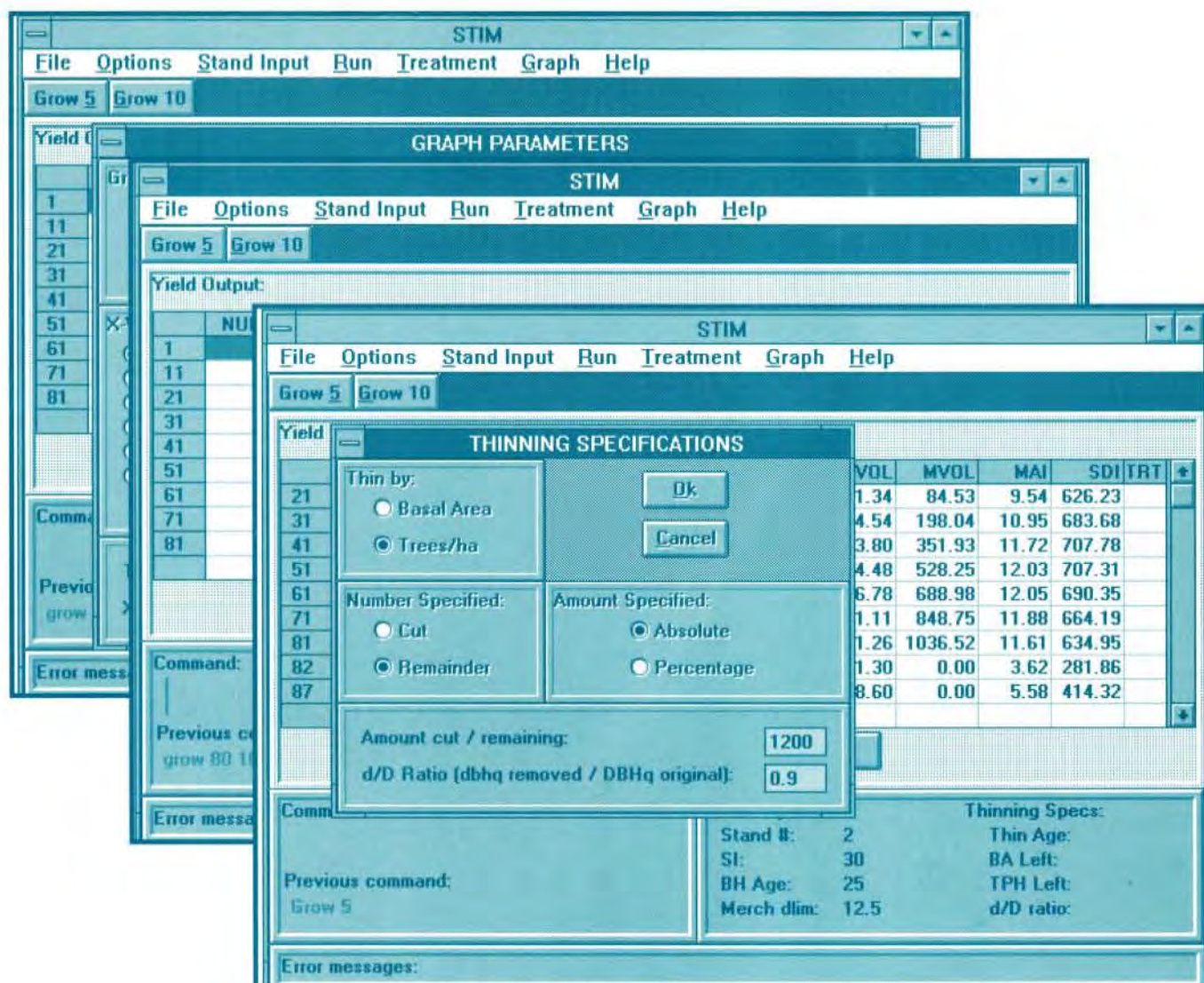# A guide to the STIM growth model

G.M. Bonnor, R.J. De Jong, P. Boudewyn and J.W. Flewelling

Pacific and Yukon Region • Information Report BC-X-353

The Pacific Forestry Centre is one of six regional and two national establishments of the Canadian Forest Service. Situated in Victoria with a district office in Prince George, the Pacific Forestry Centre cooperates with other government agencies, the forestry industry, and educational institutions to promote the wise management of the forest resources of British Columbia and the Yukon.

The Pacific Forestry Centre undertakes research in response to the needs of the various managers of the forest resource. The results of this research are distributed in the form of scientific and technical reports and other publications.

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A guide to the STIM growth model

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Contents

Abstract

The Stand and Tree Integrated Model (STIM) has been developed to make growth projections for inventory updates, for timber supply assessment, and for general management planning. It includes both a tree and a stand growth model component which make independent projections that subsequently are reconciled. A component for the projection of thinned stands is also included.

STIM is designed to operate on IBM® and compatible micro-computers. While the core of the program is written in FORTRAN, the user interface employs the Windows® environment: a main screen is presented to the user who makes choices related to data input, growth projections, management options, and output.

STIM has been implemented for western hemlock using a data set of 1339 permanent sample plots containing 5304 measurement sets. The plots are located in the Pacific Northwest.

The core of STIM is comprised of the predicting equations. These have been validated individually and jointly, sensitivity analyses have been performed, comparisons have been made between STIM and other growth models, and corrections and improvements have been made.

Résumé

Le modèle d'intégration STIM a été élaboré pour permettre d'établir des prévisions de la croissance dans le cadre de mises à jour de l'inventaire, d'évaluations de l'approvisionnement en bois et d'activités générales de planification de l'aménagement. Il comporte un volet sur la croissance des arbres et des peuplements qui établit des prévisions indépendantes qui seront par la suite rajustées et un autre sur les peuplements éclaircis.

Le STIM a été conçu pour fonctionner sur des micro-ordinateurs compatibles IBM. Le programme de base est en FORTRAN, mais l'interface utilisateur fait appel à l'environnement Windows qui présente un plein écran où sont offerts divers choix d'entrée de données, de prévisions de croissance, d'options d'aménagement et de sorties.

Le STIM a été appliqué à la pruche occidentale. Les données utilisées provenaient de 1 339 parcelles d'échantillonnage permanentes et comportaient 5 304 séries de mesures. Les parcelles sont situées dans la région nord-ouest du Pacifique.

Les équations prévisionnelles sont à la base du STIM. Elles ont été validées individuellement et collectivement et ont fait l'objet d'analyses de sensibilité. Le STIM a également été comparé à d'autres modèles de croissance et a subi les corrections et les modifications nécessaires.

Acknowledgements

The authors would like to thank the following:

Introduction

Better information on the growth and yield of second growth forests is needed for improved forest management. Foresters generally agree that much of this information can be provided by an integrated system of growth models which can be used to estimate future yield and growth of a stand, from stand establishment to harvest, given different starting conditions and silvicultural treatments. Many growth models which appear to be suitable already exist. When examined closely, however, they may turn out to be incompatible with the present inventory or to have other shortcomings.

The Pacific Forestry Centre has developed a growth model which should fit into a system of integrated models. STIM (Stand and Tree Integrated Model) can be used to estimate future growth and volume for inventory updating, determination of allowable annual cut, and management planning. The model will predict growth of a stand from establishment until harvest, starting at any intermediate point, for natural or managed stands. Although it is not designed as a silvicultural training tool, it can be used to make projections of silviculturally treated stands.

STIM has been developed for both natural and thinned stands of western hemlock (*Tsuga heterophylla* (Raf.) Sarg.). This species has been chosen because a good data set already exists which can be used to develop the model and validate the output. In the future, the model will be calibrated for other commercial species such as aspen (*Populus tremuloides* Michx.) and white spruce (*Picea glauca* (Moench) Voss), and modified to project mixtures of these two species.

The development of STIM, initiated in September 1990, is supported by the B.C. Forest Productivity Councils. The largest target client is the Ministry of Forests' Inventory Branch, which may use STIM for inventory update and projection.

The purpose of this paper is to help the user understand how STIM is structured, what the components are, how it works, and how the results have been validated. It is not a user's manual.

Model structure

Using the classification established by the Forest Productivity Councils of British Columbia (1991), STIM is classified as an empirical, integrated tree and stand growth model. It is unique in that it includes both a tree model and a stand model that make independent projections which subsequently are reconciled. The stand model predicts stand averages: top height increment is the "driver", and annual basal area increment is divided into survivor increment and mortality. The tree model is classified as distance independent: predictions are made by diameter classes or other "cohorts". These two models apply to stands with a top height of at least 5.5 m.

The components and the relationship among them is shown in the overview flow chart of the model structure (Fig. 1): Data input (A) may be from young stands having a top height of less than 5.5 m, in which case a rudimentary yield model projects the stand data to that height, or from older and taller stands. The data may be incomplete, in which case steps are taken to generate the missing data. Information about any silvicultural treatments (B) must also be supplied. The complete data set will be used in (C) and (D) to grow the stand and tree variables for the desired period. One option is to run either model alone. Normally, however, both models are used to make independent growth projections. In that case, the reconciliation step in (E) is used to ensure compatibility between the two sets of data. The resulting stand table is then summarized and output in (F).

STIM can be used with minimal input data requirements (site index and top height) or with a complete set of tree and stand data.

Results of the predictions are expressed in an augmented stand table which includes number of stems, basal area and volume per hectare, by tree classes. Additional details on the model components are given in Appendix 1.

The data

To develop STIM, data from approximately 1600 permanent sample plots in pure, even-aged stands of western hemlock (*Tsuga heterophylla* (Raf.) Sarg.) were obtained from nine forestry agencies in British Columbia, Washington and Oregon through the Stand Management Cooperative (Fig. 2, Appendix 2). These research installations and growth monitoring plots had been screened previously and were generally of high quality. However, with so many agencies supplying so much data, a considerable amount of time was spent on additional validation and summarizing of the data.

Data validation

The individual tree and plot data were edited to identify and correct errors, and to flag anomalies. For example, some trees might have missing or incorrect species codes, and some plots might be below a minimum specified size. Details are given in Appendix 3. Additional data errors were found and corrected as a result of developing and assessing the predicting equations.

With top height and change in top height being the main driving variables in the STIM model, it was important to ensure that adequate tree height measure-

ments were available for each plot. Initial editing of the data indicated that many plots had inadequate tree height data. To prevent a large number of plots from being discarded, it was decided to use the available tree height measurements to construct height-diameter equations, to use these equations to generate predicted heights for each tree in a plot, and to use only these predicted heights in all modelling efforts. Details of the methodology are given in Appendix 3.

At the end of the validation process, 1339 plots were retained for model construction. These plots had originally contained 6086 measurement sets, i.e., they had been measured 6086 times, but 782 sets had to be discarded because they had too few height measurements, so 5304 measurement sets remained (Appendix 3).

Data summary

Validation of the data produced a database. This database was summarized into tree and stand level growth and yield files. These files contained variables (Appendix 4) that described almost every aspect of stand and tree growth and yield. The stand and tree summaries were then used to develop the empirical equations for each model component.

Modelling is an iterative process: data summary and equation development identify problems with the data (e.g., insufficient coverage of a particular age range, trees that disappear between measurements, outliers in equation fitting, and need for new variables). To correct these problems, new data are acquired and validated, new summaries are compiled and new equations are developed. This cycle is repeated until some point is reached where the equations are deemed acceptable.

Predicting equations

A standard approach to develop each equation (Appendix 5) was taken: the appropriate data set was selected, scattergrams were produced to determine trends, an equation model was constructed and fitted to the data, and the behaviour of means, variances and residuals were analysed. Those equations found deficient in terms of goodness of fit, general trend, and extrapolation values were re-run until an acceptable version was obtained. Up to five such iterations were made and five versions developed.

The site-height equation is used to predict top height and top height increment, which is the "driver" variable. The site index equation is often used instead of the site-height equation but the two have different statistical properties and the resultant height-age curves are different: the site index equations have a bigger spread, particularly at very young or very old ages. In developing STIM, we attempted to ignore these differ-

ences and chose Wiley's (1978) site index equations. As expected, we found that the equations did not produce good top height estimates for stands less than 20 years of age. The estimates were sufficiently poor that we developed another set of equations intermediate between the site index and site height equations. The equations are given in Appendix 5 and the methodology is described in Appendix 6.

Model implementation: hardware and software

STIM is designed to run on MSDOS®-based personal computers (PC) with WINDOWS® 3.1 loaded. The minimum hardware requirement is for a 386 SX PC with a math co-processor and 4MB RAM, although a 486 DX PC is strongly recommended.

The STIM model comprises two parts; the core program and the user interface.

The core program is written in Microsoft Fortran and includes four key groups of FORTRAN routines, as well as various control routines to keep track of the logical flow of stand development. The four key groups are:

1. Sapling stand startup, real stand startup and various routines to estimate values not provided by the user. The only routines that are numerically complex are the Weibull recovery routines. They use numerical root finding methods to calculate the three parameters of the Weibull distribution function based on estimates of three properties: quadratic mean diameter, coefficient of variation of DBH2, and the 10th percentile of the DBH distribution.

2. Routines to grow the stand one year at a time. This entails updating each class of the tree list by adjusting stem frequency to account for mortality, and growing all DBH's and heights. Ingrowth may also be added. The steps in making an annual growth projection are to calculate growth in top height, unreconciled tree growth and mortality, ingrowth, unreconciled stand growth, and reconciled stand and tree growth.

The predicting equations (Appendix 5) form the building blocks for these routines.

3. Routines to perform thinnings to various specifications. They determine how many trees from each size class should be thinned in order to meet the user-specified criteria. Numerically, this is a root-finding problem. An alternative approach (not presently implemented) would let the user specify how many trees should be cut from each size class.

4. Routines to calculate volumes. Conceptually, this is quite simple since DBH and height are known for all elements of the tree list.

The user interface is written in Microsoft Visual Basic as a true WINDOWS application, and links

directly to the core program through a Dynamic Link Library. Of all the Fortran code, only the main program (which controls the program flow), has been rewritten in Visual Basic. All other Fortran coding remains unchanged. The user interface handles the data input, display and output, and provides for extensive manipulation by the user. The results of all tree and stand projections are stored in relational database files.

This PC based WINDOWS application, called WINSTIM, is the version of STIM made available to users, and thus forms the main product.

Model validation

The purpose of validating STIM is to identify weaknesses in the model and to assess the overall goodness of fit: are the projections close to real-life data, to empirical evidence, to expectations? Are they sensitive to variations of input variables? Having developed a set of satisfactory predicting equations, the validation (described below) begins with validation of the stand and tree models and progresses to sensitivity analyses, yield analyses, and comparison with other models.

Validation of stand and tree models

Two separate validation procedures were used: single-period, where projections were made for individual plots using as input the initial data of a single growth period, and compared against the actual plot data at the end of each period; and first-to-last, where projections (including thinnings) were made from the first plot measurement and compared with the plot data at the end of the measurement series, spanning up to 26 years. The computed residuals were summarized by classes of the independent variables, and trends were explored.

The primary purpose of the validation was to learn if the equations interacted in ways that introduced new and unexpected errors (single period), as well as to assess the potential for error propagation over longer projections (first to last). The reason that problems might be expected is that the models are a system of equations (Borders 1989): the input variables in one equation may be a prediction from another. Thus, there is no guarantee that the individually fitted equations will produce satisfactory results when used jointly, and the need for assessing the interaction among them arises. In the process of doing so, any programming errors that might cause the growth projections to "blow up", or to be substantially different from what was used in the earlier regression analyses, would also be uncovered. In validating the stand and tree growth models, several variables were examined: top height increment, basal area increment, mortality, stand density (trees per ha), ingrowth, and volume. At the end of a validation run, results were analysed and reviewed, and decisions

were made about the need to change the equations. Such changes were made, the validation was re-run, and so on until the equations were satisfactory.

The major results of the validation were:

1. The variance of the integrated model was considerably less than that of the tree model (when each was run separately), confirming that the integrated model is more robust.

2. Site index was not sufficient to explain the variability in basal area growth. Hence, five geographic regions were introduced into the basal area growth function: B.C. Wet Maritime, B.C. Dry Maritime, Coastal Washington, Coastal Oregon, and Western Cascades.

3. The single period validation indicated no significant errors or trends (at an alpha level of 0.05) in model predictions. Overall, basal area growth was underestimated by 2%, while top height increment and mortality were well predicted. The only major difference was in ingrowth basal area, with an overall 28% underestimate. This error is of minor importance, as it stems mainly from the thinned data where ingrowth was not modeled (based on the assumption that ingrowth is generally removed in operational thinnings).

4. Although the first to last validation revealed increased bias for most components (when compared to the single period), the magnitude of the errors remained similar, indicating that there were no major problems in error propogation over longer projection periods. For example, bias in basal area increment increased to a 4% underestimate, top height increment retained zero bias, while TPH mortality increased to an 11% underestimate.

Sensitivity analyses

These analyses consisted of running STIM with a basic set of input data for the 5-75 year age span, then repeating the run with one variable - or treatment regime - changed, and examine the trends to see if they were reasonable. The variables checked in this manner were:

- number of trees per ha changed from 1500 to 2500;
- site index changed from 20 to 40 m (Fig. 3);
- stand thinned at age 7 to 800 trees per ha;
- stand thinned again at age 55 to 380 trees per ha;
- stand thinned at age 7 to 300 trees per ha;

Other options were also explored, e.g. use of different mortality predictors, site index equations, and volume equations.

Some of the potential problem areas revealed by the sensitivity analyses were: low mortality at high ingrowth rates; generally unrealistic long-term projections from the tree model; and very little separation in predicted yields at older ages between high sites and

low sites. These problems were addressed by modifying the predicting equations, by placing restrictions on their use, by using a substitute equation, or by strengthening the fit through the use of additional plot data.

Comparisons with other models

To many growth modellers, the comparison with other models represents the ultimate test. Is the new model within range of the others, or "out in left field"?

STIM was compared with five other models used in the Pacific Northwest. The approach was to project for 130 years all six models using a basic input data set, then plotting several key outputs (volume, basal area, trees per ha and top height) over age. STIM placed within the range of the other models, which was the desired result. An example is shown in Figure 4. Differences among the models could be attributed partly to the data used in their construction: models giving high predictions were constructed from fully stocked research plots, while models giving low predictions were constructed from operational, growth monitoring, or inventory plots.

Applications

This chapter describes some of the major applications of STIM: after a basic growth projection, the user is shown a series of options available at the various steps in the projection sequence. The emphasis is on what the options are and the resulting output, not on how to run STIM - that is covered in the User's Manual.

A simple growth projection

Having installed STIM on the computer, the user will see the main screen. Figure 5 shows this screen with a stand generated through the "Stand Input" option in the top menu bar and grown for 80 years.

The "Stand Input" option includes three choices, of which the "Generate a Stand" choice enables the user to input stand parameters. In Fig. 5, the following values have been input: SI=30, HTOP=14, BA=20 and TPH=7000. In the absence of other input, STIM now generates the other stand and tree data.

To grow the stand, several avenues are available: the "Run" option, the "Grow" option, or the "Command" option. The last was chosen here. The result is a list of the projected values for the stand at ages 20–100 years.

Options for input of stand data

The three options of the "Stand Input" selection are:
1) Generate a sapling stand:
A screen is presented for input of data: site index (required) and, optionally, top height, trees per ha and quadratic mean diameter;

2) Generate a tree stand:
A screen is presented for input of stand data: site index and top height (required), and basal area, quadratic mean diameter, diameter at the 10th percentile, and coefficient of variation (optional).

3) Enter a tree list:
A screen is presented for input of a full set of tree and stand data: plot size, site index, breast height age, and a stand list (Fig. 6);
Data can also be input through the "command" line box.
Any missing data are generated by STIM to ensure that a full set of data is available for input into the predicting equations.

Growth options

A stand can be grown on STIM using three approaches:
1) under the "Run" option of the menu bar, select "Grow a Stand". A screen is presented for input of specifications on the number of years to grow the stand, or the size (in terms of quadratic mean diameter, top height, volume or age) to which the stand should be grown (Fig. 7);
2) the "Command" line box at the bottom left of the main screen. This option was demonstrated in Fig. 5, by typing "GROW 80 10" in the Command box.
3) the "Grow 5" or "Grow 10" options on the second bar;

Treatment: thinning

The only treatment option currently available is the thinning option. It can be accessed by selecting "Thin a Stand" on the "Run" option, or through the "Command" option. The user will be prompted about the amount and type of thinning to be done (Fig. 8). A thinned stand is tagged with a "T" in the last column (Fig. 9).

Output options

Model output can be in the form of tables (Figs. 9 and 10) or graphs: Figure 11 shows the specifications for graph production, while Figures 12 and 13 illustrate two types of graphic output. The graphs can be displayed on the monitor or printed.

Other options

On the menu bar, the "File" option includes a capability of accessing a filed set of stand and tree data, and of deleting one or more stands.

The "Options" include model control choices:
- to run both tree and stand models, or one only;
- to reconcile to the tree or stand model;
- in selecting tree volume equations;

- in calculating mortality and generating diameter distributions; and
- in specifying ingrowth height.

It also includes a capability of setting and changing default values.

The "Run" option includes a capability of entering batch commands to process batch data.

Discussion and conclusions

Model structure

STIM has a number of features which, in aggregate, make it unique. Predominant among these is the inclusion of both a tree growth model and a stand growth model that are used to make independent projections which are reconciled annually before a result is produced. This approach has several advantages:

- discrepancies can focus attention on critical model assumptions;
- the two independent projections can be used to check each other;
- if no stand table (tree list) is required or if the necessary input data are not available, the stand growth model alone may be used;

Other special features of the model are:

- gross growth rather than net growth is projected in the model. Gross growth of basal area is defined for a multi-year period as the sum of final basal areas of all survivor trees and mortality trees, less the initial basal area of the same trees; and
- top height increment is used as an independent variable in the prediction of basal area increment.

This helps to keep all of the stand dimensions in accord with each other.

Data input

As stated at the beginning of this report, STIM is designed to provide growth projections for inventory update, for allowable annual cut determination, and for management planning. Given these purposes, STIM must accept the kind of inventory data available in the area to which it will be applied. A problem common to growth models using inventory data as input is that the broad inventory data (essentially obtained from air photos) available for all stands are insufficient to run the models, while the detailed data obtained from field sample plots are only available for some stands. For example, to run STIM, the number of trees per ha must be known; it is not available from the air photos and, while it is obtained in the field plots, only some stands are sampled. The new provincial inventory will hopefully provide the data necessary to drive STIM. Until then, two unsatisfactory alternatives exist: develop equations so that trees per ha can be estimated from the air photo data, or group the stands so that each group has sufficient detailed data.

Prediction equations

The equations used to make projections of current values comprise the core of the model. STIM contains 21 such equations. Two of the most critical ones will be discussed here.

The top height increment equation is critical because it is the driver: the output of annual top height increment is used as input into many other equations. The common approach is to select an existing site index equation. For STIM, an equation developed by Wiley (1978) was chosen as the most appropriate one. During the validation phase, however, it became apparent that this equation did not match the trend of the data for young stands. The solution was to develop a new equation (Flewelling 1992) which is offered as an option to users of STIM (Appendix 6).

The survivor basal area increment equation of the stand model is critical because basal area is arguably the most important stand variable. The equation was validated and modified extensively. This process was complicated by the inclusion of the thinning module in the equation. In the end, a good fit was achieved, partly through the inclusion of factors accounting for regional differences.

The accuracy of the prediction equations also depends on the availability of data. While the database of 1339 plots is large, it does have some weak spots: few plots are in stands younger than 20 years or older than 80 years. Attempt to strengthen the database have not been successful. Thus, the regeneration model is weak and projections of the tree and stand models beyond 80 years are extrapolations.

Data and model validation

Data validation is a lengthy process and really is never truly complete. The best one can achieve is that the database is in a form that meets the standards set for the project. For STIM, editing and validating height and dbh were of paramount importance because STIM is a height-driven model, with survivor basal area increment as the key equation. Editing procedures were very rigorous for these components of the database.

The model validation worked well. It helped to identify weak spots in STIM and provided sufficient diagnostics that remedial action could be started. It was particularly important in assessing the effect of thin-

ning on growth, and in comparing the performance of the stand and the tree model.

Treatment modules

As noted, the only silvicultural treatment effect currently implemented in STIM is the thinning module. More modules will be added to the model to make it more versatile: additional treatments such as pruning, effects of pests such as defoliators, and an economics overlay to provide value as well as volume predictions. Fertilization of western hemlock has not been shown to be beneficial in all cases. That removes the economic incentive to do so and makes modelling difficult. Hence, no fertilization module is planned.

User interface

Having a user friendly interface is a key feature in "selling" a model. That led to the choice of the Windows environment and the Visual Basic language for the shell of STIM, with the core being maintained in FORTRAN. Problems in linking these two languages turned out to be minor.

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A

Data
Input

C

Stand
Growth Model

E

Recon-
ciliation

F

Data Summary
and Output

B

Treatment
Information
Input

D

Tree
Growth Model
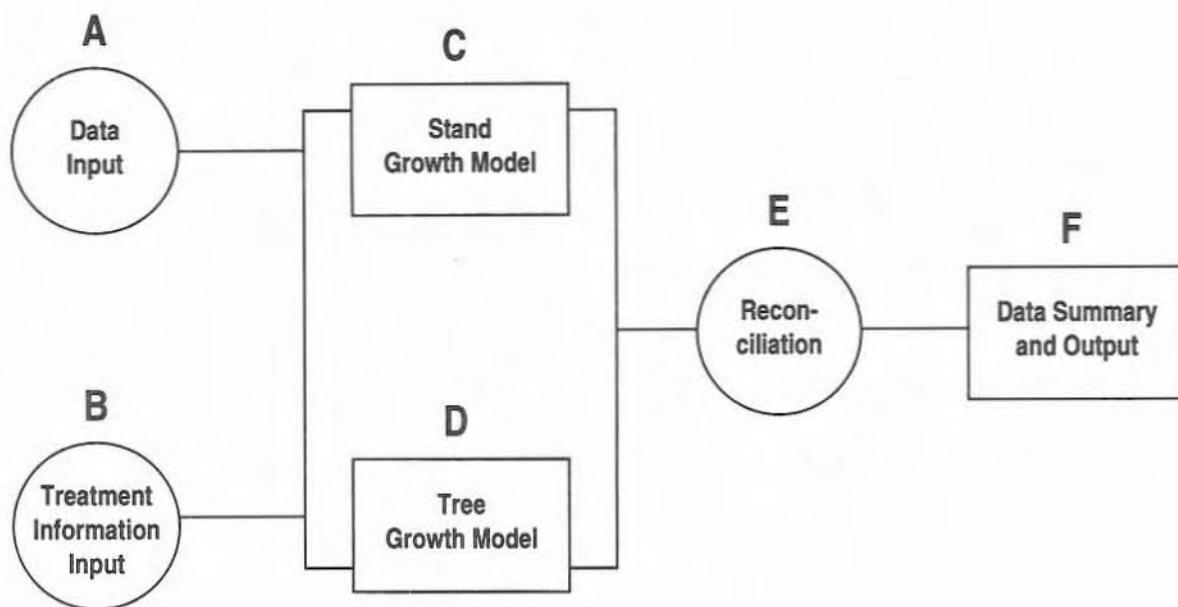
Fig. 1: Framework of STIM
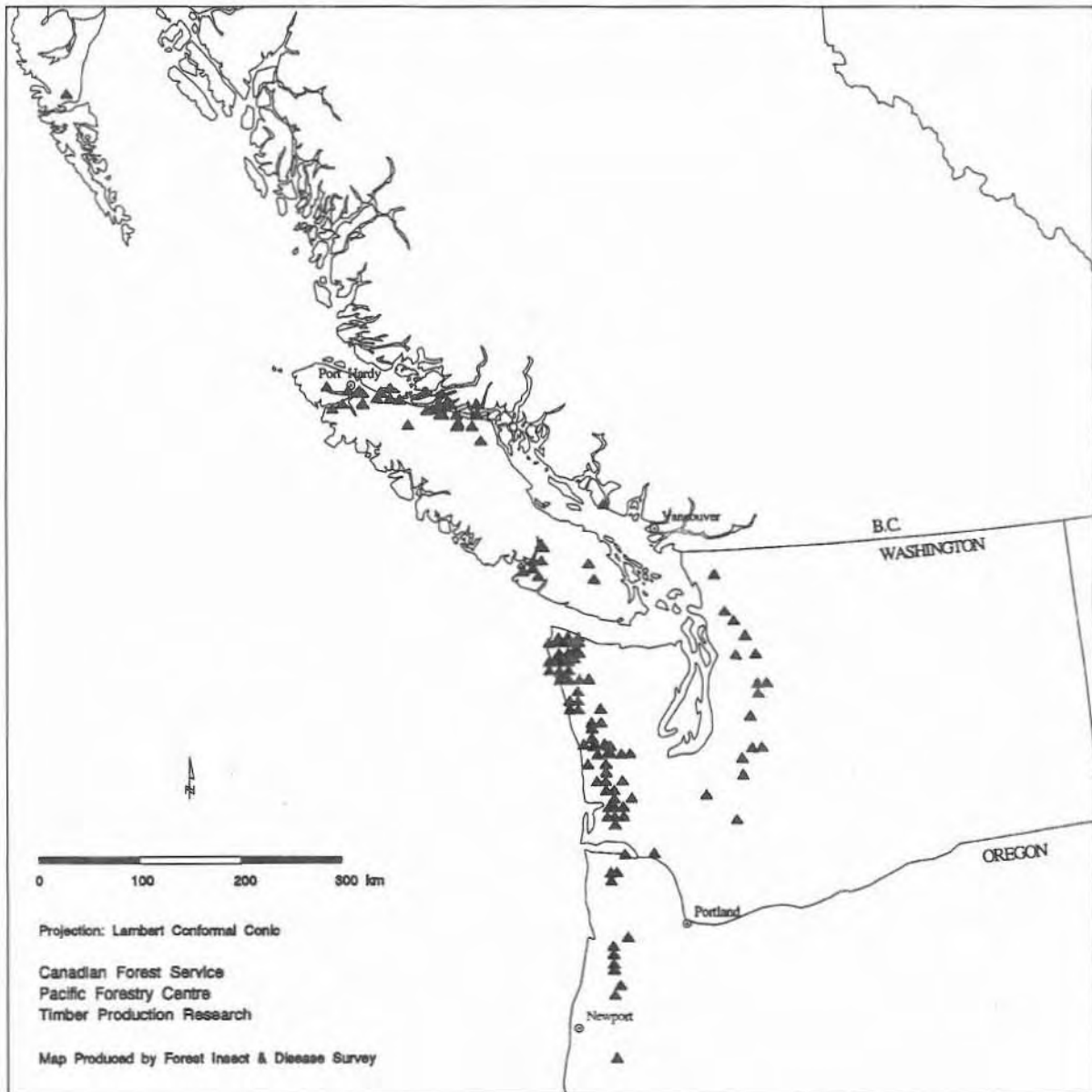
Fig. 2: Distribution of sample plots used to develop STIM

The map contains the following labels:

Port Hardy

Vancouver

B.C.
WASHINGTON

OREGON

Portland

Newport

0   100   200   300 km

Projection: Lambert Conformal Conic

Canadian Forest Service
Pacific Forestry Centre
Timber Production Research

Map Produced by Forest Insect & Disease Survey
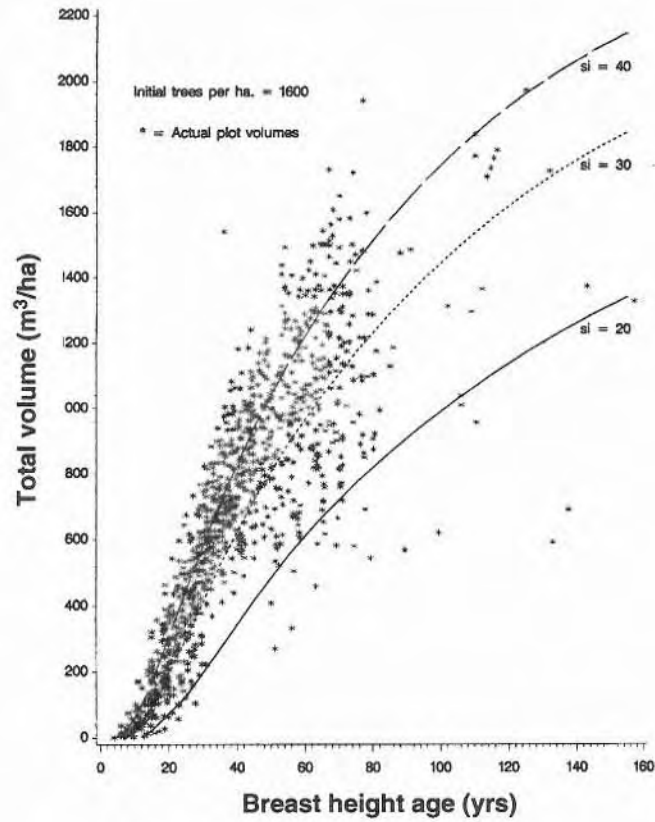
Fig. 3. Sensitivity analysis: site index
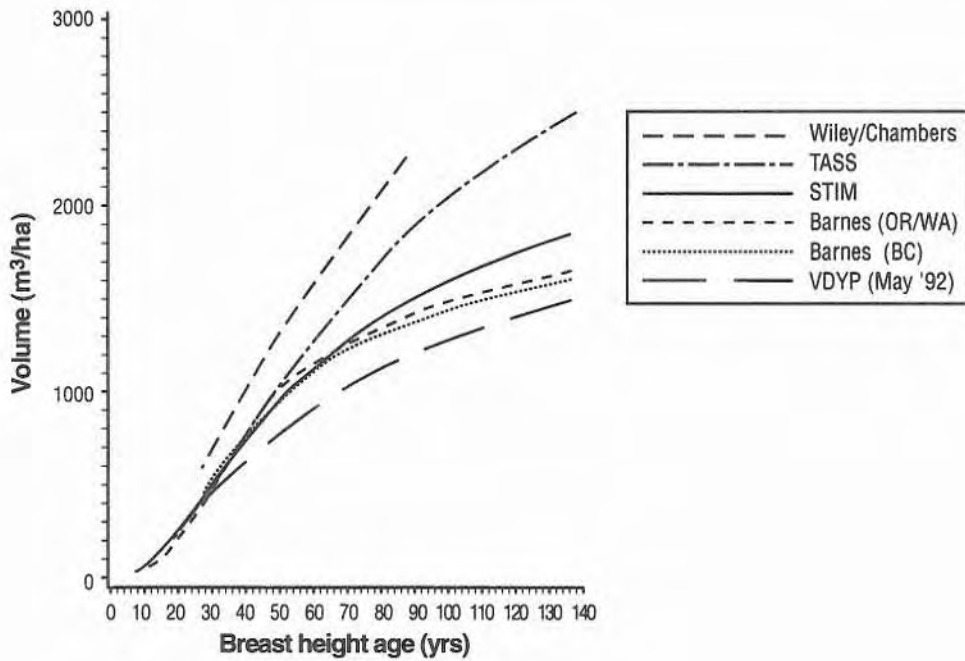
Fig. 4. Comparison of STIM with other models

Fig. 5. Main screen with stand projected for 80 years

Fig. 6. Screen for input of stand and tree data

STIM

File Options Stand Input Run Treatment Graph Help

Grow 5 | Grow 10

Yield Outpu | GROW A STAND

	NU				TVOL	MVOL	MAI	SDI	TRT
11		Number of years:	80		255.23	34.24	7.25	514.02	
21					431.34	84.53	9.54	626.23	
31					604.54	198.04	10.95	683.68	
41		Required DBHq (cm):			763.80	351.93	11.72	707.78	
51		Required Top Height (m):			904.48	528.25	12.03	707.31	
61		Required Total Vol (m3/ha):			026.78	688.98	12.05	690.35	
71		Required BH age (yrs):			131.11	848.75	11.88	664.19	
81					221.26	1036.52	11.61	634.95	
82					91.30	0.00	3.62	281.86	

Reporting Period (yrs):   Ok
10
Cancel

Command:

Previous command:
grow 80 10

Stand #:   2
SI: 30
BH Age: 20
Merch dlim: 12.5

Thinning Specs:
Thin Age:
BA Left:
TPH Left:
d/D ratio:

Error messages:

Fig. 7. Screen for input of growth specifications

STIM

File Options Stand Input Run Treatment Graph Help

Grow 5 | Grow 10

Yield | THINNING SPECIFICATIONS

Thin by: Ok
O Basal Area
● Trees/ha   Cancel

			VOL	MVOL	MAI	SDI	TRT
21			1.34	84.53	9.54	626.23	
31			4.54	198.04	10.95	683.68	
41			3.80	351.93	11.72	707.78	
51			4.48	528.25	12.03	707.31	
61			6.78	688.98	12.05	690.35	
71			1.11	848.75	11.88	664.19	
81			1.26	1036.52	11.61	634.95	
82			1.30	0.00	3.62	281.86	
87			8.60	0.00	5.58	414.32	

Number Specified: Amount Specified:
O Cut   ● Absolute
● Remainder   O Percentage

Amount cut / remaining: 1200
d/D Ratio (dbhq removed / DBHq original):   0.9

Comm

Previous command:
Grow 5

Stand #:   2
SI: 30
BH Age: 25
Merch dlim: 12.5

Thinning Specs:
Thin Age:
BA Left:
TPH Left:
d/D ratio:

Error messages:

Fig. 8. Screen for input of thinning specifications

WINSTIM - STAND LEVEL YIELD REPORT
Date: 01-27-1995

	STAND SI (m)	AGE (yrs)	DBHQ (cm)	TPH (#/ha)	BA (m2/ha)	HTOP (m)	TVOL (m3/ha)	MVOL (m3/ha)	MAI (m3/ha/yr)	SDI	TRT #
1	30	20	006.0	7000.0	020.00	014.0	0091.30	0000.00	03.62	281.86	
1	30	30	007.1	9889.0	038.84	020.2	0255.23	0034.24	07.25	514.02	
1	30	40	008.2	9440.0	050.25	025.5	0431.34	0084.53	09.54	626.23	
1	30	50	009.5	8218.0	058.00	029.9	0604.54	0198.04	10.95	683.68	
1	30	60	010.8	6853.0	063.32	033.7	0763.80	0351.93	11.72	707.78	
1	30	70	012.4	5515.0	066.75	037.1	0904.48	0528.25	12.03	707.31	
1	30	80	014.2	4319.0	068.77	039.9	1026.78	0688.98	12.05	690.35	
1	30	90	016.3	3329.0	069.88	042.5	1131.11	0848.75	11.88	664.19	
1	30	100	018.7	2565.0	070.44	044.7	1221.26	1036.52	11.61	634.95	
2	30	20	006.0	7000.0	020.00	014.0	0091.30	0000.00	03.62	281.86	
2	30	25	006.6	8993.0	030.39	017.2	0168.60	0000.00	05.58	414.32	
2	30	25	009.7	1200.0	008.78	017.2	0060.50	0000.00	05.58	102.80	T
2	30	35	014.0	1178.0	018.25	022.9	0167.63	0082.54	06.86	184.19	
2	30	45	017.5	1119.0	027.06	027.8	0302.12	0257.75	08.17	250.13	
2	30	55	020.3	1045.0	033.79	031.9	0434.40	0392.49	09.01	294.89	
2	30	65	022.6	0968.0	038.94	035.5	0557.39	0516.48	09.48	325.52	
2	30	75	024.7	0895.0	042.99	038.5	0669.67	0629.51	09.70	346.96	
2	30	85	026.7	0827.0	046.25	041.3	0771.60	0732.13	09.75	362.25	
2	30	95	028.5	0765.0	048.94	043.6	0864.03	0825.23	09.70	373.28	
2	30	105	030.3	0709.0	051.19	045.8	0947.90	0909.72	09.58	381.27	

Fig. 9. Example of output: yield report

WINSTIM - TREE LIST REPORT
Date: 01-27-1995

STAND	SI (m)	AGE (yrs)	CLASS #	DBH (cm)	TPH (#/ha)	BA (m2/ha)	HT (m)	TVOL (m3/ha)	MVOL # (m3/ha)
2	30	25	1	011.7	0462.5	005.00	017.2	0036.99	0008.79
2	30	25	2	008.4	0462.0	002.56	014.5	0016.24	0000.00
2	30	25	3	007.5	0461.9	002.06	013.5	0012.18	0000.00
2	30	25	4	007.0	0461.8	001.80	012.9	0010.16	0000.00
2	30	25	5	006.7	0461.8	001.63	012.5	0008.92	0000.00
2	30	25	6	006.5	0461.7	001.51	012.2	0008.09	0000.00
2	30	25	7	006.3	0461.7	001.43	012.0	0007.48	0000.00
2	30	25	8	006.1	0461.6	001.36	011.8	0007.03	0000.00
2	30	25	9	006.0	0461.5	001.31	011.7	0006.68	0000.00
2	30	25	10	005.9	0461.2	001.27	011.6	0006.41	0000.00
2	30	25	11	005.8	0460.8	001.23	011.5	0006.19	0000.00
2	30	25	12	005.8	0460.1	001.20	011.4	0006.01	0000.00
2	30	25	13	005.7	0458.9	001.18	011.4	0005.85	0000.00
2	30	25	14	005.7	0456.8	001.15	011.3	0005.72	0000.00
2	30	25	15	005.6	0452.8	001.13	011.3	0005.59	0000.00
2	30	25	16	005.5	0503.9	001.18	010.1	0005.20	0000.00
2	30	25	17	005.3	0454.7	001.02	009.8	0004.34	0000.00
2	30	25	18	005.2	0411.0	000.89	009.5	0003.67	0000.00
2	30	25	19	005.2	0373.5	000.78	009.2	0003.13	0000.00
2	30	25	20	005.1	0342.4	000.70	009.0	0002.72	0000.00

Fig. 10. Example of output: tree list report

Fig. 11. Screen for input of graph parameters
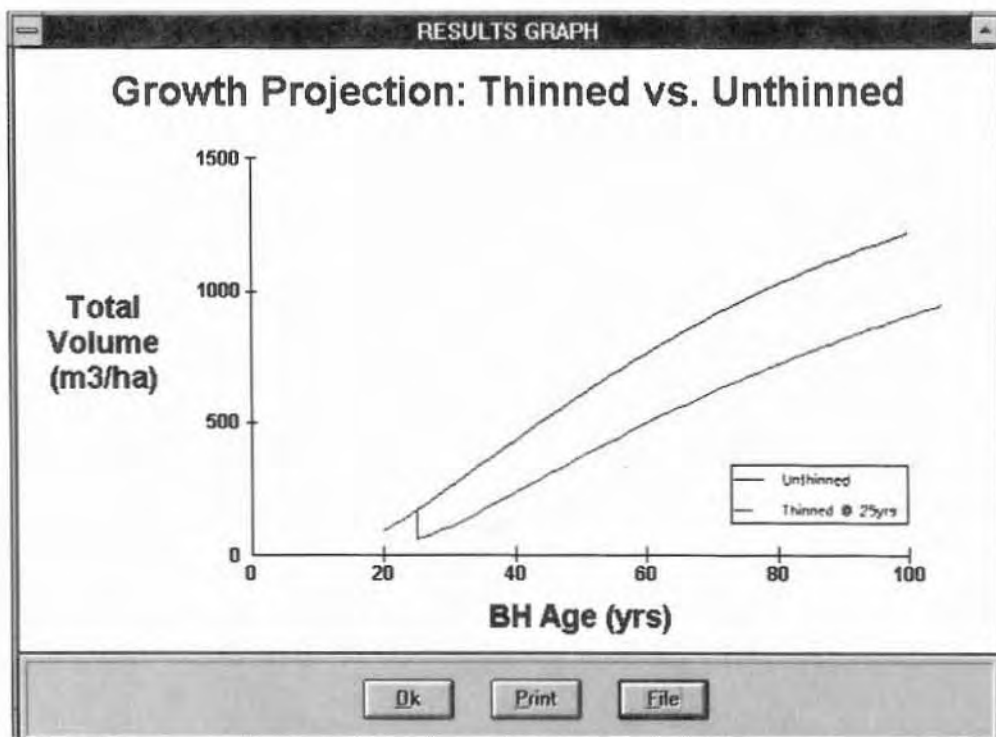

Fig. 12. Example of output: growth projection graph

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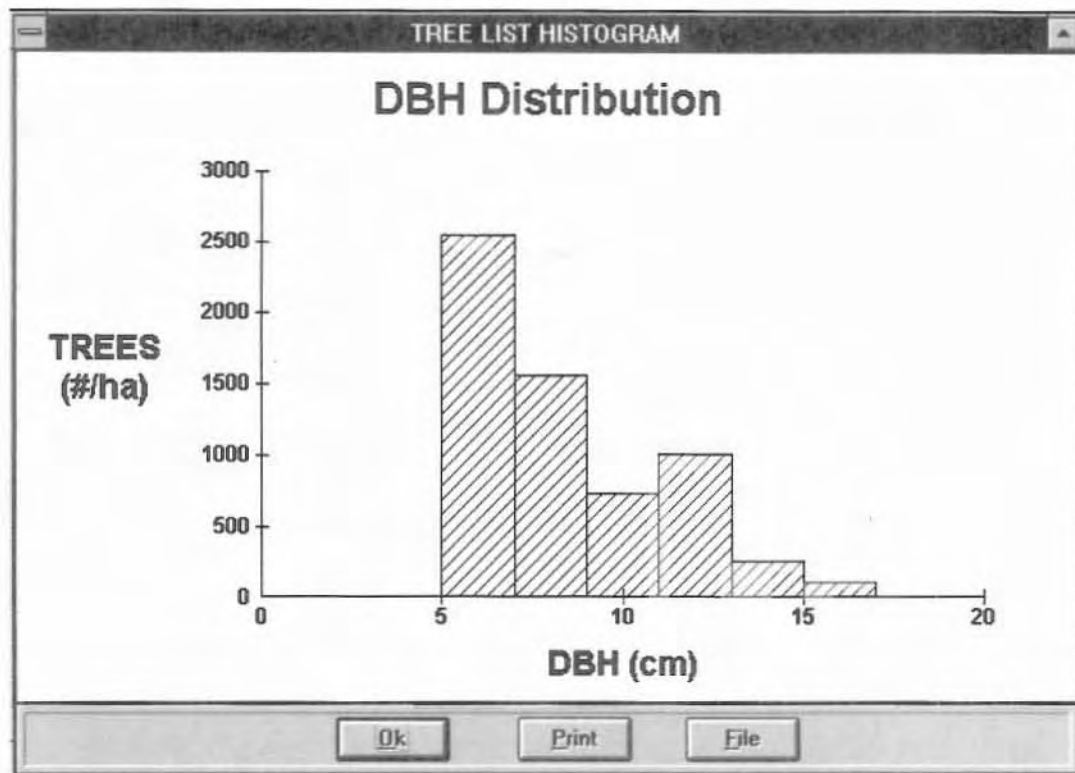Fig. 13. Example of output: histogram

Appendix 1
Details of the model components

A. Data Input (Fig. 1)

Each stand scheduled for projection is either a young (seedling) stand or an older (tree) stand. For the tree stand, the minimum input data are top height or age, and site index. A tree list or stand table is optional.

For a seedling stand, the minimum input is site index. This value is used to generate a set of data for a stand having a top height of 5.5 m. If the user can provide the number of trees per ha and quadratic mean diameter of the stand at 5.5 m, they will be used to refine the stand and tree data.

This approach is similar to the regeneration logic used by Hyink et al. (1988). It is a useful approach when data are scarce, but it is not accurate. A regeneration model would be a significant improvement.

Tree stand data provided by the user may be incomplete. Any such gaps must be filled. The most common missing attributes are those referring to the diameter distribution. If a tree list (stand table) has not been provided by the user, it is generated from available data: the stand attributes of coefficient of variation for tree basal area and the 10th percentile of the diameter distribution are empirically estimated. These, together with the quadratic mean diameter of the stand, are used to "recover" the tree parameters of a truncated Weibull distribution, the truncation point being at a diameter of 5.08 cm. From the cumulative Weibull distribution, an estimated tree list is generated. Heights for the tree list are empirically estimated unless provided by the user.

B. Silvicultural treatments

Information about silvicultural treatments such as thinning, fertilization, pruning and genetic effects must be entered. At present, only a thinning component has been implemented. A fertilization component has been deliberately omitted: research to date has not found a clear and positive correlation between fertilization and growth of western hemlock.

Thinning is accomplished by allocating the removals specified by the user to the tree list (stand table). In subsequent growth projections, the amount and type of removals are used to modify the stand growth, as described in section C3 below.

C. Stand growth model

This component is the focal point of the whole model system. It is similar to that described by Hyink et al. (1988): top height increment is first derived from height-age equations; survivor basal area is next predicted as a function of top height increment and other known variables; mortality and ingrowth are predicted subsequently.

Predictions are made in annual increments, as follows:

1) Top height is incremented by applying the one-year increment to an appropriate height-age equation (see Appendix 6).

2) The incremented top height is modified to account for any effects of stand density and management options (not yet implemented).

3) Survivor basal area increment is predicted from top height, top height increment, treatment history, quadratic mean diameter, age, geographic region, basal area and management options. The equation includes a thinning factor, which changes survivor basal area increment if the stand has been thinned. The factor is a function of stand basal area, the amount of thinning, and the change in top height since the last thinning.

4) Mortality is predicted using two alternate strategies. In the first one, basal area mortality and the average size of dead trees are predicted. In the second one, the trajectory angle defined by the net change in average stem diameter and trees per ha of a density management diagram is predicted and used instead of basal area mortality. In both strategies, the predictions are used to calculate mortality in terms of basal area and trees per ha. We recommend the first strategy.

The average size of dead trees may be predicted by an empirical equation, or it may be taken from the tree growth model (Fig. 1:D); we recommend the latter, which ensures that the predicted size of dead trees is within the diameter distribution.

5) Ingrowth is predicted in terms of diameter, height and number of trees per ha. This method of ingrowth prediction is used for both the stand and the tree model.

D. Tree growth model

The tree growth model serves several purposes: it provides data on the stem diameter distribution of the grown stand, it serves as an independent check of the stand model projections, and it can be used on a stand-alone basis.

The model operates by making projections of class averages. Typically, these averages are input by the user. If not, they will be generated by the model, in which case they will comprise 12 classes with an equal number of trees in each class. Apart from trees that die, a tree will thus remain within a class for the duration of the projection period. Similarly, apart from ingrowth, the number of classes will remain constant.

The steps of the tree model predictions are as follows.

1) The diameter growth of the trees in each class is predicted in terms of basal area, average tree diameter, basal area of the larger trees in the stand, total stand basal area, and top height increment.

2) The number of trees that die in each diameter class is predicted as the probability that a tree in a class will die (which is equivalent to the proportion of trees in a class that will die). This proportion is then multiplied by the number of trees per ha in the class to give the desired value.

3) Finally, height growth of trees in the class is predicted.

E. Reconciliation

The reconciliation process is one of adjusting the output from one model to correspond with the output from the other. Generally, the tree model output is adjusted to that of the stand model, under the assumption that the latter gives more robust projections at the stand level. The adjustments consists of
- revising the grown tree list (sum of class totals) so that the number of trees per ha agrees with the stand model projections of trees per ha;
- by a pro-rating method, the adjustments are then applied to the individual tree classes so that the quadratic mean diameter of the two models are equal;
- finally, pro-rating is used to adjust the height estimates of the revised tree list so that the top height of the two models are equal.

The reconciliation process is of course not applicable if only one of the models is run.

An example of the reconciliation process is given in Appendix 7.

F. Data summary and output

The basic data output from E consists of a stand table or grown tree list. It is augmented by height and volume calculations, log size tables and other calculations which are additional to the growth process *per se*. They will be reported together with control options used during the projection period, by different categories such as residual stand, mortality and thinnings.

Projection results may be summarized and output at the end of each year, or at the end of the total projection period. Changes in management options may be introduced into the projection period at any year, enabling the comparison of different scenarios.

A list of variable names and definitions is given in Appendix 4.

Appendix 2
The data

Most of the data used to develop STIM is a product of the Western Hemlock Cooperative Database Project, completed by the Stand Management Cooperative in 1985.

Table 2.1. Data Summary by Ownership

Cooperator	Number of plots	Number of tree records
B.C. Ministry of Forests	369	161 538
Crown Zellerbach	146	31 978
Dept. of Natural Resources (WA.)	30	35 449
ITT Rayonier	208	39 510
MacMillan Bloedel	145	67 391
U.S. Forest Service	9	3 539
University of Washington	302	164 287
Western Forest Products	207	36 989
Weyerhaeuser	246	76 593
Total	1662	617 274

Table 2.2. Number of plots by age classes

Age of plot*	Number of plots
missing	4
0 - 5	3
6 - 10	107
11 - 20	369
21 - 40	410
41 - 60	290
61 - 80	61
81 - 100	36
100 +	59

* Breast height age at first measurement.

Table 2.3. Range of input data variables

Variable	Minimum	Maximum	Mean
Basal area (m^2/ha)	0.3	154.0	49.3
Trees (no/ha)	112.0	11490.0	1642.3
Top height (m)	5.0	50.5	24.0
Quadratic mean diameter (cm)	5.0	64.8	22.1
Site index (m at 50 yrs)	8.9	66.0	32.9
Age at breast ht.	4.0	251.0	36.0
Number of measurements per plot	1	15	4.0

Appendix 3
Data validation

The data validation goal for STIM was to produce a database that was reasonably free from measurement and data input errors, that met or exceeded some minimum standards of quality, and that contained no abnormal growth trends, especially for height and diameter.

1. Data editing

For individual trees, anomalies and missing values were identified and corrected. These anomalies included tree numbers and species codes that changed between measurements, and trees that were classed as dead at one measurement and alive at the subsequent measurement. Diameter values that decreased by more than 0.3 cm between measurements, or increased to a size larger than a subsequent measurement, were flagged and later examined individually to make any corrections. Also, height values that decreased by more than 1 m were flagged and corrected if necessary.

For each plot, graphs of diameter increment versus initial diameter, height increment versus initial height, and height versus diameter were studied to identify outliers, artificially generated data, unbelievable growth, and other anomalies.

2. Plot screening

Plot size, number of measured heights, and minimum diameter limit were used to screen the plots. The minimum acceptable plot size was usually set as 0.04 ha. For research installations with good design, the minimum size was reduced to 0.03 ha. To ensure that good height-diameter curves could be constructed, measurement sets with fewer than six ground measured heights were discarded, unless they could be interpolated from adjoining sets. And finally, to ensure that all plots were summarized to the same standard, any plot where the dbh tagging limit set at greater than 5.08 cm was assessed and discarded, if necessary.

Table 3.1. Errors detected in STIM data validation

Data component	Type of error
Tree data	No species code
	Diameter out of range
	Species does not exist
	Diameter increment out of range
	Height increment out of range
	Dead tree has come alive
	Change in species
	Unusual growth trend
Plot data	Plot size too small
	DBH tagging limit too high
	Too few height measurements
	Height measurement range unsuitable

The statistics below indicate the extent to which the original database was reduced by the validation and editing procedures.

Number of plots at start of validation		1662
Deleted: plot too small	146	
Deleted: Dbh tag limit too high	64	
Deleted: too few height measurements	113	
Retained at end of validation		1339
Number of measurement sets from retained plots		6086
Deleted: too few height measurements	782	
Retained at end of validation		5304

As shown, 323 plots were deleted from the original database of 1662 plots. The remaining 1339 plots contained 5304 measurement sets after deletion of sets with too few heights. Thus, the average was 5304/1339 = 3.96 measurement sets per plot.

3. Height-diameter equations

These equations were fitted to each plot measurement set. Thus, a plot measured in 1973, 1978 and 1983 had three measurement sets, with a height-diameter equation fitted to each. Since many measurement sets had insufficient tree height measurements to fit an equation, and to retain as many plots as possible for the analyses, a decision was made that the first and last measurement set of a series (in the example above, 1973 and 1983) must contain at least six

measured heights, with at least one tree in the top height category. In-between measurement sets (1978 in the example) with fewer than six measured heights had their equations interpolated.

The fitting methodology (Flewelling and de Jong, 1994) included a procedure that minimized the errors in predicted height and predicted change in height over all measurements. The following constraints were imposed on the equations: 1) The height asymptotes had to increase between repeated measurements, 2) the predicted heights had to increase as dbh increased, and 3) any cross-over of curves between measurement sets could only occur below quadratic mean dbh.

The fits frequently utilized these constraints, as 19% of the plots required at least one asymptote constraint, 0.3% of the plots required the slope constraint, and 8.5% of the plots required a cross-over constraint.

Appendix 4
Variable names and definitions

To the extent possible, these names are to be used in describing model components and in programming. To allow for SAS programming, names are limited to eight characters.

A_BH   Breast height age of a tree (years).

AGE_BH   Breast height age of a stand (years). See Logic specs.

BA   Basal area of a stand (m^2/ha).

BA_DIE   Basal area of trees that die in a given year (m^2/ha).

BA_GR_TR   Basal area growth of a tree (m^2/yr).

BA_IN   Basal area of ingrowth trees in a given year (m^2/ha).

BAL   Sum of tree basal areas larger than the subject tree, plus 0.5 of the midpoint basal area of the subject tree (m^2/ha).

BA_ST   Basal area at the start of the first year of stand growth (m^2/ha).

BA_TR   Basal area of a tree (m^2).

BH   Breast height (@ 1.30m).

CSR_BA   Cummulative selection ratio for basal area, defined as the product (over all thinning periods to date) of the ratio of residual over initial basal area.

CSR_TPH   Cummulative selection ratio for trees per ha, defined as the product (over all thinning periods to date) of the ratio of residual over initial number of trees per hectare.

CV_BA   Coefficient of variation of basal area per tree. This is the square root of the variance divided by the mean. The variance is calculated as the average squared deviation from the mean; there is no correction for degrees of freedom.

CV_BA_ST   Predicted coefficient of variation of basal area at the first year of stand growth.

DBH_IN   Quadratic mean diameter for ingrowth trees in a given year (cm).

DBH_LIM   The minimum DBH which is to be summarized (cm).

DBH   Diameter for a tree, or quadratic mean diameter for a group of trees (cm).

DBHQ   Quadratic mean diameter of a stand (cm).

DBHQ_DIE   Quadratic mean diameter of trees which die in a year (cm).

DBHQ_IN   Quadratic mean diameter of the ingrowth trees (cm).

DBHQ_ST   Quadratic mean diameter of the first year of stand growth (cm).

DEL_BA_S   Survivor basal area one-year increment of the stand (m^2/ha/yr).

DEL_DBH	One year increment in a tree's DBH (cm/yr).
DEL_H	One year increment in a tree's (or group of trees) height (m/yr).
DEL_HTOP	One year change in a stand's top height (m/yr).
DEL_TPH	One year change in a stand's number of trees (#/ha).
DTOP	Quadratic mean diameter of the top height trees (cm).
D_TOP_i	DBH of the ith top height tree.
D_OVER_D	Quadratic mean diameter of trees cut during thinning, divided by the quadratic mean diameter of stand prior to thinning.
D10	Predicted initial dbh at the tenth percentile (cm).
H	Height of a tree (m).
H_IN	Predicted height of ingrowth (m).
HTOP	Top height of a stand, as defined in Logic specs (m).
HTOP_ST	Top height at the start of the first year of stand growth (about 6m).
M	Trajectory angle (in radians) from the start of one year to the start of the next. This is defined on a log-log graph of TPH vs DBHq. For a stand with no ingrowth and no mortality, the angle is zero. For a stand with no ingrowth but with mortality among the small trees, M is a positive number.
M_NO_ING	Trajectory angle (in radians) from the start of one year to the start of the next, where the second position is calculated without regard to ingrowth; hence TPH cannot increase.
NUM_TOP	Number of top height trees per plot.
ORIGIN	Stand origin (natural, seeded, or planted).
PR_DIE	The fraction of a tree class which will die in a one year period.
PR_DIE_T	Transformation of (PR_DIE): $PR\_DIE\_T = -\dfrac{1}{\log (PR\_DIE)}$
PR_LIVE	The fraction of a tree class which will survive in a one year period.
PRE_HTOP	Top height of most recent previous treatment, in m.
SDI	Stand density index $= \left(\dfrac{TPH}{2.471}\right) \times \left(\dfrac{DBH}{25.4}\right)^{1.605}$
SI	Site index, based on breast height age 50 years (m).
TPH	Number of trees per hectare taller than 1.37 m, with DBH > DBH_MIN (#/ha).
TPH_DIE	TPH which die in a given year (#/ha).
TPH_IN	TPH of ingrowth in a given year (#/ha).

TPH_ST   Start-up TPH. Predicted TPH at first stand age (#/ha).

TPH_P   TPH planted (#/ha).

VPH   Volume of the stand (m^3/ha).

Appendix 5
Predicting equations

1. Stand completion

a. Generalized HT/DBH equation:

The generalized ht/dbh equation provide height estimates for every tree (or group of trees). This is computed once for any simulation; for a seedling stand at the point it becomes a tree stand, or for an existing tree stand with an incomplete tree list.

$$H = 1.37 + b1 \times \exp (b2 \times DBH^{-1.0})$$

where

$b2$ = $-1 \times a1 \times \exp (a2 \times HTOP) \times \exp(a3 \times DBHq)$

and

$b1$ = the upper asymptote of the ht/dbh curve. It is determined iteratively, and equals a value that makes the top height calculated here equal to that given by the user or by the stand model.

$a1$ = 3.73881

$a2$ = 0.01915

$a3$ = 0.01346

b. Diameter distribution:

The dbh distributions are generated through a 'distribution recovery' component. *BA*, *TPH*, *CV_BA* and *D*10 are inputs into a mathematical root finding procedure which produces the *a*, *b* and *c* parameters of a Weibull function. A dbh distribution is then generated. If any of the inputs are missing (*BA*, *TPH*, *CV_BA*, or *D*10), they are estimated by empirical equations. There are many equations, both for the regeneration yield model and the stand model.

2. Regeneration yield model

a. Trees per hectare:

This component is part of the stand completion phase. If we start the growth model with a seedling stand, it may lack a forecast of what it will look like when it becomes a tree stand. This component predicts the trees per hectare that a seedling stand will have when it reaches the point where it becomes a tree stand. All that is required is a value for top height at the start of tree stand growth.

$$TPH\_ST = \exp [a + b \times \log (HTOP\_ST)]$$

where

a = 0.634999

b = 3.461780

and

if $HTOP\_ST < 5.0$, then $HTOP\_ST = 5.0$

if $HTOP\_ST > 10.0$, then $HTOP\_ST = 10.0$

b. Basal area per hectare:

This component is part of the stand completion phase. If we start the growth model with a seedling stand, it may lack a forecast of basal area per hectare at the point where it becomes a tree stand. This component predicts basal area per hectare. It uses top height and the previously predicted value for trees per hectare.

$$DBHQ\_ST = \exp\ [a + b \times \log\ (TPH\_ST) + c \times \log\ (HTOP\_ST)]$$

if $DBHQ\_ST < 5.80$, then $DBHQ\_ST = 5.80$
if $DBHQ\_ST > 10.50$, then $DBHQ\_ST = 10.50$

where

$a = 0.777963$
$b = -0.019562$
$c = 0.651146$

$$BA\_ST = \frac{(\pi \times DBHQ\_ST^2)}{40\ 000} \times TPH\_ST$$

c. Diameter at the 10th percentile:

This model will predict D10 at the point when a seedling stand becomes a tree stand. D10 is the value of the 10th percentile of diameters, sorted in ascending order.

$$D10 = \sqrt{DMIN^2 + P \times (DBHQ\_ST^2 - DMIN^2)}$$

where

$DMIN = 5.08$
$P = 0.071$

d. Coefficient of variation of basal area:

C.V. is required to develop a diameter distribution using the Weibull function. *DBHQ_ST* and *D10_ST* are predicted earlier in models for seedling stands. They are then used here to get an estimate of *C.V.*

$$CV\_BA\_ST = \frac{100 \times a \times (DBHQ\_ST^2 - D10\_ST^2)}{DBHQ\_ST^2}$$

3. Stand growth model

a. Top height increment:

Site curves developed by Wiley, and new ones by Flewelling, can both be used. In general, the calculation of annual increment is a two-step process. The first step calls for finding the age that will cause the site curves to predict the current top height given the stated site index. The second step is finding the increase in height that the site curve predicts for a one year increase in that age. The alternative is to compute growth from the site curves based on site index and age, without regard to starting height. The equations below illustrate both alternatives.

(i) Wiley's equations (Wiley 1978)

$$HTOP = .3048 \times \left(\frac{4.5 + A\_BH^2}{(B1 + B2 \times A\_BH + B3 \times A\_BH^2)} \right)$$

where

$B1 = 1.7307 + \dfrac{(0.1394 \times 2500)}{((SI/0.3048) - 4.5)}$

$B2 = -0.0616 + \dfrac{(0.0137 \times 2500)}{((SI/0.3048) - 4.5)}$

$B3 = 0.00192428 + \dfrac{(0.00007024 \times 2500)}{((SI/0.3048) - 4.5)}$

(ii) Flewelling's equations (Flewelling 1994)

Equations are of the splined type, with a variable height inflection point.

Equation form below the inflection point (used when A_BH-1<K5):

$$DEL\_HTOP = K1 \times \left(1 - (1-K2) \left(\frac{(K5 - (A\_BH-1))}{K5} \right)^{K3} \right)$$

Equation form above the inflection point:

$$DEL\_HTOP = K1 \times exp \left(\frac{(K5 - (A\_BH - 1))K1}{K4} \right)$$

where K1-K5 are constants for a given site curve, with

K1 = maximum growth rate for the given site curve at the inflection point (m/yr). Determined by numerical analysis.

$K2 = 0.2 + \dfrac{0.8}{(1 - exp(A1 + A2 \times K1))}$

$K3 = 1 + A3 \times K1$

$K4 = A4 \times K1$

$K5 = A5 \times exp(A6 \times K1)$

and

A1 = 0.299720
A2 = 0.116875
A3 = 0.074866
A4 = 0.032348
A5 = 0.006984
A6 = 0.000339

b. Survivor basal area:

Given the stand conditions at the beginning of a one year period, we can directly predict survivor basal area increment for that period. The model predicts survivor basal area increment for unthinned and thinned stands. The equation parameters change slightly for each geographic region.

$$\text{THIN\_FACTOR} = 1 + (\text{THIN}) \times (\text{THIN\_1}) \times (\text{THIN\_2}) \times (\text{THIN\_3}) \times (\text{THIN\_4})$$

where:

$\text{THIN} \quad = \quad 0 \text{ (unthinned) or } 1 \text{ (thinned)}$

$\text{THIN\_1} \quad = \quad \text{T0}$

$\text{THIN\_2} \quad = \quad 1 - \exp((-2/\text{T0}) \times (1 - \text{CSR\_BA}))$

$\text{THIN\_3} \quad = \quad 1 - \text{T4} \times \exp(\text{T3} \times \text{HT\_SINCE})$

$\text{THIN\_4} \quad = \quad \text{MAX} [1.0, \exp(-0.693 \times (\text{HT\_SINCE} - \text{T5})/\text{T5})]$

$$\text{TM} = 1 + \left(\frac{\text{THIN\_FACTOR} - 1}{2} \right)$$

$$S = S0 \times \exp\left(S1/\text{DBHQ} + S2 \times \log (\text{DBHQ}) + S3 \times \log (\text{AGE\_BH})\right)$$

$$\text{P3} = \text{MAX} [0, \text{H1} + \text{H2} \times \log (\text{AGE\_BH})]$$

$$\text{DEL\_BA\_S} = C \times (\text{TM}) \times [1 - \exp(S \times \text{BA} \times \text{TM})] \times (\text{AGE\_BH})^{\text{P2}} \times (\text{H0} + \text{DEL\_HTOP})^{\text{P3}}$$
$$\times (1 - \exp(\text{A1} \times \text{AGE\_BH})) \times (\text{SI}/33)^{\text{P4}} \times (\text{HTOP})^{\text{P5}}$$

Coefficients and values (by geographic region if five values shown - coastal Ore., coastal Wa., western Cascades of WA., B.C. wet maritime, B.C. dry maritime).

$\text{A1} \quad = \quad -0.1569$

$\quad\text{C} \quad = \quad 71.97, 72.34, 69.97, 67.84, 67.84$

$\text{H0} \quad = \quad 0.30$

$\text{H1} \quad = \quad 0.510$

$\text{H2} \quad = \quad -0.1095$

$\text{P2} \quad = \quad -0.0973$

$\text{P4} \quad = \quad 0.6$

$\text{P5} \quad = \quad -1.0$

$\text{S0} \quad = \quad -5.83, -5.05, -4.01, -4.08, -2.81$

$\text{S1} \quad = \quad -13.83$

$\text{S2} \quad = \quad -0.901$

$\text{S3} \quad = \quad -0.419$

$\text{T0} \quad = \quad 0.335$

$\text{T3} \quad = \quad -1.82$

$\text{T4} \quad = \quad 0.673$

$\text{T5} \quad = \quad 4.44$

c. Stand-average mortality:

i. Basal area

Given the independent variables, basal area mortality is predicted.
Together with an estimate of the size of dead trees (DBHd), mortality in TPH can be calculated.

$$BA\_DIE = a0 \times DEL\_BA\_S \times exp[a1 \times (BD)^{a2} + a3 \times (DBHq/25)^{a4}$$
$$+ a5 \times (BD)^{a2} \times (DBHq/25)^{a4} + a6 \times DEL\_BA\_S + a7 \times SI]$$
$$+ b0 \times BA$$

where

$$
\begin{aligned}
a0 &= 1.081 \\
a1 &= -13.75 \\
a2 &= 0.8887 \\
a3 &= -0.1842 \\
a4 &= -2 \\
a5 &= -8.166 \\
a6 &= 0.9492 \\
a7 &= 0.01 \\
b0 &= 0.00293 \\
BD &= \frac{DEL\_BA\_S}{TPH \times 100}
\end{aligned}
$$

Adjustment for stands that were thinned in the previous 12 years:

$$F0 = MAX\ [0.2,\ 0.2 + 4.0 \times (CSR\_BA - 0.8)]$$

$$FACTOR = F0 + (YR\_SINCE/12) \times (1 - F0)$$

$$BA\_DIE = (BA\_DIE\ from\ unthinned\ eq'n) \times FACTOR$$

ii. Dead-tree size

$$DBHd = 5.08 + [RLL + (RH - RLL) \times logit^{-1}\ (b1 + b2 \times SDI)] \times (DBHq - 5.08)$$

where

$$RLL = RL \times [1.0 - exp(b3 \times (DBHq - 5.08))]$$
$$logit^{-1}(x) = exp(x) / [1 + exp(x)]$$

with

$$
\begin{aligned}
b1 &= 11.80 \\
b2 &= -0.02985 \\
b3 &= -0.1141 \\
RH &= 0.739 \\
RL &= 0.4881
\end{aligned}
$$

iii. Trajectory angle

$$M = \tan^{-1}(TANM)$$

where,

if $x < xi$, $TANM = a1 + a2 \times \left(\dfrac{\exp(a3 + a4 \times x)}{1 + \exp(a3 + a4 \times x)} \right)$

if $x \geq xi$, $TANM = b1 \times (x - xi - b2)^{b3}$

x = $SDI^{[1 - \exp(c \times (MAX(DBHq, 7.5))^2)]}$

a1 = 0.0645

a2 = 2.065

a3 = $-a4 \times xi$ = -9.175464

a4 = 0.01926

b1 = $yi \times (-b2) - b3$ = 0.67435

b2 = $-yi \times b3/yip$ = -18.42497

b3 = 0.167

c = -0.0245

xi = 476.4

yi = $a1 + a2/2$ = 1.097

yip = $(a2 \times a4)/4$ = 0.00994298

d. Ingrowth:

i. Number of trees

Ingrowth is defined as trees which are greater than or equal to 5.08 cm dbh, and which in the previous year were less than 5.08 cm. Ingrowth number of trees is predicted as the product of two steps; first, the probability of ingrowth occurring; and second, the amount of ingrowth. The predicted ingrowth is the product of the probability multiplied by the estimate of the amount.

$$TPH\_IN = PROB\_ING \times a1 \times (1 + a2 \times HTOP) \times \exp(-a2 \times HTOP) \times \exp(a3 \times DBHQ)$$

where

$$PROB\_IN = \dfrac{1}{(1 + \exp(b1 + b2 \times HTOP + b3 \times DBHQ))}$$

a1 = 11700.02

b1 = -9.6939

a2 = -0.04262

b2 = 0.1425

a3 = -0.4613

b3 = 0.5974

ii. Size

The quadratic mean diameter of the ingrowth trees is predicted as an empirical function of DEL_HTOP and TPH, from the ungrown stand.

$$DBHQ\_IN = 5.08 + a \times \exp(b \times HTOP) \times \exp(c \times TPH/500)$$

$$\text{if } DBHQ\_IN > 8.0 \text{ then } DBHQ\_IN = 8.0$$

where

a = 1.5675

$$b = -0.08194$$
$$c = -0.2157$$

iii. Height

Ingrowth height is computed whenever ingrowth is estimated.

$$H\_IN = 1.37 + b1 \times \exp(b2 \times DBHQ\_IN) \times DBHq^{b3} \times HTOP^{b4}$$

where

$$b1 = 0.5304$$
$$b2 = 0.2593$$
$$b3 = -0.5829$$
$$b4 = 0.8664$$

4. Tree growth model

a. Basal area growth:

This model component predicts the basal area growth of an individual tree. In fitting the equation, the average basal area growth per tree within a decile was used. For the subject tree BAL is defined as the sum of basal area of all trees larger than the subject tree plus one-half the basal area of the subject tree.

$$BA\_GR\_TR = \exp(a + b1 \times (1-\exp(b2 \times DBH))^{b3} + d \times DEL\_HTOP + e1 \times (1-\exp(e2 \times BA^{e3})))$$

where

$$a = -18.502$$
$$b1 = 14.1683$$
$$b2 = -0.035699$$
$$b3 = 0.122309+(0.001669-0.0005786 \times THIN) \times BAL^{1.12034}$$
$$\text{and THIN} = 0 \text{ if } CSR\_BA = 1.0$$
$$= 1 \text{ if } CSR\_BA < 0.9$$
$$= 10 \times (1.0 - CSR\_BA) \text{ if } 0.9 \leq CSR\_BA < 1.0$$
$$d = 0.57684$$
$$e1 = -1.60952$$
$$e2 = -0.005708$$
$$e3 = 1.30961$$

b. Tree mortality:

This component predicts the probability that a tree in a class will die during the projected one year growth period, or the proportion of trees in the class that will die in a one year growth period.

$$PR\_DIE = \exp\left(\frac{-1}{TMF}\right)$$

where

$$TMF = k1 + k2 \times \exp(k3 \times DEL\_DBH) \times (BAL/BA)^{k4}$$
$$k1 = k11 \times \exp(k12 \times DBH)$$
$$k2 = k21 \times \exp(k22 \times DBH)$$
$$k3 = -6.53936$$
$$k4 = 7.15423$$

k11 = 0.168600
k12 = -0.002435
k21 = 0.684419
k22 = 0.041637

c. Tree height growth:

The tree height increment model predicts height growth for individual trees.

$$\frac{DEL\_H}{DEL\_HTOP} = 1 - \exp(-a1 \times X^{a2})$$

where

X = DBH / DTOP
a1 = 4.1437
a2 = 1.6486

Appendix 6
Site-height equations

There are two types of height-age relationships: site index equations and site height prediction equations (Curtis et al. 1974; Flewelling 1982). The former is used to predict site index, the latter to predict site height or top height. They have different statistical properties and the resultant height-age curves are different.

This appendix outlines the development of another relationship, intermediate to the other two, called the constant percentile height-age relationship.

The principle behind the constant percentile relationship is that a stand should maintain the same top height relative to other stands in the population: it should stay in the same percentile. Thus, if a stand in a population of eight-year old stands has a top height in the 10th percentile, it will still have a top height in the 10th percentile when the stands reach 50 years of age. If site index equations were used, the top height at age 50 would be in a higher percentile, e.g. the 20th; it would be in a lower percentile (e.g. the 5th) at age 50 if top height prediction equations were used.

Our implementation of the constant percentile relationship differs in some respects from the traditional approaches of site equations or site height prediction equations:
- top height data are estimated from permanent plot measurements (Flewelling and De Jong 1994); and
- the fitting methodology is similar to a random parameter regression technique: it finds the set of model coefficients that minimizes the error in height change for a fitted curve that seeks to pass close to the initial and final observed heights for each plot.

The resulting equations give a better approximation to the top height increments observed in the data than does Wiley's equations. Nevertheless, both sets of equations are included in STIM and the choice is left to the user.

Appendix 7
Example of reconciliation process

1. Initial input parameters and tree list:

Class	Trees per ha (TPH1) (no.)	Stem diameter (DBH1) (cm)	Basal area (BA1) (m^2/ha)	Top height (HTOP1) (m)
1	500.00	10.0	3.93	7.00
2	400.00	15.0	7.07	9.00
3	350.00	20.0	11.00	11.00
4	300.00	25.0	14.73	12.00
All	1550.00		36.73	

Site index = SI = 30

Breast height age = AGE_BH = 20 yrs

2. Output after a one-year growth projection:

Model	Class	Trees per ha (TPH2) (no.)	Basal area (BA2) (m^2/ha)	Top height (HTOP2) (m)
Tree	1	493.36	4.07	7.43
	2	399.45	7.44	9.52
	3	349.76	11.67	11.61
	4	299.85	15.72	12.68
	(sum of classes)	1542.41	38.90	
Stand		1537.29	39.44	12.678

3. Reconcile the tree output to agree with the stand output:

(a) trees per ha reconciliation

The TPH reconciliation is accomplished by adjusting the mortality values predicted by the tree model for the individual size classes, to make the sum of the values equal to the value predicted by the stand model. The adjustment is proportional to the change (here, mortality) in TPH values of the individual size classes during the projection period.

This reconciliation is accomplished in the following manner (see table below). The tree model has a mortality of 7.59 trees/ha (MORT = TPH1-TPH2). This value must be increased by an additional 5.12 trees/ha (1542.41 - 1537.29) to match the stand model output. The reduction is accomplished by proportionately increasing the individual class values of MORT, to yield a set of revised (REV_MORT) values. For example, for class 1 the mortality is revised from 6.64 to 11.11 (= 6.64 + (6.64/7.59 × 5.12)); for class 2 the revised mortality is 0.55 + (0.55/7.59 × 5.12) = 0.94, and so on. From these figures, the revised number of trees per ha (REV_TPH2 = TPH1-REV_MORT) is calculated.

Class	TPH1	TPH2	MORT	REV_MORT	REV_TPH2
1	500.0	493.36	6.64	11.11	488.89
2	400.0	399.45	.55	.94	399.07
3	350.0	349.76	.25	.41	349.59
4	300.0	299.85	.16	.26	299.74
All	1550.0	1542.41	7.59	12.72	1537.28
All	(with ingrowth)	1542.41			1537.28

(b) DBH reconciliation

The general approach is similar. DBH values of individual size classes are adjusted until the sum of the corresponding basal areas is equal to the value predicted by the stand model. Adjusted TPH (REV_TPH2)values are used. The adjustment is proportional to the change (here, growth) in diameter values of the individual size classes during the projection period.

This reconciliation for basal area is accomplished as follows (see table below).

The value k is found such that:

$$\frac{\pi}{40000} \times \sum_{i=1}^{n} TPH_i \times (DBHi + k \times \Delta)^2 = BA2$$

where

BA2 = final basal area from stand model.

Δ = DBH2-DBH1

and

TPH_i = predicted TPH in class i at end of period.

then:

NEW_DBH2 = $k \times \Delta$ + DBH1

for this example, k is approximately 1.26

thus, for class 1:

NEW_DBH2 = $1.26 \times .24$ + DBH1 = 10.30

Class	REV_TPH2	DBH1	DBH2	Δ	$k \times \Delta$	NEW_DBH2
1	488.89	10.00	10.24	.24	.30	10.30
2	399.07	15.00	15.40	.40	.51	15.51
3	349.59	20.00	20.61	.61	.77	20.77
4	299.74	25.00	25.84	.84	1.06	26.06

(c) Height reconciliation

This is done after the TPH and DBH reconciliation: height values of individual size classes are adjusted until the top height of the adjusted values matches that predicted by the stand model. Adjustment is proportional to the change in height (here, growth) of the individual size classes.

This reconciliation of top height is accomplished as follows (see table below)

The predicted height growth is modified by:

$$NEW\_H2 = k \times \Delta + H1$$

k is chosen so as to ensure that the top height implied by the reconciled tree list matches that predicted by the stand model. In the present case, the top heights predicted by each model are identical, so k becomes 1.

Class	TPH	H1	H2	Δ	k×Δ	NEW_H2
1	488.89	7.00	7.43	.43	.43	7.43
2	399.07	9.00	9.52	.52	.52	9.52
3	349.59	11.00	11.61	.61	.61	11.61
4	299.74	12.00	12.68	.68	.68	12.68