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PREDICTIVE ECOLOGY: SIMULATING LONG-TERM CHANGES IN FOREST POPULATIONS
RESPONDING TO VARIOUS REINTRODUCTION METHODS OF THE BC3F3 AMERICAN-
CHINESE CHESTNUT TREE

by

Shelby Dawn Young

Bachelor of Science, University of Arkansas Fort Smith, 2016

A Thesis

Submitted to the Graduate Faculty

of the

University of North Dakota

in partial fulfillment of the requirements

for the degree of

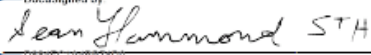
Master of Science

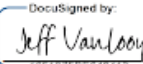
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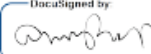
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ABSTRACT

Vida is an explicit biometric simulator tool used to predict multiple aspects of plant populations and community dynamics. Vida is a growth model combined with a reiterative algorithm. The software is written in Python and uses species-specific growth data to model virtual forest ensembles based on each species' growth parameters. Biometric modeling tools like Vida are reliable because they are based on mathematically observed biological truths, of which scientists can use to enhance the predictive power of ecological approaches in different areas. These simulation outputs can be used to demonstrate the ways a forest grows over time. The user can also model the ensemble's response(s) to various environmental disturbances using "event files" which the Vida program recognizes. We have elected to use this tool in a multi-scale study of BC3F3 American-Chinese Chestnut tree reintroduction into Beanfield Mountain of Giles County, Virginia.

Using Vida, we parameterized the Beanfield Mountain environment, introduced the BC3F3 American-Chinese Chestnut tree, observed how the environment reacted to the reintroduction, and reported on the most successful reintroduction method at that location based on Vida outputs. The completion of this research revealed that among three commonly used reintroduction techniques (random, one large center grid, and four small quads) the intervention consisting of small plots and slow, steady reintroduction coupled with clear-cutting the plots generated the most successful and sustainable reintroduction approach. Overall, the most successful method of BC3F3 American-Chinese species reintroduction at the Beanfield Mountain site is the four quads method, where the species is reintroduced using four small plots every two years. The results of this study are specific to the BC3F3 American-Chinese Chestnut tree reintroduction into a Virginia site, on Beanfield Mountain in Giles county.

CHAPTER I

INTRODUCTION

What Happened to the American Chestnut Trees?

From the late 1860's into the early 1910's, Japanese Chestnut trees had become popular decorative imports in the United States.¹ American landscapers were enticed by their lovely, full canopies, and they exhibited little resistance to importing increasing numbers from Asia. Sadly, the love of this species would ultimately doom the native American Chestnut tree. Importers were blissfully unaware of the infection beneath the trees' heartwood. After the blight fungus had already taken its toll, the root cause of the blight infections was a diseased nursery stock in Asia, where the species was imported from.² The Chestnut blight fungus, *Cryphonectria parasitica*, had traveled within the Japanese Chestnut tree and therefore immigrated from the Eastern hemisphere into the Western hemisphere.² The Japanese Chestnut trees showed no signs of infection, and ultimately are not damaged by the fungus, whereas the American Chestnut tree displayed damage of the infection in the form of large cankers, which can be seen in Figure 1, below.



*Figure 1: American Chestnut blight canker.*³

These large cankers are characteristically found on the tree trunk, and are partly caused by the tree's response to the infection.⁴ The canker housing the fungus is swollen or sunken, with the swollen type being the most lethal.⁵ At first, the tree dies above the canker, then, as the sprouts grow, they become infected and die as well. The fungus remains latent until the tree reaches sexual maturity, minimizing the chance of a susceptible species to produce viable seeds, but allows it to live until that point.

The underlying cause of the disease, and the origin of it, was eventually traced to the imported Japanese Chestnut species. In 1912, the USDA officially claimed that the Japanese Chestnut trees imported into the United States were carriers of the disease, and most likely responsible for the initial spread of *Cryphonectria parasitica* in this country.⁵ With almost no immunity against the fungus, the results were catastrophic for the native American Chestnut. An estimated 3.5 billion American Chestnut trees were lost from 1910 to 1950.⁴

In early Appalachian forests, the American Chestnut accounted for about 25% of the total number of trees.⁶ Its original range expanded over 200 million acres from Maine to Florida, mostly east of the Mississippi River.⁶ Figure 2 illustrates this large dominant range.

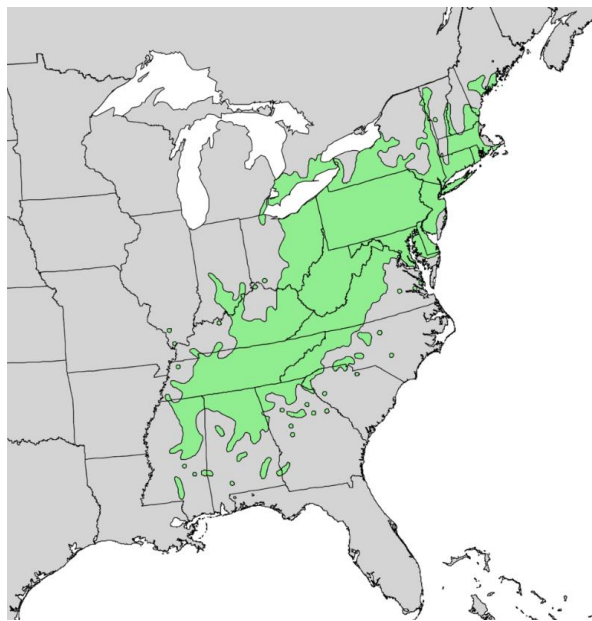


Figure 2: Natural range of the American Chestnut tree.⁷

The natural range of the American Chestnut before its devastation was quite extensive. The American Chestnut tree was a species that covered much of the landscape. The loss of this keystone species created a drastic change in the forest landscape that become more evident over time.

Why Revive the American Chestnut Tree?

The American Chestnut tree was previously a dominant species before its devastation, particularly along the East coast of the United States. Its exposure to the blight fungus in the early 1900's drastically changed the forests' species abundance distribution, the nuts the animals ate, and ultimately- the way the forest grew and evolved. One way that forest ecologists gauge the importance of different tree species in forest ensembles is by generating "importance values" for each species based on the relative frequency of the species in the surveyed area, and the basal area occupied by that species.⁹

$$importance\ value = \left[\left(\frac{relative\ basal\ area + relative\ frequency}{2} \right) * 100 \right] \quad (EQ: 1)$$

Within the area of Beanfield Mountain, many professional (and local, nonprofessional) ecologists have regularly conducted non-invasive, comprehensive site surveys to document the changes in species composition of the area. As the blight began to impact local populations of American Chestnut trees, the community began to assemble several individually kept databases until the USDAFS began keeping records on the area. Individual records can be found at local libraries in Giles county, and cover several areas within the vicinity. Many public and private databases utilize the importance value for their record-keeping, including those maintained by the USDAFS. The importance value is a standard approach used by most foresters to assess a forest ensemble. Foresters usually do not inventory a forest by counting each individual tree. Instead, they locate individuals in the forest and sample a specified area around those points. Figure 3 shows a Google Maps location of Beanfield Mountain, Virginia in Giles County.

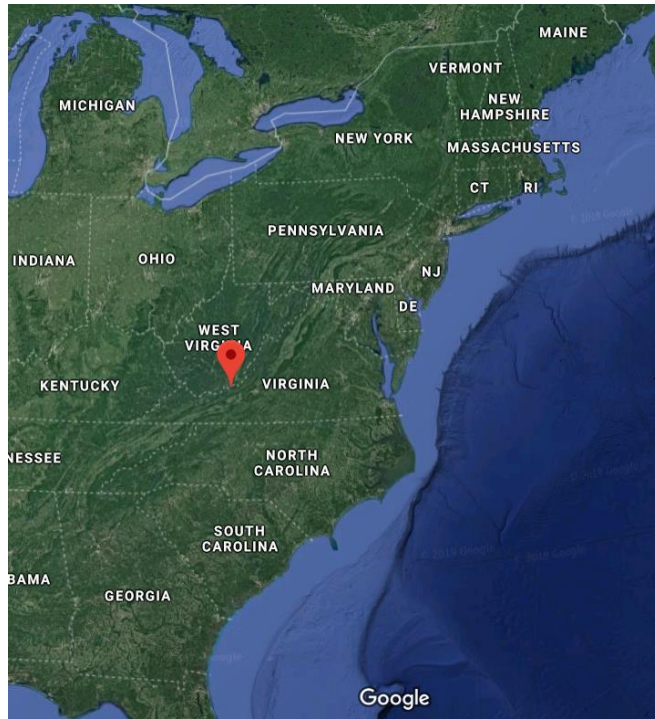


Figure 3: Google Maps location of Beanfield Mountain, Virginia in Giles County.⁸

In 1998, Stephenson and Fortney sampled large sections of the Beanfield Mountain site to obtain quantitative data needed to assess both recent (since 1970) and long-term (>50 years) ensemble changes.⁹ Altogether, they sampled ten different species of trees within the Beanfield site: Chestnut Oak, White Oak, American Basswood, Red Oak, Pignut Hickory, Red Maple, Sweet Birch, American Ash, American Chestnut, and Black Cherry. Stephenson and Fortney's importance values for 1920 are derived values based on sampling carried out in 1939. Their data for both 1939 and 1993 only considers trees with trunks that are at least 7.5 cm DBH. A cutoff value is used because it's not practical to measure every sapling on a site. Not only this, but saplings don't count as a significant amount of biomass, and many trees smaller than 15cm die from being outcompeted with other trees (lack of light, space, nutrients). This technique is not unusual. In order to analyze significant data, a cut off height is generally established. Stephenson and Fortney's results create a dynamic overview of the importance values of each species in the area. Their data of the composition of Beanfield Mountain for 1920, 1939, and 1993 is incredibly reliable, but there

is a chunk of information missing between 1939-1993. Their data was categorized in terms of importance values and can be seen in Table 1.

Table 1: Composition of the tree ensemble of Beanfield mountain in 1920, 1939, and 1993.⁹ Data is represented as importance values based on 100.

Species	1920	1939	1993
Chestnut Oak	21.3	26.8	24.5
White Oak	20	27.8	5
American basswood	3.7	5.5	1.1
Red Oak	14.7	21.1	25.8
Pignut Hickory	7.9	11.5	6.1
Red Maple			21.5
Sweet Birch			9
American Ash	1.8	2.7	
American Chestnut	2.7		
Black Cherry	3.4	4.6	7
<i>Total</i>	100	100	100

When a dominant species, such as the American Chestnut, exits the landscape, drastic reactions are seen within the remainder of the population in response to that loss. As the American Chestnut tree died out, the success of the Oak species increased. The success of the Oak species is due to the fact that their greatest competition, the American Chestnut tree, disappeared. With their greatest competition out of the way, they became more successful. Then, another interesting event happens which relates to an overall systemic reaction to habitat loss. Two tree species, Chestnut Oak and White Oak, decrease in abundance after a brief initial increase in population once the American Chestnut dies out. We believe we see this phenomena because of the shift in feeding habits of the animals in the area (squirrels, deer, bears, etc). After an initial population increase in 1939, all major species decrease in population by 1993 except for Red Oak. Red Oak acorns are higher in tannins, which give them a more bitter taste compared to other nut and acorn options.¹⁰ Since animals are not eating the seeds from Red Oak as much as the other species, its success is higher. When animals do not eat the seeds or nuts of a tree species as frequently compared to the other tree species in the area, more seeds are left over in the environment for that non-eaten species to proliferate. This is what happened to Red Oak. The Red Oak acorns are also smaller

compared to other acorn cups, relatively low in protein, while still containing starches, sugars, and fat.¹⁰

There are also average size difference between the acorns of these trees. Figure 4 shows the visual comparison between these Chestnut, White, and Northern Red Oak Acorns.

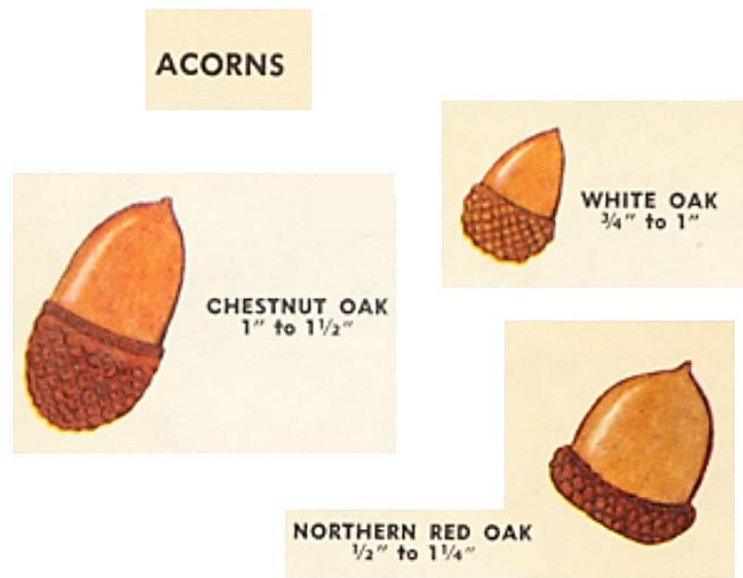


Figure 4: Variations seen between acorns of three Oak species.¹¹

Red Maple is not present at all in the ensemble until American Chestnut is eliminated from the forest. Red Maple appears in year 1993 and was not present in the earlier surveys. Red Maple acts as an invasive species and invades the Beanfield Mountain landscape after the American Chestnut is eliminated for some time. This species is not particularly detrimental; invasiveness is not necessarily negative.

As the ensemble continues to change, a new forest ensemble is created, one that no longer supports the fauna that originally thrived there. In 1920, the American Chestnut species was the most abundant species in the Virginia location. By 1939, there were no living American Chestnut trees recorded in this same area which meant that animal populations that had relied on mast from the American Chestnut needed to shift their food sources. In addition to this, as the years passed, the abundance ratios of the other species were changing in response to this loss of such a keystone species.

An innovative, up-and-coming advantage of reintroducing the American Chestnut species is gradually emerging. Mine reclamation sites can be problematic to reforest, and trees that successfully establish on these sites are often composed of undesirable species.¹³ The American Chestnut tree is a more desirable species with many charismatic features, making it a supreme candidate for enhancing reclamation sites. There is evidence that suggests the American Chestnut tree may tolerate many of the stressful physical and chemical soil characteristics typical of mine reclamation sites.¹³ Many tree species cannot handle soils that have been stripped in nutrients due to mining. The hardy American Chestnut tree is one of those species that can withstand the difficult conditions seen in mining areas. Some traits that make the American Chestnut tree a highly desirable species for enhancing mine reclamation sites are its rapid growth, adaptability to various environmental conditions, and high timber quality.¹³

Since the American Chestnut tree is a large, hearty tree, there are positive considerations pertaining to carbon sequestration. Douglass Jacobs, an associate professor of forestry and natural resources, found that the American Chestnut tree grew much faster and larger than other hardwood species, allowing them to sequester more carbon than other trees over the same period.¹⁵ Jacobs compared the growth and attributes of the American Chestnut tree to Black Walnut, Red Oak, Quaking Aspen, Red Pine, and White Pine at corresponding ages. In all cases except one, the American Chestnut tree grew faster, had three times more aboveground biomass, and sequestered more carbon than all the other species.¹⁵ This means that restoring the American Chestnut tree has large-scale benefits for CO₂ sequestration for an atmosphere that is constantly gorged with an increasing amount of CO₂.

The Hybridized BC3F3 American-Chinese Chestnut Tree

By the 1950s, nearly the entire existing American Chestnut tree population had become infected with the blight fungus; the population was considered a threatened species, making it the worst disaster in forest history.⁴ Therefore, without the possibility of genetic recombination through reproduction, it is difficult for the species to generate new trees that might be resistant. The USDA Forest Service began a

breeding program to develop blight-resistant chestnuts in 1909.¹⁶ The American Chestnut Foundation continued the restoration program to breed American Chestnut tree trees with blight-resistant Chinese Chestnut trees, which closely resemble American Chestnut trees but have slightly different seed and growth properties.¹⁶ In order to create the hybrid species, an original American Chestnut tree is crossed with a Chinese Chestnut tree several times. In the first step, an original 100% American Chestnut tree is crossed with a 100% Chinese Chestnut to produce a 50-50% American-Chinese Chestnut tree. This cross produces an F1. This F1 in this expression stands for Filial 1, the first filial generation seeds/plant offspring resulting from a cross mating. Then, the F1 offspring is crossed with another 100% American Chestnut tree to produce the BC1F1 generation. The BC expression represents the “back cross” amount and reflects how many times the organism has been back crossed, or mated, with the original parent. These generations are crossed with 100% American Chestnut trees three more times to produce a BC3F3 chestnut hybrid (94% American Chestnut and 6% Chinese Chestnut). This BC3F3 American-Chinese Chestnut species is phenotypically similar to the original American Chestnut tree but is resistant to the blight fungus. Active breeding of BC3F3 American-Chinese Chestnuts is occurring in Connecticut, Indiana, Pennsylvania and Virginia. Virginia is within the native range of the American Chestnut, and there is a large amount of growth and site data recorded over time for Virginia forests. Although repeated breeding and additional backcross generations will be necessary, since it seems the BC3F3 American-Chinese Chestnut tree is still susceptible to blight to a small degree.

There is data that supports there is minimal difference between the growth patterns between the original American Chestnut and the BC3F3 American-Chinese Chestnut. In 2010, a research team in West Virginia began growing American Chestnuts, Chinese Chestnuts, and two sections of second (BC3F2) and third (BC3F3) backcross hybrid American Chestnut trees together.¹⁷ One of their sections was in Cheat county and the other, in Gauley county. The plants were assessed after 4 years. Pure American Chestnut trees and pure Chinese Chestnut seedlings were also planted as controls for height growth, form, blight occurrence, and blight resistance.¹⁷ Changes in height from the time of planting to 2014 were similar (or the same) for 100% American Chestnut and BC3F3 hybrids on both sites.¹⁷ A

similar trend among seedling types occurred for total height. American Chestnut seedlings and BC3F3 hybrids performed similarly and showed the greatest mean total height on each site compared to all other seedling types.¹⁷ Table 2 shows how similar the height and growth are between the American Chestnut and BC3F3 compared to other varieties.

Table 2: Arithmetic means and standard errors for three measures of Chestnut trees by site and seedling type.¹⁷

Height in meters	Cheat		Gauley	
	Mean	SE	Mean	SE
Height in 2014				
American Chestnut	9.3	0.2	7.5	0.2
BC3F2	8.0	0.4	6.1	0.3
BC3F3	9.3	0.2	7.6	0.2
Chinese Chestnut	7.1		5.9	
ΔHeight from 2011-2014				
American Chestnut	6.0	0	4.8	0.3
BC3F2	5.0	0	5.1	0.6
BC3F3	6.0	0.1	4.6	0.2
Chinese Chestnut	4.6		3.7	
Total height growth				
American Chestnut	5.8	0	5.2	0.2
BC3F2	4.9	0.1	4.3	0.3
BC3F3	5.8	0.1	5.5	0.1
Chinese Chestnut	4.3		3.8	

American Chestnut seedlings and BC3F3 hybrids performed similarly and showed the most similar mean total height compared to the other seedling types over the four growing years.¹⁷ So, in order to compare an original American Chestnut to a new hybrid, the results of these early years are key, since these are the few years before the fungus manifests and the American Chestnut tree dies. There seems to be enough evidence of similarities between the two species across many planting research locations.

How Our Research Helps the Species Revival Effort

Predicting the future is never a simple task, yet any attempt at reintroducing the American Chestnut requires us to do exactly that. The exact method(s) of reintroduction, location, and impact on a

forest that has had a hundred years to reach a new equilibrium, are all things that need to be considered. Dealing with complexity in space and time are exactly where computer simulations excel.

Vida is a spatially explicit, allometric-based tree growth model that has previously been used to accurately model individual tree growth,¹⁸ and forest populations over time.¹⁹ We have successfully used Vida to hindcast and simulate the loss of the American Chestnut from the simulated space. Now, we will use it to forecast the long-term (100 years into future, 2119) changes in species diversity after successful reintroduction. Vida operates under a null hypothesis that biologically complex phenomena, including widely observed scaling relationships at the species-ensemble level, can emerge from the operation of simple and transparent rules governing competition for space and light.¹⁸

Vida, and other forest simulators, allow us to predict how a forest system will respond to changes in the species composition. This allows us to test several potential interventions needed to reintroduce the chestnuts into the wild and determine which one works best for the environment. Put another way, biometric simulators allow us to observe the outcomes of several situations and chose the best among them—almost like we are viewing parallel realities. The ability to forecast complex changes in an ecosystem has the potential to advance the knowledge of conservation techniques and ecological response efforts across several disciplines, with direct applications to American Chestnut revitalization efforts of the American Chestnut Tree Foundation.

The predominant goal of this thesis is to determine the most successful and sustainable reintroduction method for the BC3F3 American- Chinese Chestnut tree in the Beanfield Mountain, Virginia location. We plan to share our findings with entities closely associated with BC3F3 American-Chinese Chestnut tree reintroduction, such as the American Chestnut Foundation and USDA. The results of this project will also solidify the dependency of the Vida tool, as well as enhance its accumulating library of species files.

CHAPTER II

LITERATURE REVIEW

Literature Involved in Vida's Basics

Vida is a simulator tool written in Python. The program uses a spatially explicit reiterative algorithm to create projections of plant community interactions. Through means of physical principles and empirically derived relationships, Vida tests alternative hypotheses about individual functional traits governing ecological and evolutionary processes at the community level of complexity. In the Vida world, as a result of competition for light and space, growth features are based on an individual-level and scale up to produce emergent properties such as self-thinning, size-dependent mortality, realistic size-frequency distributions, and a broad spectrum of empirically observed relationships for the species examined.¹⁹ Vida also predicts the age at which reproductive maturity is achieved.¹⁹ The model operates under a null hypothesis that predictable scaling relationships at the species-ensemble level can emerge from outcomes associated with competition for space and light in a forest system. Vida ultimately demonstrates that biologically complex phenomena are predictable, scalable, measurable, and demonstratable. These foundational, widely observed scaling relationships at the species-ensemble level govern the emergent properties that develop from competition for space and light between species.¹⁹

This simulator tool embodies the original model developed by Leonardo da Vinci called the “pipe model” which consists of iterative branching systems and regular fractional division.¹⁹ Pipe models consist of a chain of processes that produce a skeletal-like system. The output of each element is related to the next. Pipe models also consists of specific mathematical concepts, like that the sum of the cross-sectional area of all tree branches above a branching point at any height is equal to the cross-sectional area of the trunk or the branch immediately below the branching point.¹⁹ Vida is a pipe model in the way it assembles trees, not just because trees have regularly dividing components, but also because Vida

models the way carbon is distributed throughout the tree during its life cycle. In response to this approach, the growth variables in Vida are parameterized together- instead of separately. For example, the mass of the canopy (M_L) and the structures that allow it to grow are governed by the following relationships:

$$M_S \propto M_T \quad (\text{EQ: 2})$$

$$M_L \propto M_S \quad (\text{EQ: 3})$$

$$D_S \propto M_S \quad (\text{EQ:4})$$

$$H_S \propto D_S \quad (\text{EQ: 5})$$

M_S is the mass of the stem (or woody mass), M_T is total mass (leaves and wood), M_L is mass of the canopy (leaves), D_S is diameter of stem (trunk width), H_S is height of stem (tree height), and α is the species-specific slope.¹⁹ Significantly correlated variables are parameterized together to represent the appropriate flow of carbon throughout the tree. Scientists can use these relationships to estimate certain variables. The various formulae below represent some of the significant relationships found within an individual plant:

$$M_S = \beta_1 M_T^{\alpha_1} \quad (\text{EQ: 6})$$

$$M_L = \beta_2 M_S^{\alpha_2} \quad (\text{EQ: 7})$$

$$H_S = \beta_3 D_S^{\alpha_3} \quad (\text{EQ: 8})$$

where β and α are species-specific constants. β and α are constants, and we can refer to M_S , M_L , and H_S as Y variables and D_S as an X variable. These formulae are not complicated to assemble, but reliable data to accurately parameterize the species is key. Vida utilizes these species specific formulae to run a forest ensemble simulation, where each species has a set of formulas representing their physical growth relationships. The core of Vida's growth calculations encompass less than ten individual variables: G_T is total growth, A_L is the projected area of a canopy, M_L is the mass of a canopy, M_S is the mass of the above-ground woody components, D_S is the diameter of the trunk at ground level, H_S is the height of the tree, and i which is the given number of iterations.

All beta values (β) are species-specific whereas alpha values (α) are within a certain range for all plants. It is important to note that not all parts of a tree grow indefinitely. When a plant is young, its growth is more linear. When a plant has passed sexual maturity, its growth becomes natural logarithmic, leveling off after the incredible, constant increase seen in the juvenile stage. Vida's formulas consider these life transitions and changes in maturity. The relationship between diameter and height accurately portrays the use of linear and then natural logarithmic formulas to accurately represent the change in growth among maturing species:

$$H_S = \beta_7 D_S^{\alpha_7} - \beta_8 \quad (\text{EQ: 9})$$

and

$$H_S = \beta_9 + \beta_{10} \ln D_S \quad (\text{EQ: 10})$$

It is not hard to see the differences between the way we formulaically express juvenile growth (top linear equation) and mature growth (bottom log function equation). The most noticeable difference is the natural log function in the mature formula. The species-specific constant (β) and exponent (α) are calculated using the Vida tool, known as the "alpha beta calculator.csv" found in the Vida-master folder.

The alpha beta calculator automatically calculates the constant (β) and exponent (α) values based on the growth data that is used as the input for the X and Y sections. Growth data in both these sections should correspond in time and significance. The constant (β) and exponent (α) values reflect the relationships between these growth values over time. The growth relationships are also modeled based on a correlative relationship and are proven to have highly significant r^2 values before corresponding together in a formula, i.e. (Growth of Leafy Mass G_L and Growth of Woody Mass G_S vs. age; regression of predicted vs. observed values gave $r^2 = 0.927$ and 0.989 , respectively), age- and size-dependent changes in their respective mass (Mass of Leafy Mass M_L and Mass of Woody Mass M_S vs. age; regression of predicted vs. observed values gave $r^2 = 0.988$ and 0.978 , respectively), and changes in stem diameter and height (D and H vs. age; regression of predicted against observed values gave $r^2 = 0.945$ and 0.998 , respectively).¹⁹

Proof of Principle

Any program attempting to accurately model the growth of individual plants must successfully mimic the detailed behavior of real populations and communities. This was done by Dr. Sean T Hammond and Dr. Karl J. Niklas in 2009 using this model.¹⁸ Hammond and Niklas analyzed the extent to which Vida, at that time called SERA, could successfully emulate the growth and allometric behavior of a community with generalized angiosperm and conifer species. Vida uses the following parameters: N (number of trees per hectare), Height (meters), Diameter (meters), M_L (Mass of leafy biomass in kilograms), M_S (Mass of woody biomass in kilograms), G_L (Annual canopy growth in one year, kilograms/yr), G_S (Annual growth of woody mass in one year, kilograms/yr), and nM_D (“banked” biomass for reproduction in one or more future growth cycles, in kilograms).¹⁸ The most useful data set for Silver Fir (with an initial density of 25,000 plants/ha), included documentation every 5 years for 95 years, starting 10 years after the initial planting. Since most data for the Silver Fir population was recorded at 5-year intervals starting at 10 years after the initial planting of the population, statistical comparisons between observed and predicted trends were limited to these discrete time intervals.¹⁸ Based

on the performance of these computer runs, the compendium was used to statistically characterize 332 angiosperm and 343 conifer dominated communities to emulate the dynamics of “generalized” angiosperm and “generalized” conifer populations.¹⁸

The extent to which Vida was successful at emulating the behavior of the Silver Fir population in the midst of a “generalized” angiosperm – conifer forest ensemble was evaluated. A confidence interval of 95% was used. The comparisons between the observed and predicted scaling exponents can be seen in Table 3.

Table 3: Comparisons between observed and predicted scaling exponents (95% confidence) of Silver Fir, generalized conifer, and generalized angiosperm.¹⁸

Silver Fir		Generalized conifer		Generalized angiosperm	
Observed	Predicted	Observed	Predicted	Observed	Predicted
0.67 (0.65,0.68)	0.66 (0.65, 0.67)	0.80 (0.75, 0.86)	0.80 (0.78, 0.82)	0.76 (0.72, 0.81)	0.75 (0.73, 0.77)
1.18 (1.10,1.27)	1.18 (1.08, 1.28)	2.04 (1.98, 2.11)	2.05 (2.04, 2.06)	2.04 (1.93, 2.15)	2.02 (2.00, 2.04)
0.72 (0.85, 0.87)	0.64 (0.19, 1.09)	1.95 (1.87, 1.96)	1.95 (1.93, 1.97)	1.79 (1.75, 1.80)	1.80 (1.79, 1.81)
0.60 (0.58, 0.61)	0.57 (0.56, 0.58)	1.00 (0.98, 1.03)	1.00 (0.99, 1.01)	1.15 (1.07, 1.23)	1.15 (1.13, 1.18)
0.99 (0.93, 1.05)	0.95 (0.94, 0.96)	0.78 (0.74, 0.81)	0.78 (0.77, 0.79)	0.73 (0.71, 0.74)	0.74 (0.73, 0.76)
1.91 (1.89, 1.94)	2.03 (1.86, 2.21)	1.93 (1.85, 2.02)	1.98 (1.96, 2.00)	1.86 (1.72, 2.00)	1.98 (1.96, 2.00)
2.54 (2.53, 2.55)	2.54 (2.53, 2.55)	2.48 (2.39, 2.56)	2.44 (2.42, 2.47)	2.63 (2.55, 2.70)	2.66 (2.62, 2.67)
2.98 (2.90, 3.06)	2.84 (2.81, 2.88)	2.59 (2.47, 2.71)	2.60 (2.59, 2.61)	3.12 (2.88, 3.35)	3.10 (3.08, 3.13)
0.85 (0.83, 0.88)	0.89 (0.79, 0.99)	0.93 (0.88, 0.97)	0.94 (0.93, 0.97)	0.83 (0.75, 0.91)	0.86 (0.80, 0.87)

In this 2009 publication, Vida was able to accurately predict the age of maturation for several species of which data for computations was available. The observed age of maturation in the wild was compared to the age that Vida predicted the species’ age of maturation would be. A recognition in the growth transition from linear to natural logarithmic triggers Vida to identify this stage as when the species switches from the juvenile stage to the mature stage- and thus, when it becomes sexually mature. The comparisons show that Vida produced reliable results when it came to predicting the age at which a tree species will become mature enough to produce seeds. This is a reliable ability that allows a user to parameterize life-like tree species. In the 2009 publication, Vida predicted the reproductive maturity age

for eight species. This is impressive, considering there can be a major difference in growth after the species becomes sexually mature. Those comparisons in the observed age of maturation and the Vida-predicted age of maturation can be seen in Table 4.

Table 4: Predicted and observed age of reproductive maturity for eight species.¹⁸ The number of individuals available to plot height vs. stem diameter is indicated by n.

Species (number)	Predicted age (yr)	Observed age (yr)
Silver Fir (18)	~24	(25-35)
Silver Birch (9)	~32	15
Japanese Cedar (12)	~10	(15-20)
Rubber Tree (7)	~2	(5-6)
Monterey pine (8)	~5	(5-10)
Scots Pine (12)	~9	(10-15)
Sal Tree (12)	~7	15
Teak (6)	~8	(8-10)

Based on tests comparing predicted and observed Silver Fir data using 95% confidence intervals of scaling exponents, y -intercepts, and regression analyses of predicted vs. observed data points, Vida successfully reproduced all observed age and size dependent trends reported for the real Silver Fir population and for the generalized angiosperm and conifer species based on three or more computer runs parameterized in the same way.¹⁸ It is important to note that, despite eight different ways plants can die in Vida simulations, the most prevalent cause of death in each computer run was light deprivation.¹⁸ In this experiment, light deprivation accounted for 85% of all deaths, while 11% of all deaths resulted from seeds that were randomly dispersed outside the world space; the remaining 4% of all deaths were the result of random and age-dependent deaths.¹⁸

This success demonstrates Vida's reliability to predict realistic outcomes of forest ensembles. Using Vida to investigate Beanfield Mountain as a potential site for BC3F3 American- Chinese Chestnut tree reintroduction is solidified by the success of Hammond and Niklas 2009 study. Vida's reliability is

further amplified from this project, with the successful parameterization of all significant species in the Beanfield Mountain ensemble.

Scaling Relationships Seen in Nature

All land plants share a key set of morphological and physiological attributes as a result of evolving from a common ancestor.²⁰ The growth and development of an individual plant and the changes that occur within a plant population or community (also known as a species ensemble) are influenced by similar ecological factors. These factors include light availability and habitat stability, as well as basic spatial and temporal influences. Several literature sources were utilized and reviewed in defining the biological allometry Vida is based on. Reviewing those sources is crucial in understanding how Vida works.

One of the most widely cited, published theories to explain the origin of many of these scaling relationships is that of West, Brown, and Enquist- referred to as the WBE theory.²¹ This theory focuses on the belief that the Earth is an individual organism made up of fractal-like transport and delivery systems, which has evolved to optimize the time and energy needed to distribute materials throughout the planet.²² Even for global change research, the WBE theory can be used to determine the parameters of variables that cannot be measured directly, like estimating belowground carbon storage based on the scaling relationship between plant roots and aboveground mass. The fact that the WBE theory has successfully predicted aspects of community dynamics proves that it is foundational. West, Brown, and Enquist also outline that hierarchical population and community interactions may be the direct consequence of the properties of the individual.²¹ Many of the scaling relationships predicted by Vida emerge from the WBE theory. The WBE Theory describes that the dependence of a biological variable Y on body mass M is typically characterized by an allometric scaling law: $Y = Y_0 M^b$, where b is a scaling exponent and Y_0 is a constant that is species-specific. An older version of the formula was written by Huxley in 1932: $Y = \beta X^\alpha$, where β is species-specific and α is the slope of the line.¹⁸ The two formulae are ultimately

indistinguishable. For juvenile growth that changes linearly with age (diameter), Vida uses the linear formula to predict the amount of growth between significant parameters: $Y = \beta X^\alpha$. For parameters that change very quickly but level off after sexual maturity is reached (Height x DBH), a natural logarithmic function more accurately models what we observe in nature. Vida and other mathematical/theoretic explanations for real-world scaling relationships, such as the WBE theory, have conceptual common ground.¹⁹ They both deal with the formulaic consequences of packaging objects in real space.¹⁹

Huxley observed the abrupt change of mass relative to the rest of the body in relation to the onset of sexual maturity in male Fiddler crabs.²³ This research is outlined in his 1932 publication entitled *Problems of Relative Growth*.²³ Huxley illustrated how the mass of the male's large claw (or chela) in relation to the total body mass was closely approximated by the formula: $Y = \beta X^\alpha$. Huxley's generalization has allowed for the establishment of modern biometric assumptions. A variety of empirical-field and theoretical modeling approaches have been used to resolve whether scaling relationships are reliable predictor variables in the face of well documented, species-specific response to different environmental conditions. A similar change is observed in the canopy mass (M_L) relative to above-ground woody mass (M_S) for individual species, and in the relationship between stem diameter (D_S) and tree height (H_S).

Numerous techniques exist which do use forest inventories to predict standing biomass.¹⁹ These statistical techniques fail to capture fine details about community structure and cannot predict random disturbances, such as fire and logging. Along with the forest inventories, statistical techniques by themselves are often biased toward the largest individuals and fail to give clear insights into the locations, spacing, and physical characteristics of the smallest individuals.¹⁹ The predictive accuracy of models, like Vida, which cover spatial and temporal scales are extremely important to ecologists that study changes in population structure. Not only this, but Vida gives us insight into the possibilities of multiple universes. Since each Vida simulation is independent from the last, each simulation run can be seen as the outcomes of this certain timeline, or universe. When another, separate simulation is run, a user can consider this new simulation a totally separate universe that's programmed with the same parameters. Running several

simulations and examining each run is essential in determining the overall story Vida is trying to tell with the parameters one has selected.

Ecological Factors

Vida has the ability to recognize several “world parameters” which designate the numerical value for the variables that correspond to the planet itself. The world preference variables that are modeled into Vida’s simulations include gravity, surface area, canopy transmittance, atmosphere, light intensity, random death, Janzen-Connell mortality, and max seeds per plant. Vida includes an ecological value called the Janzen-Connell value that reflects the amount of distance a seed is dropped from its mother plant. The Janzen-Connell hypothesis states that areas closest to a parent/seed produce areas that are inhospitable for the survival of seedlings. This is because the seedlings compete with the mother tree for resources, surface area, sunlight, etc. just as any other individual in the forest would. The Jansen value can be any value between 0.0 and infinity. Another consideration is that approximately 20% of full sunlight passing through a single tree’s canopy actually reaches the ground.¹ Therefore, Vida assumes a 20% transmission rate for simulated tree canopies. If a tree receives less than 20% of E (light energy) in a simulation, it dies due to lack of light.¹ Calculations on how shaded a given plant might be are complicated; they are mostly based on whether the understory is partly or wholly shaded by one or more overtopping canopies.¹⁹

When physically isolated from one another, individual plants establish allometric trends that differ dramatically from those observed at the level of a maturing population or community.¹⁸ This is because ecological phenomena are significant players in the development of an eclectic ecosystem. As plants increase in size, interactions among neighboring plants increase in regularity and intensity because of shading from overlapping canopies.¹⁸ As these interactions intensify from growing canopies, they reach a critical point, where dynamic properties (such as self-thinning and extensive mortality due to light deprivation) emerge out of necessity for limited resources.¹⁸ Vida delineates the amount of sun reaching

the understory in this way, designating the amount of light distribution among the canopy regularly. Each species allows a certain fraction of light to pass through its canopy (default for each species is 2%).¹⁹ Tree mortality due to insufficient light can be caused when overtopping plants shade an individual too much. If the shaded plant does not have at least 20% or more of their projected canopy area exposed to full light, it will die.¹⁹ This is a major consideration in calculating G_T . Therefore, Vida is respectful of both parent-offspring competition and leaf ecology when it comes to ecological considerations.

Vida has the capability to include large death events, such as random fires, to represent the influence of natural disasters. The user can write event files in a basic script editor using the basic outline provided in the Vida-master folder. If the user knows the frequency of these events, the event file can include as many death incidents as someone can code for. If the user wants to code for totally random death events, this is achievable as well. The inclusion of event file capabilities increases the functionality of Vida to consider dynamic large-scale disturbances to a higher degree than other standard models.

Each species file contains a species-specific seed mortality rate, which reflects the combined observations that create the rate of seedling failure in nature. It is difficult to measure exactly why/how individuals die in natural, uncontrolled habitats— and then combine all these many ways into one generalized decimal.²⁴ In order to reflect this observation in our simulated ensemble, Vida uses a unique, specified, changeable random death value that kills off a certain number of plants or seeds each simulation cycle. This value is generally species and regionally specific. The default value for this random death quotient denotes that every plant at each iteration has a 0.75% chance of dying during each iteration of a simulation, but this number can be changed to reflect any literature value the user uncovers for that species.¹⁹ This value acts as a natural representation of the many ways a tree species can randomly die in nature. When working with simulators, it's important to note that not every little variable can be accounted for. That's why many reliable simulators are “round cow” models, where variables are grouped together and generalized for the sake of simplicity. Alternatively, one can build a “kitchen sink” model where comparatively many more variables are included in order to zone-in on all possible mechanisms on a more micro scale. Vida works as a “round cow” model in many respects, and especially because of

variables like the random death quotient, where several variables are grouped together. Doing this allows a user to diagnose an issue or needed change within the software more easily. Also, there is less room for human error and design with fewer variables.

How Vida is Different, and Familiar

Vida is similar to other computer models especially those of Chave²⁵ and Niklas^{26,27}. A major similarity is that each plant is intentionally simplified to consist of a single photosynthetic surface (canopy) elevated by a single stem. However, Vida differs from previously published models in at least three important ways. First, in contrast to the Niklas^{26,27} models from 2000 and 2001, Vida requires fewer input variables among which only six scaling exponents are required to initialize a computer run. Therefore, Vida's Python-based model is a modern version of the more basic techniques, which is a major contributor to its "round-cow" model identity. Secondly, Vida is an individual-based algorithm, which makes it unique, because species identification files define the properties of individual plants belonging to that species. The resulting mathematical transparency allows a user to more quickly identify whether an output is the direct result of using specific numerical values to characterize individual plants or a consequence of inter-species interactions. Third, the Chave²⁵ and Enquist & Niklas²⁷ models represent the tree canopy as a flat disc, while Vida treats each canopy as a hemisphere of uniform thickness. This difference is very important, because a canopy described as a flat disk will cast a significantly larger projected area than a hemispherical canopy with an equivalent mass and thickness. A flat disk canopy model over-estimates the ability of a simulated plant to capture light and shade its neighbors. It also over-estimates the space that must be occupied to capture a fixed quantity of light. While contributing to more realistic measures of a plant's ability to harvest light and to shade individuals below its canopy, hemispherical canopies can also be easily modified in future versions of Vida to describe spheroid canopy geometries, or even cones.¹⁹

As in the Chave²⁵ and Niklas^{26,27} models, the angle of solar incidence is time-averaged to be 0° (i.e., light comes from directly above each plant) such that the photosynthetic area available for each plant is the projected area of the canopy. This stipulation can be relaxed to cope with daily changes in the solar angle or differences in latitude. However, one of our objectives was to simplify the real world by reducing the number of variables that can influence the outcome of our computer runs. By eliminating latitudinal and diurnal differences in the solar angle, the results of simulations can be assumed to be due to plant-plant interactions, not due to variations in ecologically important variables (such as total solar energy). An intriguing emergent property of Vida is its ability to predict the age at which reproductive maturity is achieved based on the species' shift from linear to natural logarithmic growth. This shift into sexual maturity has a domino affect. A significant change in canopy growth with respect to stem growth in turn affects the ability of a plant to harvest sunlight. This in turn alters total growth and thus the amount of biomass that can be used to construct seeds. This shift in plant height vs. stem diameter emulated by Vida has been predicted and empirically demonstrated using a zero-order biophysical theory, as used in Niklas and Spatz's 2006 approach.²⁸ In Vida, this biophysical theory is a direct consequence of empirically determined input variables based exclusively on how plant height scales with respect to stem diameter among real plants. It is noteworthy that the ability to predict when a species reaches reproductive age based on vegetative growth is consistent with prior allometric theory as well as empirical observation- as mentioned by Niklas and Enquist in 2003.²⁹

CHAPTER III

METHODS

Why Beanfield Mountain, Virginia

It is important to explain why a Virginia location was selected for reintroduction rather than a southern state that would experience less snowfall/ hazardous conditions than generally warmer areas. The original range of the American Chestnut is along the east and southeastern parts of the United States, giving us many options for our location selection. There is a soil-borne water mold that favors these warm, moist environments-- and is a particular problem in southern parts of the United States. This water mold, *Phytophthora cinnamomi*, represents a large threat to restoration of the BC3F3 American-Chinese Chestnut in the areas with climate and soil conditions favorable to the disease. These areas include a large portion of the American Chestnut tree's natural range. In addition to this, climate change has altered the temperatures in certain areas. Also, active breeding of BC3F3 American-Chinese Chestnuts is occurring in Virginia, and it is within the native range of the American Chestnut. There is also a large amount of growth and site data recorded over time for Virginia forests.

In 2007, Dr. Fei Schibig published an article listing four important factors that were shown to significantly affect American Chestnut success in Mammoth Cave National Park, Kentucky.³⁰ We also considered her findings when choosing our location. The most significant factors that she thought should be considered are:

1. Moderate location elevation, compared to surrounding elevation of around 232 meters above sea level for this area
2. Slope of land should be between 25-40°

3. The species should not be grown with 40 meters of limestone (Euclidian distance-soil acidity effects)
4. If the land was previously heavily influenced by agriculture, species will not grow

We kept Fei's conditions in mind, however these suggestions were not our most crucial location consideration factors. We were able to locate The Forest Inventory and Analysis Database for Virginia, known as FIADB, with all the data needed in order to parameterize a forest within the American Chestnut's natural range in Virginia. The FIADB database was collected from Giles County, Virginia. The location we chose for reintroduction is Beanfield Mountain, Virginia which is situated at the head of a deep horseshoe-shaped valley that extends northeast from the community of Pembroke in Giles County, Virginia. This Virginia site ranges from very steep ($>60\%$) at upper slope positions to moderately steep ($10\text{-}20\%$) at lower slope positions. Only sandstone, instead of limestone, is found there. Individual quadrats were located every 50 feet (15.2 m) along an elevation gradient that extended 1052 to 1189 meters, a little high for our species, but several lower elevation gradients were also included (<950 m). As part of the Daniel Boone National Forest, this mountain location in Southwestern Virginia was not heavily influenced by agriculture. In addition to meeting Fei's suggestions, this FIADB source oversatisfied the amount of data we needed, with extensive background detail about the locations and methods used. Beanfield Mountain, Virginia was officially our selected location. Places like Beanfield Mountain, that have a wealth of published data and local knowledge, are particularly ideal for studies involving parameterization of an environment. In order to correctly parameterize each of the ten species for Beanfield Mountain, the FIADB database was used for growth data in Giles county, Virginia. There was more than enough data to parameterize all the species featured in the Stephenson and Fortney data. However, there were times when certain species lacked a significant amount of data in Giles county alone, so we had to use more data from trees in additional Virginia locations to parameterize them. However, the data always came from the FIADB dataset, and for most species, Giles county supplied

sufficient data. The study site consisted of 56-88 individual 100-101 m² sized plots for each of the study years.² Several analyses of a single 100 m² sized plot were run to represent a scaled down ratio of the whole study site.

Analytical Process and Data Collection

Data collection for this project was thorough and precise. Multiple aspects of each species were investigated through various reputable sources to confirm reliability. Aspects such as wood density, maximum height, and Young's modulus are all critical components that each species file has the capability of reproducing. Young's modulus is a mechanical property that measures the stiffness of a material. It defines the relationship between stress and strain of something in terms of linear elasticity. Each species of tree has a particular Young's modulus which reflects its elasticity, or flexibility, of its stems. It is important for a tree to be flexible enough to withstand breaking among high winds, but also not too flexible as to compromise its natural shape, strength, and structure. Wood density is another significant factor. Tree mortality rates are associated with low wood density. Some scientists consider wood density to be the single most important wood property, because of its strong relationship to both yield and quality- as well as its large variance, which is highly species specific. If a tree invests much of its energy into wood density, there is less energy to invest into other parts of the tree- such as the leaves. Leaf properties that aid the tree in shade tolerance, such as increased size to improve respiration rate, take a lot of energy to form and maintain. There is a trade-off between growth rate and risk of damage or death in many ways, including deep shade tolerance- which is negatively correlated with wood density.

Using the FIADB data, the Stephenson and Fortney data⁹, the Vida "alpha-beta calculator" tool to calculate the alpha and beta growth values, the Vida "csv to yml" tool to assemble the species files, and the Vida "miniVida with Graphs" tool to make sure our species files did not violate any physical laws- we were able to successfully parameterize the 10 species observed in the Beanfield Mountain, Virginia site.

Table 5 shows all of the species parameterization variable values for each species that was parameterized for the Beanfield Mountain site.

Table 5: Species parameterization table with researched and calculated variable values.

Common name	Chestnut Oak	White Oak	Northern Red Oak	American Basswood	Pignut Hickory	Red Maple	American Ash	American Chestnut	Sweet Birch	Black Cherry
Germination (% seedling mortality)	10	15	8	70	37.5	13	46	35	80	50
Mass of a single seed (kg)	0.05	0.0275	0.0073	0.000031	0.0061189	0.000017514	0.0000026	0.00265	0.0071	0.00009
Mortality (% death annually)	0.38	0.693	0.92	0.895	0.4	1.06	0.46	43	1.1	1.8
Wood Density (kg/m3)	750	865	700	415	835	610	675	480	735	560
Young's Modulus (GPa)	11	12.15	12.14	10.07	15.59	11.31	12	8.48	14.97	10.3
Max Height (m)	30.4	31.3	30	30.6	31.5	24.5	32	33	32.4	30.4
Observed Age of Maturity (yrs)	20	20	25	15	30	5	20	8	15	10
photoConstant (β_9)	1.35	1.15	1.3	1.5056	0.77	1.5056	0.76	1.28	1.5056	1.5056
photoExponent (a_6)	-0.448	-0.448	-0.4602	-0.448	-0.4602	-0.448	-0.4602	-0.4602	-0.4602	-0.4602
speciesConstant1 (β_1)	0.72	0.78	0.82	0.58	0.605	0.698	0.81	0.78	0.95	0.66
speciesExponent1 (a_1)	0.9985	1.004	0.988	1.023	1.05	1.002	1.037	0.921	1.003	1.036
speciesConstant2 (β_2)	0.116	0.1	0.1	0.1164	0.1164	0.1164	0.1164	0.2	0.1164	0.1164
speciesExponent2 (a_2)	0.8819	0.8819	0.8819	0.8819	0.8819	0.8819	0.8819	0.8819	0.8819	0.8819
speciesConstant3 (β_3)	0.15	0.13	0.15	0.15	0.15	0.15	0.15	0.25	0.15	0.14
speciesExponent3 (a_3)	0.7719	0.7719	0.7719	0.7719	1.7719	0.7719	0.7719	0.7719	0.7719	0.7719
speciesConstant4 (β_4)	0.026	0.025	0.02484	0.0325	0.0278	0.0253	0.0279	0.0301	0.0218	0.0324
speciesExponent4 (a_4)	0.411	0.409	0.416	0.394	0.39	0.422	0.388	0.444	0.421	0.389
speciesConstant7 (β_5)	71.02	95.58	48.73	61.47	73.72	88.21	77.22	128.298	68.58	87.65
speciesExponent7 (a_5)	0.819	0.901	0.668	0.753	0.796	0.838	0.804	0.972	0.728	0.91
speciesConstant8 (β_8)	8.51	8.51	8.5	8.4	8.5	5.4	8.5	8.7	8.5	8.2

The species-specific constant (β) and exponent (α) are calculated using the “alpha beta calculator.csv” Vida tool, which is featured in the Vida master folder. The alpha beta calculator

automatically calculates the constant (β) and exponent (α) values based on the growth data that is used as the input for the X and Y sections. The constant (β) and exponent (α) values reflect the relationships between growth values over time.

In addition to using the previously mentioned Stephenson and Fortney article⁹ which was used to provide a generous view of the Beanfield Mountain ensemble, overstory data from Stephenson and Adams³¹ was also used. This separate project team, also led by Stephenson, conducted a matching importance analysis on Peters Mountain, which focused on just the overstory portions of a large number of areas found within the original site. This data was combined to provide an overall, data-driven view of the Beanfield Mountain forest ensemble. Stephenson and Adams' calculations were extrapolated into importance values per hectare, which matches the 100 m² sampling method from the previous Stephenson and Fortney approach.⁹ Using the overstory data to enhance our current growth data, the potential for reliably parameterizing the Beanfield Mountain site seemed imminent. Table 6 shows the understory section that was used to enhance the existing data, as well as some additional data Stephenson and Adams collected from those same sites.

Table 6: Importance values for each species in Peters Mountain, Virginia.³¹ The "Overstory" section was used to enhance the existing 1969 time period.

Species	Overstory	Understory	Saplings	Seedlings
Chestnut Oak	28.1	16.4	7.7	15
Red Oak	17.3	8.6	5.5	10.3
White Oak	13.3	7.1	2.3	5.6
Scarlet Oak	10.1	1.4	2.6	1.4
Red Maple	7	22.2	11.5	11.2
Black Oak	5.4	3.5	1.6	1.2
Pitch Pine	5.3	1.3	0.7	0.9
Pignut Hickory	3.2	5.7	3.2	3.9
Sourwood	2.9	7.3	6.6	1.8
Sour Gum	2.9	9.2	12.3	7.8
Sassafras	0.6	3.1	19	24.5
American Chestnut	0.1	3.1	11.2	4.1
Others*	3.8	11.1	15.8	12.3

“Others” are other species, which include: Whiteheart Hickory, Shagbark Hickory, Black Locust, Sweet Birch, Table Mountain Pine, Cucumber tree, Dogwood, Bitternut Hickory, Downy Serviceberry, Witch Hazel, Sycamore, and Eastern Red Cedar.³¹ Although additional species are listed in Table 6, the data still provides information on the species we’ve already researched for the area. This additional information gives us a more thorough outlook on the ensemble during a large period of time neglected in the previous data, featured in the Stephenson and Fortney article.⁹ Although data for 1969 wasn’t crucial, it filled a large gap in the timeline. Using the importance values featured in both these articles, we assimilated a range of importance values over an extensive period of time. Now, there was information for 1920, 1939, 1969, and 1993. For forecasting purposes, Vida was selected to run for 381 years (or cycles) to account for appropriate growth of pre-existing old growth trees. After the two datasets were gathered and confirmed for use, a table featuring all the combined information was assembled. This combined information is the guide that was used for the forest ensemble creation of the Beanfield Mountain based on the population dynamics of the timeline that was provided. This combined information can be seen in Table 7.

Table 7: Combined literature values of species importance values by year (1920-1993).^{9,31}

Species	1920	1939	1969	1993
American Chestnut	27.2	0	0	0
Chestnut Oak	21.3	26.8	28.1	24.5
White Oak	20	27.8	13.3	5
American Basswood	3.7	5.5	n/a	1.1
Red Oak	14.7	21.1	17.3	25.8
Pignut Hickory	7.9	11.5	3.2	6.1
Red Maple	0	0	7	21.5
Sweet Birch	0	0	3.8	9
White Ash	1.8	2.7	n/a	0
Black Cherry	3.4	4.6	n/a	7
American Chestnut	27.2	0	0	0
Chestnut Oak	21.3	26.8	28.1	24.5
White Oak	20	27.8	13.3	5

With this combined information from Table 7, the hindcasting simulation was ready to be run. Hindcasting simulations are significant because they prove, or disprove, whether a simulator produces reliable results. Being able to replicate real-world observations, proves that the simulator can be used to forecast outcomes for future events. If the hindcasting simulation results reflect real-life observations, then the forecasting abilities of the simulator are reliable. A hindcasting simulation was run with all the parameterized species featured in Table 7 for 255 years (or cycles). The results will be compared to real-world values to confirm reliability. Hindcasting simulations were run for 255 cycles to account for appropriate growth of pre-existing old growth trees.

Simulations were run with a world size of 150 m², and then after the simulation gives the raw data outputs, the inner 100 m² was selected for analysis. There are two main reasons for this action. This apparently unessential step is important- it diminishes edge effects, which can be seen in modeled simulations and nature. As edge effects increase, the boundary area allows for greater than expected biodiversity, which arises out of competition- but also because the edges act as corridors, which is an area that connects two potentially different habitats. Also, since the literature values featured in our sources included measurements that were taken in almost perfectly sized 1-hectare sized plots (100 m x 100 m = 10,000 m²), we replicated that same sample area. analysis.

Ensemble Creation

After initial analyses were run, it was apparent that the foraging habits of animals greatly influenced the growth dynamics of the system. Some modification was required, in the form of an event.yml file, to achieve valid replication results for the ensemble. Some species-specific values representing the annual fraction of seeds that fail to germinate were adjusted beginning at the year the American Chestnut succumbed to blight and died out (100% by 1938, or cycle 200). As previously mentioned, the death of a keystone species drastically affects the ensemble. Round cow models like Vida cannot forecast specific, compounding environmental micro-influences like shifts in feeding habits. In

order to aid Vida in accurately representing the forest ensemble, the user should consider the species-specific influences a computer cannot predict, and group them together in a common way. Increasing the number of seeds that die annually for each species groups together the common term of death. Changing the fraction of seeds that fail to germinate is a species-specific procedure, because there is a varying level of ecological response for each species. In the event file for the Beanfield Mountain ensemble simulations, feeding habits are the main special ecological response consideration. The fraction of seeds that fail to germinate annually were manipulated for some species the same year the American Chestnut tree completely succumbed to the blight fungus and was eliminated from the landscape at year 1938 (cycle 200). This was used to represent the shift in the animals' food choices. This approach also gives us some insight as to exactly how much the external pressure compromised the influenced species' success. This approach has the potential to allow one to question whether making these adjustments compromises Vida's reliability.

There is some debate as to whether this specific technique compromises Vida's ability to accurately display an ensemble's true nature on its own. If anything, I believe that these adjustable mechanisms highlight Vida's impressive functionality and allow us to recreate an ensemble's true nature. Using simulators to "round out" real-life observations is tricky business, because you can't possibly create a variable for every factor that exists. There are many considerations that go mathematically unincorporated in simulator programs simply because you can't consider everything in a computer model compared to real life. The approach in modeling these changes in feeding habits was to create an event.yml file, where the amount of seeds that would fail to germinate would increase. This is a "round cow" approach to modeling the dynamic changes we see in true biological systems. At the appropriate intervals, the fraction of seeds that failed to germinate was adjusted to account for the fraction of seeds that were increasingly non-successful due to being eaten by animals. Figure 5 shows the event file that was written in order to reproduce the growth patterns that were seen when considering the shift in feasting habits of the wildlife in the Beanfield Mountain area.

```

200:
- Killzone:
- x: 0.0
  y: 0.0
  shape: square
  size: 150
  target: all
  species: C_dentata
- Species:
- name: Q_alba
  fractionFailGerminate: 0.91
  randomSlowGrowth: 0.4
- Seed:
- species: arubrum_sth2.yml
  placement: random
  number: 250
- Seed:
- species: blenta_sth1.yml
  placement: random
  number: 40
201:
- Species:
- name: Q_prinus
  fractionFailGerminate: 0.7
  randomSlowGrowth: 0.0
281:
- Species:
- name: A_rubrum
  fractionFailGerminate: 0.7
  randomSlowGrowth: 0.0
289:
- Species:
- name: Q_alba
  fractionFailGerminate: 0.2
  randomSlowGrowth: 0.0

```

Figure 5: Event File for Beanfield Mountain Parameterization. "C_dentata" is American Chestnut. "Q_alba" is White Oak.

"A_rubrum" is Red Maple. "Q_prinus" is Chestnut Oak.

Our first representation of this transition in foraging habits beings in year 1939 (cycle 201) which is the year after the American Chestnut is entirely removed from the landscape. By this time, the blight fungus had drastically impacted the American Chestnut population, and the transition in feeding habits would be well underway. The fraction of seeds annually failing to germinate for Chestnut Oak needed to be increased from the initial value of 0.1 to 0.7 in order to accurately represent literature values for 1993. This means that from 1738 to 1939, there was a 0.6 ($0.7 - 0.1 = 0.6$) or 60% increase in the natural death of Chestnut Oak. Although we cannot directly correlate that this amount of change was completely caused by shifting feeding patterns of local wildlife, it allows us to group collective influences in order to accurately represent the ensemble. In the event file (featured in *Figure 5*) there are other species modified

the same way. Two Oak species and Red Maple were the only individuals modified in this way. Using Vida, the event file shown previously, and the 10 species files, the simulated Beanfield Mountain ensemble came into existence. The simulation was run for 255 cycles (or years). Five individual simulations were run, and the average number of individuals was taken from each of the analyzed year's results. Table 8 shows the averaged results of the hindcasting simulations of Beanfield Mountain, VA.

Table 8: Importance values of simulated Beanfield Mountain site, averaged over 5 individual simulations categorized by year (1920-1993).

Species	1920	1939	1969	1993
American Chestnut	34.62	0	0	0
Chestnut Oak	21.7	33.88	29.82	26.66
White Oak	13.38	20.84	14.18	9.1
American Basswood	2.97	4.11	2.998	2.1
Red Oak	15.58	24.52	26.82	28.98
Pignut Hickory	5.27	8.64	8.998	7.12
Red Maple	0	0	10.77	20.74
Sweet Birch	0	0	0.66	0.87
White Ash	2.7	3.41	2.6	2.11
Black Cherry	3.71	4.598	3.17	2.31

Taking the average of 5 simulations mitigates the variance we see among individual Vida simulations. When we compare our 1920-1993 results to the literature values, we see that Vida accurately represented many species for each time period. Sweet Birch is a smaller tree with a high mortality rate. Only 10-20% of the species' seeds grow successfully, meaning that only one or two seeds germinate annually per adult in the growing season- sometimes less.³² It was difficult to increase the importance of such a generally small, unsuccessful species, and therefore its importance values stayed low each year. Also, Sweet Birch saplings grow at about the same rate as Black cherry.³² This means Sweet Birch is in direct competition with Black Cherry, and Sweet Birch happens to be the more successful species, in both

Vida simulations and literature observations. Even though the two species have similar max heights and canopy radii, Black Cherry just outcompetes Sweet Birch in the Beanfield Mountain environment.

Black Cherry was selected as a round cow species to represent the “other species” category. Within the FIADB data for Giles County, Black Cherry was the most proliferate species featured in the “other species” category. There was also sufficient data on this species compared to the others. Therefore, we used Black Cherry data to represent the entire “other species” category. This is also another major reason why it is low in importance compared to the literature values.

The American Chestnut tree is approximately 7% more successful in our simulations versus the literature values for the first year (1920). This species is very dominant when present in nature, even with a high biological fraction of seeds that fail to germinate at 90%. When it is accurately parametrized, it is still dominant. This restates the importance of reviving this keystone species, since it affects the landscape so drastically. Each species’ importance value will vary with each simulation. In this particular case, the way the American Chestnut was parameterized and the way Vida is representing Beanfield Mountain, creates a system where American Chestnut is slightly more abundant. The less populated species also have lower importance values than the literature states, meaning this loss is made up somewhere else other than in the understory.

White Oak is slightly low in importance (about 7% low) compared to the literature values in the first years. However, in the last year (1993), Vida accurately represents the decline in the species’ population. In order to see the amount of correlation between species, we graphed the abundance of each species in pairs. This was to demonstrate the degree of correlation between each species. After doing so, it was apparent that the three Oak species strongly influenced the growth of one another, as the slope of their correlations were almost completely straight ($r^2 \approx 1$). With three Oak species competing in the same environment, it is not surprising that there are interactions between them. In this Vida version of Beanfield Mountain, White Oak is the least successful Oak species.

Before initiating the various methods of reintroduction, additional simulations were run on the Beanfield Mountain data in order to receive the negative control output. This would serve as our

prediction for the Beanfield Mountain site if no reintroduction of the American Chestnut occurred after the blight's destruction. Forecasting simulations were set to run for 381 years.

Table 9: Negative Control outcomes; importance values averaged over 5 simulations categorized by year (1920-2119).

Species	1920	1939	1969	1993	2119
American Chestnut	34.62	0	0	0	0
Chestnut Oak	21.7	33.88	29.82	26.66	18.44
White Oak	13.38	20.84	14.18	9.1	8.69
American Basswood	2.97	4.11	2.998	2.1	0.5998
Red Oak	15.58	24.52	26.82	28.98	39.32
Pignut Hickory	5.27	8.64	8.998	7.12	6.93
Red Maple	0	0	10.77	20.74	23.24
Sweet Birch	0	0	0.66	0.87	1.94
White Ash	2.7	3.41	2.6	2.11	0.28
Black Cherry	3.71	4.598	3.17	2.31	0.56

According to Vida by 2119, 100 years into the future, if we do not plant American Chestnut trees, the two most abundant species will be Red Maple and Red Oak in the Beanfield Mountain area. This is reasonable because of the animals' choice in nuts as discussed previously. Red Oak has seeds that are smaller compared to the other acorns, so they are not as ideal of a food source. Red Oak nuts are higher in tannins, which make them more bitter compared to the other Oak acorn options. Since animals are not eating the seeds from Red Oak as much as the other species, its success is higher in comparison. This contributes to its long-term success. Red Maple is in a similar situation; since the animals are not eating the seeds, it will proliferate more than the other species that are being feasted upon. Five negative control simulations were run, where no American Chestnut trees were reintroduced, and then the results of each year were averaged. Table 10 shows the individual and averaged results of the negative control forecasting simulations.

Table 10: Individual and averaged outcomes of the negative control method (no American Chestnut reintroduction) method after 100 years of growth categorized by year (1920-2119).

Species	2119	2119	2119	2119	2119	Average
American Chestnut	0	0	0	0	0	0
Chestnut Oak	17.8	18.44	20.1	18.9	15.3	18.108
White Oak	8.05	8.69	4.89	14.1	11.5	9.446
American Basswood	2.04	0.6	0	0.19	0.77	0.7198
Red Oak	39.4	39.32	43.9	31.2	38.2	38.404
Pignut Hickory	3.81	6.93	5.79	11	8.28	7.162
Red Maple	21.9	23.24	24.3	20.6	25.1	23.028
Sweet Birch	4.31	1.94	1.08	2.38	0.85	2.112
White Ash	0.38	0.28	0	1.01	0	0.334
Black Cherry	2.25	0.56	0	0.57	0	0.676

In the forecasted negative control results, there is some species loss, as you can see in the last two rows of the third and fifth column. However, these are not keystone species and are low in population. There is a chance that 100 years into the future, those smaller and less populated plans will perish from the area. When the American Chestnut is not reintroduced, Red Oak and Red Maple stay dominant. This makes sense because Red Oak and Red Maple seeds are the less desirable for eating, so their seeds proliferate compared to other species who do have the tastier seeds, which animals eat and don't always plant back in the same area.

Various Methods of Reintroduction

Reintroduction is realistically facilitated by scientists in the field using various methods. In addition to manually planting seeds, it is also possible to use more creative methods, such as walking dogs with mesh backpacks to drop seeds randomly in particular areas. To compare the

outcomes of multiple reintroduction methods and determine the most effective method, three main approaches were designed:

1. Random reintroduction: 100 seeds randomly introduced over the entire 150 m² square plot in year 2020 (cycle 281). No areas were clear cut for reintroduction.
2. Center grid reintroduction: A single 12 m² space in the middle of the 150 m² plot is clear-cut at year 2019 (cycle 280). Within this 144 m² space, 56 American Chestnut seeds are planted within a 12 m² space in a hexagonal pattern at year 2020 (cycle 281).
3. Four small quads reintroduction: Four miniature plots (each sized 6 m²) are located at regular intervals within the 150 m² square plot. All trees within these 6 m² plots are cut down, and 14 American Chestnut seeds are planted within each plot. Within the total 144 m² space, 14 seeds x 4 plots = 56 seeds are planted in total over eight years. Each plot is clear-cut the year before American Chestnut reintroduction, starting in year 2019 (280). The individual 6 m² plots are planted two years apart from each other starting in year 2020 (cycle 281).

56 seeds were planted because that amount seemed like a satisfactory amount of seeds that could be manually planted in a hexagonal pattern, while also avoiding domination of the area after germination. Clear cutting an area before reintroduction is becoming standard practice. “Clearcutting” is when mostly all of the trees are removed from a forest area. Clear-cuts allow more water to enter a stream system through underground aquifers, because water is not being taken up and released by trees in a process called evapotranspiration. Not only this, but agricultural practices have demonstrated that planting a crop in one location by itself can increase its success. The forest is redeveloped by planting new trees or seeds. Sometimes, areas are allowed to naturally regenerate. Many species regenerate poorly in shaded

areas and need full sunlight to initiate their growth process. Therefore, clearcutting is used to give new species more of a chance to grow.

Outcomes of Each Method

The first reintroduction method, the random reintroduction, was the most unsuccessful reintroduction technique, even though nearly double the initial number of seeds were reintroduced compared to the other methods. An average of only two trees survived after 100 years. Table 11 shows the averaged outcomes of the random reintroduction method, run for five simulation.

Table 11: Individual averaged outcomes of the random reintroduction method after 100 years of growth (2019-2119).

Species	2119	2119	2119	2119	2119	Average
American Chestnut	0.64	0	0.97	0.67	0.47	0.55
Chestnut Oak	23.9	17.6	20.8	17.2	21.3	20.16
White Oak	10.4	35	10.3	25.7	26.5	21.58
American Basswood	1.16	1.76	0.68	0.47	0	0.81
Red Oak	33.4	14.5	40	21.3	29.5	27.74
Pignut Hickory	7.28	3.48	10.9	4.98	4.36	6.2
Red Maple	23.2	25.9	16.1	28.4	17.2	22.16
Sweet Birch	0	0	0	1.37	0	0.27
White Ash	0	0	0	0	0	0
Black Cherry	0	1.82	0.17	0	0.74	0.55
# American Chestnut trees	3	0	5	3	1	2.4

Since no part of the ensemble was clear cut for American Chestnut reintroduction, it is understandable why it would be the least successful method. The concerning aspect about this outcome is that random reintroduction is still a commonly used method among field biologists. Vida aids in demonstrating that reintroduction is more successful when a degree of physical intervention is involved. Not only this, but at least two species go extinct in every simulation trial. This is worse than the negative control outcome, where the average outcome features no species extinction. In the

individual negative control outcomes, only three out of the five simulations featured extinctions. In regard to biodiversity, it would be better if we did nothing at all versus randomly introduce this species back into this particular environment.

The next method was the center grid reintroduction. The center grid approach produced an adequate number of surviving BC3F3 American- Chinese Chestnut trees. However, it did not produce the highest number of surviving BC3F3 American- Chinese Chestnut trees compared to other methods. Table 12 shows the averaged outcomes for the center grid reintroduction method. Each simulation was run five times.

Table 12: Individual averaged outcomes of the center grid reintroduction method after 100 years of growth (2019-2119).

Species	2119	2119	2119	2119	2119	Average
American Chestnut	1.98	3.39	1.91	4.46	3.44	3.036
Chestnut Oak	16.5	14.2	26.5	33.5	15.7	21.28
White Oak	15.8	3.82	11.4	10.2	17.7	11.784
American Basswood	0.47	0	0.47	2.26	1.32	0.904
Red Oak	31.8	51.6	34.8	27.9	37.5	36.72
Pignut Hickory	13.5	8.9	6.7	8.98	5.52	8.72
Red Maple	18.7	17.4	17.3	10.3	16.5	16.04
Sweet Birch	1.2	0.34	0.36	0.49	1.98	0.874
White Ash	0	0	0	1.89	0.24	0.426
Black Cherry	0	0.37	0.42	0	0	0.158
# American Chestnut trees	6	10	6	11	13	9.2

In regards to biodiversity, this center grid attempt created the most biodiverse outcome. The impact of species death was not as significant in this trial compared to the other methods of reintroduction. However, there is a trade-off. Not many BC3F3 American- Chinese Chestnut trees survived after 100 years. This method was found to be our “middle-of-the-road” method of reintroduction. The number of surviving BC3F3 American- Chinese Chestnut trees was higher compared to the random method, but lower than the coming final method.

The final reintroduction method features a four small quads reintroduction. This outcome produced the highest number of surviving BC3F3 American- Chinese Chestnut trees. Since the BC3F3 American- Chinese Chestnut trees is more dispersed, there is a more seamless transition into the ensemble. Table 13 shows the averaged outcomes of the four quads method, where five simulations were run as well.

Table 13: Individual averaged outcomes of the four quads reintroduction method after 100 years of growth (2019-2119).

Species	2119	2119	2119	2119	2119	Average
American Chestnut	4.25	4.65	5.91	4.43	4.35	4.72
Chestnut Oak	15.4	23.7	30	17.5	28.6	23.04
White Oak	8.19	13.2	11.8	2.94	9.42	9.11
American Basswood	0	0.86	0.57	0	1.98	0.68
Red Oak	51.8	30.7	20.5	37	11.2	30.24
Pignut Hickory	4.36	5.73	7.76	11.4	15	8.78
Red Maple	15.4	21.3	21.1	25.3	27	22.02
Sweet Birch	0.55	0.22	2.4	0.39	0.67	0.85
White Ash	0	0	0	0.84	1.53	0.47
Black Cherry	0	0	0	0.18	0.295	0.095
# American Chestnut trees	14	12	16	11	13	13.2

The four quads method achieves the goal of a seamless introduction, growing steadily over time instead of instantaneously, without dominating the ensemble. There is loss in biodiversity, but generally only in the lesser populated species groups. The fact that an average of thirteen species are present after 100 years shows that an adequate number of BC3F3 American- Chinese Chestnut trees can survive using this method without overly-compromising the existing trees. This means that the four quads method produces a highly sustainable outcome that doesn't compromise the existing ensemble. Although the individual trials of the center grid method result in a higher degree of biodiversity, the averaged results show no difference between the center grid and four quads approach. Therefore, since there are more surviving BC3F3 American- Chinese Chestnut trees in the four quads approach, it would seem to be the best option for the Beanfield Mountain area. The center grid approach is arguably a fine approach, but it

may not maximize one's efforts to the highest degree. That's the benefit of using these simulators for these conservation efforts. What could be a massive trial and error process of planting the BC3F3 American- Chinese Chestnut trees with a fragile and limited supply of seeds, now has the potential to save the conservation effort time and money by maximizing outputs immediately.

CHAPTER IV

RESULTS

Most Successful Method of BC3F3 American-Chinese Species Reintroduction

The three individual reintroduction methods that were used produced varying levels of BC3F3 American- Chinese Chestnut species success. The first reintroduction method features a random dispersal of BC3F3 American- Chinese Chestnut seeds randomly into the entire world space. Nearly double the number of seeds were planted in this method compared to the other methods (100 seeds vs 56 seeds). This is because the random reintroduction method was the only attempt that did not include any clear-cutting. Since there was no clear-cutting featured in this method, it was justifiable to plant more seeds compared to the other methods. However, this method remained the most ineffective approach. The competition between the newly reintroduced BC3F3 American- Chinese Chestnut species and the other species in the forest ensemble is too high for the reintroduction to be considered successful.

The second method consists of a center grid reintroduction. Fifty-six seeds were placed in a center grid that was completely clear-cut for the purpose of BC3F3 American-Chinese Chestnut species reintroduction. Clear-cutting an area before reintroduction is becoming standard practice. Clear-cuts allow more water to enter a stream system through underground aquifers, because water is not being taken up and released by trees in a process called evapotranspiration. Not only this, but agricultural practices have shown us that planting a crop in one location by itself can greatly increase its success. The number of surviving BC3F3 American- Chinese Chestnut trees increased to four times the amount compared to the random reintroduction method (two individuals in random → nine individuals in central grid). This center grid method produced an adequate number of surviving BC3F3 American- Chinese Chestnut trees after 100 years of growth, and created an environment where the individual trials produced the least amount of species extinction.

The third attempt includes the clear-cutting of four small squares, each the same size and equal distances apart, with 14 seeds planted in each square- for a total of 56 seeds. Each quad is six m² and is introduced two years after the previous plot. There was one individual four quads simulation that had all species survive in year 2119. This did not happen in any other individual reintroduction method simulation- except once in the negative control trials, where the BC3F3 American- Chinese Chestnut tree was not introduced at all. Even though the center grid method produced individual results which maintained a higher level of biodiversity, there was no difference in the amount of species extinctions when the averaged results were compared to the four quads approach. This means that the higher number of surviving BC3F3 American- Chinese Chestnut trees can be obtained using the four quads method without sacrificing the overall biodiversity of the ensemble after 100 years. Therefore, I consider the four quads method to be the most successful method of reintroduction because it produces the highest number of surviving BC3F3 American- Chinese Chestnut trees without compromising the diversity of the ensemble. Table 14 compares the averaged outcomes of each reintroduction method.

Table 14: Importance values of each species at the end of each reintroduction method in final year 2119; each method is averaged over 5 simulations. Five averaged results for year 2119.

Species	Random Reintro	Center Grid	Four Regions
	Avg Importance Value	Avg Importance Value	Avg Importance Value
American Chestnut	0.55	3.036	4.72
Chestnut Oak	20.16	21.28	23.04
White Oak	21.58	11.784	9.11
American Basswood	0.81	0.904	0.68
Red Oak	27.74	36.72	30.24
Pignut Hickory	6.2	8.72	8.78
Red Maple	22.16	16.04	22.02
Sweet Birch	0.27	0.874	0.85
White Ash	0	0.426	0.47
Black Cherry	0.55	0.158	0.095
# American Chestnuts	2.4	9.2	13.2

Recent estimates indicate that one-fifth of botanical species are at risk of experiencing extinction in the wild.³³ This means that out of our ten species, two species would be an acceptable amount to go extinct. With the exception of one simulation featured in the individual four quads simulations, this is achieved. However, this is achieved in all simulations of the center grid approach. This aspect makes it arguable that the four quads approach outweighs the center grid approach when biodiversity is taken into account. Lowering species extinctions as much as possible reinforces the sustainability, diversity, and integrity of the forest ensemble- which are things we do not want to sacrifice. Maintaining a high level of biodiversity after BC3F3 American- Chinese Chestnut reintroduction is a major goal of this project. All these factors considered, the four quads method should be considered as the most ideal method of reintroduction in the Beanfield Mountain site. The greatest number of BC3F3 American- Chinese Chestnut trees are produced, and the diversity of the ensemble is not compromised to a considerable degree.

Overall, the most successful method of BC3F3 American-Chinese species reintroduction at the Beanfield Mountain site is the four quads method. For the conservationist working for a client, it would be wise to present them with both the center grid and four quads option. In terms of maximizing success, the four quads method is undeniably best. In the end, the discretion of the user will determine what method of reintroduction is selected.

Future Beanfield Ensemble with Chestnut Presence

Overall, Beanfield Mountain seems like a suitable location for BC3F3 American-Chinese Chestnut reintroduction. Even though humans facilitated the American Chestnut destruction, its revival depends on human intervention. Random reintroduction of the species is only partially successful. Reintroduction methods that include clear-cutting portions of the landscape and allowing the American Chestnut to thrive during the early stages of its development benefit the restoration goal immensely. Beanfield Mountain is full of many lower abundance species that buffer against the domination of

American Chestnut. In locations where larger species have not had time to proliferate in lieu of the American Chestnut, such as areas without large charismatic oak species, the reintroduction might overpower the existing ensemble, decreasing the diversity of the land. In the Beanfield Mountain location there are three large oak species that have persisted through time and show no signs of exiting the landscape, even when the BC3F3 American- Chinese Chestnut tree is introduced.

Dependability of Vida

Vida exhibits a large degree of variability. At least five replications of each simulation are required to receive an accurate representation of Vida's calculations. The American Chestnut had extremely varying abundance, with a standard deviation of ± 4.765 among the importance values in the negative control simulations. Vida's ability to accurately represent species is impressive. The closeness in the alpha and beta values of the Oak species demonstrates proper representation of mechanisms on the individual species level. The overwhelming domination of the American Chestnut in year 1920 of each simulation, as well as its dominance in the final year 2119 outputs for the center grid reintroduction method, demonstrates that Vida can successfully model species that do become dominant in forest ensembles.

CHAPTER V

DISCUSSION

For the first method, random reintroduction, only two BC3F3 American- Chinese Chestnut trees survived after 100 years, even when double the amount of seeds are planted. When interventionists utilize the random reintroduction method, they do not clear cut anything in the forest. The aspect of limited intervention, for the sake of randomness, greatly compromises the success of the reintroduced BC3F3 American-Chinese Chestnut species. In general, random reintroduction is not as successful as other reintroduction methods. Augmenting reintroduction methods with human intervention drastically increases species success. Therefore, the decreased success of the random method compared to the other methods is unsurprising.

The center method includes an increased amount of human intervention, since a center 12 m² square is clear-cut in the middle of the plot. This method demonstrates a heightened rate of species success beyond the naturally based, random reintroduction. We would also see increased amount of species success with this method in real life compared to the random reintroduction method. This heightened success is due to the incorporation of basic agricultural practices. Clearing an area of land for seed planting is an old-fashioned technique that significantly increases species success. This is the basis of human-based agricultural practices. Around 1000 AD, the wheeled heavy plough drawn by eight oxen was used more and more to turn the heavy clay lands which became increasingly available as natives began clear-cutting.³⁴ The rise of civilization began with basic agricultural practices, which were found to increase the success of crops, and in turn increase the manageable population sizes of human societies. It makes sense that incorporating a degree of human intervention would increase the success of a reintroduced species. In regards to biodiversity, the center attempt is no better than the random reintroduction method, where at least one species goes extinct in every trial.

The four quads reintroduction represents our current state in agriculture; we are utilizing well-organized, rotational, stratified planting techniques of individual seed plots. The four quads method features four smaller scattered portions of clear-cut land which creates a situation for the BC3F3 American- Chinese Chestnut tree to spread out more effectively over the ensemble. In the center grid method, all seedlings are confined to the center and slowly spread out from the center. When the reintroduction locations are more spread out, the species has an easier time healthfully dispersing throughout the landscape. For many species, it is wise to stratify when you plant the seeds. Generally, it is better to plant the seeds of a species intermittently by at least 30 days.³⁵ This phenomena reflects the Janzen Connell index mentioned previously, where early species success is heavily influenced by the competition it has with the mother and/or other propagules. The amount of time one should wait between plantings to maximize its success is species-specific because this competition is decreased. Incorporating more modern techniques like these and minimizing the amount of perturbation to the preexisting ensemble, allows farmers to achieve adequate success without compromising the surrounding species. This approach reflects our current stage in agriculture, where basic techniques have been combined with finely-tuned methods (centuries-long products of trial and error). Crop rotation, surface irrigation, and soil preparation are all fine-tuning methods that have been combined with basic agricultural techniques. These approaches maximize crop success without causing substantial harm to the landscape or other species.

The results of this thesis enhance Vida's proof of principle, previously mentioned in the Literature Review. Any program attempting to accurately model the growth of individual plants must successfully mimic the detailed behavior of its real population and demonstrate reliable prediction abilities to forecast changes in a dynamic forest environment. A major goal of this thesis is to successfully parameterize the Beanfield Mountain site, which includes successfully mimicking the detailed behavior of its real population. Using the Stephenson and Fortney articles, a biometric representation of the Beanfield Mountain population was created. This is the third event demonstrating Vida's prediction abilities to forecast changes. Vida is proving to be quite reliable when it comes to replicating populations.

These results of this thesis enhance the WBE Theory of biometric relationships. The WBE Theory describes that the dependence of a biological variable Y on body mass M is characterized by an allometric scaling law. Each of the species included in the Beanfield Mountain ensemble was created using the “miniVida with Graphs” species parameterization tool that ensures a smooth graphical transition from juvenile linear growth to mature natural logarithmic growth was obtained for appropriate parameter interactions. The fact this ensemble reflects the real Beanfield Mountain ensemble helps reinforce that the WBE biometric theories are valid. Common, rudimentary biometric relationships that are found between species are the foundations that make them possible to model.

For each of the simulations in this thesis, a Janzen-Connell value of 1.0 was used. In order to test the effects of the variable’s use, multiple trials were run to see which outcomes produced more accurate results compared to the literature information. The outcomes using a Janzen-Connell value produced results that were much closer to the published values versus results that were produced without a Janzen-Connell value. The American Chestnut tree was much too successful in trials where a Janzen-Connell value was not used, i.e. value was zero. In several negative control trials where the Janzen-Connell was set to 0.0, the American Chestnut exceeded 55% in importance by year 1920, cycle 182. The Janzen-Connell index represents the distance a seed is dispersed from its mother tree. This observation is based on the natural phenomena that a seed will have competition with the mother that birthed it for resources, and vice versa. The closer the seed is dispersed to the mother, the more competition there is between the mother and the seedling, and the seedling will most likely die. Including this variable in order to achieve successful ensemble reproduction reinforces the fact that ecological considerations are important in biometric modeling.

The results of this thesis enhance the species catalog for the Vida software. Vida users will be able to access these species as reliable variables for engineering their ensembles. As part of increasing Vida’s usability for all types of users, this library of pre-assembled species files is building. As research is done, the species used in the analyses are saved into the Vida-master folder and updated on the GitHub repository. Each time a new species is accurately replicated, the species.yml file is saved in the Vida-

master folder in this way. During this project, ten species were correctly parameterized. This means that these ten species will be added to the official Vida-master download location on GitHub. Having access to these pre-parameterized species makes the Vida software more user friendly. Preparing a species file from scratch is doable, but not easy. Adding an increasing number of pre-assembled species files takes out a chunk of the start-up work in analyzing ensembles. This helps to maximize Vida's usability, which improves upon its previous capabilities. The fact that all ten species were successfully parameterized also reinforces the fact that all the core mathematical assumptions that build Vida's foundation are reliable. Having access to biometric simulator tools like Vida helps improve upon real-world interventions. Tree species reintroductions incorporate reliable techniques, but many options exist for the replanting method. In a world of many options, it is nice to have a guide that will increase your ability to select the best option for your needs. Predictive tools provide insight into the effects of interventions before they happen, saving conservationists time and money. The results of this thesis have explained and improved upon previous studies involving species reintroduction and biometric analysis.

There is controversy surrounding the issue of whether an invasive species has a negative connotation or not. In addition to this, there is the question- if the BC3F3 American- Chinese Chestnut tree is acting as an invasive species through the invasive act of reintroduction? Not all invasive species are considered harmful. In fact, some invasive plants that have found their way into the United States, and are essential to supplying our enormous population.³⁶ Most of our food crops, such as potatoes and wheat, are not native to the United States.³⁶ This goes to show that species introduction, or reintroduction, can have large scale benefits. However, introducing an invasive species into an environment is not always successful. Humans have tried this several times in lakes and park areas with mammal and fish species in order to control the population of another species in the area. There are almost always negative reactions that emerge in the long-term effects of these interventions. Ecosystems are maintained by a delicate balance between biotic and abiotic components. This is why simulation analysis is extremely important. Humans have perpetuated enough discord and demolition already. We are in a critical period where

limiting our further negative actions to the planet is paramount. Tools like Vida help us predict which species and methods will yield the most successful results- the methods that minimize disturbances and negative effects as much as possible.

CHAPTER VI

CONCLUSION

Vida has successfully parameterized the Beanfield Mountain location within an acceptable range for modeling purposes. The purpose of this thesis is to investigate the most successful method of reintroduction for the BC3F3 American- Chinese Chestnut tree in the Beanfield Mountain, Virginia location. Using Vida, we identify the four quads approach maximizes BC3F3 American- Chinese Chestnut success to the highest degree. This method does not harmfully compromise the diversity of the existing ensemble, in fact it enhances it. Without ecological interventions like these, reintroduction would be a gamble, and interventionists would have to guess which method would yield the desired outcome. Although Vida may not be perfectly accurate, it allows the user to simulate probable outcomes and compare them to one another. This saves ecological interventionists time and money when performing environmental projects. The trial and error tactic is exhausting and can drain resources. Vida takes some of the guess work out of environmental change impact analysis.

Areas of uncertainty in this study lie among the altered fraction of seeds that fail to germinate for some species in order to achieve appropriate results. Altering the fraction of seeds that fail to germinate in order to reflect eating habits of squirrels is not an ideal approach to accurately model the fluctuation in survival. Incorporating a death variable in addition to the fraction of seeds that fail to germinate would be a better way to represent (in the code) what is happening in the world space. However, grouping the death effects together into a single variable gives insight as to how much the overall death changes for each species as the ensemble changes over time. Vida is generally a round cow model, which is a witty metaphor justifying using highly simplified scientific models to analyze complex real-life phenomena. Round cow models function under the key principle that you should reduce a problem to the simplest form to make calculations more feasible, even though such simplification may hinder the model's application to reality. Grouping death variables together satisfies

the basic assumptions of a round cow model, but for explanation and programming purposes, it is more understandable to have a separate death variable that corresponds to dietary transitions of the animals. The fraction of seeds that fail to germinate should technically remain unchanged, since each species is known for having its own specific number of seeds that fail to germinate every annual seed-dispersal season. Some species, like Sweet Birch, have an extremely high number of seeds that fail to germinate. Whereas others, like Red Maple, have much lower seed mortality rates of 13%.³⁸ These species-specific mortality rates were used in the initial parameterization of the species and were only changed if the eating habits of the animals obviously influenced its success rate in the later years. Two Oak species and Red Maple were the only individuals that required modification in this way.

A fourth reintroduction method was almost implemented- reintroduction using controlled burns. Instead of clear-cutting an area, simulated controlled fires would be ignited, and American Chestnut seeds would be planted in the now bare areas. Theoretically, this would kickstart the growth and seedling germination rate of the BC3F3 American-Chinese Chestnut tree. Historical accounts and phylogeny suggest chestnut may have certain disturbance adaptations similar to Oak including the ability to profusely sprout following top kill.³⁸ However, the response of American Chestnut to fire has only been observed in mature individuals, not in seedlings which would be used during restoration attempts. In 2007 and 2009 a project team in Indiana simulated the morphological effects of surface fire and associated top kill on 143 Red Maple and 94 American Chestnut seedlings using a burn chamber. The litter was ignited and stems were heated using a plumber's torch, subjecting stems to temperatures of 200–300°C for 60 seconds from two diametrically opposite directions. Only sprouts \geq 7.5 cm total height were recorded.³⁸ The results suggested that both species had highly productive sprout responses following top kill by fire, producing sprouts up to 200 cm tall after one growing season. Both species also responded favorably to increased light availability and may, therefore, benefit from fire, harvesting, natural canopy mortality, or other disturbances that increase light availability at the forest floor. Their results implied that larger Oak and Chestnut seedlings can produce sprouts with considerably advanced regeneration rates in the growing season following a

prescribed fire.³⁸ However, it is still unclear whether chestnut seedlings can tolerate multiple burns that are sometimes used for understory management in oak dominated forests. At each fire introduction, BC3F3 American-Chinese Chestnut seeds would be planted in the now bare area. For the first year of growth, an increased seedling germination rate would be implemented to reflect the increase in success after the fire. A thorough literature review would be done to assign the appropriate value for the high germination rate during the first year of growth. Then, the normal fraction of seeds that fail to germinate would be reinstated. Unfortunately, not enough time was available for this trial to be implemented. Running a fourth method would have added another option for most effective method consideration, giving insight into the success of another method. This controlled fires reintroduction method is a probable area of future investigation.

The benefits of using predictive software to analyze conservation interventions are three-fold. First, comparison of different techniques and incorporation of observational data can result in improvements to reintroduction practices. Second, analyzing the outcomes of each method increases the likelihood that one will be successful. Put another way, trying more than one approach at a time can be viewed as a “bet-hedging” strategy in case any single method fails. Biological bet-hedging occurs when organisms suffer decreased fitness in their typical conditions in exchange for increased fitness in stressful conditions. Biological bet-hedging was originally proposed to explain the observation of a seed bank, or a reservoir of ungerminated seeds in the soil. Finally, endangered-plant reintroduction is still a relatively new field. These techniques are necessary to build the literature base needed for developing generalizations and theory.

Since reintroduction biology is such a relatively young discipline it continues to be a work in progress. No strict and accepted definition of reintroduction success exists, but it is known that a reintroduced species should blend in with the ensemble as opposed to dominating it. Using biometric tools with predictive capabilities allows this new science to exponentially increase in efficiency and accuracy. In addition to addressing the basic goals this thesis, the work of this study helps to reinforce the usefulness of using predictive, allometric tools in reintroduction biology. Merging nature and

technology is a major way humans are going to correct some of the crimes they have committed against mother nature. Many of these crimes, are irreversible. In the case of the American Chestnut, however- its previous dominance may be reestablished if the proper reintroduction methods are selected for each region. American Chestnut restoration is on the horizon. Access to tools like Vida can only enhance the chances of implementing the most successful, sustainable large-scale revitalization efforts.

Vida fails to consider precipitation or elevation in these trials. This compromised functionality has the opportunity to be enhanced. Especially when considering the American Chestnut tree, slope and water availability would be critical environmental factors to consider. The Vida forest emerges from the relationships found between the variables represented in the species files. The emergent properties of each species compounds into combined world effects. These world effects change the environment, and therefore- the success of each species. Modeling these dynamic changes are challenging for any forecasting software. It is quite impressive that Vida was able to accurately represent the changes in the Beanfield Mountain ensemble without considering additional parameters such as nutrient availability, temperature, moisture, etc. Using Vida to reforest and learn about forests is an invaluable resource.

GLOSSARY

Biological Bet-Hedging: occurs when organisms experience decreased fitness in their typical conditions in exchange for increased fitness in stressful conditions

Evapotranspiration: the process by which water is transferred from the land to the atmosphere by evaporation from the soil and other surfaces and by transpiration from plants.

Parameterization: The representation of one or many simplified numerical, measurable factors forming a set of boundaries that defines a system or sets the conditions of its operation.

Program: A collection of instructions that performs a specific task when executed by a computer.

Python: A general-purpose programming language that can be used on any modern computer operating system. It can be used for processing text, numbers, images, and scientific data.

Round cow model: Metaphor for highly simplified scientific models of complex real-life phenomena.

Functions under the key principle that you should reduce a problem to the simplest form to make calculations more feasible, even though such simplification may hinder the model's application to reality.

Script editor: An application used to edit or write code that is interpreted by a computer.

Simulation: The usage of a computer for the imitation of a real-world process or system which requires a model, or a mathematical description of the real system.

Software: The programs and other operating capabilities used by a computer that are comprised of a set of commands instructing a computer how to do specific tasks.

.yaml file: File created in the YAML (Yet Another Markup Language) format, a human-readable data format that is interpreted by the computer upon command; can be incorporated into many different programming languages using supporting YAML libraries, including C/C++, Ruby, Python.

APPENDIX

How to install Vida:

DEPENDENCIES/REQUIREMENTS

*Python v2.7 (<http://Python.org/download/>)

*pyYAML v3.11 (<http://pyyaml.org/wiki/PyYAML>)

*ContextFree v3.0.8 (optional. Needed to generate graphics.

<http://www.contextfreeart.org/download/ContextFreeSource3.0.8.tgz>)

Apple users can make use of Homebrew (<http://brew.sh/>) to install the command line version of cfdg using the following commands:

```
brew tap kn1kn1/cfdg
```

```
brew install cfdg
```

*ffmpeg for making videos.

Apple users can make use of Homebrew (<http://brew.sh/>) to install ffmpeg:

```
brew install ffmpeg
```

HOW TO USE VIDA

Command line options and ways to make species, event files and define planting locations:

-d	turn on basic debugging
-dd	turn on module debugging
-n <string>	simulation name

-w <integer>	world size in meters
-s <mixed>	starting population size, a list of species, locations and germination delays, or a file defining species, locations and delays in germination
-m <integer>	maximum population size
-t <integer>	maximum number of cycles
-g [<characters>]	produce graphics (see Graphic Options)
-c	keep CFDG files
-p	delete PNG files
-v [<integer>]	produce a Quicktime video, with an optional frames/second value(Macintosh only)
-r <string>	reload a previously saved simulation
-rl <string>	reload a previously saved simulation & reload the Vida World

Preferences file:

-e <string>	load an event file named <string>
-a <characters>	save a simulation state
-f <characters>	save statistical data
-x <integer>	number of times to reun the simulation

Seeding options:

Vida accepts a number of ways of placing seeds in a simulation

-s <int>	Place <int> seeds randomly in the world-space. The species
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used will be chosen randomly from those in the Species/ folder

-ss <int>	Same as -s <int>, but the seeds are placed in a grid pattern
-sh <int>	Same as -s <int>, but the seeds are placed in a hexagonal pattern
-sf <file>	Seeds placement and species type is defined in a 'placement' file

Archival options:

Vida allows one to save simulation states for later resumption

-a n	Do not save any simulation states.
-a s	Save only the starting state of the simulation
-a e	Save only the final state of the simulation
-a a	Save every cycle of a simulation

Data output options:

Vida allows one to save data about the world-space

-f n	Do not save any data
-f s	Save only the data for the initial cycle of a simulation
-f e	Save only the data for the final cycle of a simulation
-f a	Save data for every cycle of a simulation

Graphic Options:

Vida can generate graphics showing views of the simulation from various angles, using the following options

-g s	show the simulation from the side without any depth
-g t	show the simulation from the top-down
-g b	show the simulation from the bottom-up
-g bs	show the simulation from the bottom-up and from the side
-g ts	show the simulation from the top-down and from the side
-g tb	show the simulation from the top-down and from the bottom-up(images are oriented left to right)
-g bt	show the simulation from the bottom-up and from the top-down(images are oriented left to right)
-g 3d	produce a dxf file

BASIC USAGE

After changing the directory in the command prompt to the Vida-master folder, one can begin the program by simply typing:

Python Vida.py

Running Vida without any arguments will make use of default values in `Vida_Data/vdefaults.py`. One can modify how Vida's simulations are run by either altering the default values in the `vdefaults.py` file, or by entering options on the command line. The basic command line function is as follows:

```
Python Vida.py -n example -w 100 -s 100 -t 200 -m 550 -g bs -v 10 -f a
```


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