species cohorts for example). Since the dynamics of the aggregate are implied by the aggregate of the individual predictions, this strategy results in a simulator which may better characterize growth in a more diverse array of conditions than may be addressed with a lesser degree of reductionism.

The precise means of aggregation is dependent on the sampling methodology employed. The sampling methodology determines the expansion factor which quantifies the number of other trees in the stand represented by any given sampled tree. Each tree in a list of sample trees acts as a surrogate for some number of other trees in the stand for the purpose of simulation of growth and yield over some unit of area. The greater the sampling intensity, the more trees which are sampled and hence the fewer individuals that one must infer are "like" the individual in the sample. One assumes that by knowing the status of some number of individuals in the stand, and by being able to make predictions about their growth and probability of mortality, that one may be able to make reliable predictions of the aggregate.

The variables used in individual-tree models generally fall into one of four classes: tree dimension, rank, site quality and stand density. For illustration, consider a very simple individual-tree/distance-independent model based on a tree basal area increment function:

$$\widehat{\Delta ba} = \psi(w,p,S,D), \qquad [2.1]$$

where, for this particular illustration:

$\widehat{\Delta ba}$ = tree basal area increment,

w = tree diameter,

p = diameter based rank variable (e.g., Stage 1973; Hann and Larsen 1991),

S = site index,

D = diameter based density variable, such as stand basal area.

In the absence of mortality, this will be sufficient to build a very simple tree-based model. Tree growth predicted with such a model can be aggregated to the stand level by summing the growth prediction times the expansion factor (n).

In many individual-tree models, additional tree-level variables, such as crown ratio, are employed in growth functions. Addition of such variables precipitates a need for additional equations to reflect their dynamics and, as a result, the system can become quite complex. Each additional variable is dependent on a system of equations for prediction. This complexity is one of the drawbacks of this particular type of model. It can be difficult to anticipate the behavior of a whole suite of functions working together over a long projection period, even if those functions seem reasonable when viewed alone.

2.3.2 Whole-Stand Models

In contrast to individual-tree models, whole stand models are fully aggregated approaches to predicting stand growth and yield (e.g. Curtis et al. 1981; DeMars and Barrett 1987). Whole-stand models are conceptually simpler than individual-tree models. As with any modeling endeavor, the whole-stand modeling method presupposes that the modeling unit in question (in this case the stand), has a functionally definable relationship for the dynamics of those quantities of interest to be modeled. It can therefore be argued that structurally diverse stands, or those comprising a variety of species, are ill-suited to the stand level approach. As was mentioned earlier, one means of dealing with this problem is to develop a model based on some intermediate level of detail as in a diameter-class model (e.g., Hann

1980) or a model based on species cohorts (e.g., Turnbull 1963; Lynch and Moser 1986); these types of models are not truly whole stand models, nor are they individual-tree models, rather they occupy an intermediate position with respect to the level of detail.

True whole-stand models are generally driven by aggregated variables, or those which reflect an assumed homogeneity within the stand such as site index, and do not provide for tree level predictions. While the input requirements are very simple, the output is restricted to aggregate stand descriptions such as volume, number of trees, or basal area per unit area. If additional parameters are quantified to more fully describe the distribution of some variable, then more detailed output may be derived by means of idealized probability density functions.

As a simple parallel to the individual tree illustration, consider a model for stand gross basal area growth (ΔBA) for some growth interval t:

$$\Delta BA = \Psi(S,D,A). \qquad [2.2]$$

This model can also be re-expressed for basal area at the end of a t year interval (BA_{A+t}):

$$BA_{A+t} = BA_A + \Psi(S,D,A).$$

Age is frequently used in whole stand models, and therefore, age must be well defined for any stand of interest. If a stand is uneven-aged, or multistoried, stand age will not be well defined and an age-based model will be ill-suited. In this simple example, basal area can be predicted at any given point in time, assuming no mortality and assuming that density is to be expressed in terms of trees per unit area, or basal area per unit area, or both. While this is a naive system, it will serve to illustrate application in disaggregative models.

2.3.3 Disaggregative Models

Yet another method of modeling stand dynamics, which has not been as well documented or widely applied, is the disaggregative model (e.g., Opie 1972; Dahms 1983;

Harrison and Daniels 1987; Zhang 1990), which is a logical counterpart to the individual-tree/distance-independent type simulators. The resolution of both input and output can be identical for disaggregative and individual-tree models, however there are fundamental differences in philosophies and dynamics embodied by these two modeling approaches. The disaggregative model ostensibly bridges the gap between individual-tree models and whole-stand models. However, in some respects, the disaggregative approach is really a modified whole-stand model. Functionally, the disaggregative and individual-tree models are very different and these functional differences may carry with them some important implications for applicability.

In Munro's classification, a whole-stand model is one for which the stand is the basic modeling unit. In disaggregative simulators, individual-tree information is aggregated as input to the whole stand growth functions, the predicted stand growth is then disaggregated among trees in the sample tree list. The individual-tree data only affects predicted stand growth through the aggregate states.

Up to the point where growth is disaggregated, this approach is indistinguishable from the traditional whole-stand approach. The variables which drive the growth functions are simple stand-level aggregates such as stand basal area and site index. Growth is allocated among individual-trees via some assumptions about the current state of individuals as implied by a disaggregation function. The disaggregation function only serves to express changes in variability within a stand over time. The central tendency of a stand is an expression of the whole stand component of the system.

Returning to the previous illustration of a simple whole stand growth equation, a disaggregation function could employ equation [2.2] for stand growth prediction, and then derive a prediction of tree basal area growth given this equation:

$$\Delta ba = \psi'\big(w,p,\Psi(S,D,A)\big). \qquad [2.3]$$

Here, stand basal area growth, a function (Ψ) of site, age, and density, is disaggregated by a function (ψ) which is thus dependent on both tree-level data and the stand growth prediction. Conventional disaggregation functions generally do not include a rank variable; growth is allocated based on tree dimension, w, alone. It will be shown that the disaggregation function, ψ', may have certain constraints placed upon it which will dictate important elements of the model's behavior.

2.3.4 Modeling Distinctions

The individual-tree models mentioned above are distance-independent, that is, the simulator does not require information on the exact relationship between any sampled tree and its neighbors. It is assumed that, by knowing the current dimensions of the tree and how that relates to the general conditions of the surrounding stand or plot, one may make some inference about the likely growth of the tree. It is further assumed that the information lost by ignoring the specific spatial arrangement of competitors will not inhibit predictions of that cohort of individuals represented by any given individual.

The expression of growth for the given individual in the sample is representative of the average growth expressed by all those individuals being characterized by the surrogate tree in the tree list. In this sense, the individual-tree simulator has as a modeling unit, some cohort or class of trees which are represented by the individual in a sample. The state of the tree is usually described by variables such as diameter, height, crown ratio, and species. These variables are not necessarily all required, nor are they all inclusive.

If the individual-tree growth predictions are perfect, or as they approach this state, the aggregate simulation will also be perfect, unless mortality estimation is flawed. Thus the emphasis is often on the development of individual-tree equations, with the hope that as these functions perform well, so will the simulator as a whole.

As the individual tree predictions of tree growth and mortality suffer, the stand predictions may or may not suffer proportionately. If the errors incurred in prediction among any given sample of individuals somehow balance out, it is possible, in theory anyway, to obtain reliable aggregate predictions. While the stand aggregate predictions may be acceptable under such conditions, flaws in the individual-tree equations will, at the very least, be reflected in the quantification of variability with the stand.

There are a number of advantages to the disaggregation approach to predicting growth of stands. Primary among them is that the considerable past knowledge of whole-stand dynamics which can be brought to bear on the problem of simulating stand dynamics. It can be argued that more is known about gross stand growth than tree growth, as evidenced by the legacy of growth studies the United States dating back to the early part of this century. However, much of this knowledge is tied to very simple stand structures; most traditional yield studies were directed towards single-species, even-aged stands. If management objectives depart from this ideal, the disaggregation model may be less well suited.

In addition, there may be some emergent properties which are masked by modeling at some higher levels of detail (Overton 1977). Aggregate models are generally simpler to understand (Iwasa et al. 1987), and easier to develop, than more complex models functioning at a higher levels of resolution.

Yet another advantage is the flexibility some disaggregative models display. Flexibility in this context refers to the simulators ability to accept input in the form of a tree list or as aggregated stand values. This may make the disaggregative model applicable for a larger group of users than individual-tree models which require tree list input.

In a disaggregative model, stand growth predictions are dependent strictly on aggregate values. However, at higher levels of resolution, growth is dependent on both the stand growth component and tree level data through the disaggregation function. Therefore, even if the disaggregation function is flawed or limited in application, stand growth predictions should be unaffected if the function is properly constrained.

2.3.5 Model Performance

Growth models are imperfect abstractions of real world phenomena. It is intended that the individual-tree/distance-independent model effectively predict not only the aggregate (stand) dynamics, but also structural detail within the stand. This is true of disaggregative models as well. A model should ideally predict well for less aggregated cohorts such as species groups and diameter classes, so that stand structure may also be quantified.

The effectiveness of any model is determined, to some extent, by the data used in parametrization and by the artistry of the modeler who invents the abstraction to be parametrized. This is true of empirical models as well as so called process models which differ primarily in the type of information and the amount of information brought to bear on the prediction. The art of modeling involves the modeler's ability to exclude those functional elements of a system in such a way as to not impair the veracity of the model. Determination of what is irrelevant is left to the judgment of the modeler. The relevant elements are those which will suffice to adequately describe some observed phenomena.

In order to establish the adequacy of a model it is important that the objectives be stated. The objectives of any model are often given inadequate attention (Overton 1975, page 51), and this may result in misapplication. The idea of the adequacy of a model was expressed by von Neumann (1963) :

> *The sciences do not try to explain, they hardly even try to interpret, they mainly make models. By a model is meant a mathematical construct which, with the addition of certain verbal interpretations, describes observed phenomena. The justification of such a mathematical construct is solely and precisely that it is expected to work.*

In the context of growth and yield modeling, the statement that a model "is expected to work" generally refers to the ability to predict the growth of stands, or cohorts in stands, to within a specified level of error over some range of conditions. The modeler and the user may have different definitions of the acceptable level of error, but without a clear specification of the objectives of a given model, the user is left to make assumptions about the proper domain of the given model. If the user has objectives which do not form a subset of the objectives of the modeler, then the user is engaged in extrapolation.

Given that the application of some modeling constructs are to be made within the domain of the intended application, often the user's decision to choose one methodology over another is made on such grounds as data required or by the nature of stands being simulated. Utilitarian concerns aside, questions remain about which approach will provide the "best" results, where "best" is quantified in terms of the ability of a model to forecast the state of interest in a system, with associated errors falling within some tolerance level. This dilemma was phrased by (Ijiri 1971) as:

> *How should we reconcile the contradictory predictions on the same factor based on two different theories, each of which, if taken individually, appears to be "correct?"*

The ideal simulator would be one for which, given any stand, forecasts of any required trait could be made with a high degree of precision for any time horizon (Curtis 1972). Obviously, any model will fall short of this standard, to varying degrees, in at least three ways. These are: (1) Applicability limited to only some subset of stands with a limited range of characteristics which might be of interest, (2) Differing performance levels for certain characteristics of interest, and (3), Simulator "fall-down" for certain time horizons. Ideally, any discussion of model efficacy should deal with these three areas of concern.

The two methodologies being considered may differ in the applicability to ranges of stand conditions. Given the propensity of users to extrapolate, the modeling philosophy which is most flexible with respect to stand characteristics is to be preferred. Furthermore, since both of the methodologies being considered herein may provide estimates at higher levels of resolution, one aspect of the comparison of the two is the level of aggregation at which such comparisons are made. If the comparison is made at the stand level, the ability to predict states of some population of stands must be evaluated with an eye toward the time horizon for which predictions will be reliable.

2.4 Resolution

At this juncture we will consider some of the broader implications and assumptions embodied in these two divergent philosophies; one reductionist, the other holistic. There are fundamental differences and implied assumptions associated with each of these approaches to predicting growth and yield. One perspective of the differences between these two methodologies may be explained in the context of symmetry and aggregation theory, which is to be discussed later. First, it is important to understand any distinctions being made in terms of the dimensionality (or resolution) of simulators in general.

Dimensionality and resolution, though related, are not exactly synonymous terms. Resolution carries with it the concept of breaking an entity (disaggregating) into component parts. For example, one may consider trees or species cohorts to be component parts of a stand (aggregate). Resolution does not generally refer, therefore, to the number of characteristics used to define any given modeling unit or it's dynamics. Dimensionality is a fairly vague concept which incorporates both the degree to which the system is reduced to component parts, and the number of states needed to describe any given component. In matrix notation, dimension refers to the row and column size of any given matrix. Resolution may be thought of as referring to the row dimension of any given stand representation.

Therefore, for a stand represented by some matrix of values with rows representing individual modeling units, the level of resolution of this representation generally increases as the row dimension increases. For mean stand values, this dimension is one. For a tree list to be provided to an individual-tree simulator, this dimension is the number of trees sampled. In this sense a sample of one tree provides the same level of resolution as would a list of corresponding stand averages.

Decisions regarding resolution may have a great impact on simulator behavior. Resolution will affect the detail of output as well as management options. There is no widespread agreement on the appropriate means to establish the correct resolution. If use alone is allowed to dictate model resolution, then the appropriate modeling technique is that which provides the minimally acceptable resolution to the user. However if model performance is also a concern, and if resolution affects simulator performance, then one might logically consider the effect of varying the resolution of the system representation.

It may not be possible to fully comprehend, at the beginning of a modeling project, some of the demands which will be put on any given simulator. Over the years, the Prognosis model (Stage 1973) has been modified for a number of different regions in the western United States, and various "modules" have been added. This has been possible, in part, because of the structure of the simulator chosen when the project was initiated. In this respect, the individual-tree approach provides a level of flexibility which may be absent in more highly aggregated structures. Irrelevant information may be disposed of by aggregation, but if a lower level of resolution is established, information lost to aggregation cannot be recaptured.

The level of heterogeneity within a system may also influence model resolution. A greater level of homogeneity may be obtained for the modeling unit by aggregating to some species cohort (e.g. Vanclay 1991). Clearly, stand dynamics will depend heavily on the particular species mix, which may be difficult to quantify in a true whole stand model. Whole-stand models typically assume some fairly restrictive range of species compositions. Curtis et al. (1981), for example, suggest stands be composed of at least 80% basal area in Douglas-fir. Therefore, whole-stand models may be limited in application to a subset of those stands which one might enumerate as forming some super-population of interest.

It has also been suggested that model dimensionality should be dictated by length of projection (or time) because there is a reciprocal relationship between dimension and time horizon for any fixed level of accuracy (Kahne 1976). The longer the projection, the lower the proper dimensionality. This would suggest that indeed one should choose a model with the minimally acceptable resolution. However the potential for erratic behavior in models with a high degree of dimensionality may be ameliorated by placing constraints on models. This technique has been used effectively in the mortality component of the ORGANON simulator (Hann et al. 1992) in which individual-tree estimation of the probability of mortality may be constrained by an approach to a maximum size-density relation for the stand (Hann and Wang 1990).

2.4.1 Functional and Apparent Resolution

Part of the difficulty in understanding model resolution is the ambiguity of the term. There are at least two very distinct concepts with respect to the resolution of a simulator; one may refer to these as *functional* resolution and *apparent* resolution. For many simulators the functional and apparent resolution are the same, for some others they are not. In situations where functional and apparent resolution are not the same the distinction becomes critical.

Apparent resolution is the maximum required level of resolution readily seen or perceived in operation of a model. Generally, it is the apparent resolution which influences users of models. It is the perceived resolution either from input to (or perhaps output from) the model. Apparent resolution is, in fact, what Munro (1973) spoke of when distinguishing between individual-tree and whole-stand models based on the resolution of input. It should be noted that, often a simulator may require input at several different levels of resolution. Site quality, for example, is often quantified by site index, which is clearly a stand level input and may be required for either whole-stand or individual-tree models. Users may choose a given simulator based on apparent resolution, that of data being used as input, or on the capacity for producing some desired level of resolution of output.

Given the example whole-stand equation [2.2], one can see that the apparent resolution is at the stand level. However, for both the individual-tree [2.1] and disaggregative [2.3] examples, the apparent resolution is at the tree level.

The modeler is often more concerned with the resolution of the dynamic component of the model, that is the functional resolution. Functional resolution is the maximum required level of resolution which dictates the behavioral characteristics of the model. For example, if a given simulator is driven by stand level growth equations, then the functional level of resolution is limited to the stand level. The simulator may make further modifications of these projections (by disaggregating) which gives the appearance of a higher level of functional resolution.

With respect to the previous examples, individual-tree models and whole stand models have consistent functional and apparent levels of resolution. However the disaggregation model is more complicated. When one considers stand level predictions, the functional resolution is at the stand-level in equation [2.2], while tree predictions require tree-level information to be maintained in the prediction. Hence the functional resolution in disaggregative models depends on the prediction of interest. If the user is primarily interested in aggregate predictions, the disaggregative model functions as a whole stand model.

When dealing with different types of models, one might reasonably ask: what level of aggregation is most likely to provide the best predictions in situations where either will provide the required resolution of output? One may attempt to answer this question empirically, or by considering theoretical and practical strengths and weaknesses of each approach, as we will attempt to do here. In order to do this we must first consider concepts related to aggregation in order to foster a better understanding of the contrasts between modeling philosophies.

2.5 Aggregation Theory

A substantial body of work exists in the field of aggregation theory. Much of the early work was done by Theil (1954, 1957, 1959). Though Theil's work dealt with the aggregation between macro- and micro- economic units, there is a close parallel with stand vs. tree growth, and other aggregation schemes. An example of the macro- and associated micro-relations in economics are functions operating at the level of individual households and their aggregate at the regional, or national level. The general effects of aggregation on large-scale systems was presented by Aoki (1968). An insightful presentation of the topic of aggregation theory relating to economic applications was presented by Ijiri (1971). Aggregation theory as it applies to ecological models has been discussed by O'Niel et al. (1979), Iwasa et al. (1987, 1989), Gard (1988) and Rastetter et al. (1992).

Aggregation theory involves the relationship between a micro-system and a corresponding macro-system. Some systems may be viewed as a network of individual components or parts which may be considered individually (micro-level) or in aggregate (macro-level). These two components are linked by the function which aggregates from the fine scale to a coarser scale of resolution. Consider the following general model for some characteristics x and y, representative of individuals:

$$y = \psi(x), \tag{2.4}$$

where:

y is a forecast of some micro-level state,

x is the micro-level state description.

Then the function ψ is the micro-relation for y. This may then be aggregated by a passive aggregation represented by $\tilde{g}(y)$. Similarly, at a coarser level of resolution, there may be an aggregate of interest: $X = g(x)$. Then X is the macro-level state description resulting from the specified aggregation $g(x)$. For example, $g(x)$ may be a transformation from the tree level to the species cohort level for one or more stands. Furthermore, one may theorize, for a given aggregate X, the macro-relation below:

$$Y = \Psi(X). \tag{2.5}$$

Then clearly we have at least two readily identifiable estimators for the aggregate characteristic Y. They are: Ψ and a composite function, f_a, where:

$$f_a(x) = \tilde{g}(\psi(x)). \tag{2.6}$$

This composite function comprises both the micro-transition function and the corresponding aggregation function.

Conceptually, this system is illustrated in Figure 2.1, where ψ represents the micro-level transition relationship and Ψ represents the corresponding macro-level transition. The function $g(x)$ aggregates states from the micro-relation to the macro system and the function, $\tilde{g}$, is the complementary aggregation of the micro-relation, $y=\psi(x)$. These are referred to as the micro-function, macro-function, active aggregation function and passive aggregation function, respectively (Ijiri 1971). The necessary and sufficient condition for perfect aggregation (Iwasa et al. 1987) to hold is that $\Psi(g(x)) = \tilde{g}(\psi(x))$. That is, perfect aggregation exists when both structures produce the same aggregate result.

$$\begin{tikzcd}
x \arrow[r, "\psi"] \arrow[d, "g"'] & y \arrow[d, "\tilde{g}"'] \\
X \arrow[r, "\Psi"'] & Y
\end{tikzcd}$$

Figure 2.1. Illustration of passive and active aggregation schemes. The function $\tilde{g}(y)$ represents passive aggregation, and $g(x)$ is an active aggregation function.

Generally, an aggregate is a group of distinct objects gathered together. Within the context of this particular discussion, an aggregate is a group of individual living trees logically aggregated by some scheme which we have represented mathematically by the function $g(x)$. The active aggregation function, $g(x)$, is then the function which is used to aggregate tree level predictors to the stand level. In many examples the passive and active aggregation functions are the same, and may be as simple as a summation of individuals.

By no means is the individual tree the lowest level of resolution which might be considered to define the state of the system. A tree is, itself, an aggregation and could be modeled as such. The specification that the tree is the most detailed level of resolution is a matter of convenience, or necessity, depending on one's point of view. It should also be noted that the act of sampling a stand itself implies an aggregation because each individual sampled has a unit area expansion factor which assumes the sampled tree is a surrogate for others in the stand.

In discussions of models of different levels of resolution, it is generally assumed, sometimes tacitly, that one level of modeling is correct and the other is, in some sense, subservient to this. This is certainly the case for the discussions of aggregation of Theil (1957, 1959) and Ijiri (1973) wherein it appears that the micro-relation is assumed to be "correct" and the question is whether or not a macro-relation exists, or can be found, which is in harmony with the micro-relation. Disaggregation models imply just the opposite. In a disaggregation model, the individual-tree relationship is subservient to the stand-level function.

In the example basal area prediction scheme introduced earlier, the macro-relation [2.5] is gross stand basal area growth:

$$\Delta BA_A = \Psi(S,D,A).$$

The input variables into this equation are either assumed to be homogeneous, as are site and age, or represent some aggregate of the micro-level expression of the state of the system. For example, in DFSIM (Curtis et al. 1981) density is expressed as a function of stand basal area and quadratic mean diameter (QMD), $D = \frac{BA}{\sqrt{QMD}}$. Essentially, this relative density index is a function of the aggregate of tree basal area and number of trees.

To continue with the example, individual-tree growth [2.1] is the micro-relation [2.4]. And the composite function [2.6] is simply the sum of these predictions multiplied by the expansion factor: $\sum_i \psi(w_i, p_i, S, D) \cdot n_i$. If there is no mortality, the passive and active aggregation functions are the same and are dependent solely on the expansion factors.

At this point it is necessary to expand on the concept of an aggregation function. There are two different ways of looking at the aggregation function. The first is that the aggregation function is the sum of distinct tree elements, multiplied by an expansion factor to obtain aggregate growth: $\tilde{g}(\psi) = \sum_i \psi_i \cdot n_i$. In this expression, any mortality is manifested in the aggregation of tree predictions. Another view is that the aggregation is merely a summation, and the micro-transition function is then necessarily redefined as $\psi^* = \psi \cdot n$ for any tree in the list. In this expression of the system, the model is no longer a tree model but rather a model for which the modeling unit is some cohort of trees defined by n. This second way of viewing an "individual-tree" model may be more advantageous. It can be used to point out the fact that individual-tree models really vary in level of resolution, depending on sampling intensity, and that as sampling intensity reduces, the model approaches the functioning of a stand model. If taken to the extreme, where a sample of only one tree is used, an individual-tree model functions no differently than a whole stand model. It is only as sampling intensity increases that individual-tree models express variability within a stand, and stand dynamics are represented by the aggregate behavior of some number of trees.

The three types of models discussed here are summarized in Table 2.1. This highlights the distinctions which may be made when comparing these models. It is noteworthy that the functional resolution for disaggregative models depends on the particular feature of the model being considered.

Table 2.1. Summary of characteristics of three modeling techniques.

Individual-Tree Models	Whole-Stand Models	Disaggregative Models
• dependent on tree parameters	• dependent on stand parameters	• dependent on both stand and tree parameters
• complex, high dimensionality	• relatively simple, low dimensionality	• relatively simple, low dimensionality
• generally driven by stand density, site productivity, tree rank and dimension	• generally driven by stand density, stand age and site productivity	• tree component based on tree dimension, and stand parameters
• functional resolution: tree-level	• functional resolution: stand-level	• functional resolution: stand-level, for aggregate predictions, otherwise functional resolution is at the tree-level
• apparent resolution: tree-level	• apparent resolution: stand-level	• apparent resolution: tree-level
• passive aggregation	• active aggregation	• active aggregation
• reductionist	• holistic	• quasi-holistic

2.6 Symmetry

It might be reasonable to ask: Is there an equality between equations [2.5] and [2.6]? That is, one might expect that $\Psi(X) = f_a(x)$. The absence of this property will result in ambiguity in the estimation of stand growth. In terms of the example predictions of basal area increment, this may be stated as: Are there some individual-tree/distance-independent and whole stand growth models for which identical predictions of stand or aggregate growth may be maintained? As noted earlier, this is the necessary and sufficient condition for perfect aggregation as described by Iwasa et al. (1987), or as it will be termed here, perfect symmetry. Perfect symmetry is a desirable, but generally unattainable, characteristic for a non-linear transition function ψ. Collapsing or aggregating $\psi(x)$ may provide a logical symmetry across different levels of a natural hierarchy, but generally will not provide exact numerical equivalency with the macro-relation (Iwasa et al. 1987). This is generally only a concern in disaggregative models. In individual-tree/distance-independent models, Ψ is implied by aggregation and in whole stand models there is no micro-relation, ψ.

There are a number of related concepts in aggregation theory and, in some cases, there are terms employed which are easily confused. In fact, consistent aggregation (Ijiri 1971), perfect aggregation (Theil 1954) and numerical consistency (Daniels and Burkhart 1988) are, by all appearances, synonymous terms, giving rise to some degree of confusion. But the relationship between the micro-system and the macro-system may be more precisely defined in terms of the degree to which symmetry is implied by a given system of equations.

Symmetry is a term derived from the Greek word meaning "the same measure" or as it is often applied today, symmetry is a pleasing sense of proportion and/or proper allocation. A more specific definition of the term which has found application in a variety of fields is:

> *The state of some system such that a measurable quantity of interest remains invariant after a transformation.*

It is this definition which continues to be an important element in the search for understanding of the general designs of nature (Zee 1986). A number of key concepts in physics are based on the invariance to some transformation, among them Einstein's special theory of relativity. Symmetry continues to find application in a host of other areas of study, from music (Ferris 1988) to General Systems Theory (Urmantsev 1986), and Chaos Theory (Blackmore 1986).

The definition relating symmetry to invariance has direct application in growth and yield simulators. When modeling stand dynamics, we may consider transformations (aggregation or disaggregation) to different levels of resolution. It is desirable that dynamic components of any system of equations which operate at different levels of resolution be invariant to aggregation. It is natural, therefore, to question the existence of a symmetry for various modeling methodologies. Specifically, is a stand growth prediction invariant to the application of a disaggregation function $\tilde{g}(\psi'(w,p,\Psi))$?

If we consider transformations from one level of dimensionality to another, one may question whether a lower level of resolution maintains information sufficient to describe the given phenomenon, or if the loss of information resulting from aggregation is too great to describe the phenomenon with some desired level of accuracy. There are two descriptions which are crucial to this process. The first is the functional description. The second is the apparent state description. That is, we must consider the resolution with respect to the two different aspects of system representation discussed earlier.

However, in real world situations, aggregation of a system state *will* generally result in some loss of information. For example, if we reduce dimensionality of our information from n trees with q states to the average or summation of these q states, then the representation of the state of the system has been reduced from a $n \times q$ to a $1 \times q$ expression. We need to balance the information lost through this aggregation with the benefits of lower dimensionality (speed, simplicity, and perhaps better forecasts over a long time horizon). It is unlikely that we can conclude that no information, relevant to the prediction of stand growth, is lost in this process. Rather, we may be able to conclude that the information lost through aggregation is not critical to the forecast of interest, or that the information lost is not of sufficient magnitude to be a concern for any forecast.

In the integrated, consistent system of models presented by Daniels and Burkhart (1988), the term "consistent" is somewhat ambiguous. There is certainly a close relation, or some degree of symmetry, between the functions employed for different levels of dimensionality. In general these models do not display perfect symmetry. The characteristics of this symmetry, and the benefits thereof, are not immediately evident.

Leary et al. (1979) also presented a system of functions for differing levels of resolution. In both of these systems, the dimensionality is allowed to vary, thus producing transformable systems. The result is a family of functions capable of dealing with more than one given dimensional representation of the stand. As pointed out by Daniels and Burkhart, their system offered no assurance of numerical consistency. The relationship therein reflect an imperfect symmetry.

2.6.1 Imperfect Symmetry

We have considered the necessary requirements for absolute, or perfect, symmetry. However there are other means of expressing symmetry in a system. These include filtered symmetry, constrained symmetry, and characteristic symmetry. The following discussion is drawn directly from Ijiri's (1971) discussion of consistency, and relating it to the more general framework of symmetry.

A constrained symmetry is one for which symmetry occurs only under certain conditions or due to certain constraints on the variables. It should be noted that with this definition, no distinction is made between a parameter and a variable. Any restriction on the domain of the function resulting in symmetry could be applicable. For example, a set of equations may be constrained to provide symmetry for equilibrium conditions only. Within the context of growth and yield analysis, growth functions or mortality functions may be constrained to preserve symmetry with some assumed macro-function. Doing so basically engenders a disaggregation function. Examples of these are the disaggregation functions presented by Clutter and Jones (1980, equation 6) and Pienaar and Harrison (1988, equation 3). That is, a disaggregative function is constrained by the aggregate dynamics.

The distinction between this and perfect symmetry implies that there is a "correct" expression for the micro-relation, and that this expression suffers for some predictions when constrained. However, one could just as easily specify that the constrained function is, itself, correct, and there is no hidden function which is more broadly applicable.

Filtered symmetry, or consistency, can be described conceptually as being based in the decision process driven by the given system representation. Symmetry is expressed with respect to the decision making process being invariant to the level of aggregation, as opposed to system states themselves being invariant to the aggregation. If the micro-system and macro-system are consistent with respect to decisions or conclusions reached from a given simulation scenario, then the system could be said to maintain a filtered symmetry, having been filtered by the reference to resulting decision or conclusion alone. This is a symmetry which is, or could be, ephemeral and dependent on not only the given states being assumed but on the particular decision process.

A final type of symmetry one might consider is that of characteristic symmetry. A system may be said to maintain a characteristic symmetry if some quality of system behavior remains invariant to aggregation. Characteristic symmetry would seem to be at the heart of the conflict between divergent modeling philosophies. We may be willing to accept systems for which there is no perfect symmetry, if these philosophies do not produce models which are in conflict with one another qualitatively. For example, it has been noted that a number of different simulators produce very flat curves at the maximum of mean annual increment. This characteristic may be observed in both ORGANON and DFSIM. With respect to the general shape of the MAI curve, there is a characteristic symmetry between ORGANON and DFSIM. The particular macro-system in DFSIM and system of tree functions in ORGANON produce some results which are characteristically invariant, though certainly not mathematically equivalent under aggregation.

Both the Daniels and Burkhart, and Leary formulations are geared towards maintaining a characteristic symmetry. This symmetry can be defined as one in which certain characteristic traits of the micro- and macro- systems of interest are maintained with the transformation from one system to the other. That is, in growth and yield modeling we might be willing to accept any aggregation (or disaggregation) if the functions conform to accepted biological principles with respect to key attributes of the system, while not necessarily maintaining numerical equivalency across different levels of aggregation.

2.7 Aggregation in Individual-Tree and Disaggregative Models

We have now laid the foundation for a discussion of the differences between modeling strategies. Suppose that the phenomenon of interest is the state (or states) predicted for a given stand over time. Both whole-stand and individual-tree simulators provide estimates of states that a given aggregation of trees will attain over time, obviously with varying levels of dimensionality.

The individual-tree modeling approach uses a passive aggregation scheme which is a linear aggregation of the individual-tree growth function. This structure is illustrated in Figure 2.2. There is no macro-transition function $\Psi(X)$ either explicitly stated or implied. The passive aggregation function, $\tilde{g}$, is that function from which stand level growth is estimated, given the micro-relation, ψ. The active aggregation function is somewhat irrelevant in this context, inasmuch as there is no need to drive any macro-relation. However, initial state descriptions can be aggregated to the stand level. In the example individual-tree model presented earlier, the micro-relation, ψ, is defined as the individual-tree basal area growth function. The passive aggregation function determines stand basal area growth by summing predicted tree growth multiplied by the number of trees represented by each tree in the sample.

$$\begin{tikzcd}
w,p \arrow[r] \arrow[d, shift right, "g"'] & \psi(w,p,D,S) \arrow[r] & \Delta ba \arrow[d, "\tilde{g}"'] \\
D \arrow[u, shift right] & & \Delta BA
\end{tikzcd}$$

Figure 2.2. Illustration of the passive aggregation structure in an individual-tree/distance-independent model. The function g̃ represents the passive aggregation function and ψ the micro-dynamics (individual-tree functions).

The active aggregation structure of a whole stand model is shown in Figure 2.3. The active aggregation function, here, is only necessary if the initial state description is a tree-level description. Otherwise the only component to this system is a macro-transition function, Ψ. In the earlier example, the macro-relation was simply a gross basal area growth equation as a function of site quality, density and age.

$$\begin{tikzcd} w \arrow[d, "g"'] & & \\ D \arrow[r] & \Psi(S,D,A) \arrow[r] & \Delta BA \end{tikzcd}$$

Figure 2.3. Illustration of the macro-transition structure (Ψ) of the example whole stand model.

The active aggregation structure used by disaggregative simulators is shown in Figure 2.4. The growth resulting from the macro-transition $\Psi(S,D,A)$ may be disaggregated to individual-trees via a disaggregation function, ψ'. There are two distinct estimators of gross basal area growth; that obtained by means of the active aggregation scheme (ΔBA) and that obtained by passive aggregation of ψ'. They are not necessarily equal.

$$\begin{tikzcd}
w \arrow[rr] \arrow[d, "g"'] & & \psi'(w,\Delta BA) \arrow[r] & \Delta ba \arrow[d, "\tilde{g}"'] \\
D \arrow[r] & \Psi(S,D,A) \arrow[r] & \Delta BA \arrow[u] & \Delta BA'
\end{tikzcd}$$

Figure 2.4. Illustration of the active aggregation structure of a simple disaggregative simulator. The function g represents the active aggregation function and Ψ the basal area increment (ΔBA) function. The disaggregation function, ψ', is a function of both tree dimension and predicted basal area increment and can be aggregated to estimate basal area increment $\Delta BA'$.

This illustrates the importance of considering both functional and apparent resolution in a simulator. It is evident that this system maintains the full dimensionality of the tree list, while the, functional, or dynamic, component of the stand is limited to the dimensionality of the expression for site quality, density, and age. Thus, there is a tacit assumption here that the dynamics of the macro-system may be captured at the lower dimensionality of macro-relation. That is, individual-tree information is irrelevant to the estimation of stand growth. The macro-function, Ψ, may act only as an adjustment embedded in an implied micro-relation as defined by the function ψ'. For stand level projections, the disaggregative model functions at the stand level.

If tree-level information is predicted, then it functions as a constrained individual-tree model. Information present in the individual-tree characterization of the stand affects only the variability of the stand trait, not the aggregate value, unless the disaggregation function itself is not specified so as to ensure constrained symmetry (i.e., $\Delta BA=\Delta BA'$).

In addition to functional simplicity, the advantage of these simulators would seem to be that, for single-species, even-aged stands, a stand level functional resolution may indeed be sufficient. One may argue that the disaggregative simulator will maintain a sufficient functional resolution while providing the user with the apparent resolution of an individual-tree simulator without the disadvantages associated with long term projections of models with a higher degree of dimensionality.

The primary problem with a simulator whose functional resolution is at the stand level is that the dynamics may be poorly defined for stands which are not even-aged single species stands. One must assume that the macro-level function is sufficient to describe aggregate dynamics. This may be an untenable assumption for more heterogeneous aggregates. Furthermore, if the disaggregation is driven strictly by tree dimension, then one must also assume that allocation of growth within an aggregate can be fully determined by this dimension. Not only might this be a problem when there is a high degree of heterogeneity, it may also present problems in modeling thinning response. For example in simple proportional allocation based on some tree dimension, a method to be described later, there may be no distinction between different types of thinning with regard to how growth is allocated among trees. That is, thinning will produce the same proportional effect on all trees in the stand; if tree growth is boosted by thinning then all trees will show the same proportional response.

The higher level of apparent resolution in disaggregative simulators is dictated by a disaggregation function. This is simply a function which disaggregates any given trait based on the empirical distribution in the higher dimensionality of the input. These functions vary somewhat between simulators. They are all based, to some degree, on allocating growth according to the distribution of some tree dimension in the aggregate. This distribution may relate to diameter alone or some more complex function of diameter, number of trees and height. Growth may be allocated by diameter (Leary et al. 1979), basal area (Harrison and Daniels 1987), or volume (Dahms 1983, Zhang 1990). Functions are generally either based on an additive allocation or on a proportional allocation and may, or may not, maintain a constrained symmetry. The following discussion explores the particular applications of constrained symmetry as applied in disaggregative simulators.

One of the more well constrained disaggregation functions was described by Harrison and Daniels (1987). This is an additive disaggregation scheme, and may be expressed as:

$$\Delta \mathrm{ba}_{ip} - \overline{\Psi}_p = \kappa_p \cdot [\, ba_{ip} - \widehat{\mu}_p \,].$$

where:

Δba_{ip}= gross basal area growth for the ith tree in period p with expectation μ,

ba_{ip}= basal area for the ith tree in period p,

$\kappa_p = \alpha_1 \cdot exp\left(\alpha_2\, S\right) \cdot H_p^{\alpha_3}$,

$\overline{\Psi}$ = average growth per tree from the gross basal area growth function,

$\widehat{\mu}_p$ = sample mean basal area,

H_p = dominant height at period p, and

S = site index.

There are a number of important features of this particular disaggregation scheme. One is that growth is distributed among trees by an additive allocation, and this scheme is constrained so that symmetry is maintained. The sum of basal area growth for individual tree projections equals predicted stand growth rate. This is because deviations about a sample mean sum to zero. Furthermore, it can be shown that κ_p is a logical minimum for the relative average growth rate:

$$\frac{\overline{\Psi}_p}{\widehat{\mu}_p} > \kappa_p.$$

One drawback of this disaggregation function is that it is conceivable, in theory anyway, to obtain negative growth rates.

This additive disaggregation scheme also tends to provide monotonically increasing variance in tree basal area over time. In actuality, variance in basal area will be dependent on the allocation of mortality. If mortality were allocated proportionately, or if there is no mortality, then variance will increase. If mortality is allocated among smaller trees, then this may not be the case.

An example of a proportional disaggregation function is that of Dahms (1983), which allocates tree volume increment instead of basal area increment. In general, a proportional allocation rule is based on the ratio between some expression of tree dimensions w, and its stand level aggregate, W. Given this ratio then some prediction of interest, y, may be established as:

$$y = Y \cdot \frac{w}{W} = \overline{Y} \cdot \frac{w}{\overline{W}}.$$

Note that this ratio can also be expressed as a function of the means rather than the aggregates. In this second expression the ratio $\frac{w}{\overline{W}}$ may be referred to as relative tree size. Generalizations of this simple model have been developed. Zhang (1990) used a second degree polynomial of relative tree size rather than a linear function. The significance of this will be evident later. One implication of this general strategy is that the coefficient of variation of y is equal to the coefficient of variation of w. That is, if y is an expression of the growth in w, such that $y = w + \Delta w$, then the trait y will have a constant coefficient of variation over time. Also, if the coefficient of variation is constant, variance itself will increase as long as growth is positive. As with the additive disaggregation scheme, this may also depend on the allocation of mortality.

Symmetry is maintained by defining a proportional allocation function such that the proportion sums to 1.0 over the entire stand. There is no possibility of negative growth being forecast for any given element (tree) because allocation is based on a strictly positive ratio.

For the Dahms expression, w is established as:

$$w_i = d_i^{1.818} \cdot h_i^{1.786} ,$$

and growth is allocated to tree volume, by the following function:

$$\Delta v_i = \Delta V \cdot \left\{ \frac{d_i^{1.818} \cdot h_i^{1.786}}{\sum_i \left(d_i^{1.818} \cdot h_i^{1.786} \right)} \right\} ,$$

where:

$\Delta v_i =$ change in volume of tree i in the aggregation,

$\Delta V =$ change in total aggregate volume,

$d_i =$ breast height diameter of the ith tree at the start of the projection period,

$h_i =$ total height of the ith tree at the start of the projection period.

The ratio of ΔV and the sum of w_i over i is a constant for all trees. This ratio dictates the slope of the line relating volume growth and this particular function of diameter and height (w_i). Other examples of this type of allocation include the function of Clutter and Jones (1980), and Pienaar and Harrison (1988).

The proportional allocation function may be an oversimplification of the relationship between growth and tree dimension. This was found to be the case by both Leary et al. (1979), and Zhang (1990), who both used a generalization of this basic approach. While both of these functions were more flexible as to the relationship between growth and tree dimension, this was achieved at the cost of symmetry. Either, however, can be constrained so as to maintain invariance between stand and tree predictions.

There is yet another possible means of addressing the problem of oversimplification while maintaining symmetry. The disaggregation function as traditionally applied has relied on very simple assumptions of the relationship between the stand growth and the growth of any individual tree. This is not done of necessity, and there are means by which, in theory at least, a traditional individual-tree growth model could be used as a disaggregation function. The distinction between the two can be made on the basis of two characteristics: complexity and constraints. Historically a disaggregation function is much simpler than the functions used in individual-tree models. The disaggregation function is conceptually based in the allocation of pre-determined stand growth being fixed, and the individual tree growth being derived from that fixed stand growth. This usually is affected by some type of constraint embedded in the function. The individual tree allocation of growth is implied by the form of the disaggregation function assumed. Therefore this implied tree growth function is constrained by the stand growth projections.

The system by which this might be applied to growth, such as basal area increment, would be to establish the dynamics through active aggregation of the macro level. Given the earlier example of predicted stand growth [2.1], and the example tree growth equation [2.2]

The allocation of growth then can be established by the ratio,

$$\widehat{R} = \frac{\Psi(S,D,A)}{\tilde{g}(\psi)} . \qquad [2.7]$$

where the function $\tilde{g}$ aggregates the i micro-level predictions to the stand level.

A disaggregation function, ψ', can then be developed to allocate gross basal area growth to tree i by combining equations [2.2] and [2.7]:

$$\psi' = \widehat{R} \cdot \psi(w,p,S,D).$$

It is evident that this is nothing more than a scaling of the micro-relation $\psi(w,p,S,D)$, by the function $\Psi(S,D,A)$. However it also functions in precisely the same fashion as a disaggregation function.

Any individual-tree growth equation may be constrained in the preceding manner. The primary difference between this method and traditional disaggregative models is that the individual-tree models are generally more complex and may provide for greater variability in growth response and more sensitivity to individual-tree characteristics found to be related to tree growth.

This application of individual-tree growth functions does represent a distinct change in philosophy. Rather than stand growth being derived from the micro-relation (individual-tree growth), individual-tree growth becomes subservient to the defined stand growth (macro-relation).

2.8 Discussion

Existing disaggregation functions which are constrained to maintain symmetry all depend on a linear relationship between growth and some measure of tree dimension. However, in two applications of a proportional allocation of growth, some evidence was found to suggest a linear function is often inappropriate (Leary et al. 1979, Zhang 1990). In neither of these applications is symmetry constrained. The method of disaggregating growth by means of a specific growth function is intuitively appealing since the disaggregation function is itself an implied individual-tree growth function. And by application of this type of disaggregation function, one merely scales the micro-relation, based on the macro-relation. However, generalizations of model behavior are difficult if not impossible to define and the models themselves loose some of the beneficial simplicity embodied in more traditional disaggregation models. Whatever means is employed to disaggregate, users need to seriously consider the applicability of any given system, with an emphasis on the implications of assumptions which are foundational to the system.

Disaggregative models traditionally do not include a tree rank variable, and while tree rank and tree dimension are most certainly correlated, the relationship between the two is generally not linear. The relationship between tree basal area and basal area in larger trees, for example, is linear only when the distribution of tree basal area is approximately uniform. The problems with a lack of a rank variable may be illustrated if one considers a proportional allocation of basal area growth based on tree basal area. Unless the expression for density in the macro-relation (stand growth function) is somehow sensitive to type of thinning (i.e. thinning from above or below) then this structure cannot distinguish between different types of thinning in the effect on growth of any particular tree. In other words, it would matter not which trees one thins, as long as the basal area removed is kept constant, all sample trees would be predicted to respond identically.

To this point, the discussion has focused on a very simple illustration of a growth and yield model. In application, however, mortality functions will generally be included, as well as models for predicting height, crown length, or any other components which are used to predict growth in the driving function(s). In order for the earlier example of a model to predict basal area growth to be viable, mortality functions would be required. The addition of the mortality function to the system may complicate the structure of a disaggregative model substantially. One fairly straightforward means of structuring such a model is shown in Figure2.5. Here, disaggregation functions allocate both gross stand basal area growth and predicted stand mortality (*M*). This function of predicted stand mortality produces a probability of tree mortality which is then applied to *n*, yielding the number of trees lost to mortality (m) among those represented by the subject tree. These functions are represented as ψ'_1 and ψ'_2 respectively. Net stand basal area growth may then be obtained via a passive aggregation function. An example of a function which could be used to determine aggregate mortality (Ψ_2) is the self-thinning rule (Smith and Hann 1984).

$$\begin{tikzcd}
w \arrow[rr] & & \psi'_1(w,\Delta BA) \arrow[rr] & & \Delta ba \\
n \arrow[rrr] \arrow[dd, "g"'] & & & \psi'_2(n,M) \arrow[r] & n,m \arrow[ddd, "\tilde{g}"'] \\
& & & & \\
D \arrow[r] & \Psi_1(S,D,A) \arrow[r] & \Delta BA \arrow[uuu] \arrow[dl] & & \\
N \arrow[r] & \Psi_2(N,D,\Delta BA) \arrow[rr] & & M \arrow[uuu] & \Delta BA',\Delta BA'_{net} \\
& & & & M'
\end{tikzcd}$$

Figure 2.5. Illustration of the active aggregation structure of a disaggregative simulator including a mortality component. The function *g* represents the active aggregation functions, Ψ_1 and Ψ_2 the basal area increment and mortality functions. The disaggregation function, ψ'_1, is a function of both tree dimension and predicted basal area increment. The passive aggregation function, $\tilde{g}$, is used to obtain net basal area increment ($\Delta BA'_{net}$) or gross basal area increment ($\Delta BA'$) from unit area expansion factor (n) and mortality (m).

From Figure 2.5, it is evident that the macro-relation for basal area growth influences, or drives, all other functions in this simple system. Furthermore, while gross basal area growth is clearly a stand-level growth function, net basal area growth is derived by means of a passive aggregation scheme, much as would be done in an individual-tree/distance-independent model. Therefore the anticipated benefit of a disaggregative approach may not be realized with respect to net basal area growth. In this particular example symmetry is only a concern with respect to the estimation of gross basal area, since there is no parallel active aggregation scheme for net basal area.

This is by no means the only structure by which disaggregation could be employed; there are numerous options. If, for example, Ψ_1 is defined as a function predicting net, rather than gross, basal area growth, the structure changes substantially. Furthermore, tree mortality need not be expressed as a disaggregation function; Ψ_2 could be dropped from the model altogether and the disaggregation function replaced with a more traditional individual-tree mortality function.

The disaggregative approach is a structure which, in application, may exhibit elements of individual-tree/distance-independent models. The manner in which this is manifested may vary in different applications. A modeler may use this approach as a foundation for all components, or may opt for a partial application where some subset of the models are driven by this methodology.

2.9 Conclusion

Individual-tree simulators have the disadvantage of high dimensionality along with the benefit of very flexible means of describing the stand. Passive aggregation forces the modeler to depend on the specified tree models for stand growth and, furthermore, to make an assumption that any aggregate errors are not compounded over time. Indeed, experience has shown that the greatest challenge in developing an individual-tree model comes when all the components are brought together and the process of verification yields questionable aggregate behavior. This may occur despite apparently well behaved component functions.

One with a reductionist point of view may argue that a proper, or well specified, suite of driving functions ensures that the simulator will be well behaved. However, models are by definition simplifications of complex phenomena, and we cannot be certain what the effects of these simplifications will be. This may be an indication of problems with the aggregation itself which is a reflection of mortality prediction.

One method which may be used to ensure desirable long term behavior, is to constrain some component in concert with some allocative algorithm. This, in effect, causes the individual tree to take on some of the characteristics of the disaggregative simulator. As such, the same problems may arise in dealing with some structurally diverse stands. This solution to the problems introduced by high dimensionality is fraught with difficulties itself. The application of the Reineke's stand density index, as in ORGANON and some variants of Prognosis, for example, may not be well suited to either mixed species or stands without a fairly well defined unimodal diameter distribution.

The disaggregative simulator is truly in keeping with the spirit of whole stand modeling. Because of this, the disaggregative simulator requires an assumption that the stand dynamics are functionally well defined. Without this assumption, one faces a tradeoff between the advantages of lower functional resolution (lower dimensionality and presumably a more well behaved system of equations for long term projections) and the disadvantage of a poorly conceived system of equations due to the lack of homogeneity in the system being modeled. Assumptions of linearity and the lack of indices of tree rank may result in models which are over-simplified and very limited in application.

If one may assume very homogeneous conditions, such aggregate functions may be acceptable. Application of a traditional disaggregative approach to mixed-species, uneven-aged stands is not recommended because simple linear size growth relationships will likely over-simplify the process. In situations where either simulator may be appropriate, the disaggregative simulator is, in theory, to be preferred for predicting aggregate states. It is not yet evident that this theory translates well to application. That is to say, this has not been confirmed empirically. Some means of disaggregation may not apply well to certain simulations of management activity. The stand structure, as forecast by the allocation of growth via the disaggregation function, is not necessarily superior to the individual tree growth forecast.

One promising technique is the application of traditional individual-tree models in a disaggregative setting, constrained so as to ensure symmetry with some stand-level estimator of growth or mortality. This type of structure offers sensitivity to tree rank and tree dimension while still relying on predictions of stand growth for aggregate dynamics.

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Chapter 3

Evaluation of Individual-Tree/Distance-Independent and Disaggregative Prediction Methods for Douglas-fir Stands in Western Oregon

3.1 Abstract

Efficiency of a number of disaggregative methods and two individual tree methods are evaluated in terms of their ability to predict five-year basal area increment for Douglas-fir stands in western Oregon. Models were developed for predicting gross stand basal area increment and individual-tree diameter increment. In addition, models were developed to disaggregate the passive increment prediction methods to the tree level.

Passive and active prediction schemes are evaluated for both the tree level, and the stand level predictions. Generally, the individual-tree approach was superior to a disaggregative approach for both prediction of stand and tree growth. However, this superiority diminished significantly when crown ratio was eliminated from the individual-tree models. This suggests that at least some of the disparity between the two is due to the presence of crown ratio in an individual-tree passive aggregation approach. The additive disaggregation approach of Harrison and Daniels (1987) appeared to be best suited to young stands (less than 50 years of age). The linearity assumption required for this particular model appeared to suffer for older stands with larger trees. The two whole stand gross growth models used in this study were inferior to the individual-tree method for predicting gross basal area growth for one period.

3.2 Introduction

The modeling of stand dynamics can be achieved by a number of different methods which may be distinguished from one another by their associated level of resolution (Munro 1973). However differences in levels of resolution associated with contrasting modeling philosophies are often not readily apparent. The whole-stand/disaggregative and individual-tree/distance-independent simulators, although different functionally, bear some similarity to one another due to the ability of both to produce output of the same resolution. Thus, the functional disparity between these two may be obscured by the unity of apparent resolution. Examples of the former are: Dahms (1983), Harrison and Daniels (1987), and Zhang (1990). Examples of the latter include Prognosis (Stage 1973), CACTOS (Wensel et al. 1986) and ORGANON (Hann et al. 1992).

The individual-tree modeling approach is based on growth projections for each individual in a sample of trees representative of the stand, or aggregate. The functional components of these approaches, model such traits as height growth, diameter growth, probability of mortality and crown dynamics. The sample tree list is updated based on these predictions, and stand dynamics are derived from the aggregate of these predictions. This can be described as an active aggregation scheme (Ijiri 1971). Individual-tree models are capable of simulating stands diverse in structure and species composition. Furthermore, because more information is required to run individual-tree models, they have the potential for better predictions based on this more complete representation of the stand.

The whole-stand/disaggregative approach, in contrast, achieves predictions based on the dynamics of the aggregate (passive aggregation). This may be achieved by modeling gross basal area growth (e.g., Harrison and Daniels 1987) or gross volume growth (e.g., Dahms 1983). These methods reflect a whole stand approach with the added ability to take this growth projection and distribute it among trees in a sample tree list. For some simulators the step of disaggregating growth is an option based on the resolution of the input data. Until the disaggregation takes place, this is a stand growth model.

The flexibility of the disaggregative model is such that they are capable of making predictions based on stand level attributes alone, or with the more complete stand description afforded by a tree list. This is a very attractive feature, as users are not obligated to provide a tree list, but may do so if one is available. If a tree list is maintained, then the disaggregation function is the means by which the stand growth predictions are linked to tree level descriptions of the stand. In addition the disaggregation function is solely responsible for describing changes in within stand variability.

A disaggregation function may be structured in such a way as to maintain symmetry between stand and tree growth. This symmetry means that stand growth remains invariant to the application of the disaggregation function. That is, if disaggregated growth is then summed, resulting stand growth is equal to the stand-level prediction.

A symmetric growth and yield prediction system is one for which the prediction of stand growth is consistent with the aggregation of individual-tree predictions. Aggregation of tree values does not therefore affect stand-level prediction of growth. If a growth and yield simulator is built in this manner it can be said to maintain a constrained symmetry (Ijiri 1971).

Disaggregation functions vary in complexity and in their ability to maintain symmetry in predictions. In this paper we will attempt to empirically address two questions pertaining to these different methodologies: (1) Does the disaggregative approach adequately reflect the higher resolution dynamics of stands? And, (2) which approach best reflects aggregate dynamics? In order to evaluate these questions, we will focus on gross basal area increment for a single five-year growth period. Use of multiple growth periods would unnecessarily complicate the analysis by incorporating additional components and design features which vary greatly from one simulator to another and are often an expression of the modelers unique approach to the problem at hand. Because separate components of simulators do not function independently, we don't want to obfuscate the issue with other aspects of simulator design.

3.3 Data

The data used in this study are from 105 Douglas-fir stands in western Oregon. The stands are all located on Oregon State University's College of Forestry, Forest Properties; specifically McDonald Forest. McDonald Forest is located in the mid-Willamette valley just west of Corvallis Oregon. The sample is primarily composed of even-aged second-growth stands of Douglas-fir (*Pseudotsuga menziesii* (Mirb.) Franco). In some of the stands there is a minor component of other conifers, usually grand fir (*Abies grandis* (Dougl.) Lindl.). King's (1966) site index ranged from 90 to 136 feet (breast height base age=50). Stand ages ranged from 26 to 142 with breast height basal area ranging from 12 to 270 $\frac{\text{ft}^2}{\text{ac}}$.

The sampling methodology was described in detail by Hann and Larsen (1991). A grid of points were installed in each stand, at densities ranging from one per acre to one every five acres. At each point on the grid a nested plot design consisting of a 20 BAF variable radius plot for trees greater than 8.0 inches, a 1/57 acre plot for trees from 4.1 to 8.0 inches and a 1/228 acre plot for trees less than 4.1 inches in diameter was installed. All conifers greater than four inches in diameter at breast height (4.5 feet) were bored for past five-year radial increment. In addition, tree heights, diameters and crown ratios were measured. Stand and tree growth were established using these measurements.

Because the measurement of past diameter growth of trees less than four inches in diameter was not consistently obtained across the whole data set, this analysis will only consider those trees in the stand with breast height diameters greater than 4.0 inches. While this may not be the optimal method for development of a working simulator, we feel it will not dramatically affect the results of this analysis. For most of these stands, the understory trees less than 4.0 inches consist largely of suppressed non-crop trees, many of which are prime candidates for mortality in the near future. For full implementation of some of the disaggregative approaches discussed in this paper, a more complete range of diameters would be more desirable.

3.4 Analysis

3.4.1 Gross Basal Area Growth Rate Function

Two aggregate gross basal area growth rate equation forms were chosen. The first is based on age, King's site index (King 1966) and stand density index (Reineke 1933). Application of this equation does not require any tree-level information beyond breast height diameter in order to estimate stand basal area and trees per acre. The second equation replaces stand density index with an estimate of crown surface area for the stand. A number of different crown surface area estimation methods were initially applied, with the best being those of Biging and Wensel (1990). Since the crown surface area equations are dependent on more individual-tree information, such as heights and crown ratio, this equation is limited in application to stands for which such information is available.

The equations were fit using linear regression and a log-transformation of the dependent variable. This transformation was found to provide residuals which appeared to be approximately normally distributed, implying an approximate log-normal distribution for basal area growth. The first gross basal area growth equation is expressed as:

$$E(\Delta BA) = exp[\theta_{01} + \theta_{11} \cdot ln(A) + \theta_{21} \cdot \frac{S}{A} + \theta_{31} \cdot ln(SDI)], \qquad [3.1]$$

where,

ΔBA = 5-year aggregate gross basal area growth (square feet per acre),

A = stand age,

S = site index (ft),

SDI = stand density index (log of trees per acre).

The second aggregate gross basal area growth equation is expressed as:

$$E(\Delta BA) = exp[\theta_{02} + \theta_{12} \cdot ln(A) + \theta_{22} \cdot \frac{S}{A} + \theta_{32} \cdot ln(CSA) + \theta_{42} \cdot CSA^2], \qquad [3.2]$$

where,

CSA = crown surface area, proportion of unit area (Biging and Wensel 1990).

A number of variations of equations [3.1] and [3.2] were also investigated but those presented here provided the lowest mean squared error. The ordinary least squares (OLS) parameter estimates for equations [3.1] and [3.2] are shown in Table 3.1. The adjusted r-squared ($\bar{r}^2$) values for these two log-linear fits were 0.74 and 0.82 respectively.

Table 3.1. Parameter estimates (and standard errors) and residual mean squared error from the log-transformation, linear regression of models [3.1] and [3.2]. Intercept terms are corrected for log-bias with $\frac{\text{MSE}}{2}$ (Flewelling and Pienaar 1981).

Model	$\hat{\theta}_0$	$\hat{\theta}_1$	$\hat{\theta}_2$	$\hat{\theta}_3$	$\hat{\theta}_4$	MSE
1	0.943847 (0.95)	−0.654745 (0.20)	0.171678 (0.090)	0.805055 (0.065)	––	0.0617
2	2.380485 (0.81)	−0.435310 (0.17)	0.175736 (0.076)	0.879799 (0.063)	0.000595242 (0.00022)	0.0434

In general we have a predictive equation, which we will refer to as $\Psi(\mathbf{Z},\hat{\boldsymbol{\theta}}_j)$, within which expected gross stand basal area increment is expressed as a function of some vector of stand parameters, **Z**, and a vector of parameter estimates, $\hat{\boldsymbol{\theta}}_j$, j=1, 2 for models 1 and 2 above respectively.

3.4.2 Additive Disaggregation Function

While a number of approaches have been used in developing a disaggregation function, these generally either allocate growth additively or proportionately. Harrison and Daniels (1987) presented a methodology for development of a disaggregative simulator that can be used to illustrate an additive disaggregation function:

$$[\Delta ba_i - \Psi] = \kappa \cdot [ba_i - \hat{\mu}_{ba}], \tag{3.3}$$

where,

Δba_i = individual tree basal area increment of the tree i in the aggregate,

Ψ = estimated gross basal area growth for trees in the given aggregate,

ba_i = basal area of the tree i in the aggregate,

$\hat{\mu}_{ba}$ = mean basal area for sample trees in the given aggregate.

This disaggregation function is based on the assumption that tree growth is linearly related to tree size. The parameter $\hat{\kappa}$ varies from stand to stand, and is expressed as a function of site index and dominant height (H) with the following assumed relationship:

$$E(\hat{\kappa}) = \gamma_1 S^{\gamma_2} \cdot exp(\gamma_3 \cdot H). \tag{3.4}$$

The simplicity of this model is an attractive feature. The allocation function is dynamic. That is, the disaggregation coefficient $\hat{\kappa}$ changes over time with changes in dominant height.

Model [3.3] is formulated so as to provide constrained symmetry (Ijiri 1971). This symmetry insures invariance to aggregation. That is, data from a tree list may be aggregated to stand-level statistics prior to initiation of the simulator without affecting predictions of stand growth. In theory, a more generalized model may be developed by adding terms to the disaggregation function as long as any additional terms also maintain a linear relationship with basal area increment.

For each of 105 stands, κ was estimated using OLS on a model relating basal area growth and basal area:

$$\Delta ba_{ip} = \kappa_{0p} + \kappa_p \cdot ba_{ip} + \varepsilon_{ip}, \tag{3.5}$$

for tree i in stand p. The values obtained for $\hat{\kappa}_p$ ranged from 0.00389 to 0.678, with a mean of 0.1245. All of these were significantly different from zero, the largest p-value associated with t-tests of the significance of $\hat{\kappa}$ (H_0: $\kappa=0$) was 0.017, most were well below 0.001. In terms of linear association between basal area and basal area increment, there is a tremendous range as illustrated in Figure 3.1. The plots in Figure 3.1 were selected to cover a range of linear associations between tree growth and tree basal area. In general, the best linear relationships were associated with the youngest stands.

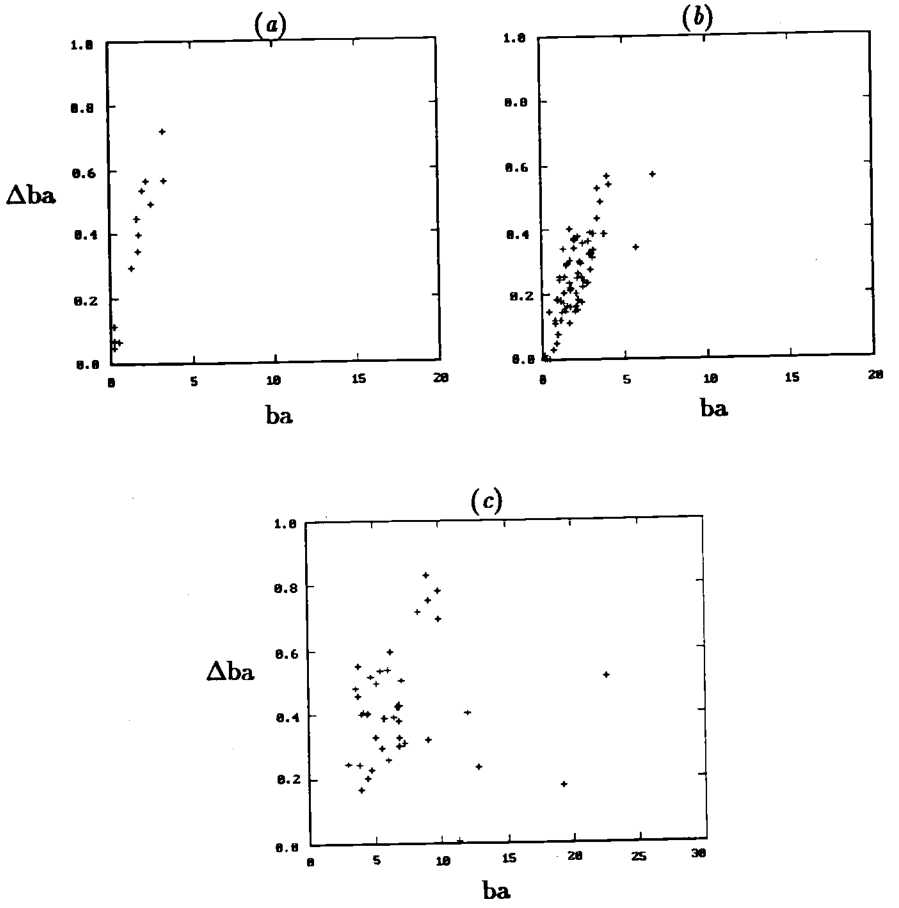

Figure 3.1. Three selected plots illustrating the relationship between basal area (in^2), and basal area increment (ft^2) for sampled trees. 3.1(*a*) shows a plot with a correlation coefficient of 0.95. 3.1(*b*) shows a plot with a correlation coefficient of 0.81. 3.1(*c*) shows a plot with a correlation coefficient of 0.16.

Considering correlation coefficient as an index of the linear association between basal area and basal area increment for each stand, we find values as high as 0.95, yet others were less than 0.10. These fits tended to be worse for older stands (Figure 3.2), possibly indicating a shortcoming in predicting tree growth for older stands. This finding was further evaluated by adding a quadratic term to equation [3.3].

On all but three of the stands, a quadratic term was significant (p-values less than 0.05) with most p-values for the quadratic term less than 0.01. This problem was evident most often in stands with large trees. Homogeneous young stands did indeed seem to maintain an approximately linear relationship. However, the presence of any large trees forming a positive skew diameter distribution seemed to accentuate the problem of nonlinearity in the equations for the disaggregation coefficient, $\hat{\kappa}$.

The linearity assumption apparently is not as reliable among older stands, where increasing variability in stand structure with stand age results in a less well-defined relationship between increment and basal area. This within stand heterogeneity may also reflect changes in management strategies over time. It is not known if the young stands of today will, in time, develop into the older stands of this data set.

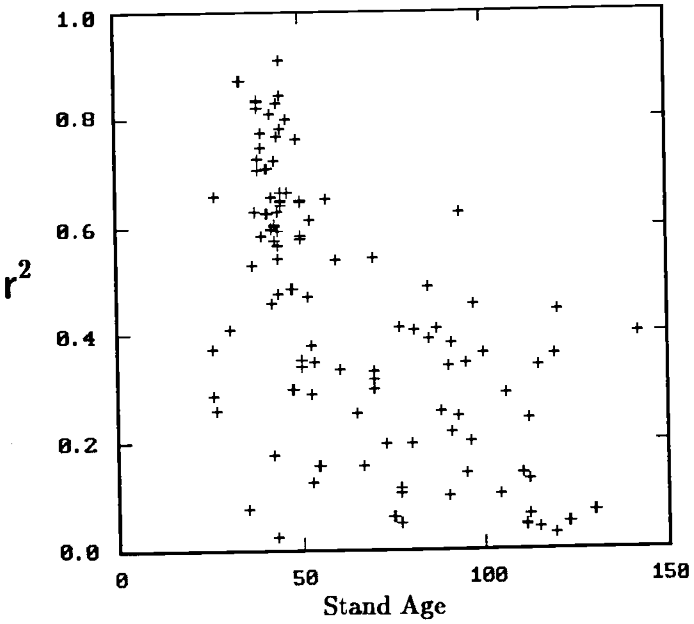

Figure 3.2. Indices of fit (r^2) plotted over stand age for the OLS fit of $\Delta ba = \kappa_0 + \kappa_1 ba$, for 105 Douglas-fir stands in western Oregon.

The disaggregation coefficient is predicted for individual stands as a function of dominant height and site index. In our analysis a similar model was also considered which used age instead of dominant height, however, the dominant height equation [3.4] provided superior fit statistics. One would expect that the disaggregation coefficient, κ would be negatively correlated with *H*, as is the case (Figure 3.3). The coefficient may be interpreted as an estimator of the ratio of standard deviations of basal area growth and basal area, that is $\kappa \simeq \frac{\sigma_{bag}}{\sigma_{ba}}$. Since tree basal area is the sum of basal area increment, and the variance of the sum should exceed the variance for any one period, one would then anticipate that κ would be less than one and would decrease as stand age (or dominant height) increases. This does appear to be the case. The values of $\hat{\kappa}$ varied from 0.00389 to 0.678 with this largest value being somewhat of an outlier, as all but four observations were below 0.40.

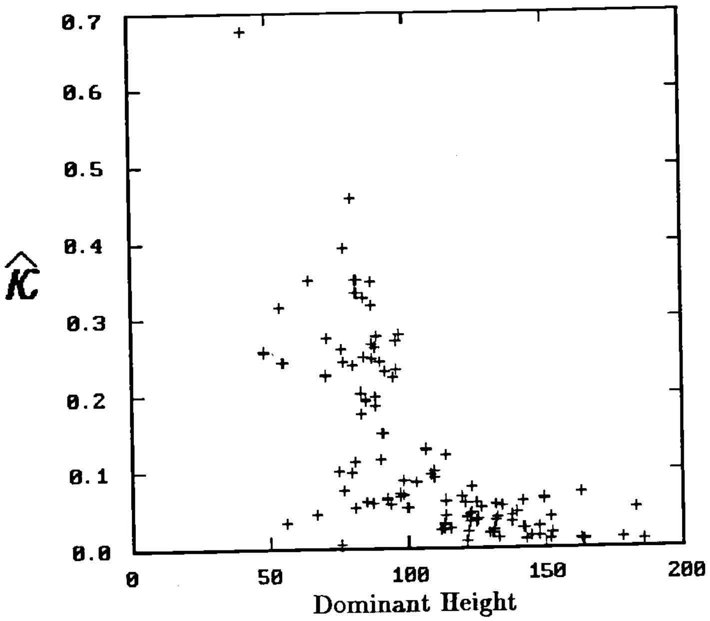

Figure 3.3. Plot of $\widehat{\kappa}$ over dominant height for 105 Douglas-fir stands in western Oregon.

There is a weak relationship between site index and $\widehat{\kappa}$ (Figure 3.4.). This relationship is not as well defined as that between $\widehat{\kappa}$ and H. Three dimensional graphical analysis of this data did not reveal any other trends which might be hidden by viewing dominant height and site index independently.

A function may be developed by obtaining estimates for the vector γ in equation [3.4]. This results in a predictive system which is sensitive to stand age and site productivity. However, since dominant height in the disaggregation function, and stand age in the gross growth function are both even-aged stand concepts, the application of this system to stands which are not even-aged is inappropriate.

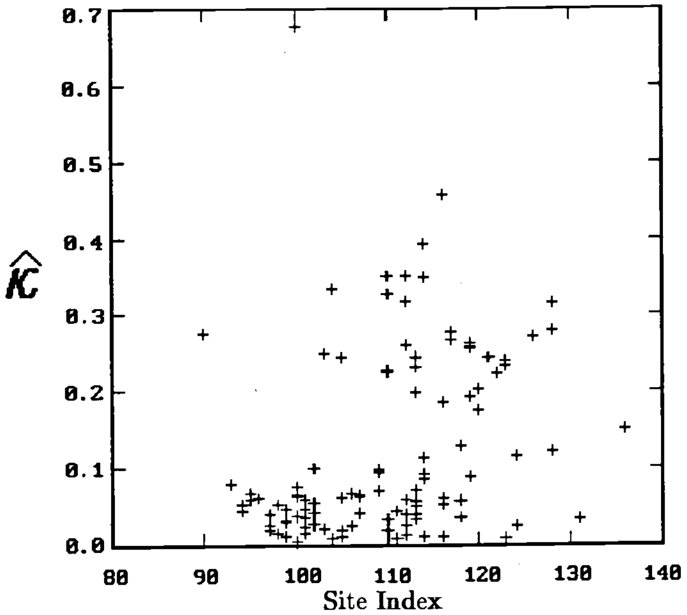

Figure 3.4. Plot of $\widehat{\kappa}$ over King's (1966) site index for 105 Douglas-fir stands in western Oregon.

The values of $\widehat{\kappa}_p$ for each of the stands (p = 1,2,...,105), were used as the dependent variable in model [3.4] above. However, in order to find a more linear solution locus, model [3.4] was reparametrized in the following manner:

$$E(\widehat{\kappa}) = exp[\widehat{\gamma}_1' + \widehat{\gamma}_2 \cdot ln(S) + \widehat{\gamma}_3 \cdot H] \ . \qquad [3.6]$$

The parameter estimates for model [3.6] were obtained using iteratively re-weighted non-linear least squares with a weight of $\frac{1}{V(\widehat{\kappa})}$, where V($\widehat{\kappa}$)=estimated variance of κ from the OLS fit. The results of this regression are shown in Table 3.2. The unweighted $\bar{r}^2$ is 0.6081.

Table 3.2. Results of nonlinear regression on disaggregation coefficient, $\widehat{\kappa}$ in equation [3.6].

Parameter	Estimate	Asymptotic Standard Error
$\widehat{\gamma}'_1$	-5.46155	4.240
$\widehat{\gamma}_2$	0.977221	0.8662
$\widehat{\gamma}_3$	-0.0182865	0.002838

The application of equation [3.6] is then:

$$\Delta\widehat{ba} = \frac{\Psi(Z,\widehat{\theta}_1)}{TPA} + \widehat{\kappa}\cdot\left\{ba - \frac{BA}{TPA}\right\}, \qquad [3.7]$$

where,

TPA = stand trees per acre,

BA = total stand basal area at breast height.

The technique suggested by Harrison and Daniels for disaggregation is not limited to the simple linear equation expressed above. The model can be generalized by adding additional terms. One possible generalization is the addition of crown ratio to the model:

$$[\Delta ba_i - \widehat{\mu}_{\Delta ba}] = \widehat{\kappa}_1\cdot[ba_i - \widehat{\mu}_{ba}] + \widehat{\kappa}_2\cdot[cr_i - \widehat{\mu}_{cr}], \qquad [3.8]$$

In this formulation the parameter κ_1 can be fit using the same equation used in the restricted model. Using the same techniques applied above, κ_1 estimates were obtained using OLS regression, and these were used in a nonlinear fit of equation [3.6] with results shown in Table 3.3. It should be noted that in the regression analysis of equation [3.8], the κ_2 term was often of marginal value. The improvements in fit statistics were not dramatic, $\bar{r}^2$ values rarely improved more than 0.10.

Table 3.3. Results of nonlinear regression on disaggregation coefficient, $\widehat{\kappa}_1$ in equation [3.8], a generalization of the Harrison and Daniels disaggregation model.

Parameter	Estimate	Asymptotic Standard Error
$\widehat{\gamma}'_1$	-3.65155	4.256
$\widehat{\gamma}_2$	0.588408	0.8721
$\widehat{\gamma}_3$	-0.0196083	0.002952

This particular generalization has the advantage that information contained in crown ratio is brought to bear on predictions of individual tree growth. Crown ratio is a variable which has been used extensively in individual-tree growth equations (Stage 1973; Wensel et al. 1986; Hann et al. 1992). The disadvantage is obviously that a simple list of diameters alone will not be sufficient to power the disaggregation component of the model; crown ratio will be required. In addition, this system would require equations for crown change.

We could find no trends for relating $\widehat{\kappa}_2$ to any stand parameters. Accordingly we employed a weighted mean for all stands as a predictor. The weighted mean was 0.4104 with a standard error of 0.019.

The application of this particular model in allocating tree growth is then:

$$\Delta\widehat{ba} = \frac{\Psi(\mathbf{Z},\widehat{\theta}_2)}{TPA} + \widehat{\kappa}_1 \cdot \left\{ba - \frac{BA}{TPA}\right\} + \widehat{\kappa}_2 \cdot \left\{cr - \overline{CR}\right\}, \qquad [3.9]$$

where,

$$\overline{CR} = \frac{\sum_i \left(cr_i \cdot n_i\right)}{TPA},$$

n_i= number of trees per acre represented by the subject tree.

Note that, as with the simpler version of this model, invariance is maintained: $\sum_i (\Delta\widehat{ba}_i \cdot n_i) = \Psi(\mathbf{Z},\widehat{\theta}_2)$. The remaining terms all sum to zero.

3.4.3 Proportional Allocation Disaggregation Function

Another means of disaggregating growth is a proportional allocation approach such as that used by Clutter and Jones (1980) and Dahms (1983). The general form of this type of model is:

$$\frac{w_i}{W} = \frac{g(u_i)}{\sum_i g(u_i) \cdot n_i}, \qquad [3.10]$$

where,

w_i = some trait of interest (e.g., volume growth, basal area),

W = predicted aggregate of w,

$g(u)$ = a function of some measured tree dimension (e.g. diameter, height).

A simple derivative of this form for basal area growth is:

$$\frac{\Delta ba}{\Delta BA} = \frac{ba_i}{\sum_i (ba_i \cdot n_i)}. \qquad [3.11]$$

By multiplying both sides of equation [3.11] by trees per acre, the left hand side could be viewed as an index of relative tree growth and the right hand side as an index of relative tree dimension. This is the general approach used by Zhang (1990), in generalizing [3.11]. In this generalization, the left hand side of [3.11] is identified as relative tree growth (*rtg*), which is the same variable used by Dahms. The right hand side is a polynomial of relative tree size (*rts*), which is explicitly defined by Zhang as predicted tree volume divided by stand volume. That is, g(u) is a tree volume function. The Zhang generalization is:

$$rtg_i = \phi_0 + \phi_1 \cdot rts_i + \phi_2 \cdot rts_i^2. \qquad [3.12]$$

The elements of the parametric vector ϕ are estimated as a function of stand parameters. Equation 3.10 above is then (approximately) a special case of Zhang's model with ϕ_0=0, ϕ_2=0, and ϕ_1=1. One problem with this generalization is that, unlike the more simplified model of Dahms, symmetry is not maintained.

A constraint can be established which will produce the desired symmetry in application of the system. This constraint may be expressed as:

$$\widehat{\phi}_0 = \frac{1}{\sum_i n_i} \cdot \left\{ 1 - \widehat{\phi}_1 - \widehat{\phi}_2 \cdot \frac{\sum_i g(u_i)^2}{\left(\sum_i g(u_i) \cdot n_i \right)^2} \right\}, \qquad [3.13]$$

We developed predictors for basal area increment using both the restricted and generalized proportional allocation model. For this application we defined the following variables:

$$rtg_i = \frac{\Delta ba_i}{\Psi(\mathbf{Z},\widehat{\theta}_1)},$$

$$rts_i = \frac{ba_i}{BA}.$$

The estimates of ϕ for these stands did not reveal any trends useful for predicting either ϕ_1 or ϕ_2. Although the two are highly correlated, as was found by Zhang, neither parameter showed any significant relationship with other stand variables. Therefore we calculated weighted means for both variables: $\widehat{\phi}_1$=0.80735 (s.e.=0.0252), $\widehat{\phi}_2$=−3.5167 (s.e.=0.250). The function for the intercept term, $\widehat{\phi}_0$ is then:

$$\widehat{\phi}_0 = \frac{1}{TPA} \cdot \left\{ 0.19265 + 3.5167 \cdot \frac{\sum_i ba_i^2}{BA^2} \right\}.$$

Predicted growth with this model then is:

$$\Delta\widehat{b}a = \Psi(\mathbf{Z},\widehat{\theta}_1) \cdot \left\{ \widehat{\phi}_0 + \widehat{\phi}_1 \cdot rts_i + \widehat{\phi}_2 \cdot rts_i^2 \right\}. \qquad [3.14]$$

3.4.4 Individual Tree Growth Rate Equation as a Disaggregation Function

An individual tree growth equation can also be used as a disaggregation function. Generally this does not maintain symmetry with any particular whole stand growth function other than that implied by the active aggregation of such a function. However, some individual tree functions may, within the context of the particular application, actually act as a symmetric allocator of growth. An example of this is use of individual-tree mortality functions in ORGANON (Hann et al. 1989). In this particular application, situations may arise wherein the individual-tree mortality functions are scaled according to an aggregate level prediction - that provided by the size-density trajectory of Smith and Hann (1984). Symmetry is maintained in these situations and this particular phase of simulator operation is actually a disaggregative approach.

Similarly, the basal area growth equation may be scaled by a whole stand basal area growth prediction, thereby maintaining symmetry with the passive aggregation scheme. Given an aggregate gross basal area growth equation, $\Psi(\mathbf{Z},\widehat{\theta})$, and an established individual-tree equation:

$$\Delta\widehat{b}a_i = \psi(\mathbf{x}_i,\widehat{\beta}),$$

where:

$\mathbf{x}_i$ = a vector of predictors for individual-tree diameter growth for tree i, [3.15]

then the proper allocation of growth can be established by the ratio:

$$\widehat{R} = \frac{\Psi(\mathbf{Z},\widehat{\boldsymbol{\theta}})}{\sum_i \left(\psi(\mathbf{x}_i,\widehat{\boldsymbol{\beta}}) \cdot n_i\right)} . \qquad [3.16]$$

A disaggregation function, ψ', then can be developed to allocate gross basal area growth to tree i by combining equations [3.15] and [3.16]:

$$\psi' = \Delta\widehat{ba}_i \cdot \widehat{R} . \qquad [3.17]$$

This is actually another proportional allocation scheme, not unlike that used by Dahms. Instead of tree dimension, however, this method uses estimated basal area growth divided by the aggregate of estimated basal area growth. Another perspective of this method is that predicted tree growth is scaled by the ratio of the two estimates of stand gross basal area growth. For this predictive model, an individual-tree model is required. For our analysis, we fit individual-tree diameter growth regressions for Douglas-fir and grand fir.

The regression for individual-tree diameter growth functions was based on the findings of Hann and Larsen (1991) for conifer species in southwest Oregon. Hann and Larsen (1991) found that the basal area growth prediction function was unreliable for very small trees, and instead used diameter increment as a response variable. Employing the fully specified model for predicting individual-tree diameter increment, parameter estimates were obtained for the model:

$$E(\Delta d) = exp[\beta_0+\beta_1 \cdot f_1(d)+\beta_2 \cdot f_2(d)+\beta_3 \cdot f_3(S)+\beta_4 \cdot f_4(bal,d)+\beta_5 \cdot f_5(BA)+\beta_6 \cdot f_6(cr)] \qquad [3.18]$$

where,

Δd = five-year diameter increment in inches,

$f_1 = \ln(d+1) \cdot 0.1$,

$f_2 = d^2 \cdot 0.0001$,

$f_3 = \ln(S-4.5)$,

$f_4 = \frac{bal}{\ln(d+5)} \cdot 0.00001$,

$f_5 = \sqrt{BA} \cdot 0.01$,

$f_6 = \ln\left\{\frac{(cr+0.2)}{1.2}\right\}$,

$cr = \frac{\text{live crown length}}{\text{total tree height}}$,

d = diameter at breast height (in.),

bal = aggregate basal area in larger trees than the subject tree (ft^2/ac),

BA = aggregate basal area (ft^2/ac).

The parametric vector β was estimated (Table 3.4) using the nonlinear least-squares technique of Marquardt (1963). This fit was iteratively re-weighted assuming that the variance of the error term was proportional to the predicted growth. This weight was found to be optimal by Hann and Larsen (1991). There are 9526 Douglas-fir and 595 grand fir sample trees in the data sets.

Table 3.4. Results of nonlinear regression on the full individual-tree diameter growth rate equation [3.18].

Parameter	Douglas-fir		grand fir	
	Estimate	Asympt. std. err.	Estimate	Asympt. std. err.
$\hat{\beta}_0$	-4.69641	0.2991	-2.34621	1.363
$\hat{\beta}_1$	3.39517	0.1752	5.94642	0.8051
$\hat{\beta}_2$	-4.28248	0.1241	-9.76101	1.465
$\hat{\beta}_3$	1.15615	0.06069	0.555335	0.2769
$\hat{\beta}_4$	-4.46313	0.2571	-2.90672	0.8624
$\hat{\beta}_5$	-2.37026	0.3960	-4.70849	1.738
$\hat{\beta}_6$	1.19951	0.02374	1.12712	0.1058

Those modelers working on disaggregative models have, by convention, avoided inclusion of crown ratio. In a disaggregative setting where crown information is generally absent, a growth function without crown ratio is more appropriate. Accordingly, we fit a reduced form of model 3.18, shown below as model 3.19:

$$E(\Delta d) = exp[\beta_0 + \beta_1 \cdot f_1(d) + \beta_2 \cdot f_2(d) + \beta_3 \cdot f_3(S) + \beta_4 \cdot f_4(bal,\ d) + \beta_5 \cdot f_5(BA)] \quad [3.19]$$

Results of this regression are shown in Table 3.5 below.

Table 3.5. Results of nonlinear regression for individual-tree diameter growth rate equation excluding crown ratio [3.19].

Parameter	Douglas-fir		grand fir	
	Estimate	Asympt. std. err.	Estimate	Asympt. std. err.
$\hat{\beta}_0$	−5.55071	0.3352	−1.82328	1.503
$\hat{\beta}_1$	3.00611	0.1976	6.27648	0.8772
$\hat{\beta}_2$	−3.67024	0.1379	−10.1022	1.622
$\hat{\beta}_3$	1.32808	0.06792	0.446850	0.3061
$\hat{\beta}_4$	−6.17127	0.2933	−2.85420	0.9310
$\hat{\beta}_5$	−7.11432	0.4319	−10.7188	1.732

3.4.4 Individual-Tree Prediction

The models developed above were then used to establish eight different predictive methods for individual-tree basal area growth (P_1 - P_8). These are defined below:

P_1: Reduced individual-tree diameter growth rate equation [3.19]

P_2: Full individual-tree equation [3.18]

P_3: Disaggregative equation [3.17], using reduced individual-tree [3.19] scaled by predicted stand basal area growth [3.1],

P_4: Disaggregative equation [3.17], using full individual-tree [3.18] scaled by predicted stand basal area growth [3.2],

P_5: Harrison and Daniels disaggregative equation [3.7], method with predicted stand basal area growth [3.1],

P_6: Simple proportional allocation disaggregative [3.11] method with predicted stand basal area growth [3.1],

P_7: Harrison and Daniels generalization [3.9] with predicted basal area growth [3.2],

P_8: Constrained generalized proportional allocation[3.14] with predicted basal area growth [3.1].

Two of these are standard individual-tree/distance-independent predictive models (P_1 and P_2); the remaining models are disaggregative with a symmetry constraint.

For P_1 and P_2, diameter increment for an individual tree is estimated as dictated and then transformed into basal area increment as $\Delta\widehat{\mathrm{BA}} = \frac{\pi}{576} \cdot \left((d+\widehat{\Delta d})^2 - d^2\right)$. Those models requiring crown ratio were paired with the whole-stand equation [3.2] because this whole stand growth model is dependent on an aggregation of individual-tree crown measurements.

The residuals (observed—predicted) from these eight predictive schemes were used to calculate the mean squared error and $\bar{r}^2$ for the complete data set. These results are presented in Table 3.6, below.

Table 3.6. Individual-tree summary statistics for the residuals of predictive methods P_1 - P_8 on the entire data set, where residual = observed — predicted.

method	$\bar{r}^2$	bias ($\hat{b}_i$)	variance (σ_i^2)	MSE
P_1	0.3903	−0.02624	0.03249	0.03318
P_2	0.4701	−0.003969	0.02882	0.02884
P_3	0.2781	−0.02384	0.03872	0.03929
P_4	0.4001	−0.01714	0.03236	0.03265
P_5	0.1260	0.03450	0.04638	0.04757
P_6	−2.9963	−0.12488	0.2019	0.2175
P_7	0.2288	0.04268	0.04015	0.04197
P_8	0.1735	0.001055	0.04499	0.04498

The summaries in Table 3.6, indicate the superiority of the full individual tree model over all other methods. The reduced individual-tree and disaggregated full individual-tree models appear to work equally well. For these data, therefore, the loss in predictive power is approximately equal for dropping crown ratio and imposing a stand level growth constraint. The reduced individual-tree model with a whole stand basal area growth constraint (P_3), shows a substantial reduction in predictive ability. Both of the more traditional disaggregative approaches (P_5 and P_6) are much worse than the individual-tree based approaches (P_1- P_4), even those which use a tree function in a disaggregative approach. The addition of crown ratio to the Harrison and Daniels method resulted in a modest reduction in the MSE, from 0.048 to 0.042. However, P_4 has a substantially lower MSE of 0.033, so if crown ratio is to be used, the individual-tree function is superior. The generalization of the Dahms model resulted in a tremendous reduction in MSE, but even with this improvement the MSE is substantially worse than any of the individual-tree based methods.

It should be noted that the presence of a negative $\bar{r}^2$ indicates that the prediction generated is worse (has a larger mean squared error) than the sample mean. In typical regression applications, residual sum of squares is constrained to be less than the total sum of squares, thus $\bar{r}^2$ is, in most instances, positive. Since these predictions are not the direct result of ordinary least squares regression, the residual sum of squares is not so constrained.

Crown ratio, or the absence thereof, appears to be an important determinant of model performance. This was also found to be the case in prediction of height growth for individual trees in the ORGANON simulator (Hann and Ritchie 1988; Hann et al. 1992). The addition of crown ratio in the generalization of the Harrison and Daniels model does result in an improvement. However, among disaggregative approaches, the use of an individual tree growth model as an allocator of growth, either P_3 or P_4, is still superior.

The generalization of the proportional disaggregation method of Dahms (P_8), while vastly superior to P_6, is still nowhere near any of the individual tree approaches.

An earlier observation was that the assumptions required for the additive disaggregation method seemed to be affected by stand age. If so, then perhaps the benefit of using an individual-tree method would be less evident among younger stands. We calculated summary statistics for the predictive methods for stands less than 50 years old (Table 3.7). While mean squared errors for the Harrison and Daniels model did improve, so did all of the individual-tree based methods. Therefore the Harrison and Daniels model is no more ill-suited to older stands than are the individual tree models. However, MSE increased for both the Dahms model and it's generalization in the younger stands.

Table 3.7. Individual-tree summary statistics for the residuals of predictive methods P_1 - P_8 for stands less than 50 years of age, where residual = observed − predicted.

method	$\bar{r}^2$	bias ($\hat{b}_i$)	variance (σ_i^2)	MSE
P_1	0.5579	−0.03160	0.01618	0.01718
P_2	0.6525	0.001373	0.01356	0.01356
P_3	0.1812	0.009058	0.03187	0.03195
P_4	0.5362	0.001138	0.01810	0.01810
P_5	−0.1373	0.03756	0.04297	0.04438
P_6	−8.4282	−0.06467	0.3638	0.3679
P_7	0.2079	0.03169	0.02991	0.03091
P_8	−0.2503	0.02233	0.04829	0.04879

An ideal prediction scheme would be one for which there was nearly a one-to-one linear correspondence between observed Δba_i and prediction, P_{im}. This was evaluated by fitting a linear regression for residual as a function of predicted for each of the m predictive methods (m=1,2,...,8).

The results of this analysis are shown in Table 3.8. The ideal predictor has a slope and intercept of zero, or nearly so. A high $\bar{r}^2_m$ is indicative of poor fit, a linear trend in the residuals with respect to predicted growth, P_m. The individual tree methods are superior to the disaggregative methods, although the Harrison and Daniels method isn't a great deal worse than employing a reduced individual-tree growth function, and inclusion of crown ratio appears to result in a better fit.

Table 3.8. Results of analysis of residuals for linear trends.

method	intercept	slope	$\bar{r}^2_m$
P_1	0.005939	−0.094930	0.0279
P_2	0.020862	−0.078417	0.0069
P_3	0.071061	−0.28200	0.0872
P_4	0.051342	−0.20763	0.0586
P_5	0.13164	−0.34918	0.0933
P_6	0.22401	−0.79734	0.7966
P_7	0.098231	−0.20571	0.0254
P_8	0.12234	−0.38922	0.1433

The cumulative distribution of the absolute value of the residuals expressed as a percent (ϵ') is displayed for P_3, P_5, and P_6 in Figure 3.5. The ideal predictor would have zero values for all residuals and therefore would display a horizontal line at the 100% level over ϵ'. From this we see that, among the disaggregative approaches without crown ratio, the Dahms method is the least effective predictor. However, either of the models with crown ratio (whole-stand disaggregative or traditional individual-tree) are superior to any without crown ratio (Figure 3.6).

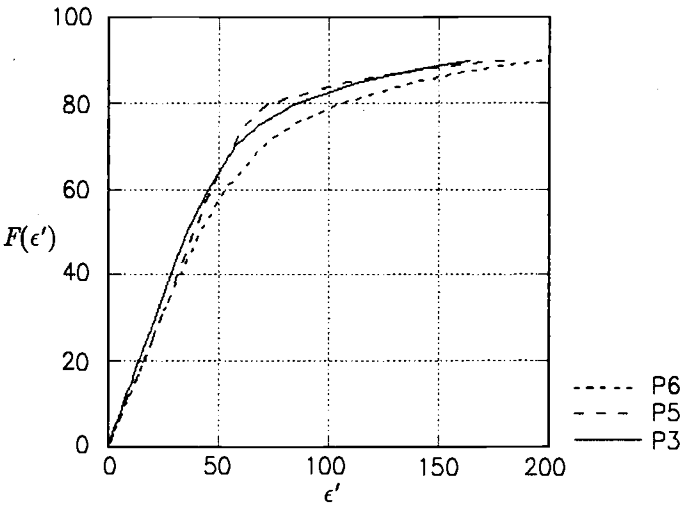

Figure 3.5 Cumulative distribution of the percent absolute deviation of residuals (ϵ') for all trees in the data set, for three of the active aggregation methods: reduced individual-tree scaled by predicted stand basal area growth (P_3), Harrison and Daniels-type model (P_5), and, simple proportional allocation model (P_6).

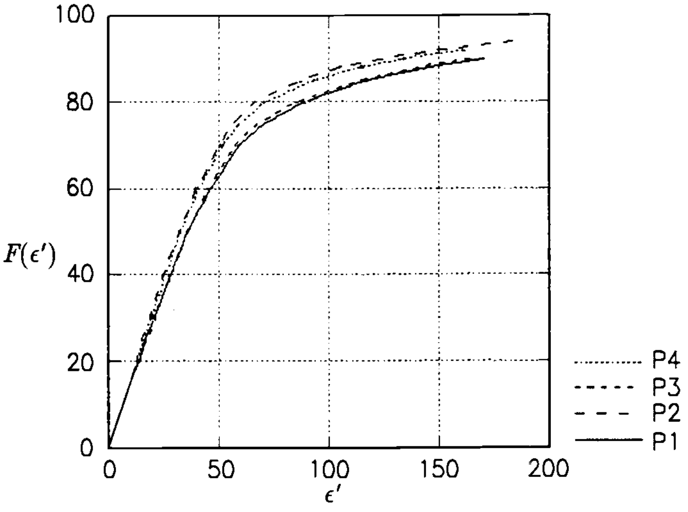

Figure 3.6. Cumulative distribution of the percent absolute deviation (ϵ') of residuals for all trees in the data set, for three predictive methods: reduced individual-tree model (P_1), full individual-tree model (P_2), reduced individual-tree model scaled by predicted basal area growth (P_3), and full individual-tree model scaled by predicted basal area growth (P_4).

3.4.4 Aggregate (Stand-Level) Prediction

Four different aggregate predictive methods may be implied by the preceding tree-level predictive schemes, these are:

AP_1: Predictions based on the aggregate of the reduced individual tree model [3.19],

AP_2: Predictions based on the aggregate of the full individual-tree model [3.18],

AP_3: Predictions based on whole stand predictive model [3.1] (with *SDI*),

AP_4: Predictions based on whole stand predictive model [3.2] (with *CSA*).

The first two of these are based on an aggregate of the predictions from the individual-tree predictive models. These predictions are made by summing the product of predicted tree growth and the per-acre expansion factor. The other two models predict the stand-level gross growth directly. Since gross-growth is used here, there is no reduction in expansion factors for mortality. The summary of residuals for these four models are summarized in Table 3.9.

Table 3.9 shows that the full specification of the individual-tree predictive method has the lowest mean squared error, however the bias is smallest with AP_4, a whole stand predictive method. For long projections, therefore, the whole stand approach may provide better predictions were this trend to hold. For short term projections, the individual-tree approach appears to be superior. It should also be noted, that the degree to which successive projections are independent may affect these conclusions. If the residuals for a given plot are highly correlated from period to period (that is, if an underestimate at time t_1 likely indicates a similar underestimate at time t_2), then the variance encountered may contain an element which is constant for the given plot over time. To the extent that this occurs, the bias may be offset by an underestimate of stand density over time, resulting in overestimate of growth.

Table 3.9. Summary statistics for the residuals of aggregate predictive methods AP_1-AP_4 for 105 Douglas-fir stands in western Oregon.

method	$\bar{r}^2$	bias ($\hat{b}_i$)	variance (σ_i^2)	MSE
AP_1	0.6914	−2.1419	19.3170	23.9050
AP_2	0.8193	−0.21905	13.9549	14.0030
AP_3	0.6517	−0.13175	26.9666	26.9839
AP_4	0.7797	−0.0033101	17.7941	17.7942

The individual-tree method without crown ratio, although not as good as the whole stand model with crown surface area (AP_4), has a lower mean square error than the whole stand model based on stand density index (AP_3). Note however that the predictive method AP_4 is dependent on the information needed for a individual-tree based prediction system. In order to calculate the crown surface area using the Biging and Wensel (1990) equations, a list of trees with crown ratio is required. In general, whole stand models, even disaggregative systems, do not maintain this information. A more standard approach, such as AP_3 which does not require crown information is only marginally better in terms of bias and is much worse in terms of variance than the individual-tree prediction with crown ratio (AP_2).

The cumulative distribution of the absolute value of relative residuals expressed as a percent shows that the distributions are very similar, and that the individual tree method, AP_2, has nearly 100 percent of the predictions within 40% of the actual growth. This is a great improvement over the predictions made at the tree level. The other observation that may be made is that, at the stand level, these predictive schemes generally look better. Whether one looks at $\bar{r}^2$, or the percentage of predictions which are within some percent of the actual growth rate, the aggregation is superior.

Despite the knowledge gained over years of stand growth and yield studies, and that stand growth is generally well defined for even-aged stands, the individual tree approach was superior predictive technique for this one growth period (Figure 3.7). Figure 3.7 also illustrates the general improvement in estimating stand growth versus tree growth among the individual-tree prediction methods when compared with Figure 3.6. This does not necessarily mean that this trend will hold over a long projection. However much of the difficulty in obtaining reasonable long-term projections with a individual-tree approach may be due to mortality functions. Existing individual-tree probability of mortality functions may not aggregate reliably. The effects of mortality prediction are beyond the scope of this study and unconstrained mortality estimation techniques are certainly not a necessity for individual-tree architecture.

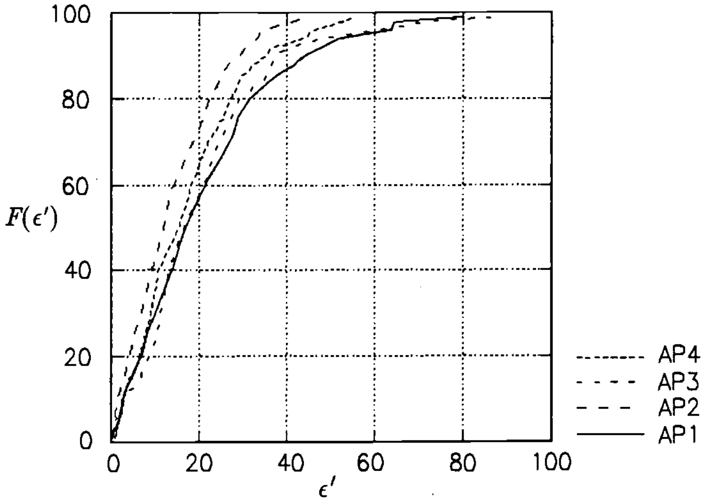

Figure 3.7. Cumulative distribution of the absolute value of residuals (ϵ'), expressed as a percent, for stand level predictions on 105 Douglas-fir stands: Aggregate of reduced individual-tree model (AP_1), aggregate of the full individual-tree model (AP_2), whole stand predictive model [3.1] (AP_3), and, whole stand predictive model [3.2] (AP_4).

3.5 Conclusion

We could find nothing in these data to suggest that the disaggregative approach is able to predict tree or stand basal area growth as well as an individual-tree approach. Crown ratio appears to be an important component in prediction of both tree and stand gross growth; the full individual-tree model consistently out performed both additive, and proportional allocation, disaggregative models. Use of the individual-tree functions in a disaggregative modeling approach did not result in any improvement in predicting stand or tree growth over the more traditional application of unconstrained individual-tree growth models.

We found that, of the two disaggregative approaches employed, the additive allocation system patterned after Harrison and Daniels (1987) was far superior to the simple proportional allocation, based on basal area. The constrained generalization of this proportional allocation, patterned after the work of Zhang (1990) was a great improvement over the simplified proportional allocation. While, it appears that the linearity assumption demanded by the Harrison and Daniels model does not hold as well for older stands in this data set, the effect of stand age on predictions is also evident for individual-tree predictive methods.

Since these stands are mostly even-aged and are dominated by a single species, we can't say what the results would be for more complex stands. However, one would expect that the whole stand models, in general, would suffer in their ability to predict growth for such stands. If disaggregative models were to work well anywhere, it should be in even-aged single-species stands, such as those in this study. The superiority of individual-tree approach for gross growth estimation may not hold for predicting net growth; this is partially dependent on mortality estimation, which may be an area where disaggregative methods will be beneficial.

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Chapter 4

Conclusion

The discussion of disaggregative and individual-tree/distance-independent modeling reveals a core problem for modeling in any discipline: How to determine the proper dimensionality for the functioning of a system. Conventional wisdom holds that longer projection periods require lower dimensionality in order to maintain reasonable predictions, and, therefore, simpler models are more appropriate for long projection periods. The disaggregative approach is a method which places a premium on model simplicity and expression of aggregate behavior. It is dependent on the development of a tenable whole stand model and a disaggregation structure which will provide the desired behavior of individuals in a stand.

Several problems with these models may be found. Some do not maintain perfect, or constrained symmetry between stand an disaggregated growth. Furthermore, the simplicity of traditional disaggregation models may be a handicap. Assumptions of linearity between tree growth and tree dimension, as well as the lack of any effect of tree position, may render them ineffective at expressing the variability within a stand over time. Yet, this is the primary goal of any disaggregation function.

In even-aged Douglas-fir stands, we found that of the traditional disaggregative models were incapable of predicting five-year growth of individual trees, or stands, as well as the passive aggregation of individual-tree/distance-independent models.

The application of typical individual-tree models in a disaggregative framework offers some promise. However all disaggregative approaches are handicapped by the need for a working whole stand growth model. The finding that unconstrained individual-tree models are superior predictors of stand growth is somewhat surprising, but it gives support to a reductionist perspective of modeling. It should be noted that this analysis focused only on tree growth, not on mortality. Yet mortality estimation is often a weak link in individual-tree/distance-independent growth models. Perhaps mortality estimation is a more fertile ground for disaggregative approaches to modeling than is the estimation of dimensional changes among individual-trees, since it is a necessary component for net growth.

The findings of this analysis are limited by the narrow range of species, stand conditions and time frame. There are many opportunities for further research in this area, given data of sufficient detail. In particular, long-term permanent plot data with periodic remeasurements over a wide range of stand conditions will be needed to better evaluate the differences between individual-tree and disaggregative models.

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