

**A NEURAL NETWORK GROWTH AND YIELD MODEL
FOR NOVA SCOTIA FORESTS**

by

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DALHOUSIE UNIVERSITY

INDUSTRIAL ENGINEERING

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List of Abbreviations

ASP	Aspect (Prognosis)
BA	Basal Area
BAL	Basal Area Larger
CCF	Crown Competition Factor (Prognosis, PROGNAUS)
CF	Correction Factor (STEMS)
CR	Crown Ratio
CRC	Crown Ratio Code (STEMS)
DBH	Diameter at Breast Height
EL	Elevation (Prognosis)
FVS	Forest Vegetation Simulator
H/D	Height/diameter Ratio (PROGNAUS)
HAB	Habitat Classification or Intercept (Prognosis)
HT	Height
LC	Land Capability
LOC	Location Classification (Prognosis)
LOD	Live or Die
MSE	Mean Squared Error
NSDNR	Nova Scotia Department of Natural Resources
P	Probability of Mortality (STEMS)
PCT	Percentile of the tree in the stand basal area distribution (Prognosis)

PSP	Permanent Sample Plot
R	Mortality Rate (Prognosis)
RMSE	Root Mean Squared Error
S	Stocking density in stems/acre (Prognosis)
SI	Site Index
SL	Slope (Prognosis)
SPP	Species Specific Intercept (Prognosis)
STEMS	Stand and Tree Evaluation and Modeling System
SQI	Site Quality Index
SQL	Structured Query Language (in Access)
V	Volume
VBA	Visual Basic for Applications (in Excel and Access)

Software Trade Names

Access	Microsoft [®] Access
Excel	Microsoft [®] Excel
MATLAB	Mathworks [®] Matrix Laboratory

Abstract

Forest growth models are important to the forestry community because they provide means for predicting future yields and exploring different forest management practices. The purpose of this thesis is to develop an individual tree forest growth model applicable for the province of Nova Scotia. The Acadian forest of Nova Scotia is a prime example a mixed species forest which is best modelled with individual tree models. Individual tree models also permit modelling variable-density management regimes, which are important as the Province investigates new silviculture options. Rather than use the conventional regression techniques, our individual tree growth and yield model was developed using neural networks. The growth and yield model was comprised of three different neural networks: a network for each survivability, diameter increment and height increment. In general, the neural network modelling approach fit the provincial data reasonably well. In order to have a model applicable to each species in the Province, species was included as a model input; the models were able to distinguish between species and to perform nearly as well as species-specific models. It was also found that including site and stocking level indicators as model inputs improved the model. Furthermore, it was found that the GIS-based site quality index developed at UNB could be used as a site indicator rather than land capability. Finally, the trained neural networks were used to create a growth and yield model which would be limited to shorter prediction periods and a larger scale.

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Chapter 1: Introduction

The purpose of this thesis is to develop an individual tree forest growth and yield model applicable for the province of Nova Scotia. Individual tree models permit the modelling of mixed species forests of which the Acadian forest in Nova Scotia is a prime example. As the Province investigates new silviculture options, individual tree models also permit modelling of variable-density management regimes. Rather than using the conventional regression techniques, our individual tree growth and yield model will be developed using neural networks. There are many species in the Acadian forest and there is not enough data to model each of these species separately. By including tree species as a model input a single model can be used for all species of the Acadian forest. It turns out we can take advantage of this to model the less represented species without much loss in the ability to model the better represented species.

In this thesis, we will review different individual tree models, neural networks, and neural network approaches to individual tree growth models. The different model structures which were used for the different individual models will be discussed. Next, we will examine the available data for Nova Scotia. Given the data we have obtained and by observing the model structures of other individual tree models, we discuss the reasons for having built a growth model that consists of three neural networks: one each for predicting tree survivability, diameter growth, and height growth. The methods by which the data was prepared and how the network models were fit will also be presented, followed by results for the data fitting. Methods for using the fitted networks in a growth model will be discussed, followed by conclusions and recommendations.

In this thesis we show that neural networking is an acceptable modelling technique for a Nova Scotia growth model. Using this technique, we show that species can be used as a model input in a model applicable to all species as opposed to creating multiple species-specific models. We also show that the networks are better fit when we use inputs to characterize both the level of stocking and site measurements in the stands. We demonstrate that a GIS-based site measurement is an alternative to land capability because, as a model input, it performed better than land capability and it is available for

the whole Province. Finally, we demonstrate that the trained neural networks to develop a growth model.

Chapter 2: Background

Forest growth models are important to the forestry community because they provide means for predicting future yields and investigating different forest management practices. They provide an efficient way to explore various silvicultural and harvesting options and examine the effects they have on the state of the forest (Vanclay, 1994). Growth models are especially important in forestry since testing various management practices on actual plots of forest is impractical. Long range planning is an essential part of forest resource management; this requires accurate estimates of both current levels and expected resource levels after various management alternatives (Belcher, Holdaway, & Brand, 1982).

2.1 Modelling Tree Growth

Traditionally, forest management has relied on yield tables to estimate expected timber harvests and to make management decisions. Yield tables were developed using pure and even-aged stands (Hasenauer, Merkl, & Weingartner, 2001) and are therefore really only conducive to stands harvested by clear-cutting. The province is committed to enhancing the Acadian forest which is typically uneven aged and of mixed species (Nova Scotia Department of Natural Resources, 2008). Overall, we would like to shift away from clear-cutting practices which causes stands to consist of trees with a variety of ages and species.

There are many different approaches to growth modelling in forestry. In addition to stand-level models, growth models may also be developed at the individual tree-level. Although stand-level approaches are quite simplified, they have been robust. Stand-level parameters such as stocking, basal area and volume are used to predict growth of the stand (Vanclay, 1994). Because there is no prediction for the individual tree, stem size distributions are often used for better comprehension of the stand. But, similar to yield tables, stand models are unable to easily represent uneven-aged and multi-species stands and do not easily lend themselves to test different thinning or planting patterns. Along with ever-improving computing abilities, there has been increased development of tree-level growth models (Porté & Bartelink, 2002).

Although there are many factors that affect tree growth, individual tree models must know, at the very least, the size of each tree in a stand to make growth predictions. As will be reviewed in the literature, many modellers choose to model tree growth using a variety of tree and stand characteristics. Aside from the level of resolution, forest growth models may be empirical or mechanistic, deterministic or stochastic, and spatially dependent or independent (Vanclay, 1994; Porté & Bartelink, 2002). Initially, growth models were developed from data (empirical); but in the interest of developing tree growth theory, growth models were made based on the underlying physical and chemical processes influencing tree growth (mechanistic). Mechanistic models are typically used for research purposes (i.e. the effects of climate change) rather than forest resource management (Porté & Bartelink, 2002). Deterministic growth models estimate the expected amount of growth in a tree or stand given certain initial characteristics. Stochastic growth models attempt to account for the natural variation of tree growth because, in reality, the growth of trees with similar characteristics will vary. This being stated, a single stochastic prediction is not useful as it is only one experiment outcome of a variety of possibilities; a series of stochastic experiments must be completed to provide understanding of the nature of forest growth (Vanclay, 1994). Spatially dependent models use the distance between trees to understand the interactions amongst adjacent trees. However, tree-location data is not always available and spatially independent models must then be used (Porté & Bartelink, 2002). There will be no discussion as to what type of model is best since the model type is clearly dependent on what the model will be used for and what information is available for developing the model.

2.2 Forests and Forest Modelling in Nova Scotia

The majority of the forest in Nova Scotia is Acadian Forest, with a small amount of Boreal Forest in the Cape Breton Highlands (Mosseler, Lynds, & Major, 2003). The Acadian Forest is characterized by its shade-tolerant species; these species include, but are not limited to, red spruce, balsam fir, eastern hemlock, white pine, yellow birch, sugar maple and American beech. The majority of the Acadian forest is occupied by red spruce and balsam fir. Mosseler, Lunds and Major (2003) state that much of the old growth from the region has been cleared within the last few centuries for agriculture and timber harvesting, thus leaves a very young forest in Nova Scotia. The Acadian Forest has since

been heavily managed which accounts for the many plots in the province that are currently even-aged and less than 100 years old (Townsend, 2004).

In Nova Scotia, the two areas of interest driving the need for growth models are economics and sustainability. From an economic standpoint, reliable growth models are required to predict outcomes of different silviculture and harvesting practices to obtain the best yields (note that unharvested stands do not supply the highest yield of timber). From a sustainability point of view, a reliable growth model is required to develop new silvicultural and harvesting practices which promote a healthy forest. The Nova Scotia Department of Natural Resources (NSDNR) has developed growth models for both hardwood and softwood stands. These models are only applicable to single-species even-aged stands and may only undergo previously researched treatments (O'Keefe & McGrath, 2006). Although these models may be useful for many current stands, they will only continue to be useful if future stands remain pure and even-aged. As the province moves away from clear-cutting practices to meet economic and sustainability demands, these models become less applicable. Therefore, NSDNR requires tree-level models for Nova Scotia.

2.3 A New Modelling Approach for Nova Scotia

Individual tree models are commonly non-linear regression models fit for a single species (Peng & Wen, 1999). In Nova Scotia, there are many different tree species and, as a result, there exist stands that include many different tree species. To model a multi-species stand, each tree species in the stand would typically require a different model. Fitting models for every species in the forest is very challenging because there would need to be a sufficient amount of stratified data available for each species. This is especially difficult in the Acadian Forest because it encompasses so many types of species. In Nova Scotia, there are considerable tree data available through the Department of Natural Resources. First, there is an inventory database of permanent sample plots (PSPs) which gives a good representation of the forest. There are also research PSPs established by the province for testing different treatments; these plots lack the variation of the inventory PSPs. Together, these data sets are well suited for modelling the most abundant species in the province (i.e. red spruce or balsam fir) since

there are plenty of data available to do so. However, there are many species that are not well represented in the database (i.e. red oak) and there is insufficient data for developing a growth model for these species. A description of the gaps in the data set will be discussed in Chapter 4. In effect, the NSDNR data set is only sufficient to enable species-specific regression models for a few species.

Thus we are left with the problem of how to create a model that can represent all trees in the province, including the infrequent species. One way of doing this is to use the full spectrum of species to develop a single model rather than having separate models for each species. Considering that tree growth for all species depends upon the same factors (we discuss these factors in Chapter Chapter 5:), we can assume that all trees grow somewhat similarly but they are influenced by their species. If we include species as a model input, it will allow for all trees to be represented within the same model and still be capable of differentiating between species.

By including species as a model input, the concept of the traditional growth model has changed and the fitting of the data becomes more challenging. In regression modelling, the modeller would be now responsible for finding basis functions to include each of the species inputs. Neural networking is a modelling approach that can be used when there is understanding of which factors influence an output, but it relieves the modeller of the responsibility of determining basis functions for the model. As long as the modeller does not require a nice equation for the model, neural networks can be a useful modelling tool.

In this project, we will develop an individual-tree based neural network model based upon the NSDNR's data to model individual tree growth.

Chapter 3: Literature Review

For this project, it is important to review well-regarded individual tree models for the purpose of building the neural network models. Clearly, in order to build a neural network model it is also important to review the theory behind neural network modelling. Different applications of neural networks in growth modelling will also be reviewed along with the advantage and disadvantages of neural network modelling.

3.1 Individual Tree Models

Although our data does not support the development of species-specific regression models Nova Scotia, it is very helpful to understand them for the purpose of building the neural network model. There are a wide variety of individual tree models available for review, a few of which will be reviewed. The United States Department of Agriculture Forest Service uses the Forest Vegetation Simulator (FVS) as its framework for growth modelling. FVS is an individual-tree and distance-independent growth simulator. It is actually a group of growth simulation models that vary by geographic region (United States Department of Agriculture Forest Service). Two well-known growth models included in FVS are Prognosis and STEMS; these models will be reviewed in sections 3.1.1 and 3.1.2, respectively. Both of these models use data at the beginning of a growth period to predict tree characteristics at the end of a specified growth period. It is also worth examining Monserud's PROGNAUS model for Austria, since there has been plenty of forest research done in Europe. PROGNAUS also predicts future tree characteristics from initial data and will be reviewed in section 3.1.3. All three of these individual tree models will be compared in section 3.1.4.

3.1.1 Prognosis

Prognosis is a widely accepted distance-independent, individual-tree, forward-projection growth model. It was originally developed for the northwestern states by Albert Stage in 1973 and modified by William R. Wykoff in 1983 (Peng & Wen, 1999). The Prognosis model is intended to provide a unified growth modelling approach applicable to all types of stands: the model applies to stands of single- or mixed-species and a variety of age and size. Prognosis was first implemented for the lodgepole pine since data was readily available and there were stand-level models available for comparison (Stage, 1973).

According to Stage (1973), a robust stand-growth prediction should consist of three main parts: (i) a model to represent the development of individual trees, (ii) a model to represent the regeneration (including ingrowth) of the stands, and (iii) a model to represent the transition from regeneration to individual trees. As the latter two parts still required much research, Stage's focus of the Prognosis model was solely on the development of individual trees.

The Prognosis model breaks down tree development into diameter increment, height increment, crown dimensions, and mortality rates. These model components depend on a combination of tree size, vigour, competition with other trees, and site characteristics; each of these model components is developed for a single species. Tree and stand characteristics are determined directly or indirectly from a tree list which is presented to the model (Wykoff, Crookston, & Stage, 1983); the tree list is a record of each tree and its attributes within a stand. In practice, tree lists exclude smaller trees and saplings by only measuring trees exceeding a minimum diameter (Nova Scotia Department of Natural Resources, 2002). Apart from offering characteristics for each tree in the list, the tree list may be used to calculate the density of a stand. Stand density can be used to understand the competition within a stand without knowing the exact locations of each tree (Vanclay, 1994).

The Prognosis model depends on a variety of measurements and classifications. The most basic tree measurement is tree size. Tree size is defined by diameter at breast height (DBH) and height (HT). If height for a tree is missing, Prognosis uses the diameter-based equation to get an estimate for height:

$$HT = e^{(C_0 + C_1 \frac{1}{DBH+1})} + 4.5 \quad (1)$$

where C_0 and C_1 are species-specific coefficients. Crown ratio (CR) is used as an indicator of tree vigour; if crown ratio is missing from the data it is also estimated. Competition with other trees is measured by the sum of the basal areas of larger trees (BAL), the percentile of the tree in the stand basal area distribution (PCT), and crown competition factor (CCF). Crown competition factor is an estimate of the percentage of an acre that would be covered by the crown if it were openly grown; CCF is species-

dependent and is estimated from DBH and stand density. Finally, stand measurements required by the model are slope (SL), aspect (ASP) and elevation (EL). Classifications of habitat (HAB) and location (LOC) are also used in Prognosis.

The diameter increment (ΔDBH) model does not directly model diameter increment. In fact, ΔDBH is calculated from the modelled squared inside-bark diameter increment (ΔDBH_{ib}^2). The reason the model predicts the increment of inside-bark squared diameter rather than diameter is because, according to Stage, the relationship between the logarithms of ΔDBH_{ib}^2 and DBH is linear and the residuals of this relationship discretely vary homogeneously for the range of the relationship. This homogeneous variance of the residuals, or homoscedasticity, is required for regression analysis (Sachs, 1984). Thus, the model predicts $\ln(\Delta DBH_{ib}^2)$ for each tree based upon $\ln(DBH)$ as well as many aforementioned variables:

$$\begin{aligned} \ln(\Delta DBH_{ib}^2) = & HAB + LOC + b_1 \cos(ASP) SL \\ & + b_2 \sin(ASP) SL + b_3 SL + b_4 SL^2 + b_5 EL \\ & + b_6 EL^2 + b_7 (CCF/100) + b_8 \ln(DBH) \quad (2) \\ & + b_9 CR + b_{10} CR^2 + b_{11} (BAL/100) \\ & + b_{12} DBH^2 \end{aligned}$$

where b_1 through b_{12} are species-specific coefficients. If available, Prognosis will use the data from the previous growth period to calibrate the model. ΔDBH may also be calibrated using the measurements of increment core samples from the trees.

As previously discussed, Prognosis uses a species- and diameter-dependent height equation to obtain missing height measurements (Equation 1). Using the differential of this equation, one can derive a relationship for height increment (ΔHT) based upon height, diameter, and diameter increment. With a few modifications, Prognosis predicts a ten year height increment according to:

$$\begin{aligned} \ln(\Delta HT_{10}) = & HAB + SPP + b_1 \ln(HT) \\ & + b_2 \ln(DBH) + b_3 \ln(\Delta DBH_{10}) + b_4 HT^2 \quad (3) \end{aligned}$$

where HAB and SPP are habitat and species dependent intercepts, b_2 is a species-specific coefficient, and coefficients b_3 and b_4 are habitat dependent. For smaller trees, however, Prognosis uses another height increment equation because it is better for calibration purposes; this equation does not include ΔDBH because taking increment cores from very small trees can be detrimental to the tree. Unfortunately, regardless of the tree size, there is discontinuity between the two ΔHT equations; therefore, Prognosis uses switching functions are used to transition between the two equations.

Crown ratio is the ratio of the height of the tree crown to the total height of the tree. Although crown ratio changes slowly over time (Wykoff, Crookston, & Stage, 1983), crown ratios should be updated after each growth period since crown ratio is required to update diameter and height (Equations 2 and 3). Wykoff, Crookston and Stage (1983) acknowledge that due to the subjectivity involved crown measurement the availability of consistent crown ratio data is limited (this will be discussed in more detail in Section 3.1.3). This makes modelling changes in crown ratio rather difficult and imprecise. In light of these problems in modelling crown ratio, Prognosis still predicts the new crown ratio according to:

$$\begin{aligned}
 \ln(CR) = & HAB + b_1BA + b_2BA^2 + b_3\ln(BA) + b_4CCF \\
 & + b_5CCF^2 + b_6\ln(CCF) + b_7DBH \\
 & + b_8DBH^2 + b_9\ln(DBH) + b_{10}HT \\
 & + b_{11}HT^2 + b_{12}\ln(HT) + b_{13}PCT \\
 & + b_{14}\ln(PCT)
 \end{aligned} \tag{4}$$

where b_1 through b_{14} are species-dependent regression coefficients.

Prognosis uses a couple of equations to predict mortality, both of which calculate a mortality rate. Mortality rate is the percentage of trees that die in a stand over a specific period; in Prognosis, mortality rates are computed on an annual basis (Wykoff, Crookston, & Stage, 1983). The simplest equation for mortality predicts the mortality rate (R_d) based on diameter only:

$$R_d = \frac{1}{1 + e^{(b_0 + b_1 DBH + b_2 DBH^2)}} \quad (5)$$

where b_1 , b_2 , and b_3 are species-specific coefficients. R_d is appropriate in most situations; however, in instances where mortality is increased by competition and suppression, the diameter-based equation underestimates the mortality rate. Therefore, Prognosis also uses a density-dependent mortality equation:

$$R = 1 - \left(1 - \frac{S_0 - S_{10}}{S_0}\right)^{0.1} \quad (6)$$

where S_0 is the current stocking density, in stems (number of trees) per acre, and S_{10} is the predicted stocking density after 10 years. Wykoff, Crookston and Stage (1983) consider that stands may be densely stocked by either the number of stems or its basal area. Therefore, Prognosis uses two methods of calculating S_{10} depending on whether stand wants to return to normal stocking levels, or whether the stand is approaching its maximum basal area. Prognosis uses the measurements of tree diameter, stand basal area, and maximum stand basal area to determine which mortality rate (or combination of mortality rates) to use.

Finally, the Prognosis model calculates stem volume from diameter and height according to:

$$V = b_0 + b_1(DBH)^2HT + b_2(DBH)HT \quad (7)$$

where b_0 , b_1 , and b_2 are species-dependent coefficients.

3.1.2 STEMS

The United States Department of Agriculture developed a Stand and Tree Evaluation and Modeling System (STEMS) for the states in the Great Lakes region. It is an individual-tree distance-independent model. STEMS consists of two FORTRAN programs: one to project the tree growth and the other to create user-defined output files and summary tables (Belcher, Holdaway, & Brand, 1982). Only the forward projection program of the model will be reviewed.

The STEMS growth model predicts annual diameter growth, probability of mortality, and crown ratio growth for each tree. The model also includes a tool in which different management options can be applied to the stands and a regeneration decision tree to bring new trees into the stand; the regeneration decision tree is determined from data. Belcher, Holdaway and Brand (1982) only had sufficient data to model regeneration for the initial growth after a stand has been clear-cut. Therefore, regeneration for uneven-aged stands was not modelled.

The annual diameter growth is estimated as a fraction of the potential diameter growth of the tree. The potential diameter increment is the expected annual diameter growth if the tree was free to grow without competition from its neighbours. This potential change in diameter is then multiplied by a modifier component which estimates competition in the stand.

$$\text{Annual } \Delta DBH = \text{Potential } \Delta DBH \times \text{Modifier} \quad (8)$$

The potential diameter increment equation depends upon diameter, crown ratio code (CRC) and site index (SI) of the plot:

$$\text{Potential } \Delta DBH = b_1 + b_2 DBH^{b_3} + b_4 SI \cdot CRC \cdot DBH^{b_5} \quad (9)$$

where b_1 through b_5 are species specific regression coefficients. The competition modifier component is comprised of a series of functions:

$$\text{Modifier} = 1 - e^{-B_0} \left(\frac{BA_{max} - BA}{BA} \right)^{\frac{1}{2}}$$

$$B_0 = f(DBH/\overline{DBH}) \cdot g(\overline{DBH}) \quad (10)$$

$$f(DBH/\overline{DBH}) = b_1 (1 - e^{b_2 DBH/\overline{DBH}}) b_3 + b_4$$

$$g(\overline{DBH}) = c_1 (\overline{DBH} + 1)^{c_2}$$

where BA_{max} is the maximum basal area per acre expected for the species, BA is the current basal area, \overline{DBH} is the average diameter of the stand, and $b_1, b_2, b_3, b_4, c_1, c_2$ are regression coefficients. Trees on less dense stands will have larger modifier values.

Having a measurement for crown ratio is important for the model to respond to changes in stand density and to measure competition in the stand. As referred to in the diameter increment equation, STEMS uses a crown ratio code. CRC is simply the classification of crown ratio based on estimates of crown ratio percentages; STEMS uses ten different crown ratio classes: 0-10%, 10-20%,..., 80-90%, 90-100%. These estimates for crown ratio percentage are classified according to:

$$CRC = \frac{b_1}{1 + b_2 \overline{BA}} + b_3(1 - e^{-b_4 DBH}) + CF \quad (11)$$

where \overline{BA} is the average stand basal area per acre over 10 years, b_1 through b_4 are species specific regression coefficients, and CF is a correction factor.

STEMS predicts the probability of mortality, P , for an individual tree for a 1-year period based upon tree size (DBH) and vigour (ΔDBH); similar to Equation 5, mortality is predicted using a logistic function:

$$P = \frac{1}{1 + e^{(b_1 + b_2 \Delta DBH^{b_3} + b_4 DBH)}} + b_5 \quad (12)$$

where b_1 through b_5 are species-specific coefficients. Once calculated, STEMS uses the probability of mortality in two different ways, where the choice is user-defined. For probabilistic mortality, a random number is generated from a uniform distribution between 0 and 1 and if the tree's probability of mortality is larger than this number then the tree is killed in the simulation. In deterministic mortality, the number of trees per acre that the tree represents, also known as the expansion factor, is reduced by the probability of mortality. If the expansion factor is reduced to 1 tree per acre, then the mortality type is switched to probabilistic so that the tree cannot represent less than one tree per acre. Both mortality methods should give the same outputs for a large amount of plots and shorter projection periods. For longer projection periods, although the probabilistic mortality is less computationally challenging, it may eventually produce unrealistic results. Recall that Prognosis calculates mortality rates on a stand basis and is thus limited to modelling deterministic mortality. Because STEMS represents tree

mortality on an individual tree basis it is able to use both probabilistic and deterministic mortality.

3.1.3 PROGNAUS

Monserud has been involved in many aspects of tree modelling including growth models, harvesting models, and validation testing (Monserud & Sterba, 1996). He has incorporated many of these models in the development of the PROGNAUS model: the Prognosis for Austria individual-tree growth model. Components of this model include predictions for basal area and height increments, crown ratio and tree mortality. Together with Sterba, Monserud developed a basal area increment model and an individual tree mortality model (Monserud & Sterba, 1996; Monserud and Sterba, 1999). With Hasenauer, he developed a height increment model and a crown ratio model (Hasenauer & Monserud, 1996; Hasenauer & Monserud, 1997).

Similar to Prognosis, Monserud and Sterba chose to use a logarithmic model for basal area increment because of its homoscedastic relationship with the logarithm of DBH; PROGNAUS predicts the logarithm of basal area increment over 5 years by a function of tree size, competition and site characteristics:

$$\begin{aligned} \ln(\Delta BA) = & a + b_1 \ln(DBH) + b_2 DBH^2 + b_3 \ln(CR) \\ & + c_1 BAL + c_2 CCF + s \times SITE \end{aligned} \quad (13)$$

where a , b_1 , b_2 , b_3 , c_1 , c_2 , and s are mostly species specific coefficients. Tree size is represented by the diameter and crown ratio measurements; the squared diameter term is useful because (if b_2 is negative) it prevents unlimited growth for large diameter trees. Because it is easier to have spatially-independent data, competition is limited to spatially-independent variables. Therefore, only stand density and rankings are possible. Again, similar to Prognosis, PROGNAUS uses two variables to represent competition: the sum of basal areas of larger trees and crown competition factor. Site characteristics include both qualitative and quantitative site measurements; for example: elevation, slope, aspect, soil group, and vegetation type (Monserud & Sterba, 1996).

Hasenauer and Monserud's crown ratio model is important because crown ratio will be indicative of tree vigour and will also be used to update the tree measurements. Crown

ratio is related to tree vigour because it is closely related to crown length; some consider crown length to be a measure of the photosynthetic potential of a tree (Hasenauer & Monserud, 1996). Overall tree growth can be attributed to photosynthates and hormones which are produced only in the crown; therefore, crown length and crown ratio reflect a tree's growth potential. Hasenauer and Monserud also point out the difficulty of modelling crown ratio because of its subjectivity; this is especially true for asymmetric crowns because it is tricky to identify the base of the crown. Furthermore, obtaining accurate measurements for height is often difficult in itself (Hasenauer & Monserud, 1997). Again, despite the problems of modelling crown ratio, PROGNAUS models the crown ratio proportion with a logistic function where crown ratio ranges from 0 (no crown) to 1 (full crown). Crown ratio is dependent upon size, competition and site:

$$CR = \frac{1}{1 + e^{-(a+b_1H/D+b_2HT+b_3DBH^2+c_1BAL+c_2 \ln(CCF)+d \times SITE)}} \quad (14)$$

Here, tree size is represented by both height and diameter. The height/diameter ratio (H/D) was also considered useful since H/D is an indicator for the taper of a tree. Both the taper of the tree and the crown ratio respond to increasing stand density, therefore crown ratio is related to taper in the sense that trees with more taper have a higher crown ratio than those with less taper. Again, for simplicity, competition measurements are restricted to distance-independent measures. Similar to the diameter increment model, BAL and CCF are used. Site measurements are meant to reflect the topography of the plot only and include elevation above sea level, slope, and azimuth measurements.

Just as in the model for crown ratio, height increment prediction for 5 years is based upon the assumption that height growth is a function of tree size, competition and site:

$$\ln(\Delta HT) = a + b_1 \ln(DBH) + b_2 HT^2 + b_3 CR + c_1 CCF + c_2 BAL + d \times SITE \quad (15)$$

where a , b_1 , b_2 , b_3 , c_1 , c_2 , and d are mostly species specific coefficients. Regression analysis was done for the logarithm of height increment to stabilize the variance (Hasenauer & Monserud, 1997).

Similar to STEMS, PROGNAUS's mortality model uses the logistic equation to model the probability of mortality for each tree, P . With inputs describing tree size, vigour, and competition, PROGNAUS uses maximum likelihood methods to fit data to a non-linear equation for the P :

$$P = \frac{1}{1 + e^{b_0 + \frac{b_1}{DBH} + b_2 CR + b_3 BAL + b_4 DBH + b_5 DBH^2}} \quad (16)$$

where b_0 through b_5 are species-specific coefficients. Although there are other factors which can contribute to the mortality or survivability of a tree, Monserud and Sterba (1999) attempted to keep independent factors to a minimum to avoid overparameterization. They state that diameter alone is a reliable measure of a tree's size. Mortality greatly depends on tree size (specifically diameter) because the larger the tree, the greater its chances are for competing for resources; this would indicate that mortality of a tree decreases as the tree diameter increases. In an older forest, the oldest trees may begin to die of senescence and it is therefore possible that tree mortality rates can increase at the largest diameter classes. The size of the tree can also be recognized as the tree's response to site and age and a model containing diameter will implicitly consider site and age effects. BAL is important in mortality prediction because it gives an understanding of competition with other trees. CR is important to consider in tree mortality because it is an indicator of the vigour of the tree.

3.1.4 Comparison of the Different Growth Models

By comparing the each of the reviewed individual growth regression models – Prognosis, STEMS and PROGNAUS – it is apparent that each of the models relies on many species-specific coefficients that must be derived from complex parameter estimation techniques. These parameters are typically estimated from large data sets. A good data set will include a reasonably large number of observations for each class of diameter, height, age, etc. Similarly, a good data set will include an acceptable number of observations for each species. Data collected for inventory purposes will inherently only have sufficient data for the most abundant species in the forest. In effect, the models are only suitable for the abundant tree species. This means that the less abundant species are regularly left with insufficient data to generate a reliable model.

Prognosis, STEMS, and PROGNAUS each forward project diameter, mortality and crown ratio as part of their model components. Both the Prognosis and PROGNAUS models also predict height increment while the STEMS model does not have a height increment component.

Diameter predictions were all made by modelling diameter increments directly or indirectly. In their diameter increment models, Prognosis and PROGNAUS use logarithmic equations to calculate a squared diameter increment from which diameter increment may be calculated; justification for modelling squared diameter instead of diameter increment was made because of the homoscedastic relationship between the logarithms of diameter and squared diameter increment. On the other hand, STEMS uses a non-linear relationship to predict potential diameter change and then modifies it. In the STEMS literature, there was no mention of the possibility for modelling squared diameter increment. Similar inputs for all three models include initial diameter, crown ratio, competition with respect to basal area, and site measurements.

Only Prognosis and PROGNAUS include height increment components for their models. Just as in the diameter increment models, both programs use logarithmic relationships to predict height increment. Similar inputs for each of these models include initial size (height and basal area), a measure for vigour (crown ratio or diameter growth rate) and some form of site measurements.

Prognosis, STEMS, and PROGNAUS each contain a crown ratio prediction equation; each of these equations are non-linear and have quite different structures than one another. Of these three equations, only PROGNAUS models crown ratio directly. Prognosis predicts the change in crown ratio while STEMS predicts the range of crown ratio range by classifying the expected crown ratio by percentage. Both the developers of Prognosis and STEMS admit that crown ratio is difficult to model over time and that crown ratio of a tree changes slowly in time (Belcher, Holdaway, & Brand, 1982; Wykoff, Crookston, & Stage, 1983). They also state that crown ratio is a measurement for which extensive data is hard to get. However, the developers agree that crown ratio is important to model because it is important to have a measure of vigour to model tree growth.

Despite having acknowledged the difficulties of modelling mortality (these are further discussed in Section 5.2.1), the developers of Prognosis, STEMS, and PROGNAUS each use a mortality prediction component as mortality (or survivability) is necessary in growth modelling. PROGNAUS and STEMS predict the probability of mortality for an individual tree over a growth period using a logistic function with common inputs of initial diameter and vigour measurements (crown ratio and previous diameter increment). Depending on the stand characteristics, Prognosis has a few different equations for predicting annual mortality rate of a stand. Similar to the other growth models, the Prognosis mortality models depend on the initial diameter of the tree.

3.2 Neural Networks

Neural network modelling is a method of approximating an input-output process. A neural network essentially outputs a linear combination of functions based upon a set of inputs. Through optimization methods, referred to as training in the neural network literature, neural networks have the ability to learn the shape of very complex response surfaces by minimizing the error between the actual and the modelled outputs. To understand how neural networks are trained, it is important to first understand the general structure of neural networks

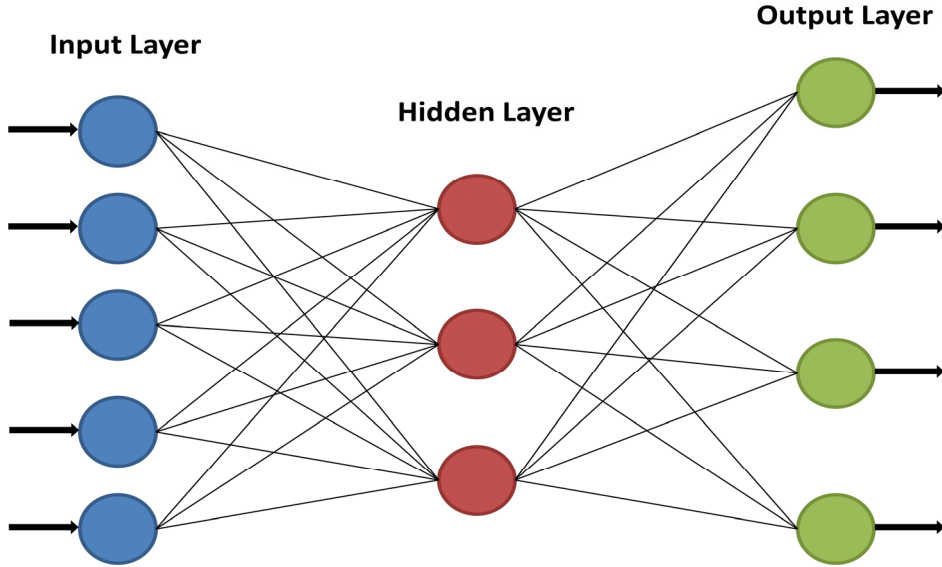


Figure 1 General structure of feed-forward neural network

A basic feed-forward neural network (Smith, 1993) consists of multiple layers where the nodes in the adjacent layers are fully connected (Figure 1). There exist many other configurations of neural networks; however, these configurations will not be reviewed in this thesis since they will not be used. In the basic feed-forward neural network, normalized data enters the network through the input layer where there is typically an input node for each input to the model. The middle and output nodal layers are comprised of computational nodes – they are called the hidden and output nodes, respectively. The model outputs leave the network via the layer of output nodes for which there is an output node for each model output. The number of hidden nodes may vary depending on the complexity required by the model. Every connection in the network has a strength, or weight, and each computation node also has an offset, or bias weight. This bias weight can simply be considered as a weight on a constant input. Consider a network with I input nodes, J hidden nodes, and K output nodes. Each hidden node calculates a weighted sum of the input values (Equation 17) and passes it through a function, f (Equation 18):

$$u_j = a_{0j} + \sum_{i=1}^I a_{ij}x_i \quad (17)$$

$$y_j = f(u_j) \quad (18)$$

where u_j is the weighted sum at hidden node j , x_i is the input of input node i , a_{0j} is the bias weight at the hidden node j , a_{ij} is the connection weight from input node i to hidden node j , and y_j is the output of hidden node j . The function, f , is generally a sigmoid function, for example, a logistic function or a tan-sigmoid function (Equation 19 and Figure 2). A sigmoid function is an S-shaped curve with upper and lower bounds, is always increasing, and is differentiable (Smith, 1993). Other options for f include linear and unit step functions.

$$f(u) = \frac{e^u - e^{-u}}{e^u + e^{-u}} \quad (19)$$

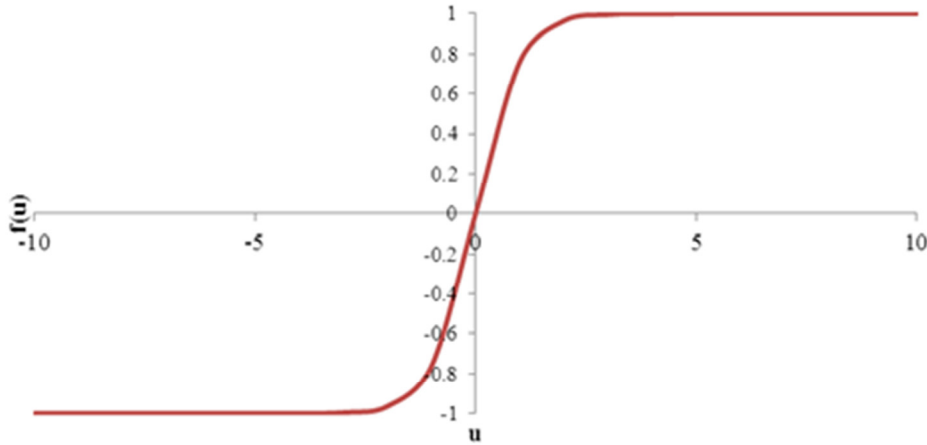


Figure 2 The tan-sigmoid function

Similar to the hidden nodes, the output nodes calculate the weighted sum of the hidden node outputs (Equation 20), and then pass it through a function, g (Equation 21):

$$v_k = b_{0k} + \sum_{j=1}^J b_{jk} y_j \quad (20)$$

$$z_k = g(v_k) \quad (21)$$

where v_k is the weighted sum at output node k , b_{0k} is the bias weight at the output node k , b_{jk} is the connection weight from hidden node j to output node k , and z_k is the output of

output node k . Function g is also often a sigmoid function, but is not required to be the same as f . Both functions f and g may be referred to as activation functions.

This forward process through the network is called the mapping mode. Given the appropriate weights, the mapping function can take on many shapes, and it is because of this flexibility that neural networks are capable of approximating nonlinear or noisy response surfaces (Barton, 1998). Also, because these mapping functions are so versatile, neural networks have many applications including function approximation, pattern recognition, and classification (Jain, Mao, & Mohiuddin, 1996).

Clearly, a very important task in fitting neural network models is finding the best possible weights; this can be done by fitting the network with a data set of known input-output values (with N samples). A conventional way of measuring the data fit is by mean squared error (MSE); when using MSE as a measure of network fit, the goal of network fitting would be to find the set of weights that minimizes the mean squared error:

$$\text{Min} \frac{\sum_{n=1}^N \sum_{k=1}^K (z_{kn} - t_{kn})^2}{NK} \quad (22)$$

where z_{kn} is the network output and t_{kn} is the target output at output node k and sample n .

Initially, the network weights are assigned small random numbers and the inputs are mapped through the network. The error with respect to the network output ($\partial E / \partial z$) is simply the difference between the modelled and known outputs. Using partial derivatives, the error with respect to the weights connected to the output nodes ($\partial E / \partial b$) can be calculated by the chain rule:

$$\frac{\partial E}{\partial b} = \frac{\partial E}{\partial z} \frac{\partial z}{\partial v} \frac{\partial v}{\partial b} \quad (23)$$

This is rather simple since the error on these weights (b_{0k} and b_{jk}) is affected only by error from a single output node. However, the rest of the weights (a_{0j} and a_{ij}) are affected by the error from each of the output nodes and the error from each output node must be propagated back to each weight a_{0j} and a_{ij} :

$$\left(\frac{\partial E}{\partial y} = \sum_{k=1}^K \frac{\partial E}{\partial z_k} \frac{\partial z_k}{\partial v_k} \frac{\partial v_k}{\partial y}\right) \quad (24)$$

$$\frac{\partial E}{\partial a} = \frac{\partial E}{\partial y} \frac{\partial y}{\partial u} \frac{\partial u}{\partial a}$$

This is done for each input-output sample in the data set where the error at each weight is accumulated with every example. This process of propagating the error back through the network is called backpropagation. Given the accumulated error at each weight, the direction and magnitude of change that is made to each weight is derived by search algorithms such as Conjugate Gradient or Levenberg–Marquardt in order to minimize the error.

It is the process of mapping inputs through the network, comparing the network outputs to the desired output, backpropagating the error through the network, and changing the weight accordingly that comprises a neural networking iteration. These iterations are executed until a target minimum mean squared error is attained or until a maximum number of iterations are performed. At this point, the network may be used for mapping inputs to estimate output values. Once a neural network is trained, a new set of data is often used to evaluate how well the model performs (Smith, 1993).

The first step of building a neural network model is to determine the structure of the network. For each quantitative model input, there should be an input node in the network. In the case of qualitative or categorical data (i.e. species), the inputs must be represented numerically to be input in the network. In the case where there is more than one category, there must be an input node for each category represented in the data (for example, each species group will require an input node), and the data must be represented by a binary vector (Brouwer, 2004). If the categorical data is represented by only one input node, a categorical scale will be used and the network assumes the variable is continuous. This is unwise if there is no meaningful relationship between the categories.

Similar to the input nodes, each quantitative output variable can be represented by an output node. However, classification output variables will require a different approach since the output will be a continuous variable (Smith, 1993). One way to adapt this

continuous output variable into a binomial one is to have a threshold where one outcome will be distinguished from another. This is especially difficult when the training data contains examples of similar inputs producing different outputs because outputs will often not be clearly distinguishable. To account for this noise, the threshold may be randomly generated (Belcher, Holdaway, & Brand, 1982). The problem with doing this is that when a classification model is used to predict a binomial outcome, it is only one experiment of many possibilities; the model would need to be run many times to get a proper understanding of the model behaviour. For example, if a coin is flipped only a few times, one can easily have three identical outcomes and misunderstand the expected behaviour of flipping a coin; the more times the experiment is performed, the better the expected behaviour may be understood. Therefore, the output of a classification matrix is often interpreted as a probability of occurrence (Smith, 1993).

In the case where there are multiple outputs, the modeler must make the decision to have either a single model with several outputs (Figure 1) or multiple models with a single output each. The advantage of using a single model with multiple outputs is if the modeler still intends to develop a classification network. Otherwise, with continuous outputs, there is an advantage to using multiple single output networks because each network will be focused on achieving the best possible fit for its output.

Determining the number of hidden nodes is a slightly more complicated process. The network can better model a complex relationship with the more hidden nodes that are in the network. However, the modeller must be careful to not overparameterize the data with too many hidden nodes or else the model will begin to fit the noise in the data set and the network will not be appropriately applied to data in general. If the training is allowed to continue for too many epochs, the network may begin to fit the noise in the data. Therefore, there must be a balance between the number of hidden nodes and maximum number of training epochs.

3.3 Applications of Neural Networks in Growth Models

Neural networks have become a modelling technique used in a variety of different areas of forest resource management including land classification, spatial data analysis, and forest growth and dynamics. Because modelling in forest resource management often has

qualitative components and other complexities, there was a drive to find alternative modelling techniques to the traditional statistical modelling approaches. Since mortality modelling has proven difficult to model, it is for this reason that in growth modelling neural networks have been mostly applied to mortality modelling (Peng, C., and Wen, X., 1999). There are problems with this that we will discuss in Chapter 8.

Guan and Gertner (1991) and Hasenauer et al. (2001) have both created neural network single species mortality models and compared them to conventional regression models. Both studies found that neural networks could better fit the data and predict mortality probabilities according to tests like the mean squared error and chi-squared. It was thus concluded that neural network mortality models were viable alternatives to the conventional methods. Both of these models used only a few input parameters. Hasenauer et al. (2001) remind us that with the increase of input parameters, the network model can only improve, because if the added inputs are not useful for improving the model fit, the training process inherently ignores the added inputs by assigning their weights with very small numbers.

3.4 Advantages and Disadvantages of Using Neural Networks in Growth Models

Especially for the Acadian forest, one great advantage of using neural networks to model growth is that species may be included as a model input while relieving the modeller of the responsibility of determining basis functions which would be required for a statistical model; this is especially advantageous with a complex data set. Also, we would expect the neural network models to more or less match the performance of regression models. Another important advantage of neural networks is that they are capable of modelling complex and less understood relationships such as individual tree mortality.

Other advantages of using neural networks are as follows (Tu, 1996):

- Although regression methods can describe complex relationships, these complexities must be identified by the modeller; therefore, complex relationships can often be left unrecognized. Since neural networks automatically adjust the network weights to reflect the relationship between the independent and

dependent variables, the neural network inherently detects any complex nonlinear relationships.

- As the number of input variables are desired to be used in the model increase, the number of possible interactions between inputs increase. This can become quite overwhelming when testing a regression for all possible two way interactions, while neural networks detect these interrelationships with the hidden layer of nodes.
- There are a variety of training algorithms available to create a neural network. Some algorithms can offer improved convergence and convergence time.
- Neural networking may be used for modelling various relationships. This is useful when the nature of the data is unknown.
- Oftentimes, nonlinear regression analysis is very complex, especially with noisy data sets. Because neural networks are capable of fitting noisy data sets, difficult regression analysis is avoided by using neural networking.

Disadvantages of using neural networks are as follows:

- Causal relationships are not easily defined in neural networks, and there are no discrete interpretations of the network weights. This causes neural networks to effectively be ‘black boxes’ whereas regression models are able to identify causal relationships between independent and dependent variables. Therefore, networks are not recommended when the goal of the model is to define interactions between variables.
- Training of neural networks can be quite expensive. Years ago, the computational time required for a network to converge could take up to weeks. With the improved computing power within the last decade, however, computational time is no longer a critical issue.
- Because neural networks are so effective at modelling complex nonlinearities, they may overfit the training data and perform poorly on other data. Available techniques should be used to avoid overparameterizing the network.
- Neural networks are still a fairly new modelling technique. Lack of formal statistical model evaluation techniques can trigger doubt in the model.

- Neural network models are more difficult to use in the field than regression models. To apply regression models, one must simply use the equation derived from the regression. To use a trained network, a copy of the trained network must be available as software or the weight matrix must be used to calculate outputs; although this is not a serious disadvantage, neural networks are less portable than an equation.

Chapter 4: The Nova Scotia Data Sets

The data used for creating the model was obtained from Dr. John Kershaw at the University of New Brunswick (UNB) which had been collected by the Nova Scotia Department of Natural Resources (NSDNR). The Province has a well-established system of permanent sample plots in place for measuring both inventory and for research purposes. These data sets will both be described. We have also received data from Dr. Fan-Rui Meng, also of UNB, who, together with Dr. Charles Bourque and their research group, have developed site quality estimates for the entire Province.

4.1 Inventory Permanent Sample Plots

The purpose of the establishment of inventory plots in Nova Scotia has been to determine mortality and growth of the natural forest and to estimate merchantable volume in the forest (Nova Scotia Department of Natural Resources, 2002). The database was established for inventory purposes but, because it is extensive, has many other potential uses: biodiversity, ecosystem management, forest inventory, forest protection, wildlife habitat.

Beginning in 1965, plot locations were randomly selected throughout the province by latitude and longitude. By 1970, the province of Nova Scotia had established 1765 forest inventory plots. The program expanded in 1996, and by 1999 the province was monitoring 3250 inventory plots. These more recently established plots were selected by randomly generating grids in GIS and adding the grid to the database if it was classified as forested. The database therefore includes all ownership type of lands, for example, crown, private, and parks. The inventory plots are circular and identified by a centre-stake and boundary trees. When possible, the centre-stake was established by the pre-selected location. If there were no trees in the pre-selected plot, the centre-stake was established at the nearest location that would allow for a forested plot. With a radius of 11.35m from the centre stake, boundary trees and rocks were marked with paint; each plot covers 1/10th of an acre. All merchantable trees within the plot – trees that are at least 9.1cm at breast height (1.3 m above ground) – were painted and tagged with an identification number. Established plots are meant to be used as they would have otherwise been used, so land owners were instructed not to treat them specially.

For each marked tree, data for species, diameter at breast height (DBH), height, living status, crown class and health were collected. Some of the more recent measurements also include the tree height to the base of the crown. Diameter measurements were obtained at breast height, to the nearest millimeter using diameter tape. Height measurements were obtained to the nearest 0.1 meter. Since tree height estimates depend on the angle observed from tree top to base, the measurement was always attempted at least the tree height away from the tree. The living status of the tree was classified as either (i) live, (ii) dead and standing, (iii) ingrowth, (iv) cut, or (v) dead and down. The crown class was classified to get an idea of how dominant the tree is in the stand (i.e. dominant, intermediate, or suppressed) (Nova Scotia Department of Natural Resources, 2002).

From each plot, three trees were chosen and used to determine the land capability of the plot. Each chosen tree was of the same majority species, was larger than 9.1cm at DBH, and did not appear to have any damage. The total height of each of the chosen trees was measured, and increment cores were taken at breast height to determine the age of the tree by ring counting (Nova Scotia Department of Natural Resources, 2002). Using the age and height of the trees, land capability can be extracted from the province's established yield curves. If no suitable trees were available for making land capability measurements, a photo interpreted land capability was used. Photo interpreted land capability has been converted from the Canadian Land Inventory's agricultural soil capability classes (established between 1960 and 1985) and additionally adjusted for any complexities identified in the photographs (Nova Scotia Department of Natural Resources, 2006) (Agriculture and Agri-Food Canada, 2010). Other site measurements in the inventory data include land cover, drainage, slope and aspect.

Once established, the plots were remeasured every five years. Plots were remarked on every visit so that they would not be lost. Any trees that had grown into the plot were included and assigned a new identification number.

In the database received from Dr. Kershaw, there are 585,271 measurements in the inventory data set. Table 1 lists the attributes which were measured according to NSDNR (2002), and the attributes which were in the database received. Table 1 also

presents the number of records which included data for each attribute. Missing records from expansion factor can be filled since each plot is the same size, and missing records for tree species can be filled if the tree has already been identified in another sample year. Some empty fields for the crown class and height to base of crown data can be attributed to dead trees, although much of the height to base of crown data is incomplete.

Table 1 Measured and received attributes of the NSDNR inventory PSPs

Measured attributes	Received attributes	Number of records (of 585,271)
Plot, stand and tree	Plot, stand and tree	585 271
Year	Year	585,271
Species	DBH (cm)	579,559
Tree status	Height (m)	533,580
DBH	Height to base of crown	185,466
Quadrant location*	Crown class	465,339
Damage agents	Species	584,965
Main product for tree*	Expansion factor	584,965
Height	Stump Age	15,895
Height to base of crown*	Site Index	8,787
Health of tree*		
Crown class*		
Land Capability		
Ground cover		
Slope, Drainage, Aspect		
Stump Age		

‘*’ denotes for live trees only

Two important attributes which were described by NSDNR and were not in the data set received from Dr. Kershaw were land capability and tree status. These were obtained from an older version of the data set from the summer of 2005; some of the

measurements for the newer trees and newly established plots were not in this older data set.

4.2 Research Permanent Sample Plots

There are also research plot data available from the province. The research plots were established to test different treatments including different thinning and fertilizer prescriptions. The research plots have also been used to develop older growth models for the province (O'Keefe & McGrath, 2006). The plots were selectively chosen in locations that were considered to be fully stocked and where treated plots could be located next to control plots. Furthermore, the research plots varied in size and were required to include a minimum of thirty trees. Also, since the research plots were not established for merchantable inventory purposes, the research plots include trees as small as 4cm in diameter.

The data from the research plots include the same measurements that were described for the inventory plots, with a couple of exceptions. The research data only include height measurements for a sample of 15 trees per plot and do not include site index or land capability. The plots were, however, measured for age. As the research plots are generally fully stocked, mono-specific, and even-aged, land capability and site index may be interpolated from the provincial yield curves. The research data also includes specific treatment data, such as thinning (i.e. basal area removed) and fertilizer amounts.

In total, there are 277,413 records in the data set received from Dr. Kershaw. Table 2 lists the attributes included in the research PSP data set as well as how many measurements are filled for each attribute. Most attributes of interest are, for the most part, complete; although, height and crown class data is only available for some trees in the research PSPs.

4.3 Site Quality Index

Dr. Meng and Dr. Bourque have estimated a site quality index (SQI) using data in GIS. The benefit of developing this index is that it will provide estimates of the site capability for the entire Province and could possibly be used in the place of site index or land capability. Building upon work done by Bourque et al. (2000), SQI captures the

controlling mechanisms for tree growth through physical features of the landscape, temperature profiles, precipitation data, solar radiation maps, soil nutrient regime and soil moisture regime. From Dr. Meng, we have received SQI estimates for the inventory PSPs only.

Table 2 Attributes received for the NSDNR research PSPs

Received attributes	Number of records (of 277,413)
Plot, stand and tree number	277,413
Year	277,413
DBH (cm)	277,413
Height (m)	90,135
Crown class	146,268
Species	277,413
Expansion factor	273,103
Stump Age	277,375
Breast Height Age	277,413
Basal Area removed (m ² /ha)	64,601
Residual Basal Area (m ² /ha)	3,987
Nitrogen fertilizer treatment (kg/ha)	222,943
Potassium fertilizer treatment (kg/ha)	222,943
Phosphorus fertilizer treatment (kg/ha)	222,943
Year of treatment	218,349

4.4 Data Overview

Together, the inventory and research PSPs provide 862,684 tree measurements. For our model, we require measurements of the trees for two consecutive samples in order to determine any growth that occurred between measurements. From these records, there are 397,242 consecutive tree records from which our network models can be developed. The consecutive pairs were sampled approximately five years apart; this means that, on average, there are five growing seasons between samples. However, depending on which

month in which the samples were actually taken, the number of growing seasons can range from four to six. Unfortunately, these sampling dates were also not included in the current data set and had to be obtained from the 2005 version of the data set. Because the dates were obtained from the older database, sampling dates for the newest measurements are missing.

The research plots are generally quite different from the inventory plots. The majority of these differences can be attributed to the different processes by which the PSPs were selected and, in general, it can be found that the trees in the research plots are less varied than those of the inventory plots. Table 3 outlines the main differences between the inventory and research PSPs. In the research data set that we obtained from Dr. Kershaw, there were no tree status data for the research plots. Again, we had to go back to an older version of the database to obtain tree status for as many research plots as possible.

Table 3 Differences between Inventory and Research PSPs (O'Keefe & McGrath, 2006)

Database Attribute	Inventory PSP	Research PSP
Plot Selection	Random	Selective
Plot Size	Fixed round plots	Variable
Minimum Tree Size	9.1cm	4cm
Height Measurements	All heights measured	Sample of 15 heights
Plot Condition (age, species, basal	Variable	Generally Uniform
Treatments	Unknown	Known
Site Quality Index	Known	Unknown

With respect to modelling, one issue with this data set is that it is not well stratified. Considering the consecutive pairs of measurements which are required for our model development, in Figure 3 we can see that species such as Balsam Fir (bf) and Red Spruce (rs) are very well represented in the data while species such as Red Oak (ro) and Eastern Hemlock (eh) are not well represented in the data (a list of all species group abbreviations is available in Table 6). Table 4 shows the data distribution for Red Spruce over different diameter classes and stand stocking levels; from Table 4 we can observe that for Red

Spruce there are many combinations of diameter and stocking for which there are not much data. Table 5 shows a similar distribution for Red Oak. In Table 5 we can observe that most classes of Red Oak are underrepresented in the data set.

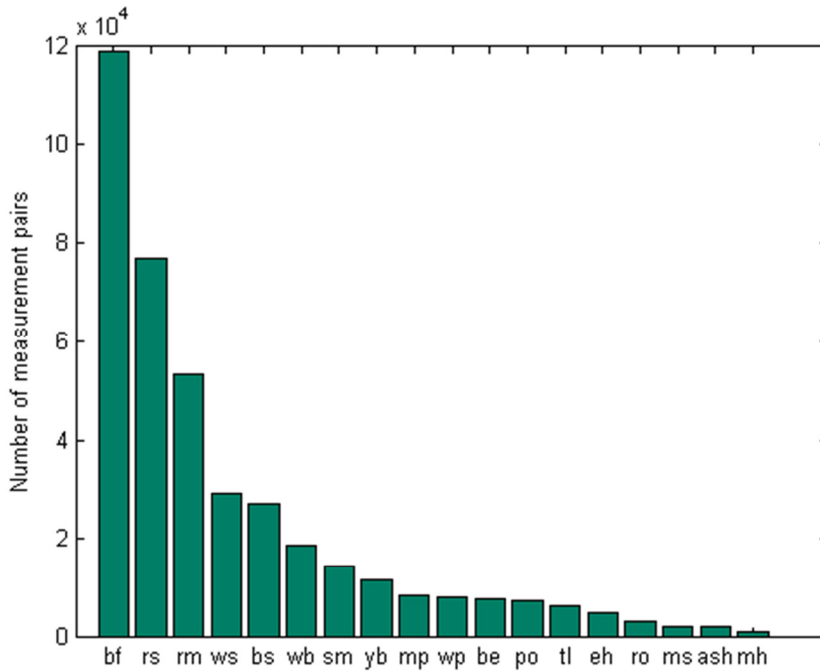


Figure 3 Distribution of data, assembled by growth species groups

Table 4 Data distribution over diameter and stocking factor classes, Red Spruce

DBH (cm)	Stocking factor						
	<0.2	0.2-0.4	0.4-0.6	0.6-0.8	0.8-1.0	1.0-1.2.	≥1.2
<10	2061	1762	1653	1137	717	233	63
10-20	5324	16174	17145	8985	3797	917	142
20-30	647	2666	4417	3672	1389	291	26
30-40	82	356	889	1045	433	88	16
40-50	7	62	160	247	94	20	3
50-60	1	10	29	40	21	3	0
≥60	0	0	6	10	1	0	0

Table 5 Data distribution over diameter and stocking factor classes, Red Oak

DBH (cm)	Stocking factor						
	<0.2	0.2-0.4	0.4-0.6	0.6-0.8	0.8-1.0	1.0-1.2.	≥1.2
<10	37	19	13	10	2	0	0
10-20	331	583	798	232	104	28	1
20-30	17	106	205	165	76	20	1
30-40	2	23	22	46	27	10	1
40-50	0	2	2	3	2	1	1

One final issue with this data set is that it is, by nature, a very noisy data set. Given trees with the same or similar inputs, there are many possible growth outcomes. For example, tree with certain characteristics could live through the next growth period while another tree with the exact same characteristics could die. Furthermore, we need to consider that what we observed in the data was only one outcome of many possibilities. Therefore, it is important to understand that it is not possible to make accurate predictions at the tree level. We will really only be able to model average tree survivability and growth which is only applicable on a larger scale.

Chapter 5: Model Design

The general design of our individual tree model is based upon inputs for the individual tree models discussed in Chapter 3 and modified to include species as a model input.

5.1 Model Structure

A complete tree growth model will require three different models: (i) a model to represent the development of trees, (ii) a model to represent the regeneration of the stand, and (iii) a model to represent the transition from regeneration to tree phase (Stage, 1973). Similar to the Prognosis model, the model developed in this thesis will only attempt to model the development of individual trees.

In our model, the development of trees will be characterized by predicting the tree survivability and growth over a certain period; tree growth will be represented by diameter and height increments over a certain period. Unlike the representations of tree development as seen by Prognosis, STEMS and PROGNAUS, we will model growth with neural network models; diameter increment, height increment, and probability of survival will each be modelled with its own network (Figure 4). With each output having its own network, future sensitivity analysis would be more straightforward. Again unlike the conventional growth models, tree species will be included as a model input rather than creating different sets of networks for each species.

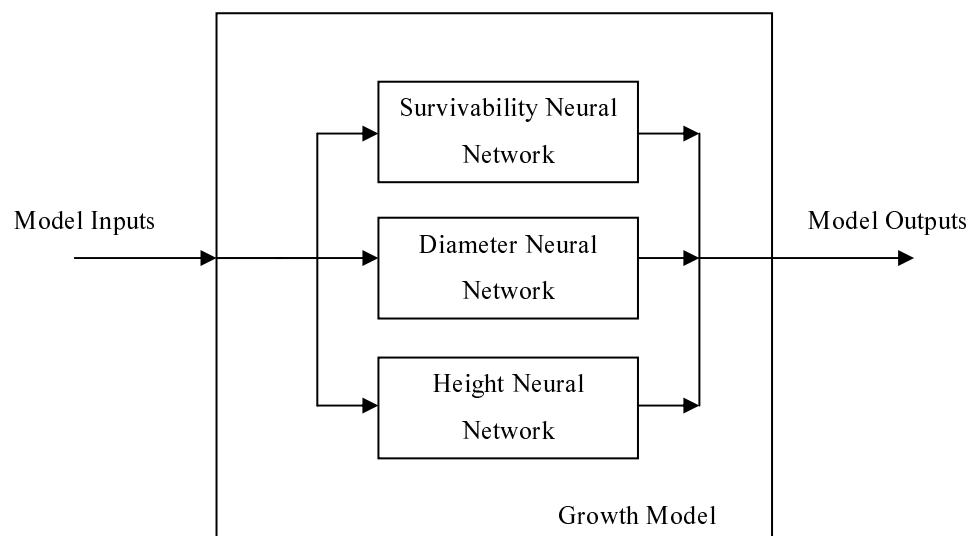


Figure 4 General Structure of proposed model

It should be noted that while each of the Prognosis, STEMS, and PROGNAUS models include a crown ratio component, our proposed model will not. One reason each of these models requires a crown ratio component is because crown ratio is an input for the other model components; crown ratio must be modelled and updated if tree development is to be predicted past one growth period. Recall that crown ratio is used as an input to the growth model because it indicates vigour and competition. Crown ratio is also desirable to predict because it gives an idea of merchantable timber. Unfortunately, crown ratio is difficult to measure for each tree and is thus hard to come by – especially over large land areas. Unlike the Province’s PSPs, most tree data is obtained from aerial photography where it can be difficult to determine height, let alone crown ratio. Since our growth model is meant to be simple and usable over a broad land base, we will not use crown ratio in our model. Crown ratio is not necessary for indicating competition if we use a measure like basal area larger. Tree vigour may also be measured by other means, such as the diameter increment of the previous growth period. To get diameter increment of the previous growth period in the model, the data used for training the networks would need to be sacrificed. Also, if we consider the application of a growth model, it would not be realistic to know the previous diameter increment for all of the trees being modelled. Therefore, in the interest of keeping as much data as possible for network training and to keep the model simple, we will not consider tree vigour in our model. Thus, for this thesis, we have limited ourselves to modelling tree diameter, height and survivability. With these model components, we should still get a good average growth model.

5.2 Model Outputs

5.2.1 Survivability

Growth predictions are very sensitive to the survivability component of the model, which becomes less reliable over larger growth periods. Although it is critically important in growth modelling, survivability – or mortality, as it is often modelled – is still the least understood component of growth models. For stand-level models, mortality prediction was much simpler because it required only a prediction for mortality rates in the overall stand. With the shift to individual tree models, however, mortality has become much

more difficult to predict at the tree-level; survivability modelling has been identified as one of the most difficult tasks in growth models (Hasenauer, Merkl, & Weingartner, 2001).

One difficulty of modelling survivability is that tree survival is a binary variable; typically, when a tree is alive it has a value of 1 and when it is dead it has a value of 0. Some survivability models will classify a tree to be alive or dead at the end of each growth period (Hasenauer, 2006); this is also known as probabilistic mortality (described in Section 3.1.2). Neural networks are capable classifying data, and could be used for classifying trees as alive or dead at the end of a growth period. However, we need to be aware that if we create a classification network, it is only one outcome of a number of possibilities. For example, if we observe 100 trees with similar characteristics and 95 of them survive to the next period, it is reasonable to portray the frequency of survival as a probability and say that the probability of survival is 0.95 for trees in this class. One must recall, however, that this is only one outcome. Consider the situation where a fair coin is flipped 100 times and 46 heads are observed; if we derived probability from the frequency of occurrence, then we would say that the probability of flipping a head is 0.46. Knowing that the probability of flipping a head on a fair coin is 0.5, we can understand that this method of deduction is slightly flawed. To better understand what the average outcome would be, the survivability model would need to be simulated many times. One way to avoid this situation altogether is to stay away from using classification networks or probabilistic mortality. If we instead predict the probability of mortality and use it to model deterministic mortality (described in Section 3.1.2), then we can understand the expected outcome without having to run a number of simulations. Similarly, we must consider that our data is only one example of many possible outcomes. In order to capture as many different scenarios as possible, we require a very large data set from which we can develop the model.

Another difficulty in modelling mortality is model calibration. Mortality is a relatively rare event, and may occur for various different reasons; for example, trees die from competition with other trees, extreme weather events, forest fires, disease, and insects.

To gather enough data to capture enough mortality events and their various causes we will again require a very large amount of tree data (Hasenauer, 2006).

One final difficulty in modelling mortality is model validation. It is impossible to validate continuous outputs with discrete data sets. From stand-level modelling, we know a rather realistic method of capturing mortality is to determine average mortality rates, which can be partitioned by size or site. An advantage to partitioning mortality rates by size is that we know the expected general behaviour. For most species, the smaller trees have a very high mortality rate since smaller trees are less competitive than larger trees; the mortality rate should decline rapidly as the diameter class of the tree increases. This trend, however, does not apply indefinitely. Because the size of a tree is related to the age of a tree, trees that will die of “old age” will generally be on the larger side and it can therefore also be expected that after a certain point, the mortality rate will increase with size classes (Monserud & Sterba, 1999). This being said, the forests of Nova Scotia are relatively young and will likely not show the high mortality rates at very large diameters as hypothesized by Monserud and Sterba. For example, the maximum life of a hemlock trees is approximately 400 years, and harvest rotations in the province are less than 100 years. By partitioning the average mortality rates by diameter, we may compare the modelled mortality rates to the actual mortality rates.

For our model, we will use a neural network to predict the probability of survival for each tree based upon a set of independent variables. These probabilities will then be used to determine mortality rates, partitioned by size, for several species to examine the mortality behaviour and to compare with the actual mortality rates. To further examine the survivability network, confidence intervals for different categories of data will be determined and compared to the actual number of trees survived.

5.2.2 Diameter Increment

Aside from modelling it directly, diameter increment may also be determined from other different model outputs such as basal area increment, future diameter, or future basal area. As all of these options are mathematically related, it may be argued that there should be no preference between these modelling approaches and that each approach should perform equally well. However, some argue that modelling basal area increment

is more representative of tree growth (Vanclay, 1994). Both Prognosis and PROGNAUS models predict basal area increment and defend this approach because it because the relationship between the logarithms of squared diameter and DBH has homogeneous variance. STEMS models the diameter increment directly.

In our early work, we attempted to model diameter increment directly. A suggestion from Dr. Kershaw (personal communication, September 28, 2009) made us realize that basal area increment was what Stage used and was likely to perform better. To better understand the nature of the diameter and basal area data, tree diameter and basal area from the end of a growth period were plotted against the same measurements at beginning of the growth period (Figure 5 and 6, respectively). In Figure 5, the variability decreases with diameter increase. In Figure 6, we observe the homogenous variance that Stage and Monserud reference when justifying basal area increment model outputs. Also, the basal area plot shows a tighter relationship between old and new measurements than the diameter plot does. Therefore, just as was done in Prognosis and PROGNAUS, this model will predict growth in diameter by means of a basal area increment neural network.

Basal area can be estimated from the DBH measurements by approximating trees to have circular cross sections:

$$BA = \pi \left(\frac{DBH}{2} \right)^2 \quad (25)$$

This is an idealized measurement since most trees do not have perfectly circular cross sections. In this thesis, when we refer to basal area, we are actually referring to the idealized basal area.

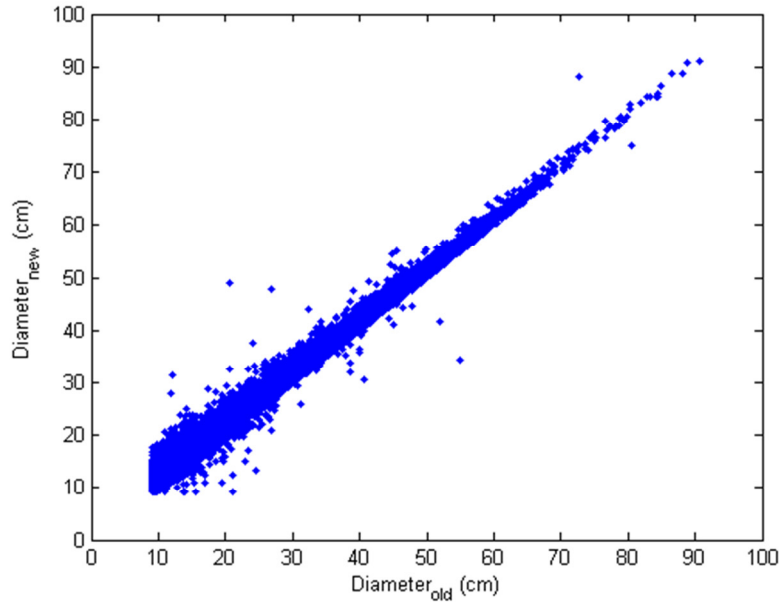


Figure 5 Diameter at the end versus the beginning of the growth period

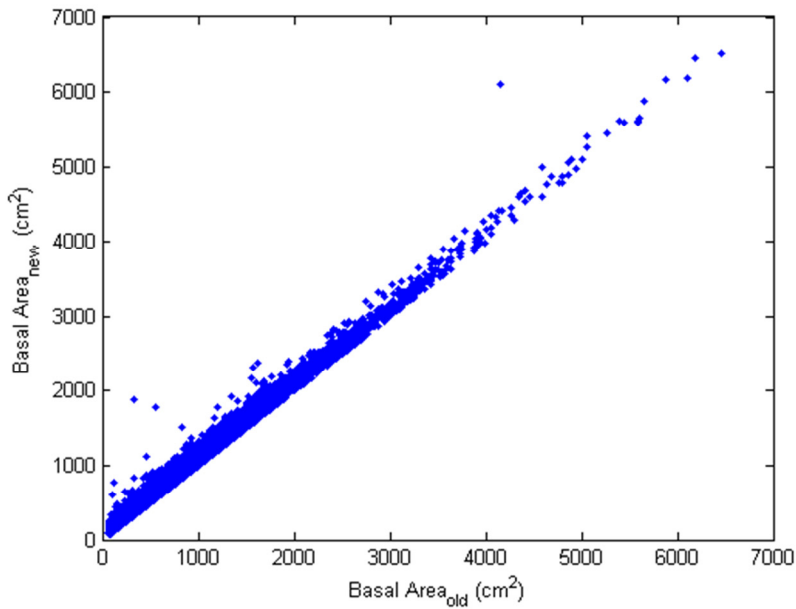


Figure 6 Basal area at the end versus the beginning of the growth period

Recall from Section 3.2, the goal of fitting a neural network is to find the weights for which the mean squared error between the actual and modelled outputs is minimized. Therefore, we will use the mean squared error as a measure of goodness of fit. Keeping in mind that during the training process of the neural networks the weights are initialized with random numbers, it must be understood that the mean squared errors can vary if they

are not initialized with the same numbers. Therefore, the mean squared errors may only be comparable if we ensure that the seed for the random number generator is the same for every training run.

5.2.3 Height Increment

Tree height is a much more difficult attribute to measure than DBH. Both Prognosis and PROGNAUS model height increment. Recall that the error associated with the height measurements in our data set are measured within 0.1m. With respect to height, this is a very reasonable amount of error since tree height can only be measured indirectly. However, with respect to height increment, an error of 0.1m is much more significant. Therefore, height increment data can have quite a large coefficient of variation and can be much more difficult to model.

In a similar approach to modelling basal area increment instead of diameter increment, we have come to realize that volume increment could be modelled rather than height increment. First, we require volume measurements in which to do this. Although there are widely accepted species-specific equations for tree volume based on height and diameter (Wykoff, Crookston, & Stage, 1983), in our model we want to avoid using species-specific equations and we also want to keep the model as simple as possible. Therefore, we have idealized the tree volume to be a cone in the same spirit that basal area is idealized as a circle:

$$VOL = \frac{HT \cdot BA}{3} \quad (26)$$

Just as we have done with basal area, volume is an idealized measurement since the shape of trees are not perfectly conical. In this thesis, when we refer to the volume of the tree, we are referring to the idealized volume.

To better understand the nature of the height and volume data, the trees at the end of a growth period were plotted against the trees at the beginning of the growth period for both height (Figure 7) and volume (Figure 8). For the volume measurements, we observe a more homogenous variance and tighter relationship than we do with height

measurements. This model will predict growth in height by means of a volume increment neural network.

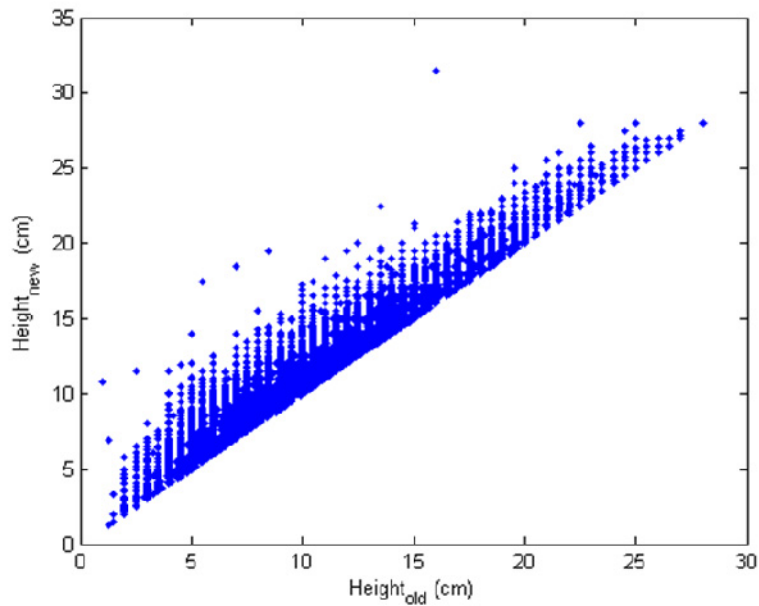


Figure 7 Height at the end versus the beginning of the growth period

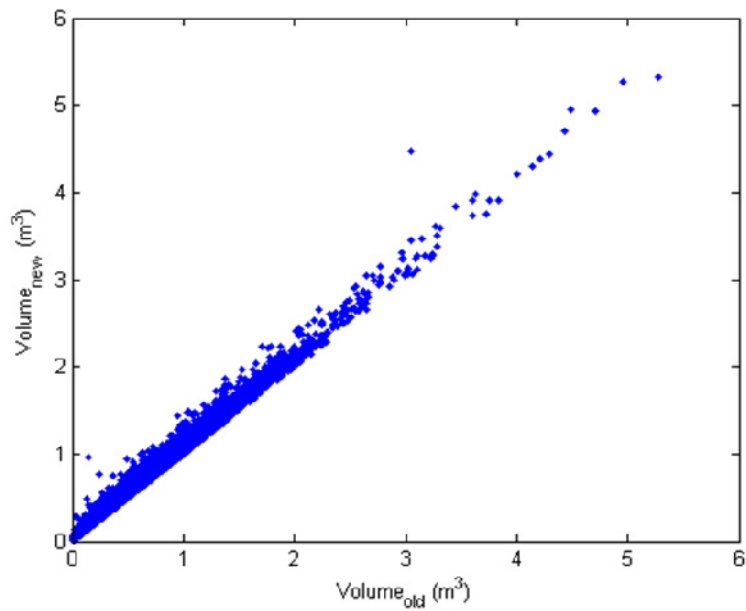


Figure 8 Volume at the end versus the beginning of the growth period

5.3 Model Inputs

In general, each network model will be fit using the same inputs. If the network output is not very dependent on a specific input, the network will inherently ignore the input by assigning its associated weights with very small values during the training process. For the most part, our inputs resemble those used for the Prognosis, STEMS and PROGNAUS growth models. An important difference is the use of species as an input vector.

5.3.1 Tree-Level Inputs

5.3.1.1 Tree Size

One major influence of the growth of a tree is its size. Larger trees tend to compete better for nutrients and light and are, in general, more likely to survive than smaller trees. Two common measurements of tree size are DBH and height.

All three of Prognosis, STEMS and PROGNAUS use initial diameter and squared initial diameter as a model inputs. These models use squared diameter terms to prevent unlimited growth for large diameter trees (Monserud & Sterba, 1996). For simplicity, we only want one measure for tree diameter in our model; therefore, we will use initial basal area according to Equation 25. Similarly, rather than use height as an input, the idealized volume will be calculated (Equation 26) and used instead. The main reason for choosing basal area and volume as inputs over diameter and height is simply because their respective relationships with basal area and volume increment are tight, as we had observed in Sections 5.2.2 and 5.2.3.

5.3.1.2 Competition

Similar to Prognosis, STEMS and PROGNAUS, we need an input that indicates competition between the trees. Because the data do not contain exact spatial coordinates of the trees, the model is restricted to using a distance-independent competition measurement. Knowing that larger trees compete better for nutrients, competition between can be represented by calculating the sum of the basal areas of the trees that are larger (BAL) than the individual tree. BAL is meant to give an idea of crown cover, or shading, for a tree and, in many ways, is analogous to available light (Vanclay, 1994).

BAL essentially ranks the tree on its ability to compete given the total stand cover is known. Both hardwood and softwood BAL should be represented separately since they have much different crowns and, thus, crown cover (Figure 9).



Figure 9 Hardwood (left) and Softwood trees (Image courtesy of Glen Nicholson)

5.3.1.3 Growth Species Vector

There are approximately fifty different species included in the database. Although it is desirable to include species as an input to the networks, to add fifty inputs for each network would be excessive especially since many of these have very little representation (recall Figure 3). Therefore, all Acadian Forest species will be classified into one of eighteen ‘growth species’ groups where species of similar growth characteristics were grouped together (Table 6). The classification was meant to match the growth species groups being used by Dr. John Kershaw and his research group at UNB.

Grouping the species means that the network model will require 18 input nodes to account for the different growth species. A binary growth species vector will be assigned to each tree where all inputs will be 0 except at the node which represents the tree’s growth species, where the input will be 1.

5.3.2 Stand-Level Inputs

5.3.2.1 Stand Cover

Total basal areas give an idea of the total crown cover of the stand. Again, because hardwood and softwood trees have much different crowns, stand basal areas are best divided into hardwood and softwood. Together with the BAL indicators, total basal area of the stand gives an idea of the ability of an individual tree to compete.

5.3.2.2 Site Measurement

Tree survivability depends greatly on the genetic makeup of the tree as well as the tree's environment. Because genetic data is not often available and cannot be made widely available, modellers ignore the genetic makeup of the trees out of necessity. Modellers also tend to ignore extreme environmental factors. Extreme environmental effects such as wind, drought, insects and disease have a large effect on the survivability of trees but are not predictable at the stand level.

In both Prognosis and PROGNAUS, site is reflected only by elements of topography such as elevation, slope and aspect. These land characteristics are important to tree growth because they affect the controlling mechanisms of tree growth such as soil water content and incident solar radiation, among other environmental conditions. However, including these topographical details alone in a growth model will not provide much insight into the nature of the environmental mechanisms controlling tree growth because much information (i.e. precipitation, soil nutrient levels, and solar radiation) is not included (Bourque, Meng, Gullison, & Brigland, 2000). Recall that the SQI from UNB includes topographical information as well as solar, nutrient, and climate information.

In both the NSDNR data and the STEMS model, the controlling mechanisms of the stand are captured by characterizing the growth of the dominant trees on that specific stand. The site of the stand is typically characterized by land capability (LC) or site index (SI). LC is a measure of the volume of wood that may be produced by a hectare of land in one year without degrading the land while SI is a measure of the height of the dominant tree(s) at age 50 (Nova Scotia Department of Natural Resources, 1993). LC and SI are determined for a single species and are generally based upon a single species stand. As

Table 6 Growth species groups (Nova Scotia Department of Natural Resources, 2002)

Species Group	Group Symbol	Included Species	Common Name
ash	ash	<i>Fraxinus nigra</i>	black ash
		<i>Fraxinus americana</i>	white ash
beech	be	<i>Fagus sp.</i>	beech
		<i>Fagus grandifolia</i>	american beech
balsam fir	bf	<i>Abies balsamea</i>	balsam fir
black spruce	bs	<i>Picea mariana</i>	black spruce
eastern hemlock	eh	<i>Tsuga canadensis</i>	eastern hemlock
miscellaneous pine	mp	<i>Pinus banksiana</i>	jack pine
		<i>Pinus resinosa</i>	red pine
		<i>Pinus sylvestris</i>	Scotch Pine
poplar	po	<i>Populus balsamifera</i>	balsam poplar
		<i>Larix sp.</i>	larch
		<i>Populus tremuloides</i>	trembling aspen
red maple	rm	<i>Acer rubrum</i>	red maple
red oak	ro	<i>Quercus rubra</i>	red oak
red spruce	rs	<i>Picea rubens</i>	red spruce
sugar maple	sm	<i>Acer saccharum</i>	sugar maple
tamarack	tl	<i>Larix decidua</i>	european larch
		<i>Larix laricina</i>	tamarack
white birch	wb	<i>Quercus robur</i>	grey birch
		<i>Betula papyrifera</i>	white birch
white pine	wp	<i>Pinus strobus</i>	white pine
white spruce	ws	<i>Picea glauca</i>	white spruce
yellow birch	yb	<i>Betula alleghaniensis</i>	yellow birch
miscellaneous hardwood	mh	<i>Alnus rugosa</i>	Alder (speckled)
		<i>Ailanthus altissima</i>	ailanthus
		<i>Malus sp.</i>	apple
		<i>Prunus serotina</i>	black cherry
		<i>Prunus virginiana</i>	choke cherry
		<i>Cornus sp.</i>	dogwood
		<i>Betula populifolia</i>	english oak
		<i>Crataegus sp.</i>	hawthorn
		<i>Ostrya virginiana</i>	ironwood
		<i>Sorbus Americana</i>	mountain ash
		<i>Acer spicatum</i>	mountain maple
		<i>Prunus pensylvanica</i>	pin cherry
		<i>Amelanchier sp.</i>	serviceberry
		<i>Acer pensylvanicum</i>	striped maple
<i>Ulmus americana</i>	american elm		
<i>Salix sp.</i>	willow		
miscellaneous softwood	ms	<i>Larix kaempferi</i>	japanese larch
		<i>Picea abies</i>	Norway spruce
		<i>Picea strobus</i>	sitka spruce

'-' denotes unclassified

hardwoods and softwoods grow differently, LC and SI are classified by softwood and hardwood. The determination of LC and SI requires physical property data from each stand, and is really only useful for the stand for which the LC and SI were measured. Yield curves from which LC and SI can be determined in Nova Scotia are shown in Figure 10.

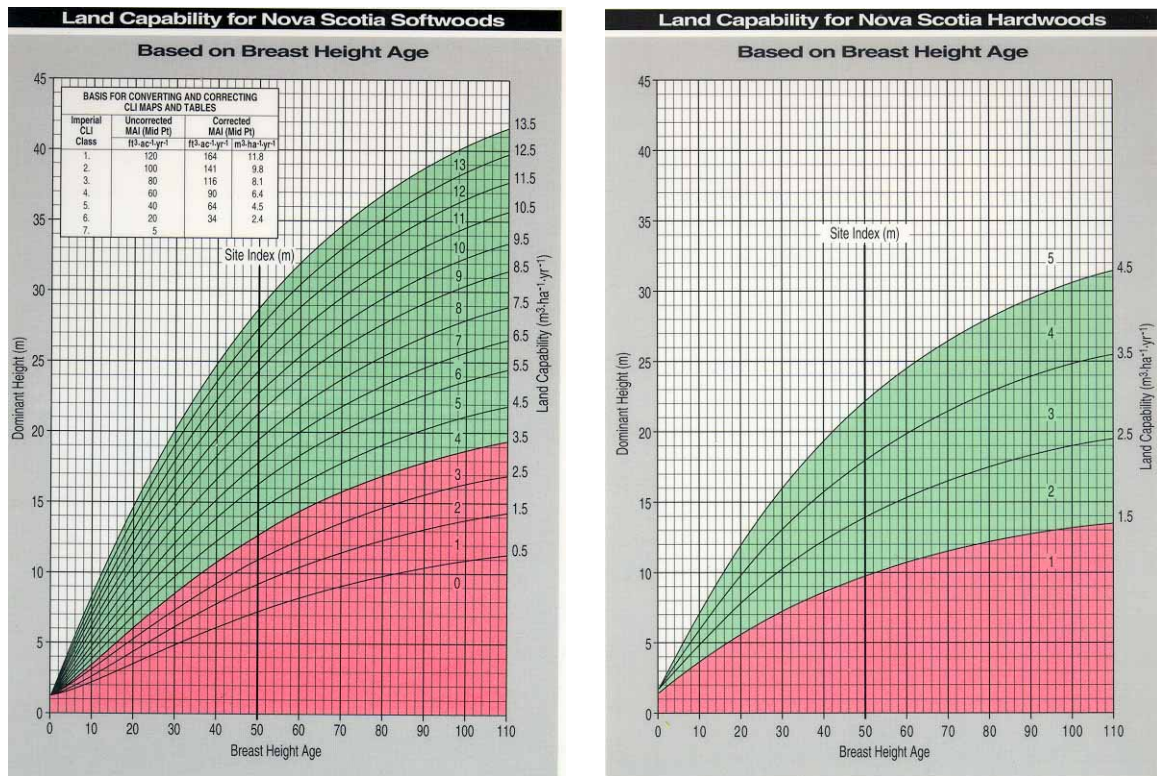


Figure 10 SW and HW yield curves for Nova Scotia (Nova Scotia Department of Natural Resources, 1993)

Since LC is available for a majority of the PSPs in the NSDNR data, the growth models can be trained including LC as a model input, and compared to growth models trained without any site measurement at all. Similarly, with the SQI data obtained from UNB, growth models will be trained using SQI as a site measurement rather than LC. As there are no site measurements immediately available for the research plots, research PSP data will not be used for models comparing site measurements.

5.3.2.3 Stand Age

Although we must assume that our stands are uneven-aged, it is still useful to have an idea of the general age of the stand. Stand age is useful to know since the growth of the

stand will slow down with older trees. On the other hand, if the trees in the stand are younger, the growth of the stand will be relatively fast.

Given that we know that LC is calculated from dominant height measurements, if we have the dominant height and site quality measurement for a stand, we can understand if we are working with a younger or older stand. In the yield curves in Figure 10, we can see that with a tree height and stand LC, a tree age can be interpolated. Therefore, to get an idea of stand age, we will use dominant height as a model input.

5.3.2.4 Number of Growth Seasons

Survivability, diameter increment, and height increment are each time dependent measurements which are determined from consecutive measurements of trees. Recall that in our data set measurements were taken every five years, however the number of growth seasons between measurements may vary depending on the dates on which the samples were taken. For example, if a plot was measured in November of one year and then remeasured in April five years later, the survivability rates and growth increments of the trees are for four growth seasons. To account for the variations in time between sampling dates, the number of growth seasons between samples will be estimated and used as a model input. It was assumed that trees in Nova Scotia grow evenly from May through August, so the months May through August each count as a quarter of a growth period; this was done so that partial growth seasons could be estimated. In our data set, the number of growth seasons in our data set range from 4 to 6.

5.3.2.5 Stocking of the Stand

To generally understand how well a stand is stocked, we will use a somewhat arbitrarily created stocking factor. The level of stocking in the stand could be useful for the survivability network since well-stocked stands are expected to have higher mortality rates than poorly stocked stands. Because hardwoods and softwoods have different crowns and compete differently, the hardwood and softwood stands also have different maximum levels of stocking. On average, the maximum basal area for a hardwood stand is approximately 30m²/ha (Nova Scotia Department of Natural Resources, 2000) while the maximum basal area for a softwood stand is approximately 60m²/ha (Nova Scotia

Department of Natural Resources, 1993). Therefore, the proportion of the stand that is fully stocked can be approximated by:

$$\text{stocking factor} = \frac{BAH}{30 \text{ m}^2/\text{ha}} + \frac{BAS}{60 \text{ m}^2/\text{ha}} \quad (27)$$

One problem with Equation 27 is that these full stocking estimates are not based on mixed-species stands, and therefore stocking factor will likely not be as accurate for mixed-species stands.

Chapter 6: Building the Model Components

Given the data that has been received from the NSDNR, there was still much data preparation that was required before the neural networks could be trained. The approaches of data preparation and network training are discussed in this chapter.

6.1 Data Preparation

The Nova Scotia inventory and research PSP data sets were obtained in a Microsoft Access database from Dr. John Kershaw of UNB. The received database had undergone some initial data cleaning at UNB. To prepare the data for neural network training, a combination of Visual Basic for Applications (VBA) subroutines and Structured Query Language (SQL) statements were used.

Idealized basal area and volume were estimated from diameter and height measurements according to equations 25 and 26. Each tree was also assigned a growth species classification vector, depending on the species of the tree. Then, based upon the growth species vector, the total stand basal areas for softwood and hardwood trees were calculated for each sample year; to allow for stands of different sizes to be comparable, total basal area was estimated on a per hectare basis. The sums of hardwood and softwood basal areas of trees larger than the individual trees were then determined for each sample year and were also estimated on a per hectare basis. Stocking factor was calculated using the total softwood and hardwood basal areas according to Equation 27. Dominant height was determined by simply taking the average of the tallest three trees of the stand in each sample year.

Next, the trees were classified as going to live or die (LOD) in its upcoming growth period. Determining LOD for a tree in the data was fairly straightforward because tree status observations were made. If a tree existed in the database for two consecutive sampling periods, and it was observed to be living for both samples, it was deemed to have lived over the growth period and assigned an LOD value of 1. If a tree existed in the database for two consecutive sampling periods, where it was observed to be living during the earlier sample and dead for the later sample, then it was deemed to have died over the growth period and assigned an LOD value of 0. All other data, including trees that had been cut over the growth period, were ignored.

Of all the trees which were marked as having lived, the proportional basal area increment and volume increment were calculated. Since each of these increments may occur over slightly different growth periods, the number of growth seasons were also estimated to the nearest growing month.

Finally, data sets were organized into three tables for each network, and then further divided into training data and check data; three-quarters of the data were used for training purposes, while the remaining data were used for checking the networks. Any increments that were within 10^{-4} of zero were assigned increments of zero. Any negative or impossibly large growth increments were ignored. All trees from the research plots with DBH less than 9.1cm were ignored to be consistent with the inventory data; it should be mentioned that these smaller trees were ignored only after they were considered for total stand basal area estimates. Cleaning of the data is described in more detail in Appendix A. Once the data sets were partitioned and cleaned, they were exported to MATLAB for neural network training.

6.2 *Training the Networks*

MATLAB contains a straightforward and relatively inexpensive neural networking package. In general, the data was normalized, the network parameters were defined, and the networks were trained with the normalized training data. Both the normalized training and check data were then run through the trained networks and then unnormalized. Each network was fit, or trained, using the error backpropagation method (described in Section 3.2) with the Conjugate Gradient algorithm to minimize the error space (Demuth & Beale, 2004). Although MATLAB offers search algorithms which can converge faster than Conjugate Gradient methods (i.e. Levenberg–Marquardt and Quasi-Newton), they could not be used in training of our networks because our data set is too large and demands too much memory.

The objective used in training the networks in MATLAB is to find the best network configuration which minimizes the mean squared error. As stated in Section 5.1, it was decided that tree growth was to be characterized by multiple single output networks. The number of input nodes, hidden nodes, and maximum training epochs must still be determined. Including the 18 unit species vector, each network could have from 26 to 28

inputs, depending on whether stocking factor and/or land measurements are used as model inputs. To determine the number of hidden nodes to use in each network, the mean squared error of both the training and check data were observed and compared for networks with varying numbers of hidden nodes; the training MSE indicates how well the model fits the data and the check MSE indicates how well the model works for data which was not used in training. Effectively, the check MSE gives an indication as to how well the network generalizes.

To be consistent, each network was trained with the same maximum number of epochs. Figure 11 shows the typical training performance for networks having a maximum of 1000 epochs (note that the performance is a normalized MSE). In this figure we can observe that the majority of the convergence occurs within the first 50 epochs, therefore, we assumed that 1000 epochs were a sufficient training period in which we can observe the majority of the convergence.

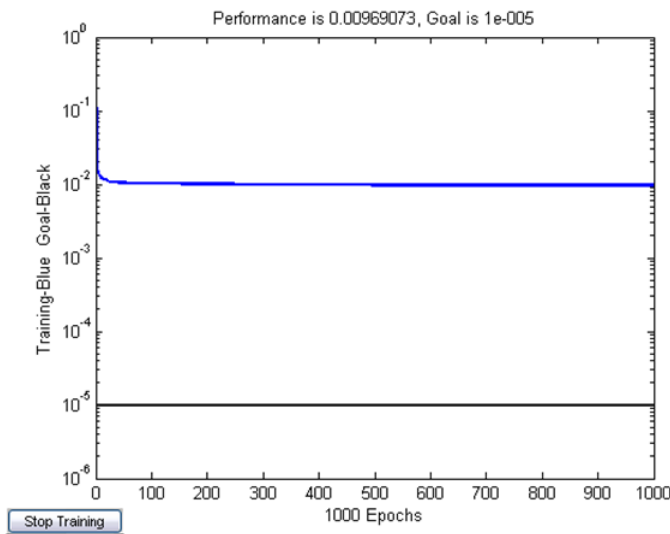


Figure 11 Typical performance of network training (1000 epochs)

With an assumed standard for maximum training epochs, different network configurations of various input and hidden nodes will be trained and compared by their mean squared errors. The best fit network configuration should have the smallest MSE. Given the chosen network configuration, different maxima of training epochs will be tested to be sure that 1000 epochs is still a sufficient amount of training.

Once the user-defined model components have been decided, we checked that the model is able to perform at the species level. In the case of the survivability network, the mortality rates were be calculated for four different growth species (note from Figure 3 that these species are the best represented in our data set): balsam fir, red spruce, red maple and white spruce. For the diameter and height models, species-specific networks were be trained using only the red spruce data and were compared to the all-species network. Clearly, the all-species model is not expected to outperform the single-species model, but we were able to observe whether the all-species model works reasonably well for the well-represented species.

Given the best network configurations, the weights from each of the trained networks were used to develop a growth model in Excel.

Chapter 7: Results

In total, thirty-five different networks were trained; from the thirty-five, only three networks (one for each survivability, diameter growth, and height growth) were chosen to use in the overall growth model. Most of these networks were allowed to train for a maximum of 1000 epochs with a normalized MSE goal of 10^{-7} . The training time for the networks ranged from 30 to 45 minutes on an Intel[®] Pentium[®] 4 CPU 3.2 GHz computer – the networks with more nodes and weights took the longest to train. The activation function used at each hidden and output node was a tan-sigmoid function. To ensure that the seed for the random number generator was the same for each run, MATLAB was restarted before each training run. Examples of the MATLAB code used for training the neural networks are shown in Appendix B.

7.1 Survivability Model Component

Fourteen different configurations for the survivability network were trained; each of the networks included the following inputs: (1) individual tree basal area, (2) volume, (3-4) the sum of softwood and hardwood basal areas of larger trees, (5-6) total stand softwood and hardwood basal areas, (7) dominant height of the stand, and (8-25) the growth species vector. Both together and separately, stocking factor and site quality index were tested as model inputs to see if they improved the MSE; land capability was not tested in the survivability networks since site quality index was observed to be a reasonable land measure (to be discussed later). The survivability network was also tested with configurations of 3, 4, 5, and 6 hidden nodes. The general structure of the survivability model is shown in Figure 12.

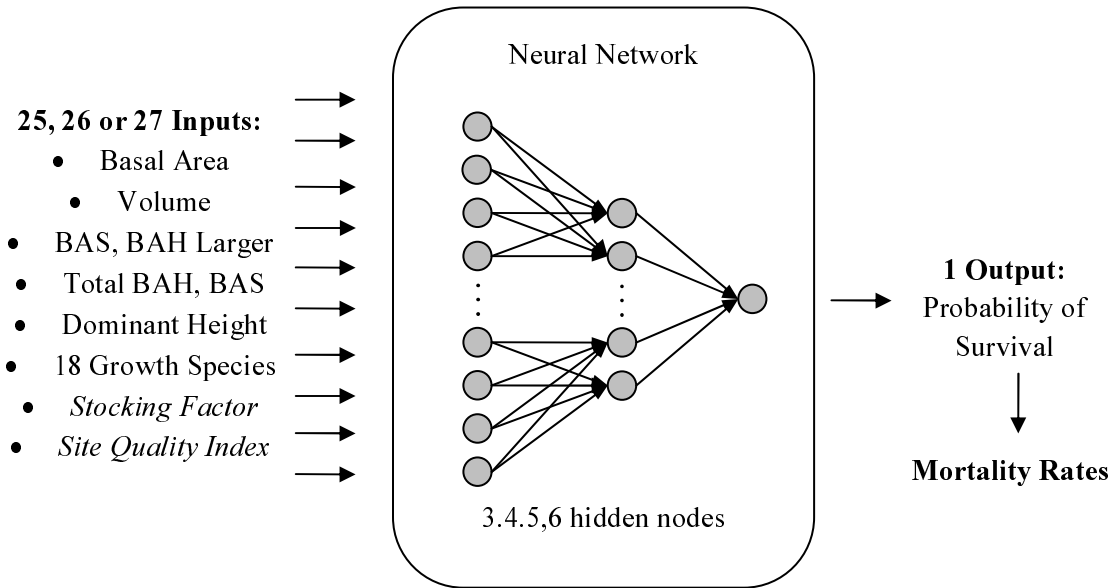


Figure 12 Outline of survivability model component

The MSE was calculated from the error between the modelled probability of survival and the discrete survival event. Table 7 and Table 8 show the MSE for both the training and check data for the fourteen different network configurations (each trained for 1000 epochs). From these tables, we can observe that the MSE for each network is essentially the same at around 0.078. Although it is expected that each of these networks would perform at similar levels, from Tables 7 and 8, we can generally observe the model fits improve (MSE decreases slightly) when SQI is included as a model input, therefore, SQI will be included in the survivability component of the growth model. From these tables we can also see that there is no apparent trend in the fits when the model includes an input for stocking level. Therefore, the effects of the stocking factor input were further investigated using networks with and without stocking factor inputs. To be consistent, the two networks with five hidden nodes were chosen to compare the effects of the stocking factor input; although each network is expected to have similar performance, the networks with five hidden nodes were chosen because they had the smallest MSEs.

Mortality rates were calculated based upon basal area and then averaged for different diameter classes for balsam fir, red spruce, white spruce and red maple trees; the diameter

classes were: 9.1-10cm, 10-20cm, 20-30cm, 30-40cm, 40-50cm and greater than 50cm. The purpose of calculating mortality rates were to compare the modelled and actual mortality, to observe the trend in mortality, and to check the effects of including the stocking factor input. Therefore, the rates were calculated for the two survivability networks with 5 hidden nodes which included the SQI model input; the only difference between the chosen network configurations was that one included stocking factor as a model input while the other did not.

Table 7 MSE for various configurations of the survivability network (without stocking factor input)

Mean Squared Error – without stocking				
Number of hidden nodes				
	3	4	5	6
No land Data	0.0785 (0.0816)	0.0783 (0.081)	0.0783 (0.0809)	- -
Site Quality Index	0.0784 (0.0802)	0.0779 (0.0799)	0.0778 (0.0798)	0.0778 (0.0799)

The two MSE values are for training data and check data (in brackets)

Table 8 MSE for various configurations of the survivability network (with stocking factor input)

Mean Squared Error –with stocking				
Number of hidden nodes				
	3	4	5	6
No land Data	0.0784 (0.0806)	0.0784 (0.0807)	0.0782 (0.0806)	- -
Site Quality Index	0.0781 (0.0804)	0.0781 (0.0816)	0.0777 (0.0797)	0.0778 (0.0818)

The two MSE values are for training data and check data (in brackets)

The average mortality rates were modelled reasonably well by both networks in the sense that the modelled and actual average mortality rates were typically quite close (Figure 13 through Figure 16). In these figures, we can observe that the model was able to distinguish between the different growth species groups; for example, the model was able to pick up the generally higher balsam fir mortality rates as opposed to the smaller mortality rates of red spruce, red maple, and white spruce.

In the case of balsam fir, red spruce, and red maple (Figure 13 through Figure 15), both models demonstrate the expected behaviour where the mortality rates decline as the trees get larger with one exception: the average mortality rate of the smallest balsam fir trees is not higher than the larger balsam fir trees. This is acceptable because the true mortality rate for the smallest diameter class would be higher since we do not include trees smaller than 9.1cm DBH in our model. The mortality rates for white spruce (Figure 16) do not exhibit the expected mortality behaviour, but it does follow the mortality trends of the data set.

When we examine the network which includes the stocking factor input, we can see that the modelled mortality rates are typically a little smaller than the rates predicted by the network which does not include the stocking factor input. Overall, neither of the networks consistently predicted mortality rates better than the other, therefore it does not provide further insight as to whether the stocking factor improves the model. If we consider the mortality rates for the trees in the most frequent diameter class of 10-20cm – Figure 13 through Figure 16 show the number of available data for each diameter class, ‘# total samples’, as well as the available data specific to the species and diameter class, ‘# species samples’ – we can see that the mortality rates predicted by the network for each species are nearer to the actual mortality rates when they include a stocking factor input. The instances where the stocking factor input does not improve the modelled mortality rates are the combinations of species and diameter classes that are much less represented in the data. Therefore, it was decided that including a stocking factor input does improve the model. The growth model will use the survivability network which includes stocking factor, SQI and 5 hidden nodes for its survivability component.

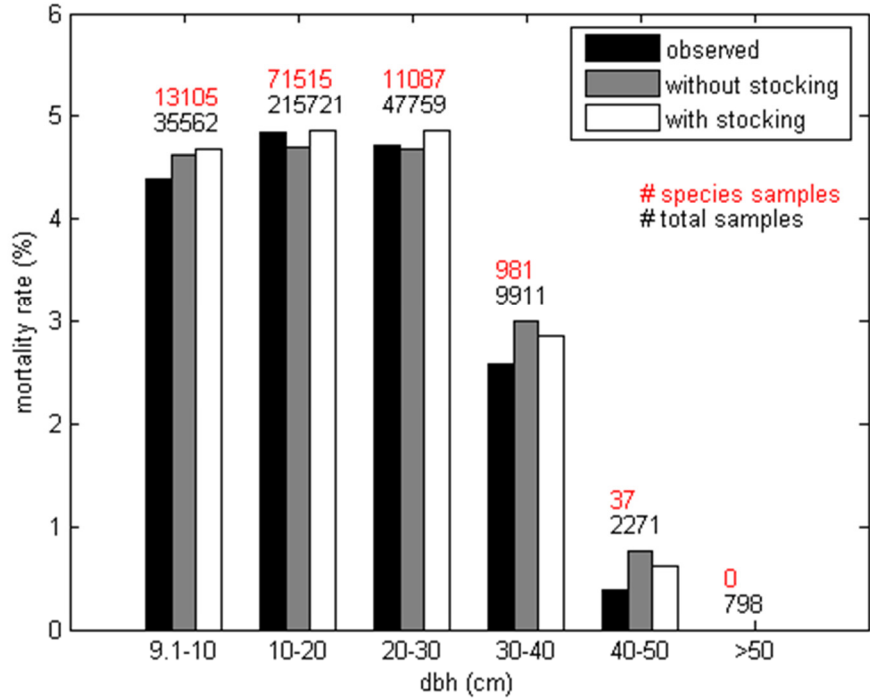


Figure 13 Observed and predicted mortality rates for different diameter classes, Balsam Fir

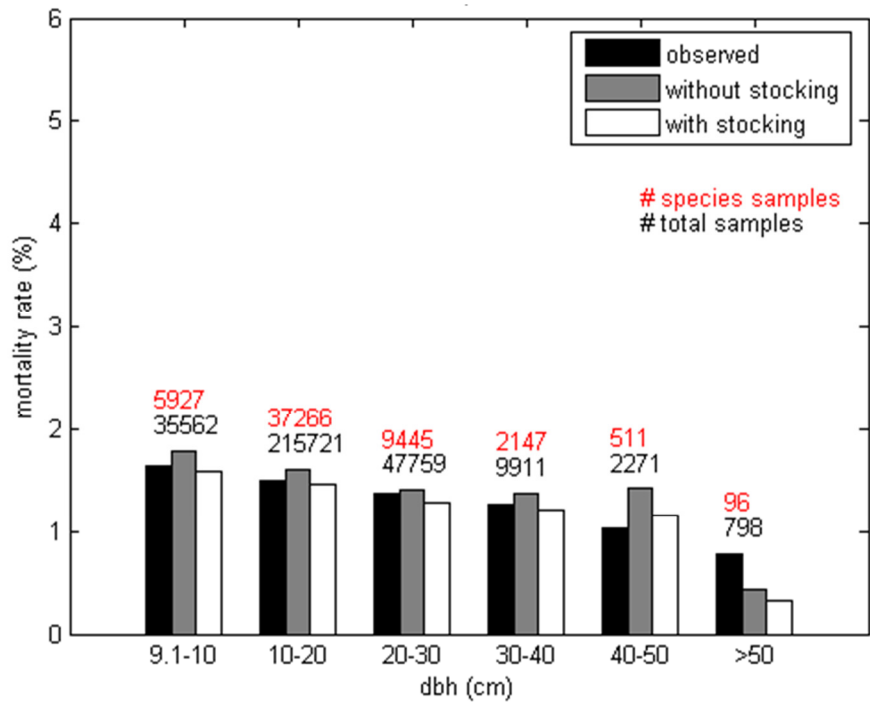


Figure 14 Observed and predicted mortality rates for different diameter classes, Red Spruce

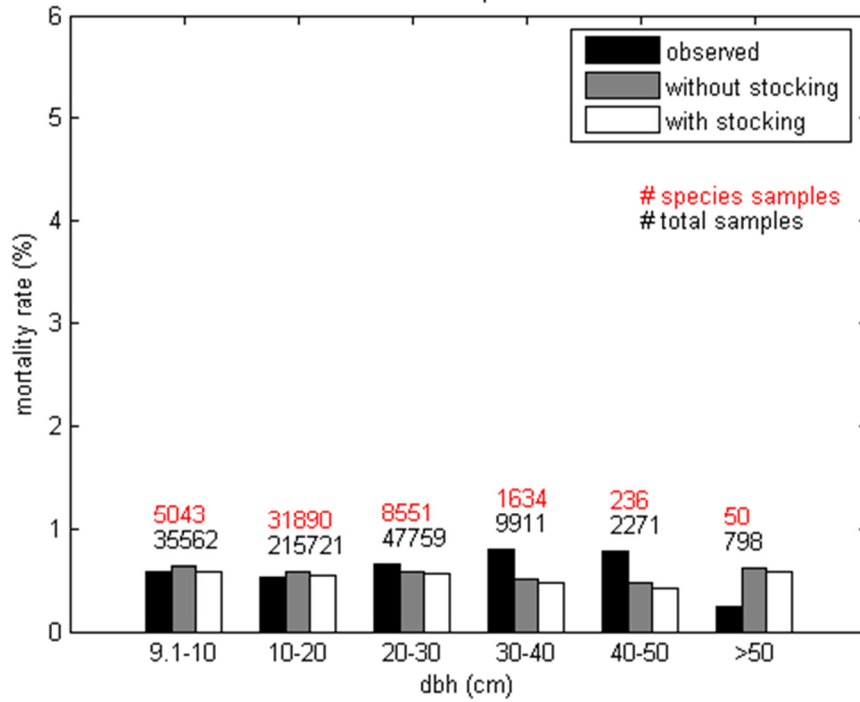


Figure 15 Observed and predicted mortality rates for different diameter classes, Red Maple

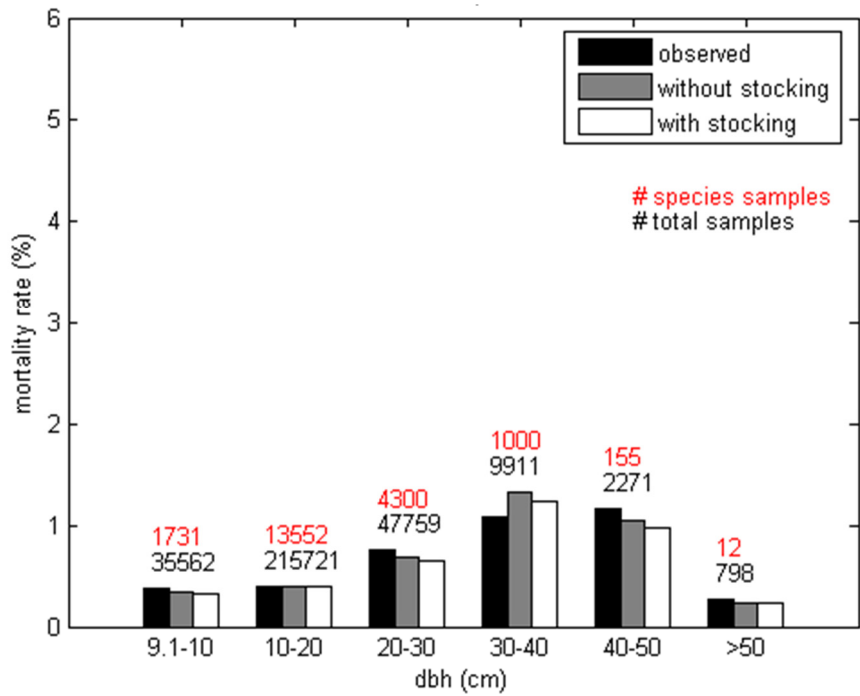


Figure 16 Observed and predicted mortality rates for different diameter classes, White Spruce

Finally, given our chosen survivability network, it was tested whether 1000 epochs was a sufficient amount of training. This was examined by training the network for different maximum epochs: 500, 1000 and 2000 (Table 9); we observed here that the MSE barely changes for the varying training times. Therefore, we can assume that 1000 epochs is a sufficient amount of training.

Table 9 MSE for the chosen survivability network configuration at various maximum epochs

Mean Squared Error		
Maximum Epochs		
500	1000	2000
0.078	0.0777	0.0776
(0.0798)	(0.0797)	(0.0801)

The two MSE values are for training data and check data (in brackets)

To further examine the survivability network, confidence intervals for different categories of data will be determined and compared to the actual number of trees survived. In order to calculate the confidence intervals for different categories of the data, the mean and variance for each category had to be determined. In a category of n trees, each tree has a probability of survival, p_i , where $i = 1, 2, \dots, n$. If each tree's survivability is treated as a Bernoulli random variable, its mean is p_i and its variance is $p_i(1-p_i)$ (Gunn & Nelson, 2005). Therefore, the number of trees expected to survive in the category, $E(x)$, and its variance, $V(x)$, may be calculated from the sum of n Bernoulli random variables (Equations 28 and 29).

$$E(x) = \sum_i p_i \quad (28)$$

$$V(x) = \sum_i p_i (1 - p_i) \quad (29)$$

The data was partitioned into several different categories: small diameter trees (DBH < 15cm), medium trees (15cm ≤ DBH ≤ 30cm), large trees (DBH > 30cm), hardwoods and softwoods. Given that n for each category is large enough, we can assume a normal distribution. With a normal distribution, mean, and variance for each category, the

confidence intervals were calculated using the survivability network outputs (Table 10). The actual number of trees that survived for each category was also calculated.

Table 10 Confidence intervals for survivability predictions of different categories of data

Category	E(X)	V(X)	Confidence Interval	Actual Survived
Small trees	220145	19045	80%: (219968,220322)	219875
			95%: (219875,220415)	
			99%: (219790,220500)	
Medium trees	60485	4676	80%: (60397,60573)	60226
			95%: (60351,60619)	
			99%: (60309,60661)	
Large trees	3867	123	80%: (3853,3881)	3811
			95%: (3845,3889)	
			99%: (3838,3896)	
Hardwood	96022	4573	80%: (95935,96109)	95735
			95%: (95889,96155)	
			99%: (95848,96196)	
Softwood	188475	19271	80%: (188297,188653)	188177
			95%: (188203,188747)	
			99%: (188117,188833)	

Table 10 shows that for both the small trees and the softwood trees, the actual number of survived trees falls within the 99% and 95% confidence intervals, respectively. Although the actual number of survived medium, large and hardwood trees do not fall within the 99% confidence intervals, they each miss the lower bound by at most 0.7%. This is not surprising since the confidence intervals are very narrow due to the large sample sizes used in each category.

Considering that tree survivability is very complex, the observed mortality rates and confidence intervals for different categories of the data show that the trained network models tree survivability reasonably well.

7.2 Diameter Growth Model Component

To model diameter growth, nine different configurations of basal area increment networks were trained; each of the models included the following inputs: tree basal area, volume, the sum of softwood and hardwood basal areas of larger trees, total stand softwood and hardwood basal areas, dominant height of the stand, the growth species vector and stocking factor. The purpose of building these basal area increment networks was to test whether the site measurements (land capability and UNB's site quality index) improved the model fit and, if so, to determine if the SQI is a reasonable replacement for land capability. The basal area increment network was also tested with different numbers of hidden nodes (3, 4, or 5) to determine how many hidden nodes give the best fit. The general structure of the diameter growth model is shown in Figure 17.

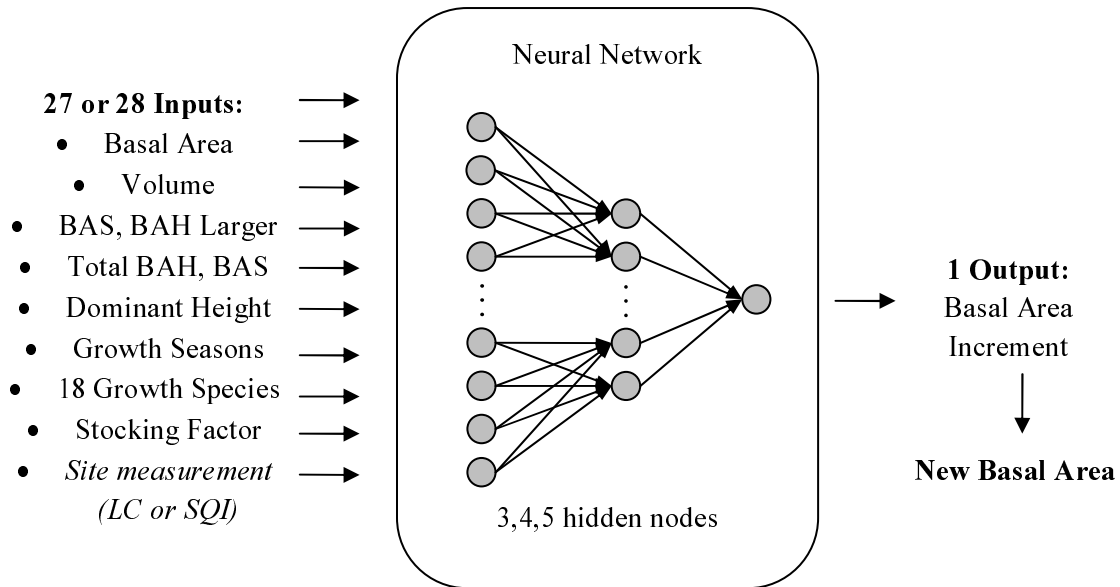


Figure 17 Outline of diameter growth model component

Using the modelled increment, the basal areas at the end of the next growth period were calculated. The mean squared error was calculated for each network by comparing the modelled new basal area to the actual basal area at the end of the following growth period. Similar to the survivability networks, these networks were each run for 1000 epochs. Rather than present the MSE, Table 11 shows the root mean squared error (RMSE) for both the training and check data for the nine different network configurations; RMSE was presented instead of MSE so that the error could be

considered in terms of basal area. In general, we can observe in Table 11 that the RMSE for each network is roughly the same at around 24cm^2 (this translates to roughly 5cm DBH). Since RMSE is an average error measurement, 24cm^2 error was compared to the basal area of an average size tree (we would expect error to increase and decrease with tree size). From the provincial *Forestry Field Handbook* (Nova Scotia Department of Natural Resources, 1993), we can figure that an averaged age tree (50 years old) on a fully stocked average capability stand (land capability of 5) will have a diameter of 15cm. This average sized tree has a basal area of nearly 180cm^2 ; this translates to a reasonable error of about 14%.

Although the RMSEs in Table 11 are essentially the same, we can, however, observe that for each configuration land measurement network inputs slightly improve the RMSE; furthermore, we can observe SQI improves the fits slightly more than LC. Another observation which can be made is that for each configuration of inputs, the networks with 4 hidden nodes yielded slightly better RMSE – although it is not possible that 4 hidden nodes can get a lower MSE than 5 hidden nodes, the networks with 5 hidden nodes likely require more training time. Overall, the configuration of the best fit network included SQI as a model input and had 4 hidden nodes. At this point, it is tempting to conclude that SQI is a reasonable site measurement replacement for land capability. However, from the diameter growth networks alone, we cannot make this conclusion because site measurements are so related to tree heights (recall that site index and land quality measurements are derived from stand dominant height). Therefore, the height increment model component will need to be considered before making any decisions regarding SQI.

Given that the best diameter growth network includes SQI as a model input and has 4 hidden nodes, it was tested to ensure that 1000 epochs was sufficient training. This was done by using a different number of maximum epochs: 500, 1000 and 2000 (Table 12). When the training was doubled from 500 to 1000, the RMSE was reduced by 1.8%. When we then doubled the training again to 2000, the RMSE was reduced by only 0.8%. Although we might expect the MSE to improve with even more training, it is not expected to improve significantly. Therefore, the training time of 1000 epochs for the nine networks was considered reasonable.

Table 11 RMSE for various configurations of the diameter growth network (training = 1000 epochs)

	Root Mean Squared Error – New Basal Area (cm ²)		
	Number of Hidden Nodes		
	3	4	5
No land data	24.44 (26.75)	24.37 (26.70)	24.55 (26.89)
Site Quality Index	23.64 (26.27)	23.53 (26.14)	23.66 (26.24)
Land Capability	23.85 (26.55)	23.59 (26.15)	23.81 (26.34)

The two MSE values are for training data and check data (in brackets)

Table 12 RMSE for the chosen diameter growth network configuration at various maximum epochs

	Root Mean Squared Error – New Basal Area (cm ²)		
	Maximum number of epochs		
	500	1000	2000
	23.96 (26.67)	23.53 (26.14)	23.33 (25.95)

The two MSE values are for training data and check data (in brackets)

Using the predictions from the chosen basal area increment network, the new basal areas for each individual tree were calculated. The modelled new basal areas were sorted and plotted with the basal areas that actually occurred. When the modelled and actual basal areas were compared, it was found that there was a lot of noise in the data. Therefore, to get an understanding of the trends in the data, the noise in the data was reduced through standard exponential smoothing (also referred to as low pass filtering):

$$s_1 = x_0$$

$$s_t = \alpha x_{t-1} + (1 - \alpha)s_{t-1}, t > 1 \quad (30)$$

where x_t is the original data and s_t is the smoothed data. Figure 18 shows the new basal areas for the data, the smoothed data, and the modelled basal areas (sorted by the modelled values). To observe any bias in the model, the data was plotted against the modelled basal area (Figure 19). These figures are representative of the check data only. In the plots, we can see that the trend of the data fits quite well with the modelled values

for new basal area. Furthermore, there does not appear to be a significant bias in the model.

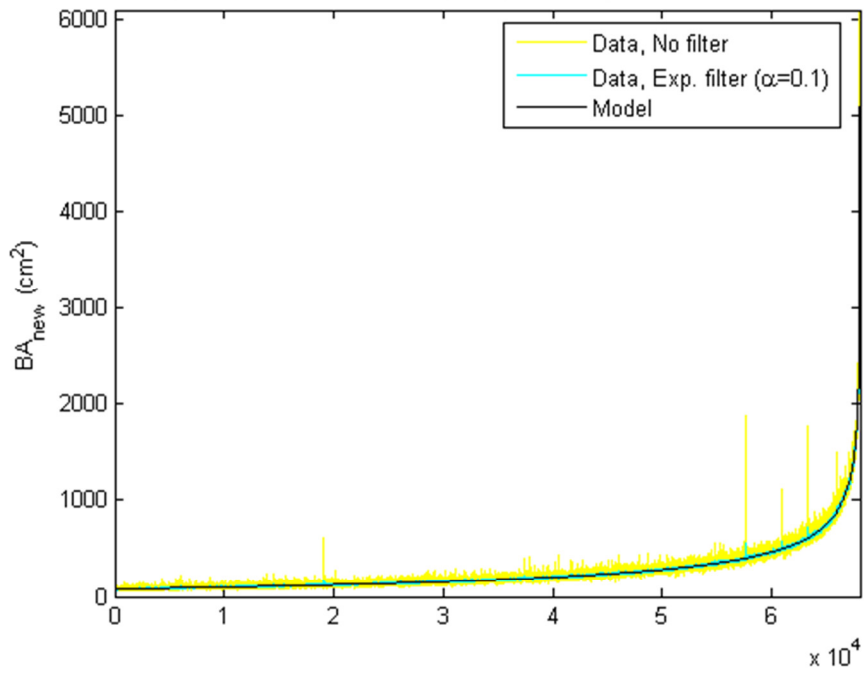


Figure 18 Modelled and actual new basal areas for the check data only, sorted by modelled values

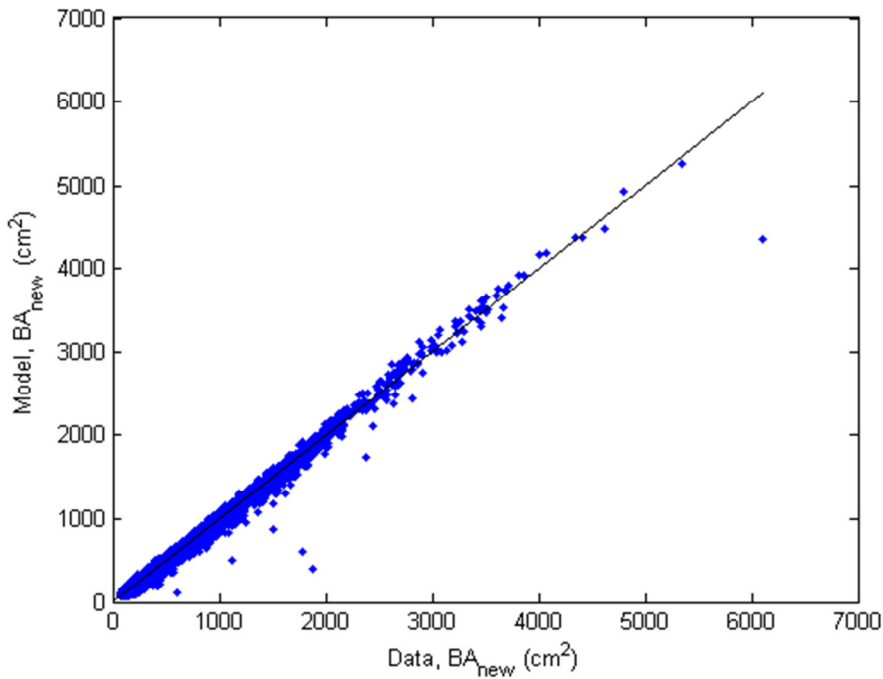


Figure 19 Modelled versus actual new basal areas - for the check data only

To be sure that the model is able to perform at the species level, the red spruce data was run through our all-species basal area increment network; this resulted in an MSE of 551.34 cm^4 . The outputs of this model were plotted against the outputs of a network model trained only with red spruce data (Figure 20). The MSE of the red spruce trained network was 519.99 cm^4 . Clearly, judging by the MSEs, we can tell that the red spruce network models the red spruce trees better – this was to be expected. In Figure 20, we can see that our all-species model slightly underestimates the new basal area compared to the red spruce network (this is most obvious for the larger trees) however the model outputs are still reasonably close. Therefore, the all-species model appears to be capable of reasonably modelling a well-represented species.

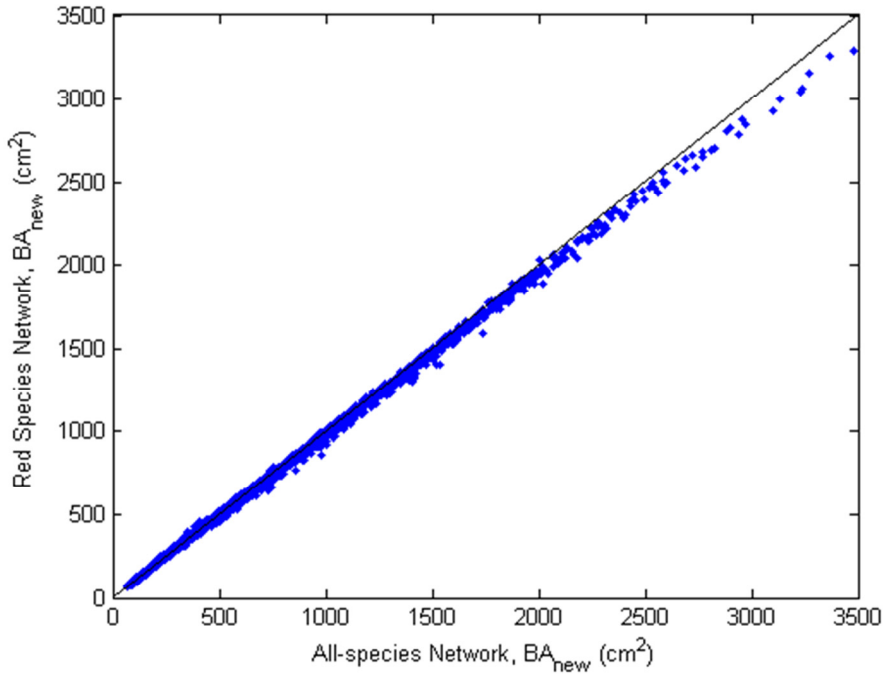


Figure 20 Comparing the new basal areas as modelled by the red spruce and the all-species networks

7.3 *Height Growth Model Component*

Similar to the diameter growth model, height growth was modelled by training nine different configurations of volume increment networks; each of the networks included the following inputs: tree basal area, volume, the sum of softwood and hardwood basal areas of larger trees, total stand softwood and hardwood basal areas, dominant height of the stand, the growth species vector and stocking factor. Again, the purpose of building each of these networks was to test whether the site measurements improved the model fit and to determine if SQI is a reasonable replacement for land capability. The height increment network was also tested with a various number of hidden nodes (3, 4, or 5) to determine the best number of hidden nodes to use in the model. The general structure of the diameter increment model is shown in Figure 21.

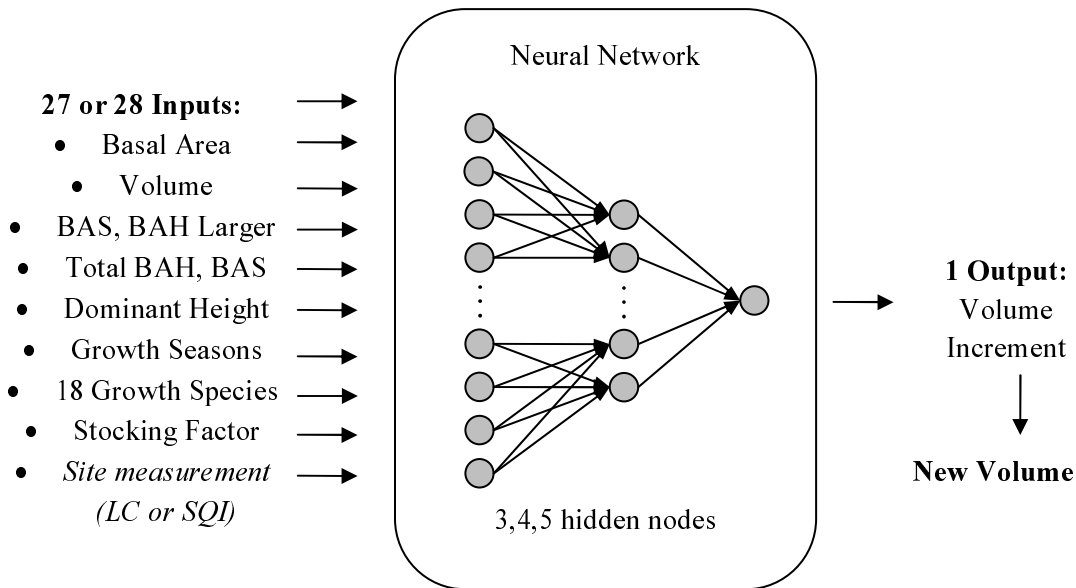


Figure 21 Outline of height increment model component

From the volume increment network outputs, the volume expected at the end of the next growth period was calculated. For each network, the mean squared error was calculated by comparing the modelled new volume that actually occurred at the end of the growth period. Table 13 shows the RMSE for both the training and check data for the nine different network configurations; these networks were each run for 1000 epochs, just as was done with the survivability and diameter growth networks. Overall, the RMSE was roughly $16,000 \text{ cm}^3$ in each of the networks. Again, we will compare this error to an average sized tree. Continuing with the average sized tree from section 7.2, from the *Forestry Field Handbook* (Nova Scotia Department of Natural Resources, 1993) we can also find that an average aged red spruce tree on an average stand will be roughly 16m high. This average sized tree has a volume of approximately 94000 cm^3 ; this translates to a tolerable error of about 17%.

Although the RMSEs in Table 13 are essentially the same, a network to use for the growth model had to be identified. In general, observations of the results in this table are not as simple as they were in the survivability and diameter growth networks. There is no obvious pattern as to what number of hidden nodes or which land measure works best. First, because it is such a widely available measure, preference was given to the SQI networks. Since we can observe that the SQI network with five hidden nodes had not

achieved an RMSE as low as the network with four, it indicates that the network with five hidden nodes should have been trained for a longer time and was therefore not used. Finally, the SQI network with 4 hidden nodes was chosen for the growth model since it had a lower RMSE than the network with 3 hidden nodes.

Table 13 RMSE for various configurations of the height growth network

	Root Mean Squared Error – New Volume ($\times 10^4 \text{cm}^3$)		
	Number of Hidden Nodes		
	3	4	5
No land data	1.66 (1.75)	1.61 (1.72)	1.62 (1.74)
Site Quality Index	1.62 (1.74)	1.59 (1.71)	1.64 (1.76)
Land Capability	1.62 (1.74)	1.61 (1.74)	1.59 (1.69)

The two MSE values are for training data and check data (in brackets)

Again, having chosen a network configuration, it still needed to be confirmed that 1000 epochs was a sufficient training length; the network was therefore tested for different maximum epochs: 500, 1000 and 2000 (Table 14). When the training was doubled from 500 to 1000, the RMSE was reduced by 4.8%. When the training was doubled again to 2000, the RMSE did not reduce at all. Therefore, 1000 epochs was deemed to be an acceptable amount of training.

Table 14 RMSE for the chosen volume increment network configuration at various maximum epochs

	Root Mean Squared Error – New Volume ($\times 10^4 \text{cm}^3$)		
	Maximum number of epochs		
	500	1000	2000
	1.67 (1.80)	1.59 (1.71)	1.59 (1.71)

The two MSE values are for training data and check data (in brackets)

The modelled volumes were sorted and plotted with the actual volumes of the following growth period (Figure 22). Again it was found that there was a lot of noise in the data, and exponential smoothing was used (Equation 30). To observe any bias in the model,

the data was plotted against the modelled new volume (Figure 23). These figures are also representative of the check data only. In the plots, we can see that the trend of the data fits quite well with the modelled values for new volume. Furthermore, there does not appear to be a significant bias in the model.

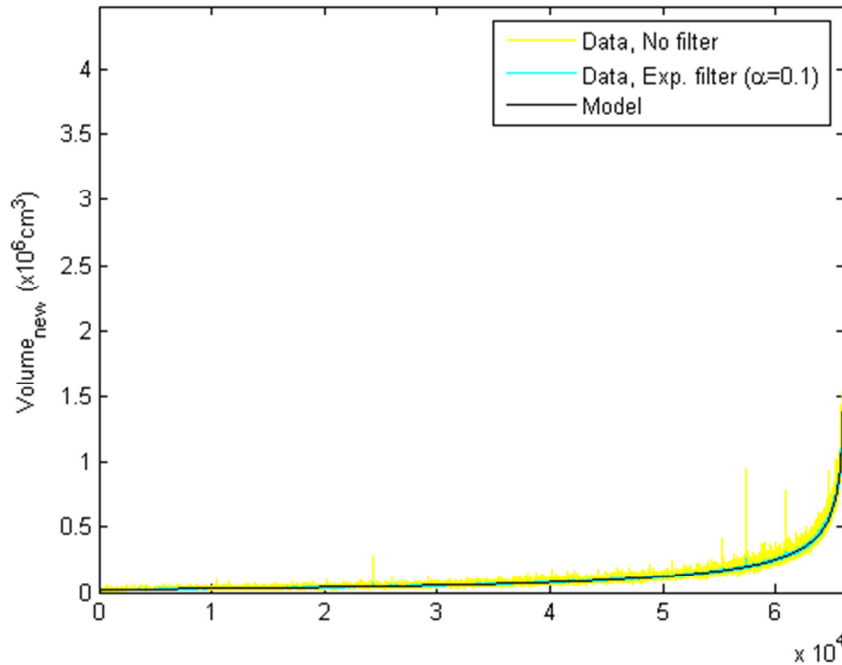


Figure 22 New volumes (modelled, smoothed, actual) sorted by modelled values, using site quality index

To be sure that the model is able to perform at the species level, the red spruce data was run through our all-species volume increment network; this resulted in an MSE of $2.698 \times 10^8 \text{ cm}^6$. The outputs of this model were plotted against the outputs of a network model trained only with red spruce data (Figure 24). The MSE of the red spruce trained network was $2.469 \times 10^8 \text{ cm}^6$. Judging by the MSEs, we can tell that the red spruce network better models the red spruce data; again, this was to be expected. In Figure 24, we can see that the volume outputs from each of the models are quite close and we can conclude that the all-species network is capable of modelling at the species level.

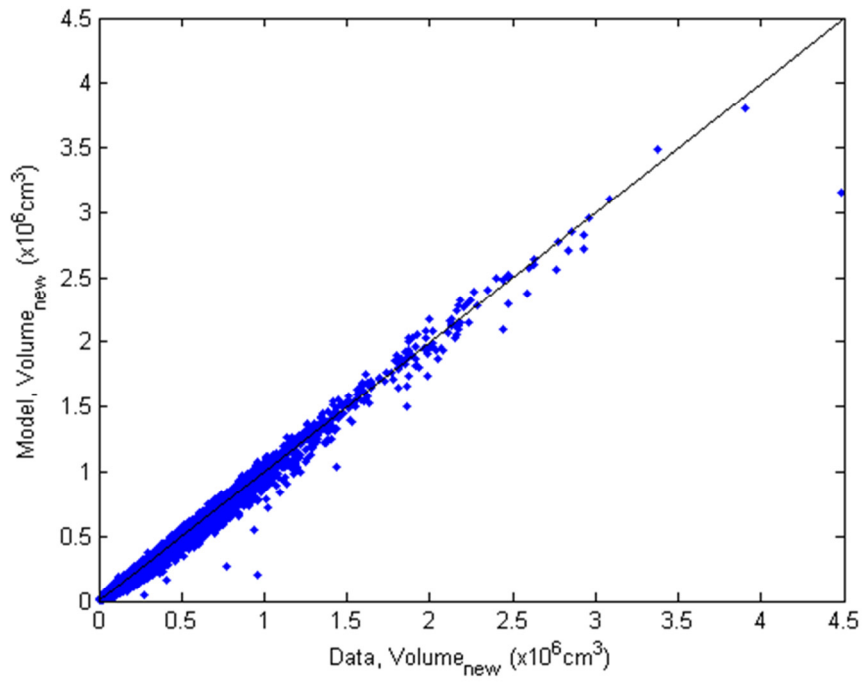


Figure 23 Modelled new volume versus actual new volume, using site quality index

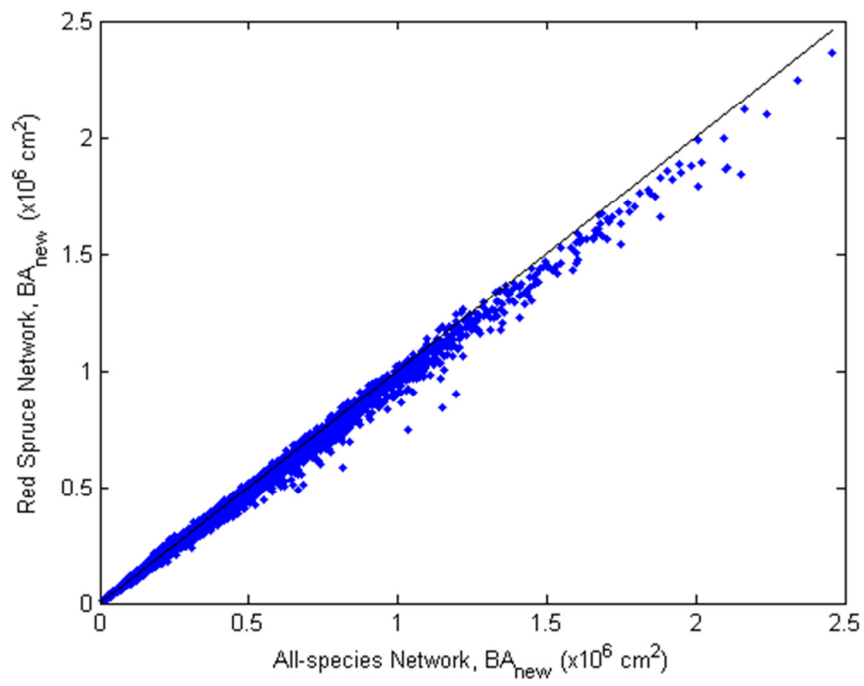


Figure 24 Comparing the new volumes as modelled by the red spruce and the all-species networks

Chapter 8: Growth Model

Recall that the purpose of building the survivability, diameter increment, and height increment networks was to unite them to create a growth model. The general idea of the growth model is to provide a tree list to the model, grow the trees over a certain time, and update the tree list using the model predictions. For simplicity, the tree lists will be presented in a Microsoft Excel workbook and updated using VBA subroutines. All weights, as well as the maxima and minima to be used for normalization, were exported from MATLAB to Excel. Detailed code for this model is shown in Appendix C.

8.1 Implementing the Growth Model

The tree list presented to the model will include all trees in the stand with a DBH of at least 9.1cm (to match the data used in the training of the networks). The original tree list should include the diameter, height and species of each individual tree. The area and SQI of the stand must also be known. Information on which species are included in each growth species groups should also be accessible to the program. Given all of this information, each of the tree-level and stand-level model inputs can be determined. Along with the weights of the previously trained networks, the maximum and minimum of each network input were imported into Excel so that the data can be appropriately normalized, passed forward through each network, then appropriately unnormalized.

Simulating the growth of the tree list is straightforward for the first growth period because it was known that each tree was alive when the list was acquired and therefore the calculations of the network inputs is clear. However, using the model predictions from the first growth period to update some of the inputs for the next growth period was not as straightforward. The difficulty lies in understanding how to properly use the model predictions of survival. Since our approach is deterministic, we do not want to classify a tree to have lived or died; instead, we assume that the probability of survival is the portion of the tree that survives and we are essentially working with partial trees. Clearly, unchanging attributes such as tree species and site quality indices are carried forward to the next period. Although we are only growing parts of trees over time, basal area and volume will simply be updated by using the increment network predictions for the previous growth period. The probability of survival must be considered, however,

when inputs are determined from aggregated measures. Cumulative inputs such as total basal area, basal area larger, and stocking factor will be calculated by using the sum of the products of survival probability and tree-level basal areas. Since dominant height is only based on the heights of a few trees in the stand, the probability of survival is not considered when it is updated. The model assumes a growth period of five years, to the nearest month. Finally, the growth model only considers the trees that were in the original tree list and does not have a function to bring new trees into the stand. Therefore, new growth that actually occurred in the stands was ignored.

8.2 Results of the growth model

Five different inventory stands were selected to observe the modelled and actual stand basal areas over several growth periods¹. Inventory stands were selected since they only included trees of 9.1cm DBH or greater. To make observations on various types of stands, the five stands chosen included (i) a poorly stocked² stand with mostly hardwood trees, (ii) a poorly stocked stand with mostly softwood trees, (iii) a well-stocked³ stand with mostly hardwood trees (iv) a well-stocked stand with mostly softwood trees and (v) a moderately stocked⁴ stand with a mixture of hardwoods and softwoods. In order to maximize the number of growth periods observed in the data, only stands established before 1970 were selected. Of the stands that fit in the outlined criteria, the chosen stands were randomly selected.

Figures Figure 25 through Figure 29 show the actual and modelled stand basal area (both hardwood and softwood) for each of the aforementioned stand types. Considering that it is highly unlikely that any individual stand will match the model, the modelled basal areas were generally reasonably close to the actual basal areas. Overall, the softwood predictions were within 20% of the actual basal areas and the hardwood predictions were typically within 40%, except in cases of extreme change as we can observe for the actual

¹ The modelled growth period is assumed to be 5 years, the actual growth period may vary slightly

² Poorly stocked stand: stocking factor <0.2

³ Well-stocked stand: stocking factor > 0.8

⁴ Moderately stocked stand: stocking factor = 0.4-0.6

softwood basal area in Figure 28. These differences become smaller as the prediction period becomes shorter. As might be expected, the poorly stocked and moderately stocked stands show growth trends (where trees of that type initially existed). The well-stocked hardwood stand demonstrated a decrease in stand basal area while the well-stocked softwood stand showed basal area growth.

We can further examine the growth model at the tree level. Appendix E shows the tree list for the moderately stocked mixed species stand and its growth over the first growth period. As would be expected from the younger trees of Nova Scotia, we can observe that the larger trees generally have a larger probability of survival. We can also observe that the model differentiates between tree species; for example, grey birch typically has a larger probability of survival than trembling aspen.

Overall, the growth model performs reasonably well for a couple of growth periods using these smaller scale inventory plots. Because we are using deterministic survivability and are therefore only predicting average growth, the model would be expected to perform better on a larger scale. The model might also be expected to perform better and if it included a function to include new growth in the model.

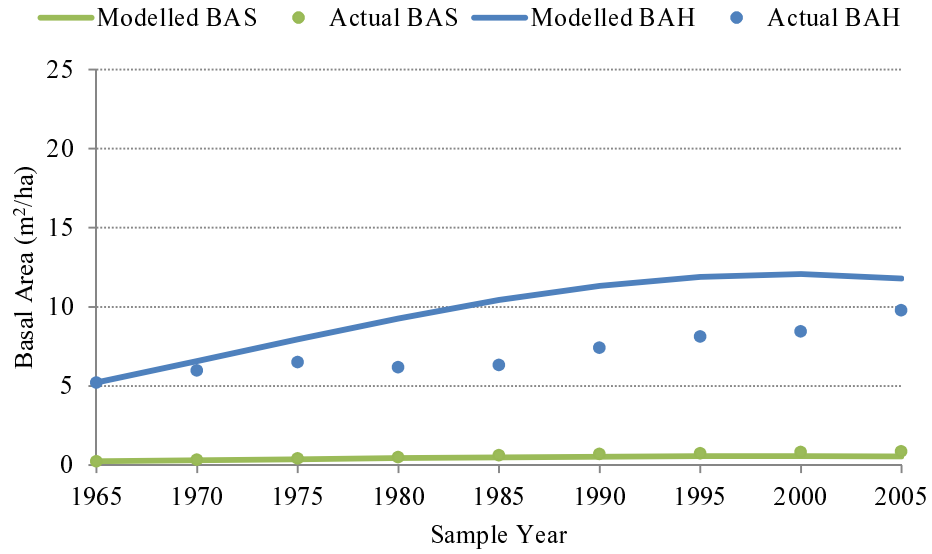


Figure 25 Actual and modelled BA growth for a poorly stocked HW stand

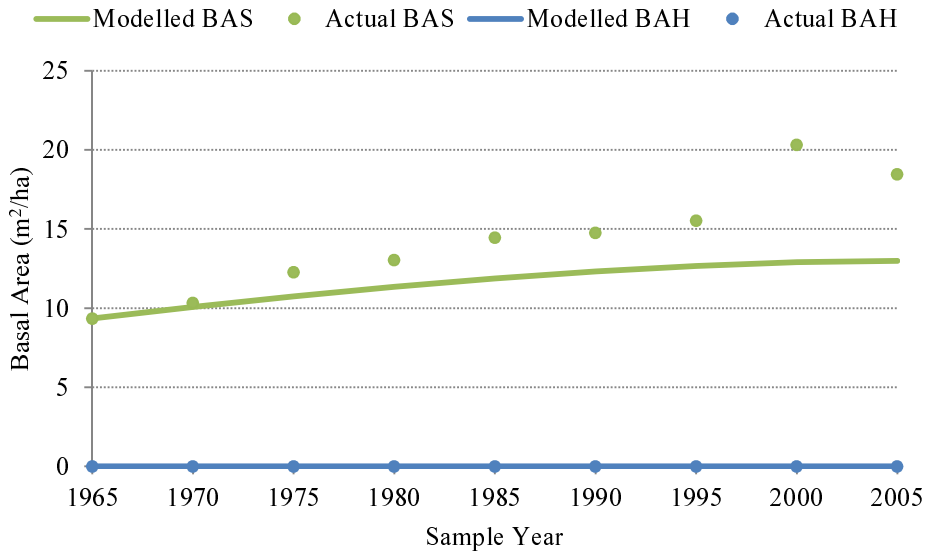


Figure 26 Actual and modelled BA growth for a poorly stocked SW stand

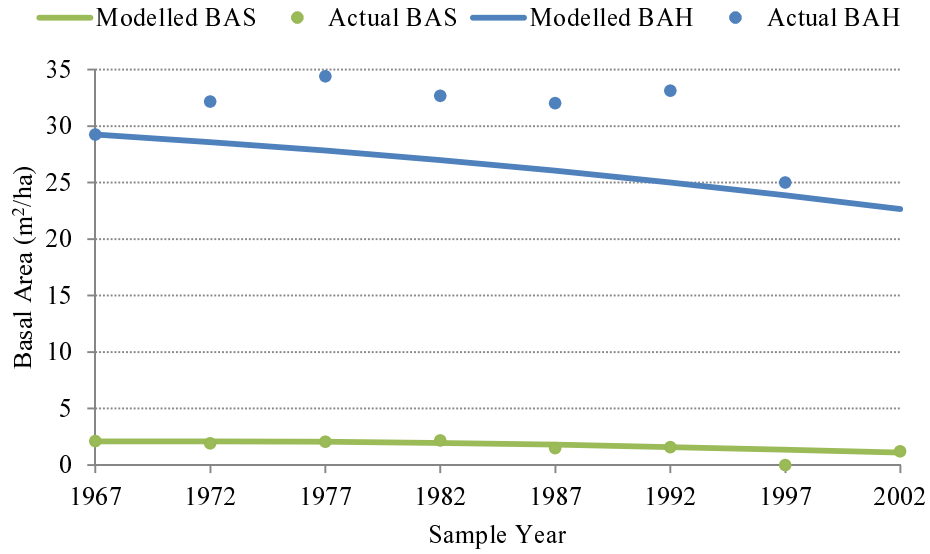


Figure 27 Actual and modelled BA growth for a well stocked HW stand

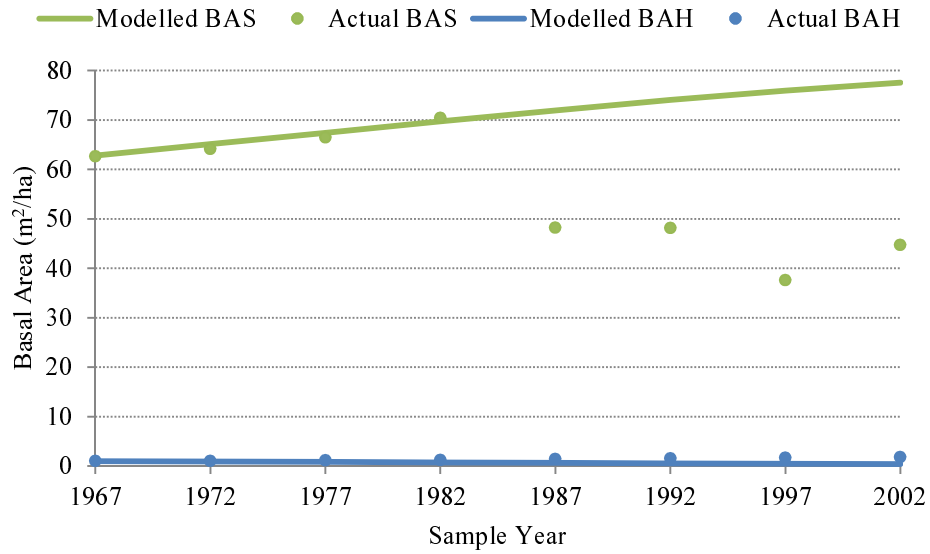


Figure 28 Actual and modelled BA growth for a well stocked SW stand

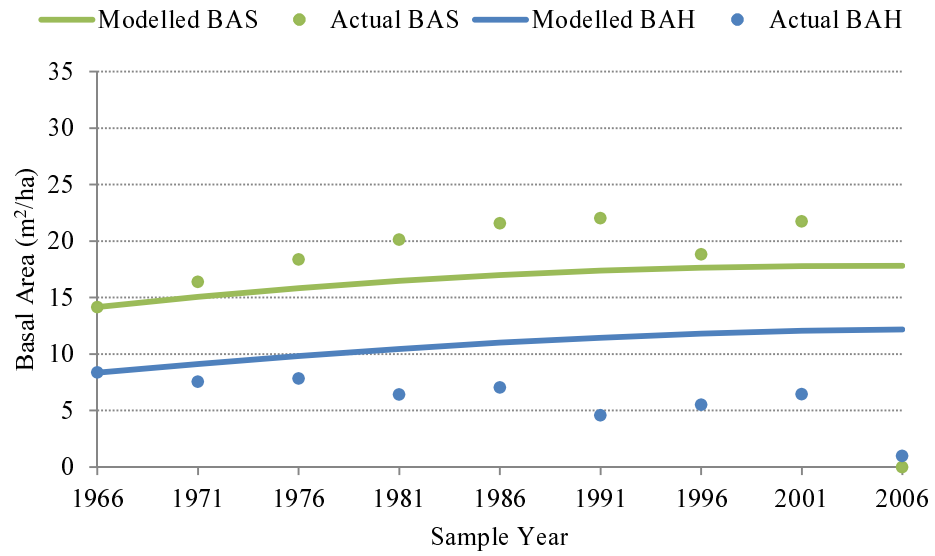


Figure 29 Actual and modelled BA growth for a moderately stocked mixed stand

Chapter 9: Conclusions

Overall, we were able to create a limited growth model with neural network components that model tree survivability, diameter growth and height growth. The growth model could be used to represent average stand evolution with no ingrowth and with characteristics similar to those used in the network training (for example, Acadian forest stands with trees of $DBH \geq 9.1\text{cm}$). Shorter-term predictions (within a few growth periods) are best. Although there are limitations to the growth model, the individual neural network components proved to fit the data quite well.

Of the fourteen different survivability network configurations tested, the best survivability network had 27 inputs, 5 hidden nodes, and 1 output. We were able to observe that when stocking levels were represented in the model inputs, the networks were able to predict mortality rates better for the most abundant diameter classes than when stocking levels were not included. We also found that including SQI as a model input improved the model when compared to having no land data input at all. From the survivability networks we were able to observe that the model could distinguish between growth species with the growth species input vector; this is important since, in Nova Scotia, the nature of our data requires us to consider a single model for all species rather than multiple species-specific models. Finally, upon the calculation of different confidence intervals for different categories of trees, it was found that the observed number of trees survived in the category was either within or very near to the 99% confidence interval.

Next, in preparation for training the diameter increment network, we observed from the nature of the data that diameter increment would best be modelled indirectly by having idealized basal area increment as the network output. Of the nine different diameter increment network configurations tested, the diameter increment network chosen for the growth model had 28 inputs, 4 hidden nodes, and 1 output. Of the nine different networks, the RMSEs were all roughly the same and seemed reasonable when compared to the basal area of an average sized tree in Nova Scotia. In comparing the nine networks, we could observe that site measurement inputs (land capability and site quality index) improved the model fits from using no site measurement data; furthermore, we

found that site quality index improved the fits more than land capability. Considering that site quality measurements are available for the whole province, SQI is recommended for use over land capability. Finally, when the modelled new basal areas were compared to the exponentially smoothed data, we could see that the trends of the data were the same as that of the model.

As for the height increment network, many of the observations made were similar to the diameter increment network. Due to the nature of the data, height increment would best be modelled indirectly by predicting volume increment and calculating height by using the predicted basal area. Again, there were nine different network configurations modelled from which we could observe the RMSEs were essentially the same for each network. When compared to an average sized tree in Nova Scotia, the RMSE for the volume networks were adequate. Favouring site quality index as a model input over land capability, the chosen height increment network had 28 inputs, 4 hidden nodes and 1 output although the network configuration with the best fit was with a land capability input. Finally, when the modelled new basal areas were compared to the exponentially smoothed data, we could see that the trends of the data were the same as that of the model.

Chapter 10: Discussion

Although it is not possible to use a data set that does not exist, it should be acknowledged that there would be improvements to the network fits if the data set was better designed for growth modelling. As discussed in Chapter 4:, there were many species, diameter classes, and stocking levels which were underrepresented in the data. It is expected that the model would perform better for all species, sizes and stocking levels if the data is stratified. It would also be good to obtain site quality indices for the research plots so that more data could be used for the training of the final networks.

Recall that during the preparation of the data approximately 75% of the data was used for training, while the remaining 25% was used as check data. It is recommended that a larger portion of the data be used for training. Given that there could be more training data available, it would be worth exploring the effects of using previous diameter increment model input as a measure of tree vigour attribute. Since vigour is an important indicator of tree survivability, it may possibly improve the fit of the survivability network; this would, however, depend on whether the intended user had access to previous diameter increment data for the trees to be modelled. Since stocking level was rough calculation and its contribution to the model was not overly convincing, it might also be interesting to consider other ways of characterizing stocking levels of a stand.

The performance of basal area and volume increment networks could be further analyzed by determining the RMSEs for different size classes to determine the relative error on each size class. This would be more indicative than the RMSE values observed in this thesis which applied to the full spectrum of tree sizes.

It would also be worthwhile to explore different optimization techniques used in the neural network training process. The scaled conjugant gradient method was used in this thesis; however, there are much more sophisticated search methods. Although there were different search methods available in MATLAB (such as Levenberg–Marquardt) they could not be used because our data set was too large. Implementation of other optimization techniques will require manipulation of the MATLAB code or use of another neural networking tool.

Finally, there is still a lot to consider for the Excel growth model. From what we can tell, it is only appropriate for modelling reasonable tree growth for, at most, a few growth periods. These observations were made on the smaller scale inventory plots, and it would be interesting to observe the growth model on a much larger stand (this was not available in our current data set). For longer-term predictions, the growth model will also require a function to bring new growth into the stand. Further examination of how to aggregate dominant height may also be useful.

Works Cited

- Agriculture and Agri-Food Canada. (2010, June 28). *CanSIS - Canada Land Inventory (CLI) Overview*. Retrieved November 21, 2010, from <http://sis.agr.gc.ca/cansis/nsdb/cli/intro.html>
- Belcher, D. M., Holdaway, M. R., & Brand, G. J. (1982). *A description of STEMS - The Stand and Tree Evaluation and Modeling System*. St. Paul, Minnesota: Forest Service - US Department of Agriculture.
- Bourque, C. P.-A., Meng, F.-R., Gullison, J. J., & Brigland, J. (2000). Biophysical and potential vegetation growth surfaces for a small watershed in northern Cape Breton Island, Nova Scotia, Canada. *Canadian Journal of Forest Research*, 30, 1179-1195.
- Brouwer, R. K. (2004). A Hybrid Neural Network for Data That is Both Categorical and Quantitative. *International Journal of Intelligent Systems*, 19, 979-1001.
- Demuth, H., & Beale, M. (2004). *Neural Network Toolbox for use with MATLAB: User's Guide*. Natick, MA: The Mathworks, Inc.
- Guan, B. T., & Gertner, G. (1991). Modeling Red Pine Tree Survival with an Artificial Neural Network. *Forest Science*, 37(5), 1429-1440.
- Gunn, E. A., & Nelson, M. (2005). *A Neural Network Approach to an Individual Tree Model in Nova Scotia*. (Working Paper).
- Hasenauer, H. (2006). Concepts Within Tree Growth Modelling. In H. Hasenauer (Ed.), *Sustainable Forest Management* (pp. 3-17). Berlin: Springer-Verlag.
- Hasenauer, H., & Monserud, R. A. (1996). A crown ratio model for Austrian forests. *Forest Ecology and Management*, 84, 49-60.
- Hasenauer, H., & Monserud, R. A. (1997). Biased predictions for tree height increment models developed from smoothed 'data'. *Ecological Modelling*, 98, 13-33.

- Hasenauer, H., Merkl, D., & Weingartner, M. (2001). Estimating tree mortality of Norway spruce stands with neural networks. *Advances in Environmental Research*(5), 405-414.
- Jain, A. K., Mao, J., & Mohiuddin, K. M. (1996). Artificial Neural Networks: A tutorial. *Computer*, 29(3), 31-44.
- Monserud, R. A., & Sterba, H. (1996). A basal area increment model for individual trees growing in even- and uneven-aged forest stands in Austria. *Forest Ecology and Management*, 80, 57-80.
- Monserud, R. A., & Sterba, H. (1999). Modeling individual tree mortality for Austrian forest species. *Forest Ecology and Management*, 113, 109-123.
- Mosseler, A., Lynds, J. A., & Major, J. E. (2003). Old-growth forests of the Acadian Forest Region. *Environmental Review*, 11, S47-S77.
- Nova Scotia Department of Natural Resources. (1993). *Forestry Field Handbook*. Truro, NS.
- Nova Scotia Department of Natural Resources. (1993). *Nova Scotia Softwood Growth and Yield Model – Version 1.0 User Manual*. Truro, NS: Nova Scotia Department of Natural Resources.
- Nova Scotia Department of Natural Resources. (2000). *Nova Scotia Forest Inventory Based on Forest Inventory Permanent Sample Plots Measured between 1994 and 1998*. Truro, NS: Nova Scotia Department of Natural Resources.
- Nova Scotia Department of Natural Resources. (2002). *Forest Inventory Permanent Sample Plot Field Measurement Methods and Specifications*. Truro, NS: Nova Scotia Department of Natural Resources.
- Nova Scotia Department of Natural Resources. (2006). *Photo Interpretation Specifications*. Truro, NS: Nova Scotia Department of Natural Resources.

- Nova Scotia Department of Natural Resources. (2008). *Nova Scotia's Code of Forest Practice: A Framework for the Implementation of Sustainable Forest Management*. Truro, NS: Nova Scotia Department of Natural Resources.
- O'Keefe, R. N., & McGrath, T. P. (2006). *Nova Scotia Hardwood Growth and Yield Model*. Truro, NS: Nova Scotia Department of Natural Resources.
- Peng, C., & Wen, X. (1999). *Recent Applications of Artificial Neural Networks in Forest Resource Management: An Overview*. Menlo Park, CA: AAAI Press.
- Porté, A., & Bartelink, H. H. (2002). Modelling mixed forest growth: a review of models for forest management. *Ecological Modelling*(150), 141-188.
- Sachs, L. (1984). *Applied Statistics: A handbook of Techniques*. New York: Springer-Verlag.
- Smith, M. (1993). *Neural Networks for Statistical Modeling*. New York: Van Nostrand Reinhold.
- Stage, A. R. (1973). *Prognosis Model for Stand Development*. Ogden: United States Department of Agriculture Forest Service.
- Townsend, P. (2004). *Nova Scotia Forest Inventory based on Permanent Sample Plots Measured between 1999 and 2003*. Truro, NS: Nova Scotia Department of Natural Resources.
- Tu, J. V. (1996). Advantages and Disadvantages of Using Artificial Neural Networks versus Logistic Regression for Predicting Medical Outcomes. *Journal of Clinical Epidemiology*, 49(11), 1225-1231.
- United States Department of Agriculture Forest Service. (n.d.). Retrieved November 7, 2010, from <http://www.fs.fed.us/fmnc/fvs/>
- Vanclay, J. K. (1994). *Modelling Forest Growth and Yield: Applications to Mixed Tropical Forests*. Wallingford, UK: CAB International.

Wykoff, W. R., Crookston, N. L., & Stage, A. R. (1983). *User's guide to the Stand Prognosis Model*. Ogden, UT: United States Department of Agriculture.

Appendix A Data Cleaning

The first step in cleaning up the data set was to ignore the plots in the research data for which there was no expansion factor recorded (or plot area). Since inputs such as stand basal areas and basal areas larger were calculated on a per hectare basis, trees from plots for which we had no areas were unusable. Again in the research plots, there were occasionally two samples taken in a year. For simplicity, only the first measurements of that year were used for determining tree growth.

Next, the gaps in the species data where the trees had been measured at another time were filled. There were a couple of cases where the species of the tree was unknown; these measurements were ignored since they would not have been useful in the total basal areas and basal areas larger measurements because the tree type (hardwood or softwood) would have been unidentifiable.

When the consecutive tree samples were paired to determine whether a tree lived or died, the progression of diameter growth for each tree was examined. In tree growth, we expect that while a tree is alive, the diameter will continue to increase. If it was found that the diameter was shrinking by more than 0.001 cm for more than two growth periods, the tree was added to a list of bad trees to be ignored in the data. The VBA code for this procedure is run in Access:

```
Sub I_LiveOrDie1()
    Dim SQL1 As String
    SQL1 = "CREATE TABLE BadTrees(PlotID Integer, Tree Integer)"
    Call CurrentDb.Execute(SQL1)
    'Open Connection
    Dim Connection As New ADODB.Connection
    Set Connection = CurrentProject.Connection
    Dim m, plotID1, plotID2, tree1, tree2 As Integer 'm is indicator for bad data
    Dim dbh1, dbh2 As Single
    'Open LiveOrDie table as recordset
    Dim rsBad As ADODB.Recordset
    Set rsBad = CreateObject("ADODB.Recordset")
    With rsBad
        .Source = "BadTrees"
        .ActiveConnection = Connection
        .CursorLocation = adUseServer
        .CursorType = adOpenKeyset
        .LockType = adLockOptimistic
    End With
End Sub
```

```

        .Open
    End With

Dim rsCheck As ADODB.Recordset
Set rsCheck = CreateObject("ADODB.Recordset")
With rsCheck
    .Source = "SELECT * FROM Tree_Information ORDER BY PlotID, tree, year"
    .ActiveConnection = Connection
    .CursorLocation = adUseServer
    .CursorType = adOpenKeyset
    .LockType = adLockOptimistic
    .Open
End With
m = 0

Do While rsCheck.EOF = False
    plotID1 = rsCheck("PlotID")
    tree1 = rsCheck("tree")
    dbh1 = rsCheck("dbh")
    rsCheck.MoveNext
    If rsCheck.EOF = True Then
        Exit Do
    End If
    plotID2 = rsCheck("PlotID")
    If plotID1 = plotID2 Then
        tree2 = rsCheck("tree")
        If tree1 = tree2 Then
            dbh2 = rsCheck("dbh")
            If dbh2 - dbh1 < -0.001 Then
                m = m + 1
            End If
        Else
            If m > 1 Then
                rsBad.AddNew
                rsBad("PlotID") = plotID1
                rsBad("tree") = tree1
                rsBad.Update
            End If
            m = 0
        End If
    Else
        If m > 1 Then
            rsBad.AddNew
            rsBad("PlotID") = plotID1
            rsBad("tree") = tree1
            rsBad.Update
        End If
        m = 0
    End If
End While

```

```

    Loop
    rsBad.Close
    Set rsBad = Nothing
    rsCheck.Close
    Set rsCheck = Nothing
    Connection.Close
End Sub

```

Any basal area or volume increments that were within 10^{-4} of zero were assigned increments of zero. Any negative growth was also ignored. The VBA code for this cleaning is:

```

Sub R_CleanUpData(ByVal TableName As String)
    Dim SQL1 As String
    Dim SQL2 As String
    Dim SQL3 As String
    SQL1 = "DELETE FROM " & TableName & " WHERE BAchange is NULL"
    SQL2 = "DELETE FROM " & TableName & " WHERE BAchange < 0"
    SQL3 = "UPDATE " & TableName & " SET BAchange = 0 WHERE abs(BAchange)<0.0001"
    Call CurrentDb.Execute(SQL1)
    Call CurrentDb.Execute(SQL3)
    Call CurrentDb.Execute(SQL2)
End Sub
Sub R_ExecuteCleanUpData()
    R_CleanUpData ("DiameterTrain")
    R_CleanUpData ("DiameterCheck")
End Sub

```

There were a couple of impossibly large diameter growths (>70cm) that were found in the data and they were also removed from the data.

Finally, once the data were imported into MATLAB, only for the basal area and volume networks and the purpose of comparing site measurement inputs, all cases where LC and/or SI were null were ignored from the data:

```

[r1 c1] = size(HeightTrain);
[r2 c2] = size(HeightCheck);

for i = c1:-1:1
    if
        (isnan(HeightTrain(8,i)) || HeightTrain(8,i)==0 || isnan(HeightTrain(9,i)) ||
        HeightTrain(9,i)==0)
        HeightTrain(:,i)=[];
        TrainTPY(:,i)=[];
    end
end

```

```
end

for i = c2:-1:1
    if
        (isnan(HeightCheck(8,i)) || HeightCheck(8,i)==0 || isnan(HeightCheck(9,i)) |
        |HeightCheck(9,i)==0)
            HeightCheck(:,i)=[];
            CheckTPY(:,i)=[];
        end
    end

end
```

Appendix B MATLAB Code for Neural Network Training

In MATLAB, there were three main network training programs for each of the neural networks created. The MATLAB code for each the survivability, diameter increment and height increment networks are respectively shown in this Appendix.

MortalityModel.m:

```
%This program uses imported tree growth data to train a neural network
and
%uses more imported tree growth data to check the neural network
%p is network input
%t is network output
%MortalityTrain is the training data
%MortalityCheck is the check data

%user-defined parameters
num_nodes = 5;
max_epoch = 1000;

%determine the number of rows and columns in the matrix
[r1 c1] = size(MortalityTrain);
[r2 c2] = size(MortalityCheck);

%define p (input) and t (output)
p = MortalityTrain(1:(r1-1),:);
t = MortalityTrain(r1,:);

%normalize data and define network
[pn,minp,maxp,tn,mint,maxt] = premmx(p,t);
net = newff(minmax(pn), [num_nodes 1], {'tansig', 'tansig'},
'trainscg');

%initialize weights and biases, according to network definition
net = init(net);
net.IW{1,1} = net.IW{1,1}/10;
net.LW{2,1} = net.LW{2,1}/10;

%set training parameters and train network
net.trainParam.show = 10;
net.trainParam.epochs = max_epoch;
net.trainParam.goal = 1e-5;
net.trainParam.lr = 0.05;
net.trainParam.min_grad = 1e-10;
[net,tr] = train(net,pn,tn);

%simulate neural network and postprocess data
an = sim(net,pn);
a = postmmx(an,mint,maxt);

%use trained network on test values
p2 = MortalityCheck(1:(r2-1),:);
```

```

t2 = MortalityCheck(r2,:);

[p2n,minp2,maxp2] = premnmx(p2);

a2n = sim(net,p2n);
a2 = postnmnx(a2n,mint,maxt);

%MSE
e = t - a;
e2= t2-a2;
MSE = mse(e);
MSEcheck = mse(e2);

```

GrowthModel.m:

```

%This program uses imported tree growth data to train a neural network
and
%uses more imported tree growth data to check the neural network
%p is network input
%t is network output
%DiameterTrain is the training data
%DiameterCheck is the check data

%user-defined parameters
num_nodes = 4;
max_epoch = 1000;

%determine the number of rows and columns in the matrix
[r1 c1] = size(DiameterTrain);
[r2 c2] = size(DiameterCheck);

%define p (input) and t (output)
p = DiameterTrain(1:(r1-1),:);
t = DiameterTrain(r1,:);

%normalize data and define network
[pn,minp,maxp,tn,mint,maxt] = premnmx(p,t);
net = newff(minmax(pn), [num_nodes 1], {'tansig', 'tansig'},
'trainscg');

%initialize weights and biases, according to network definition
net = init(net);
net.IW{1,1} = net.IW{1,1}/10;
net.LW{2,1} = net.LW{2,1}/10;

%set training parameters and train network
net.trainParam.show = 10;
net.trainParam.epochs = max_epoch;
net.trainParam.goal = 1e-5;
net.trainParam.lr = 0.05;
net.trainParam.min_grad = 1e-10;
[net,tr] = train(net,pn,tn);

```



```

%simulate neural network and postprocess training data
an = sim(net,pn);
a = postmmx(an,mint,maxt);

%define input and output for check data
p2 = DiameterCheck(1:(r2-1),:);
t2 = DiameterCheck(r2,:);

%normalize the check data (input)
for r = 1:(r2-1)
    if (maxp(r) - minp(r))>0
        p2n(r,:) = 2*(p2(r,:) - minp(r)*ones(1,c2)). / ((maxp(r) -
minp(r))*ones(1,c2)) - 1;
    else
        p2n(r,:) = 0;
    end
end

%test check data on trained network and postprocess
a2n = sim(net,p2n);
a2 = postmmx(a2n,mint,maxt);

% calculate new ba from proportional change of ba
a2 = (a2.*p2(2,:) + p2(2,:));
a = (a.*p(2,:) + p(2,:));
t = (t.*p(2,:) + p(2,:));
t2 = (t2.*p2(2,:) + p2(2,:));

%calculate MSE
e = t - a;
e2 = t2 - a2;
MSE = mse(e);
MSEtrain = mse(e2);

```

HeightModel.m:

```

%This program uses imported tree growth data to train a neural network
and
%uses more imported tree growth data to check the neural network
%p is network input
%t is network output
%HeightTrain is the training data
%HeightCheck is the check data

%user-defined parameters
num_nodes = 4;
max_epoch = 1000;

%determine the number of rows and columns in the matrix
[r1 c1] = size(HeightTrain);
[r2 c2] = size(HeightCheck);

%define p (input) and t (output)
p = HeightTrain(1:(r1-1),:);

```

```

t = HeightTrain(r1,:);

%normalize data and define network

[pn,minp,maxp,tn,mint,maxt] = premnmx(p,t);
net = newff(minmax(pn), [num_nodes 1], {'tansig', 'tansig'},
'trainscg');

%initialize weights and biases, according to network definition
net = init(net);
net.IW{1,1} = net.IW{1,1}/10;
net.LW{2,1} = net.LW{2,1}/10;

%set training parameters and train network
net.trainParam.show = 10;
net.trainParam.epochs = max_epoch;
net.trainParam.goal = 1e-5;
net.trainParam.min_grad = 1e-10;
net.trainParam.lr = 0.05;
[net,tr] = train(net,pn,tn);

%simulate neural network and postprocess data
an = sim(net,pn);
a = postmnmx(an,mint,maxt);

%use trained network on test values
p2 = HeightCheck(1:(r2-1),:);
t2 = HeightCheck(r2,:);

%normalize check data
for r = 1:(r2-1)
    if (maxp(r) - minp(r))>0
        p2n(r,:) = 2*(p2(r,:) - minp(r)*ones(1,c2)) ./ ((maxp(r) -
minp(r))*ones(1,c2)) - 1;
    else
        p2n(r,:) = 0;
    end
end

%test check data on trained network and postprocess
a2n = sim(net,p2n);
a2 = postmnmx(a2n,mint,maxt);

% calculate new vol from percentage change of vol
a2 = (a2/100.*p2(1,:) + p2(1,:));
a = (a/100.*p(1,:) + p(1,:));
t = (t/100.*p(1,:) + p(1,:));
t2 = (t2/100.*p2(1,:) + p2(1,:));

%calculate MSE
e = t - a;
e2 = t2 - a2;
MSE = mse(e);
MSEtrain = mse(e2);

```

Appendix C Weights for Trained Neural Networks

The table below outlines which model inputs were associated with which input node for each of the three networks chosen for the model. Table 22 shows the maxima and minima used to normalize the inputs for each network.

Description of input nodes of the final networks

Input Node (i)	Input Description
0	Bias weight (not a model input)
1	Basal Area (cm ²)
2	Volume (cm ³)
3	BA of softwoods in the stand (m ² /ha)
4	BA of hardwoods in the stand (m ² /ha)
5	Basal Area larger – softwood (m ² /ha)
6	Basal Area larger – hardwood (m ² /ha)
7	Dominant Height (m)
8	Site Quality Index
9	Number of Growth seasons
10	ash
11	be
12	bf
13	bs
14	eh
15	mh
16	mp
17	ms
18	po
19	rm
20	ro
21	rs
22	sm
23	tl
24	wb
25	wp
26	ws
27	yb
28	Stocking factor

The following six tables show the weights for each the survivability, diameter increment and height increment networks.

Survivability network - weights from input node i to hidden node j

a _{ij} i	j				
	1	2	3	4	5
0	-1.3627	-0.6886	-0.0224	0.6597	-1.5599
1	1.1473	1.1214	-0.1826	-0.7314	0.2429
2	0.4089	-1.3501	-0.2083	-1.9628	0.5169
3	0.3187	-0.2889	0.5651	0.0275	-0.2912
4	0.2645	-0.4334	0.5768	-0.3707	-0.2816
5	-0.4563	0.1679	0.4333	-0.1000	-0.6660
6	-0.0280	0.9070	-0.6094	0.4650	-0.7343
7	-0.3676	0.4852	-1.1447	-0.1385	0.4618
8	-0.0429	0.3101	-0.7190	-0.0976	-1.1755
9	0.0000	0.0000	0.0000	0.0000	0.0000
10	-0.3634	-0.1441	0.2643	0.1549	-0.0140
11	0.0061	0.4756	-0.1790	0.5196	-0.4672
12	-0.2480	-1.0522	-0.2964	-1.3900	0.1592
13	-0.4210	-0.0224	-0.0983	-0.5372	0.2141
14	-0.1867	0.0142	-0.1955	0.8995	-0.1102
15	0.1465	0.2534	-0.0848	0.2493	-0.0674
16	0.1834	0.1374	0.1314	0.2658	-0.0578
17	-0.1505	-0.1090	-0.0192	0.0559	0.0656
18	-0.4881	0.1115	-0.0049	0.1826	0.1566
19	-0.8459	-0.1486	0.1454	0.2187	0.4037
20	-0.2830	0.1232	-0.2051	0.3102	-0.2274
21	-0.1765	-0.1286	0.2185	0.6255	0.6428
22	0.1425	-0.0992	0.3610	0.4065	0.5308
23	0.4165	-0.2620	0.3924	-1.0105	0.1569
24	-0.4467	0.0974	-0.2811	-0.1104	0.0149
25	0.0378	-0.0588	0.3158	0.7510	-0.3087
26	0.6830	-0.1762	0.1859	-1.1376	0.4235
27	-0.0087	0.1003	-0.2100	0.6867	-0.2371
28	0.5142	-0.3274	0.8020	-0.2387	-0.3312

Basal area increment network - weights from input node i to hidden node j

a_{ij}	j			
	1	2	3	4
0	-1.3644	0.7059	0.7121	-1.3014
1	-0.0115	0.6931	0.4252	-0.1421
2	-0.1474	1.5866	1.7393	-0.7522
3	0.0538	0.3843	1.0050	0.3077
4	-0.3044	0.4556	0.0654	0.4455
5	-0.5014	0.1166	-1.1056	0.0192
6	0.0865	-0.8899	0.3793	-0.2641
7	-0.0613	0.1760	0.0546	0.0494
8	0.0508	0.0080	0.2857	0.7246
9	0.2523	0.0078	0.0022	0.0019
10	-0.0996	0.1398	-0.8015	-0.6259
11	-0.2891	-0.2471	-0.0407	-0.0021
12	0.0221	-0.3824	-0.1849	-0.2097
13	-0.2402	-0.4726	-0.1154	-0.2736
14	-0.0284	-0.3539	0.0063	-0.0230
15	0.0415	0.1454	-0.3099	-0.1452
16	-0.1321	-0.5674	0.1436	-0.2677
17	-0.1360	-0.3177	-0.2640	-0.0610
18	0.2853	-0.0326	-0.3076	-0.0416
19	-0.1092	-0.0291	-0.4673	-0.3145
20	-0.2233	0.1332	-0.2660	-0.0414
21	-0.0527	-0.4324	0.0331	-0.1496
22	-0.2131	-0.0992	-0.5288	-0.3053
23	-0.1443	-0.3834	0.1454	-0.0696
24	-0.2257	-0.0212	-0.3750	-0.1855
25	-0.0170	-0.4122	0.0922	0.1829
26	-0.1563	-0.3915	-0.0816	-0.0512
27	-0.0498	0.2093	-0.4355	-0.1984
28	-0.1248	0.6874	0.7516	0.8987

Volume increment network - weights from input node i to hidden node j

a _{ij} i	j			
	1	2	3	4
0	-1.6428	-0.6410	-0.3975	-1.6669
1	-1.2238	-0.1202	0.2751	-1.1785
2	-1.4863	-1.1864	-1.1745	-1.6438
3	-1.0606	0.1011	0.3340	-0.3591
4	-0.4358	-0.4768	0.5333	-0.1439
5	0.9926	-0.6501	-0.2295	0.5386
6	0.5665	0.8835	-0.5347	-0.1601
7	0.6173	-0.5485	0.0185	-0.7639
8	-0.4012	0.0637	0.6719	-0.1326
9	0.0379	-0.0204	0.0094	0.0045
10	0.3797	-0.3485	-0.5111	0.7090
11	0.0790	-0.0634	0.0525	0.1289
12	0.2676	0.4520	-0.1766	0.1174
13	0.2001	0.4402	-0.2059	0.1802
14	0.1566	0.4504	-0.0173	-0.0987
15	0.2769	-0.0380	-0.1232	0.1315
16	-0.1414	0.4476	0.0102	0.1063
17	0.1772	0.2035	0.0179	0.1828
18	0.2981	0.0797	-0.0571	0.1491
19	0.2100	-0.3169	-0.2132	0.4115
20	0.0809	-0.2234	0.1349	0.0370
21	0.1488	0.5339	-0.1255	0.0677
22	0.1490	-0.1205	-0.1814	0.4433
23	0.0307	0.4337	0.0468	-0.1197
24	0.0826	-0.1633	-0.0619	0.2809
25	0.1422	0.5378	0.1080	-0.1370
26	0.1375	0.4445	-0.0313	0.0766
27	0.1601	-0.4294	-0.0864	0.3467
28	-1.1481	-0.4369	1.0739	-0.4737

Survivability network - weights from hidden node j to output node k

b_{jk}	k
j	1
0	-0.6609
1	1.5682
2	-2.0100
3	-1.1491
4	2.1032
5	-1.2483

Basal area increment network - weights from hidden node j to output node k

b_{ij}	j
i	1
0	-0.0467
1	0.7500
2	-1.7903
3	-1.8839
4	1.5436

Volume increment network - weights from hidden node j to output node k

b_{jk}	k
j	1
0	-0.3071
1	1.6618
2	0.7942
3	1.9847
4	1.5019

Minima and Maxima at the input nodes for each network

Input Node` (i)	Survivability		Basal Area Increment		Volume Increment	
	Min	Max	Min	Max	Min	Max
1	65.03	6461.1	63.61	6461.1	63.61	6461.1
2	1699	5.28E+06	2168	5.28E+06	2168	5.28E+06
3	0	70.36	0	70.36	0	70.36
4	0	50.95	0	50.95	0	50.95
5	0	70.2	0	70.2	0	70.2
6	0	50.74	0	50.74	0	50.74
7	3	27.33	3.66	27.33	3.66	27.33
8	2	27.4	6.3	27.4	6.3	27.4
9	0	0	4	6	4	6
10	0	1	0	1	0	1
11	0	1	0	1	0	1
12	0	1	0	1	0	1
13	0	1	0	1	0	1
14	0	1	0	1	0	1
15	0	1	0	1	0	1
16	0	1	0	1	0	1
17	0	1	0	1	0	1
18	0	1	0	1	0	1
19	0	1	0	1	0	1
20	0	1	0	1	0	1
21	0	1	0	1	0	1
22	0	1	0	1	0	1
23	0	1	0	1	0	1
24	0	1	0	1	0	1
25	0	1	0	1	0	1
26	0	1	0	1	0	1
27	0	1	0	1	0	1
28	0.00268	1.69	0.00268	1.69	0.00268	1.69

Appendix D VBA Code for Growth Model

The Excel growth model consists of a workbook with several worksheets. The tree list and stand data is entered into a worksheet called ‘Current Tree List’ (see figure below). The worksheet called ‘Species’ contains a list of all species of the Acadian Forest which has each species classified as hardwood or softwood and associates them with a growth species group. The worksheet ‘MinMax’ contains the minimum and maximum values used for variable normalization in the training of the network. These values were imported from MATLAB. The worksheets ‘MortWts’, ‘BAWts’, and ‘VolWts’ contain the weights associated with the survivability, basal area increment, and volume increment networks, respectively. These weights were also exported from MATLAB.

Land Information		Stand BA (m ² /ha)	
Area (ha)	0.04047	BAS	18.51264
		BAH	3.293274

p(survival)	Diameter (cm)	Height (m)	Species
1	9.1	8.5	BS
1	9.1	8.5	RS
1	9.1	8.5	TL
1	9.1	8.5	TL
1	9.4	7	BF
1	9.4	8	TL
1	9.7	7	RM
1	9.7	8	RM
1	9.9	3.5	BF
1	10.2	4.5	BS
1	10.2	6	RM
1	10.2	6.5	RM
1	10.2	7.5	RM
1	10.2	8	RM
1	20.8	7.5	BF
1	23.4	8.5	BF

Grow Trees

This program models individual tree survivability and growth according to feed-forward neural networks which were trained in Matlab using PSP data from NSDNR.

To use the program, add tree data to the tree list; tree data should include the diameter, height, and species for all trees in a stand with dbh >= 9.1cm. Since all trees in the tree list should be alive, they will all have a probability of survival of 1. See 'Species' worksheet to find species codes.

Add the area of the plot, in hectares, to the cell B2.

Finally, highlight/select all data in the tree list (only) and press 'GrowTrees' button.

'Current Tree List' worksheet for Excel growth model

A VBA subroutine called ‘Grow_Trees’ is linked to the button in the ‘Current Tree List’ worksheet. Once clicked, the button activates an input box for the user to input the desired number of growth periods over which they will then update the tree list for the number of specified growth periods. The VBA code associated with the subroutine ‘Grow_Trees’ is included in this Appendix.

Option Explicit

'This growth model consists of three neural networks for: (i) modelling survivability, (ii) modelling basal area increment and (iii) modelling volume increment

'NNet INPUTS: ba (cm²), vol (cm³), BAS (m²/ha), BAH (m²/ha), BAS_Above (m²/ha), BAH_Above (m²/ha), Dominant Height (m), SQI, seasons, 18 growth species, stocking

'NNet OUTPUTS: LOD (probability), deltaba(cm²)/ba(cm²), deltavol(cm³)/vol(cm³)*100

'counters

Dim n As Integer 'example index
Dim i As Integer 'input node index
Dim j As Integer 'hidden node index
Dim k As Integer 'output node index
Dim net As Integer 'network index

'network variables

Dim ins As Integer 'number of input nodes
Dim hids As Integer 'number of hidden nodes
Dim outs As Integer 'number of output nodes
Dim y() As Single 'hidden node output
Dim z() As Single 'output node output
Dim a As Range 'weights between input and hidden nodes
Dim b As Range 'weights between hidden and output nodes

'input variables:

Dim rngIn As Range 'input from excel
Dim p() As Single 'network inputs calculated from user inputs
Dim maxp() As Single 'max values for normalization
Dim minp() As Single 'min values for normalization

'output variables (end of each growth period):

Dim rngMortality As Range 'fraction of tree remaining
Dim rngDiameter As Range 'new diameter
Dim rngHeight As Range 'new height
Dim rngBA As Range 'stand basal areas

Sub Grow_Trees()

 'define variables

 Dim trees As Integer 'total number of examples
 Dim m As Integer 'input node index
 Dim minz As Single 'min value for output normalization
 Dim maxz As Single 'max value for output normalization
 Dim bas As Single 'basal area softwood
 Dim bah As Single 'basal area hardwood
 Dim stocking As Single 'stocking factor
 Dim baslarger As Single 'basal area larger - softwood
 Dim bahlarger As Single 'basal area larger - hardwood
 Dim sw As Single 'softwood ba variable
 Dim hw As Single 'hardwood ba variable
 Dim species() As String 'species vector
 Dim PlotArea As Single
 Dim heights() As Single 'vector of height variables
 Dim domht As Single 'dominant height
 Dim sp_index As Integer 'species index
 Dim wsName As String 'worksheet name
 Dim max_period As Integer 'maximum number of growth periods
 Dim growth_period As Integer 'growth period index
 Dim mort() As Single 'probability of survivability
 Dim s_hids As Integer

```

Dim d_hids As Integer
Dim h_hids As Integer

'define network structure
ins = 28 'number of input nodes
outs = 1 'number of output nodes
s_hids = 5 'number of survivability hidden nodes
d_hids = 4 'number of diameter network hidden nodes
h_hids = 4 'number of height network hidden nodes

wsName = "Current Tree List"

'get initial tree list
Set rngIn = ActiveWindow.RangeSelection

'get user input for total number of growth periods
max_period = 1 + Application.InputBox("Number of growth periods (growth
period = 5 years)")

'initial growth period
growth_period = 1

'determine number of trees and plot area
trees = rngIn.Rows.Count
PlotArea = Worksheets(wsName).Range("B2").Value

'dimension variables
ReDim p(trees, ins + 1) As Single
ReDim maxp(ins) As Single
ReDim minp(ins) As Single
ReDim species(18) As String
ReDim heights(trees) As Single
ReDim mort(trees) As Single

'create species array
species(1) = "ash"
species(2) = "be"
species(3) = "bf"
species(4) = "bs"
species(5) = "eh"
species(6) = "mh"
species(7) = "mp"
species(8) = "ms"
species(9) = "po"
species(10) = "rm"
species(11) = "ro"
species(12) = "rs"
species(13) = "sm"
species(14) = "tl"
species(15) = "wb"
species(16) = "wp"
species(17) = "ws"
species(18) = "yb"

'assign some initial network inputs:

'assign species matrix to each tree
For n = 1 To trees
    For sp_index = 1 To 18
        If species(sp_index) =
Application.WorksheetFunction.VLookup(rngIn.Cells(n, 4).Value,
Worksheets("Species").Range("A2:D83"), 4) Then

```

```

                p(n, 9 + sp_index) = 1
            End If
        Next sp_index
    Next n

    'calculate initial ba and vol
    For n = 1 To trees

        p(n, 1) = 3.14159 * (rngIn(n, 2) / 2) ^ 2 'initial ba in cm^2
        p(n, 2) = p(n, 1) * rngIn(n, 3) * 100 / 3 'initial vol in cm^3

        mort(n) = rngIn(n, 1) 'initial tree fraction

        p(n, 9) = 5 'number of growth seasons - assumed to be 5

        p(n, 8) = Worksheets(wsName).Range("B3").Value 'site quatliy index
(SQI)

        p(n, ins + 1) = n 'tree ID to keep original order
    Next n

    'loop through each growth period
    For growth_period = 1 To max_period

        bas = 0
        bah = 0
        baslarger = 0
        bahlarger = 0
        sw = 0
        hw = 0
        stocking = 0

        'calculate aggregate bas and bah
        For n = 1 To trees

            If Application.WorksheetFunction.VLookup(rngIn.Cells(n,
4).Value, Worksheets("Species").Range("A2:C83"), 3) = "SW" Then
                bas = p(n, 1) * rngIn(n, 1) + bas
            Else
                bah = p(n, 1) * rngIn(n, 1) + bah
            End If
        Next n

        bas = bas / PlotArea / 10000
        bah = bah / PlotArea / 10000
        stocking = bas / 60 + bah / 30

        Set rngBA = Worksheets(wsName).Range("D2:D3")
        rngBA(1) = bas
        rngBA(2) = bah

        If growth_period = max_period Then
            Exit Sub
        End If

        'calculate dominant height
        For n = 1 To trees
            heights(n) = rngIn.Cells(n, 3)
        Next n
    
```

```

Call SortArray(heights)
domht = (heights(trees) + heights(trees - 1) + heights(trees - 2))
/ 3

'assign bas, bah, stocking and dominant height to input matrix
For n = 1 To trees
    p(n, 3) = bas
    p(n, 4) = bah
    p(n, 28) = stocking
    p(n, 7) = domht
Next n

'calculate bas and bah larger (credit: Rob O'Keefe, DNR)
Dim l As Integer
Dim sbg, hbg As Single
For n = 1 To trees
    sbg = 0: hbg = 0
    For l = 1 To trees
        If p(l, 1) > p(n, 1) Then
            If p(l, 12) + p(l, 13) + p(l, 14) + p(l, 16) +
p(l, 17) + p(l, 21) +
                + p(l, 23) + p(l, 25) + p(l, 26) = 1 Then
                sbg = sbg + p(l, 1) * rngIn(l, 1)
            Else
                hbg = hbg + p(l, 1) * rngIn(l, 1)
            End If
        End If
    Next l
    p(n, 5) = sbg / PlotArea / 10000
    p(n, 6) = hbg / PlotArea / 10000
Next n

'Create output worksheet
wsName = CStr(growth_period * 5) & " years"
Worksheets.Add().Name = wsName
Worksheets("Current Tree List").Range("A1:D1000").Copy
Worksheets(wsName).Range("A1:D1000").PasteSpecial (-4163)
Worksheets(wsName).Range("A1:D1000").PasteSpecial (-4122)
Worksheets(wsName).Range("A1:D1000").PasteSpecial (8)

Set rngIn = Worksheets(wsName).Range("A7:D56")

'define output
Set rngMortality = Worksheets(wsName).Range("A7:A56")
Set rngDiameter = Worksheets(wsName).Range("B7:B56")
Set rngHeight = Worksheets(wsName).Range("C7:C56")

'run normalized data through network and 'denormalize' network
output to worksheet

'survivability network: get weights and max/min values for
normalization
Set a = Worksheets("MortWts").Range("C3:G31")
Set b = Worksheets("MortWts").Range("J3:J8")
hids = s_hids
minz = 0
maxz = 1
For m = 1 To ins
    minp(m) = Worksheets("MinMax").Cells(2, m + 1)
    maxp(m) = Worksheets("MinMax").Cells(3, m + 1)
Next m

```

```

For n = 1 To trees
    Call ForwardPass
    mort(n) = ((maxz - minz) * (z(1) + 1) / 2 + minz) * mort(n)
    rngMortality(n) = mort(n)

Next n

'diameter network: get weights and max/min values for
normalization
Set a = Worksheets("BAWts").Range("C3:F31")
Set b = Worksheets("BAWts").Range("I3:I7")
hids = d_hids
minz = Worksheets("BAWts").Range("L1")
maxz = Worksheets("BAWts").Range("L2")
For m = 1 To ins
    minp(m) = Worksheets("MinMax").Cells(4, m + 1)
    maxp(m) = Worksheets("MinMax").Cells(5, m + 1)
Next m

For n = 1 To trees
    Call ForwardPass
    p(n, 1) = ((maxz - minz) * (z(1) + 1) / 2 + minz) * p(n, 1)
    rngDiameter(n) = Sqr(p(n, 1) / 3.14159) * 2

Next n

'height network: get weights and max/min values for normalization
Set a = Worksheets("VolWts").Range("C3:F31")
Set b = Worksheets("VolWts").Range("I3:I7")
hids = h_hids
minz = Worksheets("VolWts").Range("L1")
maxz = Worksheets("VolWts").Range("L2")
For m = 1 To ins
    minp(m) = Worksheets("MinMax").Cells(6, m + 1)
    maxp(m) = Worksheets("MinMax").Cells(7, m + 1)
Next m

For n = 1 To trees
    Call ForwardPass
    p(n, 2) = ((maxz - minz) * (z(1) + 1) / 2 + minz) / 100 *
p(n, 2) + p(n, 2)
    rngHeight(n) = p(n, 2) * 3 / p(n, 1) / 100

Next n
Next growth_period

End Sub

Sub ForwardPass()

'Define variables for weighted sums
Dim u As Single
Dim v As Single

'Redefine node outputs with dimensions
ReDim y(hids) As Single
ReDim z(outs) As Single

'Map the inputs through the network

```

```

    For j = 1 To hids
        u = a(1, j)
        For i = 2 To ins + 1
            If maxp(i - 1) > minp(i - 1) Then
                u = u + a(i, j) * (2 * (p(n, i - 1) - minp(i - 1)) /
(maxp(i - 1) - minp(i - 1)) - 1)
            End If
        Next i
        y(j) = tansig(u)
    Next j

    For k = 1 To outs
        v = b(1, k)
        For j = 2 To hids + 1
            v = v + b(j, k) * y(j - 1)
        Next j
        z(k) = tansig(v)
    Next k

```

End Sub

Function tansig(uv) As Single

```

    If uv < -88 Then
        tansig = -1
    ElseIf uv > 88 Then
        tansig = 1
    Else
        tansig = 2 / (1 + Exp(-2 * uv)) - 1
    End If

```

End Function

Sub SortArray(vArray As Variant)

```

    Dim lLoop1 As Long
    Dim lLoop2 As Long
    Dim lMin As Long
    Dim lTemp As Single

    For lLoop1 = LBound(vArray) To UBound(vArray) - 1
        lMin = lLoop1
        For lLoop2 = lLoop1 + 1 To UBound(vArray)
            If vArray(lLoop2) < vArray(lMin) Then lMin = lLoop2
        Next lLoop2
        lTemp = vArray(lMin)
        vArray(lMin) = vArray(lLoop1)
        vArray(lLoop1) = lTemp
    Next lLoop1

```

End Sub

Appendix E Growth Model Results for a PSP, an Example

Species	Original Tree List			5 year prediction		
	Tree fraction	DBH (cm)	Height (m)	Tree fraction	Diameter (cm)	Height (m)
GB	1	9.1	7.5	0.9343	9.6659	8.2371
GB	1	9.4	7.5	0.9372	9.9871	8.2317
TA	1	9.4	11.5	0.8872	10.4536	12.5695
GB	1	9.4	8.5	0.9375	9.9847	9.3243
WS	1	9.7	3	0.9563	10.6551	3.4467
GB	1	9.9	9	0.9398	10.5100	9.8512
TA	1	9.9	9	0.8894	11.0086	9.7951
TA	1	10.2	10	0.8950	11.3325	10.7992
WS	1	10.2	5	0.9561	11.1507	5.7092
TA	1	10.2	10	0.8950	11.3325	10.7992
GB	1	10.2	8.5	0.9432	10.8289	9.2947
TA	1	10.4	10.5	0.8967	11.5523	11.3054
GB	1	10.7	8.5	0.9453	11.3599	9.2818
TA	1	10.9	9.5	0.8992	12.1104	10.1800
RM	1	11.2	10	0.9684	12.0738	10.9866
TA	1	11.2	7.5	0.9014	12.4561	8.0145
GB	1	11.4	7.5	0.9496	12.1121	8.1791
WS	1	11.9	5	0.9548	12.9294	5.6571
GB	1	12.2	7	0.9521	12.9561	7.6139
TA	1	12.2	10.5	0.9090	13.5324	11.0593
WS	1	12.4	8	0.9545	13.4251	8.9902
TA	1	12.7	10	0.9112	14.0712	10.4829
GB	1	13.2	7.5	0.9549	14.0038	8.1257
RS	1	13.5	6.5	0.9439	14.5741	7.2279
TA	1	13.5	10.5	0.9165	14.9307	10.9072
TA	1	13.7	10.5	0.9186	15.1541	10.8757
TA	1	14.5	10.5	0.9215	16.0062	10.8061
WS	1	14.5	7.5	0.9530	15.5957	8.3339
RS	1	15	5.5	0.9456	16.1442	6.0866
RS	1	15	5	0.9453	16.1488	5.5376
RS	1	15	7.5	0.9468	16.1260	8.2740
WS	1	15.5	7	0.9575	16.6519	7.7446
TA	1	17.8	12	0.9280	19.4401	12.1182
WS	1	19	9	0.9549	20.2720	9.8118
WS	1	19	12.5	0.9537	20.2224	13.5536
TA	1	19.8	9.5	0.9303	21.5442	9.5345
BF	1	20.3	9	0.8093	21.6527	9.4947
WS	1	20.3	10	0.9558	21.5804	10.8384
RS	1	22.4	13	0.9536	23.6971	13.9314
RS	1	22.4	9	0.9493	23.7771	9.7307
RS	1	23.6	12	0.9529	24.9485	12.8711
RS	1	24.6	12	0.9534	25.9746	12.8696
TA	1	28.4	10.5	0.9424	30.2224	10.4055
RS	1	28.4	14	0.9569	29.7298	14.8318
WS	1	31.2	11.5	0.9401	32.6603	12.2271

Plot Area = 0.4047 ha, SQI = 13.167

Appendix F Growth Model – Digital Files

Available in the Department of Industrial Engineering at Dalhousie University is a compact disk which includes a digital version of all components used to develop the growth model, the growth model that was developed, as well as a digital version of this written thesis. Specifically, the disk includes:

- An Access database including the multiple VBA subroutines and SQL queries used for preprocessing data
- A MATLAB script (.m) files used to train networks with the preprocessed data
- A MATLAB data (.dat) files which include the parameters for the trained neural networks
- An Excel workbook including the growth model developed
- A text file outlining the files included on the disk