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DEVELOPING STRATEGIES TO INITIALIZE LANDSCAPE-SCALE VEGETATION MAPS FROM FIA DATA TO ENHANCE RESOLUTION OF INDIVIDUAL SPECIES- SIZE COHORT REPRESENTATION IN THE LANDSCAPE DISTURBANCE MODEL, SIMPPLLE

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SPECIES-SIZE COHORT REPRESENTATION IN
THE LANDSCAPE DISTURBANCE MODEL,
SIMPPLLE

by

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B.Sc. Forest Resource Management, University of Montana, 2007

A thesis submitted in partial fulfillment of the requirements for the degree of

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in
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Developing Strategies to Initialize Landscape-Scale Vegetation Maps from FIA Data That Can Enhance Resolution of Individual Species-Size Cohort Representation In the Landscape Disturbance Model, SIMPPLLE

Chairperson: John Goodburn

Abstract:

The ability of forest resource managers to understand and anticipate landscape-scale change in composition and structure relies upon an adequate characterization of the current forest composition and structure of various patches (or stands), along with the capacity of forest landscape models (FLMs) to predict patterns of growth, succession, and disturbance at multiple scales over time. Comprehensive vegetation maps, which classify patch polygons or raster cells into forest cover types, can be developed from available inventory data (e.g., FIA Grid) in combination with remotely sensed data, but a simple categorical forest type, even one incorporating average size, may not provide adequate resolution for tracking individual species and age cohorts over time in an FLM. This project, undertaken in Eastern Montana forest types, sought to develop strategies for utilizing extensive inventory data from the U.S. Forest Inventory and Analysis (FIA) program to initialize patch-level vegetation information for use in the landscape disturbance model SIMPPLLE (Chew et al 2004). The information provided to SIMPPLLE, includes not only a forest cover dominance type that crosswalks with the Northern Region's VMAP labels, but also incorporates further species and size information to the cohort level. By processing FIA data through the stand-level growth model FVS (Forest Vegetation Simulator), tracking of individual cohorts could be summarized to enhance resolution and realism in the SIMPPLLE model. Further, by simulating patch level dynamics within FVS for up to 300 years for representative stands, and segregating growing stock by cohort, it was possible to enhance the complexity of stand development pathways to be used within SIMPPLLE model. Specifically, I enable the tracking of individual cohorts (species and 5" breast-height diameter size class) to be passed on to the SIMPPLLE model, while still allowing for large-scale modeling of disturbances and between-patch interactions, which are the scales of interest within the SIMPPLLE FLM.

Contents	Page
Acknowledgements.....	iv
List of Tables.....	v
List of Figures.....	vi
Ch. 1 Introduction.....	1
Ch. 2 Model & Inventory Background.....	7
SIMPPLLE.....	7
FVS (Forest Vegetation Simulator).....	10
FIA (Forest Inventory and Analysis.....	12
VMAP (USFS Region One Existing Vegetation Map).....	14
Ch. 3 Methods.....	16
Assigning VMAP Dominance Groupings.....	16
Creating Cohort Classifications.....	21
Database Construction to Allow for Analysis.....	22
Analysis of VMAP Groupings.....	26
Modeling Species Cohorts.....	27
Ch. 4 Results.....	32
Ch. 5 Discussion.....	38
Literature Cited.....	43
Appendices.....	48
A Keyword File for Computing TPA, BA, CFV, and QMD.....	48
B Keyword File for Computing QMD by Species.....	49
C Plot Distribution Charts within VMAP Groupings.....	51
D Species Variability within Each DOM6040 Grouping.....	55

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List of Tables	Page
3.1 - Lookup Table for FIA and VMAP Attribution	23
3.2 - Lookup Table for SIMPPLLE Habitat Grouping	24
3.3 – DBH Grouping in SIMPPLLE Terms	25
4.1 - Number of Plots in Each VMAP DOM6040 Grouping	32
4.2 - Example Stand From Species Variability Analysis	34

List of Figures

2.1 - SIMPPLLE Interface	9
2.2 - Suggested Area for Eastern Montana (EM) Variant Use	12
2.3 – FIA Plot Design	13
2.4 - VMAP Vegetation Layer Placed Over a DEM	14
2.5 - Process of Converting Plot Data into Species Cohort	15
3.1 - Selected FIA plots in Suppose	19
3.2 - FVS Simulation Preparation	20
3.3 - R1 Existing Vegetation Classifier	21
3.4 - Newly Created Database with VMAP Labels	25
3.5 - Species Variability of TPA of Individual Stands	27
3.6 – Species Variability by National Forest and Ranger District	28
3.7 - SIMPPLLE 2.5 and Earlier Pathways Structure	29
3.8 - SIMPPLLE 3.0 Pathways Structure	30
4.1 - VMAP DOM6040 Groupings of FIA Plots within Eastern Montana	33
4.2 – Species Presence in VMAP Groupings	36

Chapter 1 – Introduction

Increasingly, forest resource managers and planners must consider large landscapes over century and longer time scales to address the potential effects of natural and human-induced disturbances on the future composition and structure of various patches across a forested mosaic. Current conditions across landscapes are typically provided via comprehensive vegetation maps of forest cover types, developed from available inventory data in combination with remotely sensed data. These spatially-explicit, polygon or raster level data also provide input conditions for forest landscape models (FLMs). Recent efforts to increase the realism of FLMs have focused on tracking individual species-size cohorts within polygon-patch scales to address novel disturbance and climate conditions, as well as better represent forest processes at various scales. However, even with increasing computing power, a balance must be sought between advancing complexity, while being computationally efficient for landscape-scale simulation.

Simulation models are valuable, because forests continually change due to a number of processes at multiple scales. Timber harvest may affect individual forest stands, whereas regional processes such as climate change affect entire landscapes (Wang et al. 2013). Stand-level processes such as competition for available resources affect individual tree function, but such processes also affect landscape-level processes such as fire, or infestations of insects or disease. Given the multiple scales of these biotic and abiotic

processes, it has become increasingly important to capture these landscape functions in forest modeling to predict these changes over large spatial scales. Furthermore, it is also increasingly important to capture these landscape functions at individual species levels given that each species potentially responds differently to the local environmental and biotic conditions (Cushman et al. 2010).

Predicting how forest structure and composition will change over time requires the use of modeling natural and human-induced processes. Many computer-based models have been developed to predict changes across vegetated landscapes including the modeling systems SIMPPLLE, VDDT, LANDSUM, and LANDIS (Chew 1995; Kurtz et al. 1999; Keane et al. 1997; He & Mladenoff 1999). These models vary widely in their complexity and functionality. Models such as LANDSUM and VDDT are successional state and transition models that use classification systems in structural stages and cover types within potential vegetation types (Keane et al. 2006; Barrett 2011). SIMPPLLE utilizes a more simplistic approach by using multiple pathways to simulate succession. (Chew 1997). All of these models, however, predict change in structural and vegetative classifications over time (Barrett 2011). Vegetative classifications are used to aggregate homogenous vegetation units across large landscapes in order to model large-scale-patterns and processes more efficiently. However, it is not feasible to model individual trees and plants across large landscapes due to computer processing capabilities so certain characteristics and variables are used to classify the vegetation. Many of the classifications within these models use some sort of proxy, whether it is species types and canopy structure to aggregate similar type groupings (Barrett 2011).

As cited in the literature, there are many benefits to modeling at fine, more resolved scales (Cushman et al. 2013; Wang et al. 2013). Yet it is not always achievable to model individual trees for large areas when considering the computing power of many operating systems. To address this problem, individual trees need to be scaled up to larger scales, while maintaining some characteristics of their composition (species and size classes), to enable FLM's to better simulate species and structure at scales within the stand (Wang et al. 2013; Strigul et al. 2008). Therefore, it is important to find a balance of modeling at landscape scales while capturing individual species cohort response to forest processes.

Cushman et al. (2010) argue for describing vegetation as biological communities with potential for multivariate gradients of species composition, where each individual species will respond uniquely to particular combinations of factors. They also question the use of classified vegetation maps to explain the structure and composition of vegetative communities due to their apparent limited ability to forecast biological patterns at the landscape level (Cushman et al. 2010). They go on to argue that the vegetation maps do not explain a large proportion of the variation of tree individual species abundance. If they do not provide an accurate characterization of the variance of species arrangements, then how can they be expected to predict the dynamics of vegetative communities over time.

Disaggregating vegetation maps to include species cohort information has recently been incorporated into other forest landscape models (FLMs) besides SIMPPLLE. For example, Landis Pro, the latest model in the suite of Landis tools, has undergone a similar transformation in modeling framework using inventory data to initialize model

parameters (Wang et al. 2013). Wang et al. (2013) used FIA data to directly initialize Landis Pro, as well as to calibrate the model predictions using the inventory data. Their study looked at how species age cohorts derived from FIA will inform and improve model outputs. They demonstrated that modeling at large scales is possible while adding stand-scale complexities. They were also able to show that, through this process, they could more realistically predict patterns of succession, in terms of forest structure and composition (Wang et al. 2013).

One of the major challenges of forest landscape models (FLMs) has been the effort to model at finer scales within the bounds of computing capacity (Yang et al. 2011). In most FLMs, the landscape is divided into raster cells or polygons. The patch-level processes, such as competition and succession, are modeled in each individual cell, while the landscape-level processes (e.g., seed dissemination, disturbance, and silvicultural actions) are typically simulated over a group, or subset, of spatially explicit cells (Dijak 2013). It is difficult and extremely time consuming to attribute and populate each spatially-explicit raster cell to represent the actual landscapes, while achieving any realistic representations of stand complexity (i.e. species and ages) (Ballestore & Qui 2012). For much of the history of forest landscape modeling, stands have been simulated as an aggregate of the complex tree species and age/size compositions (Wang et al. 2013). And until recently, long-term, large scale inventory data has played little to no role in informing these models.

The imputation of FIA data into landscape level analysis has allowed for the initialization of model parameters, as well as the setting of constraints (Dijak 2013). FIA datasets can

provide detailed records for millions of individual trees and stands, which allow initializing landscape-level models directly with systematically sampled inventory data to calibrate stand parameters. Using the available datasets, it is possible to disaggregate stand-level information further into separate species-size cohorts based on individual tree and stand data. Through modeling of species-size cohorts separately, we can presumably gain a higher level of realism and modeling accuracy. Modeling at this scale also allows simulations to be conducted within the confines of computational capabilities. We can increase realism in stand response to forest processes by modeling at species cohorts levels while allowing the model to function within reasonable constraints.

The basis for this project is to refine the SIMMPPLE FLM to project individual species cohorts rather than an aggregate of stand attributes. It is rooted in this idea that we cannot accurately predict landscape level processes based solely on current vegetative maps, given the importance of capturing these dynamics at individual species levels. I provide an innovative way to disaggregate plant communities into separate tree species-size components using forest inventory data. In order to achieve these levels of modeling detail, I incorporated inventory data from FIA, including intensified grid data for Eastern Montana National Forests. I was able to develop individual species cohorts for separate forest stands to be incorporated into a revised version of SIMPPLLE, version 3.0. I am attempting to provide a more accurate characterization of species arrangements in the forest canopy to potentially improve modeling outputs. Given that each species respond individually to forest processes, and that different size cohorts are differently affected by various biological factors, I expect that the addition of tracking cohorts separately will improve our modeling accuracy and provide more realistic outputs.

The first goal of this project was to develop a strategy to enable FIA data to be used to initialize classification of species dominance, as well as the structural attribution (i.e. size and density) for all stands across a landscape to be modeled in SIMPPLLE FLM. Further, in processing the FIA data through FVS, it was critical to create a classification label that could cross walk with VMAP (USFS Region 1 vegetation coverage map) to facilitate developing representative stands. The second goal was to disaggregate stand-level information from FVS outputs into individual species cohorts (species/size groups) and project future composition and structural changes. The final goal was to develop new successional pathways in SIMPPLLE 3.0 that could be more realistic, individualistic, complex, and flexible.

Chapter 2 – Model and Inventory Background

SIMPPLLE

SIMPPLLE is a forest landscape model developed by Dr. Jimmie Chew of the Rocky Mountain Research Station. SIMPPLLE is an acronym from SIMulating Patterns and Processes at Landscape scaLEs. The model was created to function as a management tool to help us understand how vegetative processes interact through succession and disturbance. SIMPPLLE uses classified vegetation to process landscape-level changes and produce spatially explicit outputs. The model is stochastic in nature and utilizes expert knowledge for local calibrations (Chew et al. 2004). SIMPPLLE uses a graphical interface to represent the successional pathways as well as disturbance pathways (Figure 2.1).

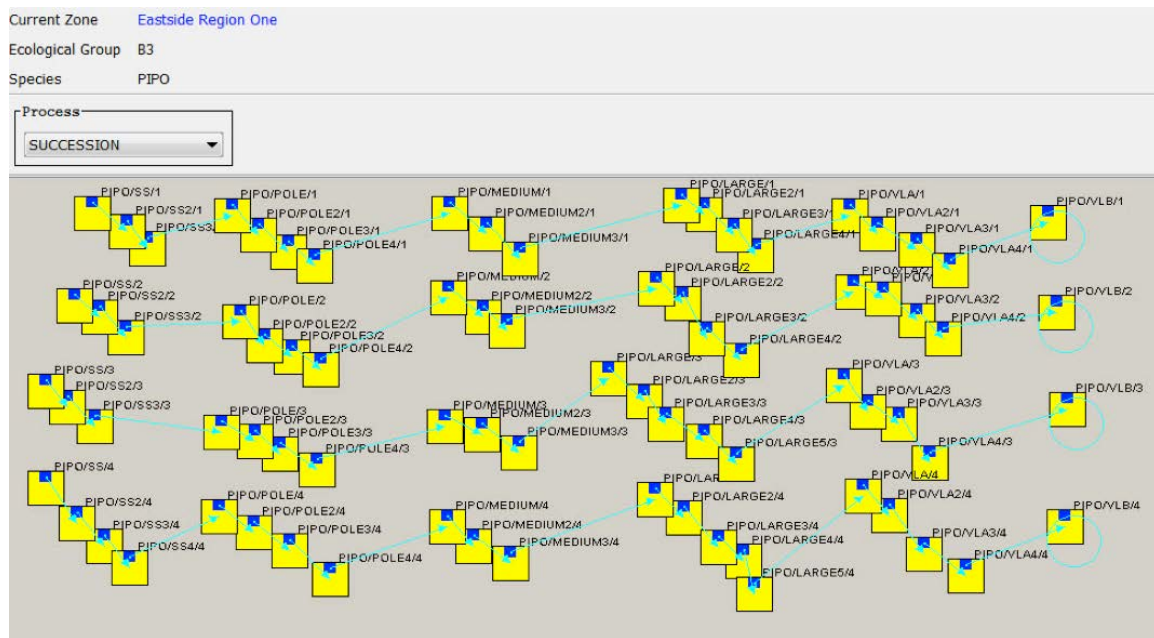
A wide range of user groups employ SIMPPLLE, including US Forest Service planners and analysts, BLM and state forest managers, and various research institutions. However, the primary focus of the model is that of a management tool. Since SIMPPLLE was adopted by the Rocky Mountain Research Station (RMRS) and delivered to the USFS Northern Region in 1997, it has been used for a variety of forest plan revisions, management plans, watershed assessments, and planning and evaluating fuels treatments at landscape scales.

SIMPPLLE has the ability to model from thousands to millions of acres, for both strategic and tactical planning. The model was created for use in the design and evaluation of management alternatives. SIMPPLLE can be used to quantify change in vegetation attributes, the levels of disturbance, and the occurrence probability of various forest processes. It may also be used to simulate representations of historical conditions for comparison to current conditions.

The emphasis within the SIMPPLLE model is to produce a means to represent and integrate the attainable knowledge on disturbance processes and vegetation patterns. The model relies on expert input on relationships between disturbance processes and vegetative patterns (Chew et al. 2004). Each of the vegetative units is expressed individually and each process is calculated for that individual unit, based in on relations to neighboring cells. SIMPPLLE runs through multiple simulations to produce an average range of conditions, including a maximum and minimum value (Chew et al. 2004).

The user interfaces on SIMPPLLE versions 2.5 and earlier have based ecological grouping pathways on species combinations, density level, and diameter at breast height (DBH) groupings (e.g. Pole, Medium, Large). These can be collectively called “states,” each with a specific set of attributes. For example, a particular state may be given a label of PIPO/POLE/3, which would identify a unit of Ponderosa pine with an average DBH between 5-10”, and within a density between 40-70%. Figure 2.1 illustrates the user interface of SIMPPLLE v. 2.5. Each state is connected to another state using a blue line that highlights their pathway. In this example, succession is the default process and depending on the ecological grouping, would have a unique pathway created from empirical data and expert input.

Figure 2.1 – SIMPPLLE Interface- Showing successional pathways in the user interface. *Simpplle contains multiple pathway interfaces that describe a specific Habitat Type Group, Species, and Process (i.e. succession, disturbance) and illustrates the projected transitional state. Each cell represents 10 yrs. with age and size moving left to right and density increasing top to bottom.*



SIMPPLLE uses existing vegetation attributes to describe each unit. The description of each unit is a combination of habitat type, dominant species, size-class and structure-class, and a measurement of density. These attributes are aggregated to describe an individual vegetative unit (Chew et al. 2004). Over time these units transition from one state to another depending on the description of the successional pathway and disturbance processes. Transitions are determined by potential vegetation states and the time spent in each size class. The unit will transition to another state once it has succeeded through that defined time period. For example, Figure 2.1 shows succession pathways within the SIMPPLLE FLM. This example illustrates PIPO states as they transition every 10 years. The blue arrows track the pathway as the stand moves from smaller size-class states to larger size-class states.

SIMPPLLE 2.5 and earlier versions have used an aggregate of attributes to describe each unit or stand. These stands transitioned through the model, as singular units comprised of all tree species and sizes, as opposed to individual cohorts of the stand acting independently. The goal of this project was to create a version of SIMPPLLE (i.e., SIMPPLLE V. 3.0) that could track vegetation dynamics at a cohort level, rather than modeling the aggregation of patch-level attributes.

This project involves updating SIMPPLLE to model landscapes at a finer, more accurate scale using individual species cohorts to transition through processes built into the model. SIMPPLLE is also changing from simulating an abstraction that is an aggregate of species to simulating the individual species cohorts that make up each plant community. This has allowed for a means to utilize cohort information to assign vegetation dominance groupings, not only at the initial state, but at each future simulated time-step, comparable to how classification rules are used to process inventory data or FVS projection data. Running actual plot data from FIA through the FVS, the Forest Vegetation Simulator, developed the cohort-level pathways.

The Forest Vegetation Simulator (FVS)

The Forest Vegetation Simulator (FVS) is distance-independent, individual-tree forest growth and yield model (Stage 1973) and serves as the primary forest growth tool of the U.S. Forest Service. FVS is a tree-level simulation model with the capacity to model many thousands of stands (Crookston & Dixon 2005). The model is widely used in many ways throughout the United States to aid forest management decisions. Though many

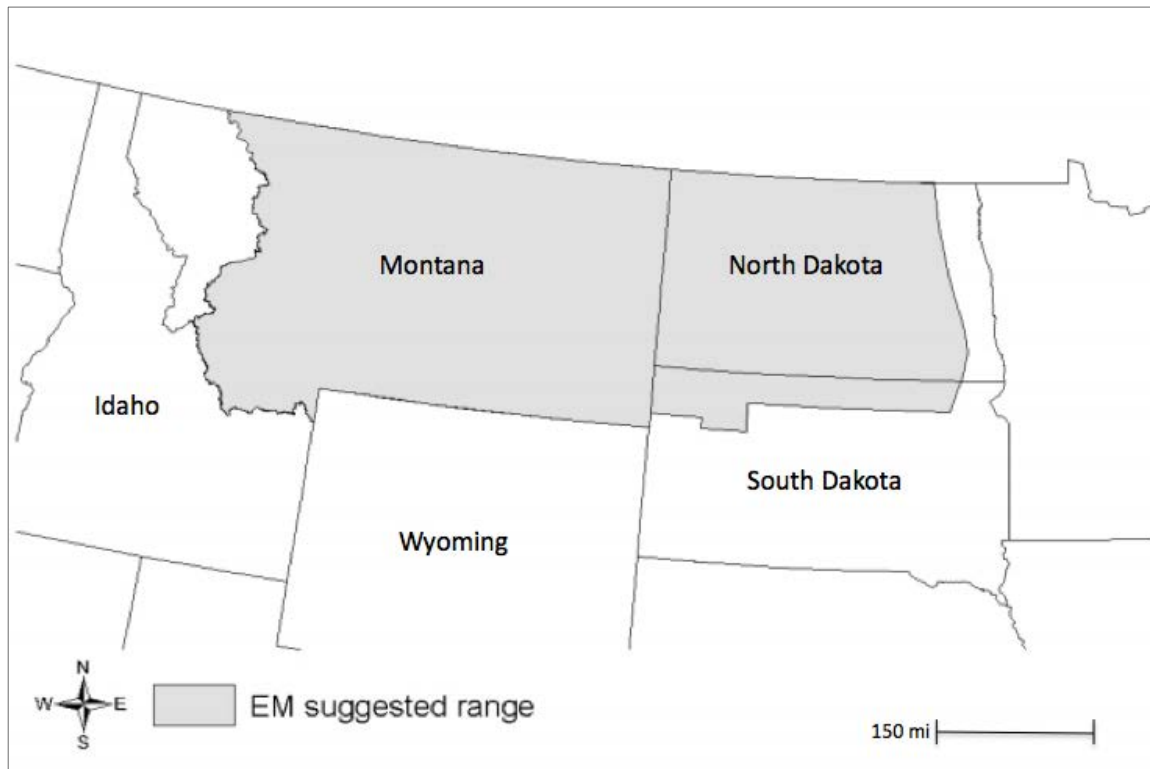
extensions have been created for use within the FVS framework, it is rooted in modeling growth and yield and predicting stand dynamics (Crookston & Dixon 2005).

The FVS model relies on a set of attributes, which are classified by density, species type, diameter, height, and crown ratio. The main stand attributes incorporated into the FVS model include slope, aspect, elevation, stand density, and habitat type (Crookston & Dixon 2005). FVS can then interpret inventory data along with stand or site information to estimate current stand conditions and future growth and yield.

FVS is locally calibrated to geographic regions through variants. There are two variants available for Region One of the U.S. Forest Service, the Inland Empire variant (IE) and the Eastern Montana variant (EM). For the purposes of this project, the EM variant was used (Figure 2.2). The main components within these variants include height and diameter increment growth, mortality, and regeneration (Crookston & Dixon 2005). Each variant is locally calibrated to specific regions using empirically driven growth data. This project utilized the growth increment function for the EM variant.

FVS is operated through a user interface for the model called “Suppose”. The Suppose interface allows users to adjust model functions and specify desired outputs. FVS also allows users to load certain commands, or “keyword files” in to Suppose in order to customize the inventory data and model outputs. Keyword files are written commands that allow users to add functions and processes (e.g., root diseases) to the model and to modify the way that output data is presented. For this project, a set of keyword files was created both to classify the stand data and to produce outputs categorized in species and size-class groupings (*Appendices A & B*).

Figure 2.2 - Suggested Area for Eastern Montana (EM) Variant Use. The EM variant contains local calibrations to the FVS model to increase output accuracy and account for regional sensitivities.

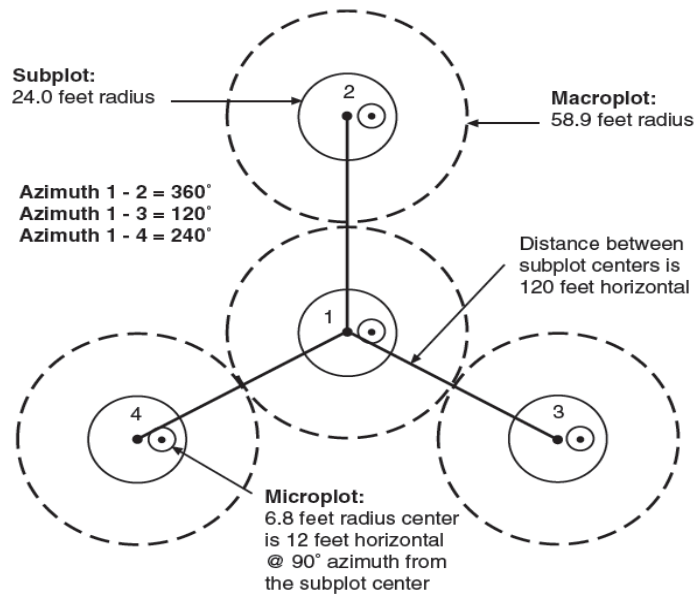


Forest Inventory and Analysis

Forest Inventory and Analysis (FIA) data was used to create FVS stands in order to complete the analysis of this project. FIA is a national program that has sampled and gathered plot-level data across the entire U.S. A spatially-distributed sampling design is used for all lands that features a consistent plot with four fixed-area subplots (Bechtold & Patterson 2005) Each FIA subplot has an additional 24-foot fixed-radius subplot to measure trees 5.0 inches DBH and larger. Each of the subplots total approximately 1/6 acre. Also included in the plot are microplots within the subplot where saplings 4.9 inches DBH and smaller are measured. The area of the four microplots total 1/75 acre. Also included in the subplots are four macroplots with a fixed-radius of 58.9 ft. to capture

large trees 40.0 inches DBH and larger (Bechtold & Patterson 2005) (Figure 2.3). The tree data collected can then be used to estimate individual tree volumes, which are then aggregated to estimate plot level volumes.

Figure 2.3 - FIA Plot Design (Bechtold & Patterson 2004) -



In addition to tree measurements taken at each FIA plot, site data is also collected in the general vicinity. These attributes include physical characteristics of the site such as percent slope, elevation, and forest habitat type (Bechtold & Peterson 2005). These site characteristics are important for guiding the combination of FIA plots and vegetative cover maps.

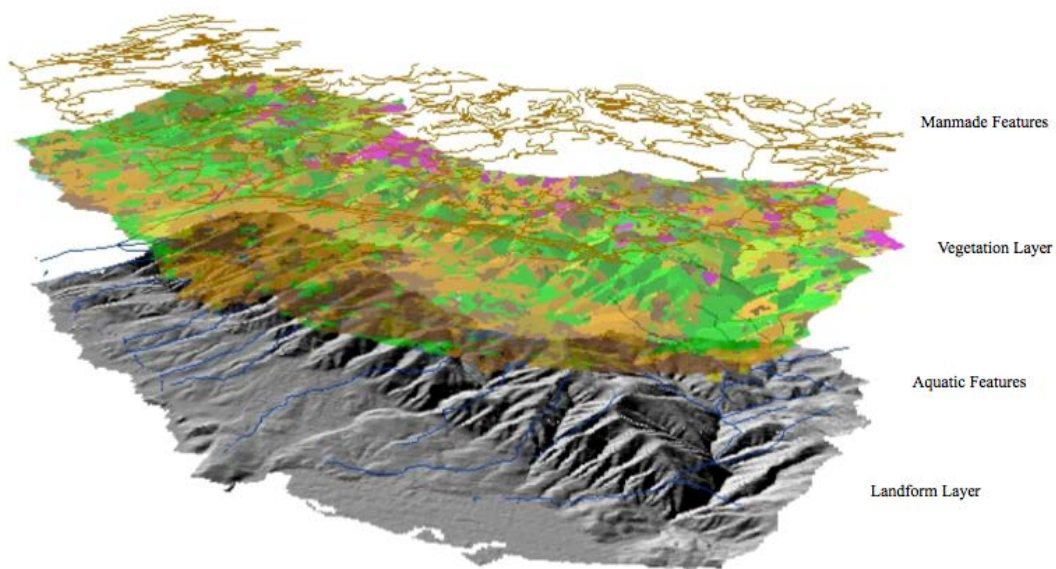
FIA data has increasingly been used in conjunction with FVS simulation for forest planning and analysis efforts, thanks in part to a US Forest Service created Mapmaker tool, which translates FIA data into FVS-ready databases (Shaw 2009). Processing inventory plot data through FVS allows for the growth simulation of FIA plots, which are developed into FVS “stands”, which can then be used for modeling at larger scales, by

incorporating many hundreds of stands. This project utilized this Mapmaker function to create FVS-ready stands from FIA plots located in Eastern Montana.

USFS Region One Existing Vegetation Map (VMAP)

For early versions of SIMPPLLE, as with most other forest landscape models, aggregated stand data was modeled based on vegetative maps that were grouped into vegetation units. The vegetation maps, or GIS layers, are often created by USFS planning teams using remotely sensed data to create large coverages of stands for use in landscape-scale planning efforts (Figure 2.4). The stand units (or patches) are delineated based on certain forest types to create unique forest boundaries. In USFS Region One, where this project took place, the “wall-to-wall” vegetation map that has been created across each National Forest in the region is called VMAP.

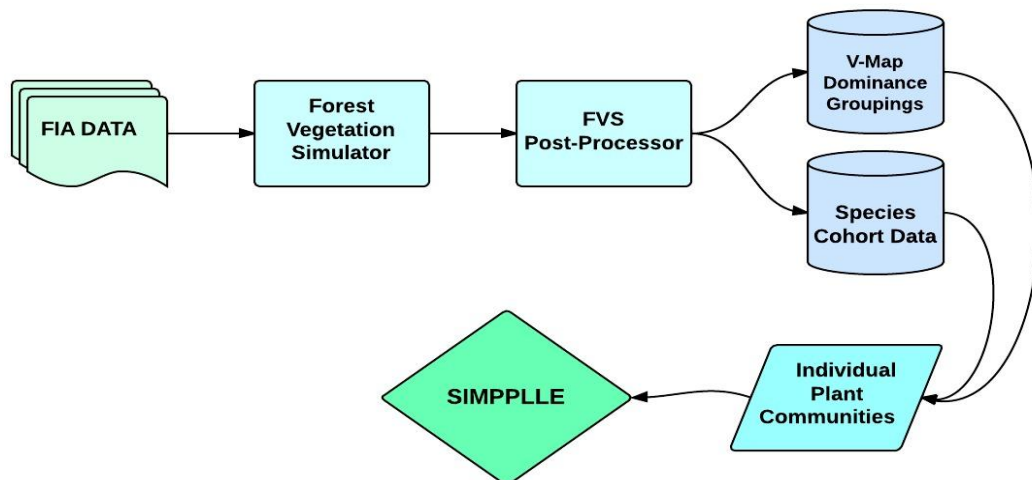
Figure 2.4 - VMAP Vegetation Layer Placed Over a DEM- Illustrates the multiple layers involved in modeling SIMPPLLE. This includes a VMAP layer (middle) with multiple stand groupings associated with specific attributes.



VMAP is a GIS-ready vegetation layer that contains a set of stands with discrete boundaries that contain unique attributes describing each stand. These attributes range from descriptions of stand characteristics, such as species dominance, density, and size, to the quantification of site characteristics, such as site potential, potential vegetation, and physical description (i.e. elevation) (Barber 2009). Stand polygons are generally attributed as having a species dominance grouping, based on percent occupancies of individual species.

This project incorporated the use of all four components introduced above: SIMPPLLE, FVS, FIA, and VMAP. Forest Inventory and Analysis (FIA) data was processed through the Forest Vegetation Simulator (FVS) to create representative stands. These stands could be expressed as sets of individual species cohorts, and then imported into SIMPPLLE (Figure 2.5). Further details of the use of these four component parts of the project are provided in the Methods section below.

Figure 2.5 - Process of Converting Plot Data into Species Cohort – FIA DATA is formatted and processed through FVS and assigned specific post-processors to attach VMAP dominance grouping labels and keyword files for species cohort information, which is then analyzed and imputed into SIMPPLLE



Chapter 3 – Methods

Assigning VMAP Dominance Groupings

FIA forest inventory data was used to develop individual stand communities, to classify stands across landscape scales, and to help identify representative stands. Analysts from the Northern Regional Office helped gather all of the FIA plots across each of the National Forests in Eastern Montana. In addition to the regular grid of FIA plots, we also made use of intensified grid data for Eastern Montana, collected by the USFS Regional Office in order to supplement and intensify FIA data using similar sampling methods. Intensified grid data uses similar plot designs to FIA inventory data but at finer spatial resolutions between plots to supplement the existing FIA grid. Only forested plots were selected for use in this analysis. In total, I was able to gather 1643 plots for analysis, including both FIA and intensified grid plots. These plot data will henceforth be collectively referred to as the FIA data.

These inventory plot data were prepared in FVS-ready formats, in that they were arranged in a database that allowed for the direct input into FVS. Plot data were processed into FVS-ready formats using the USFS data translation tool, MapMaker. Following translation, the data were arranged in formats that are compatible with the Suppose interface of FVS (Crookston 1997) and imported into a Microsoft Access database. This Access database consisted of three separate files: (1) a location file that contains stand level attributes pertaining to the inventory location (forest and region); (2) a stand list file which contains stand data (i.e. stand density, habitat type); and (3) tree

data files which describe individual tree attributes such as species, height, diameter at breast height (DBH), and crown classification (Shaw 2009). These MS Access tables are grouped and formatted to be recognized by FVS using a location (.loc) file in the Suppose interface. This location file simply directs FVS to the database and is contained in the same folder along with the FIA database.

The first major task involved in this project was to initialize the classification of species dominance and structural attribution (i.e. size and density) for all stands across a forest landscape for use in SIMPPLLE, based on FIA plots available. FIA data needed to be processed through FVS to enable a classification label that cross walks with VMAP, and to develop representative stands. To accomplish this task, inventory data were organized and put into an FVS-ready database, and then processed through FVS utilizing some post-processors designed to attach VMAP labels to each stand (based on attributes within the forest inventory data). FVS post processors are stand-alone applications that use input data (or inventory data) and produce specific outputs depending on your desired needs for the model (Van Dyck 2008). Post processors rely on a set of keyword files that instruct that model how to use and interpret stand data and produce specialized outputs.

This project utilized a vegetation classifier that was specifically developed for the USFS Region One. For the Inland Empire and Eastern Montana variants of FVS, the Region One (R1) Existing Vegetation Classifier post-processing tool was created to classify each plot simulated through FVS with VMAP attributes based on the current stand data (Keyser 2008). The R1 Existing Vegetation Classifier uses the process of grouping similar stand types into classes based on certain characteristics. The vegetation classification for the output describes the vegetation types and structural classes and

characteristics (Berglund et al. 2010). I was able to utilize this post processor in order to categorize and group the processed inventory data with VMAP labeling.

The term “representative stand” is used to describe a stand that represents a vegetation unit or VMAP polygon, as was used in this analysis. The stands, which are derived from FIA plots, are assigned to a vegetative unit based on a set of characteristics or stand attributes. The vegetative units used in this analysis were based on VMAP dominance groupings. VMAP provides consistent, empirically-based vegetation classifications for each National Forest in the USFS Northern Region (Berglund et al. 2010). VMAP classifications are represented by “dominance type groupings” that describe configurations of species located within each stand based on a certain level of confidence.

I selected to use only one type of VMAP dominance grouping for this project. The “dominant 6040 group,” or DOM6040, which was to be the main attribute used to determine stand similarities and thus create representative stands. This grouping is based on two thresholds of tree canopy cover, 60% and 40%. If a single tree species is observed to have greater than or equal to 60% of the total abundance for all of the trees present, then the group is assigned that species label (e.g. PIPO). If the dominant tree species abundance falls between 60% and 40% of total stand occupancy (i.e. canopy coverage, basal area, trees per acre), then that group is assigned the main species name with a suffix attached, designating a species mix (e.g. PIPO-IMIX or PIPO-TMIX). In this classification, IMIX refers to intolerant mix of species, whereas TMIX refers to tolerant mix of species. If no single tree species accounts for greater than 40% of stand abundance, the group is assigned the label of simply the appropriate mix, HMIX (hardwood mix), IMIX, or TMIX (Barber 2009).

Using the FVS R1 Existing Vegetation Classifier post-processing tool, I was able to attach a VMAP label to each of the FIA plots in Eastern Montana forests that were processed through FVS. Once the FIA plots were assigned VMAP grouping labels, you could evaluate the range of cohorts found in stands associated with a given dominance grouping. These groupings, derived from FIA plots, were used as the basis for creating a “representative stand.”

In FVS Suppose, the location files were connected to the FIA database. Once the FIA plots (FVS stands) were selected, they needed to be calibrated for use in Suppose (*Figure 3.1*).

Figure 3.1 - Selected FIA plots in Suppose- Showing FVS Suppose with Eastern Montana stands derived from FIA plots using MapMaker tool.

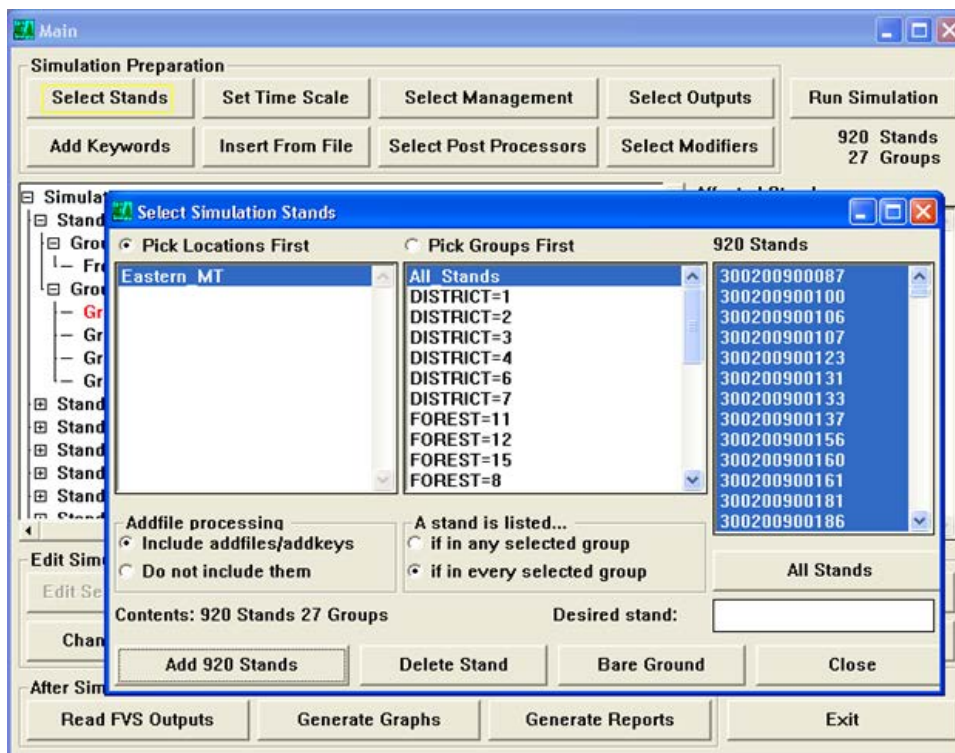
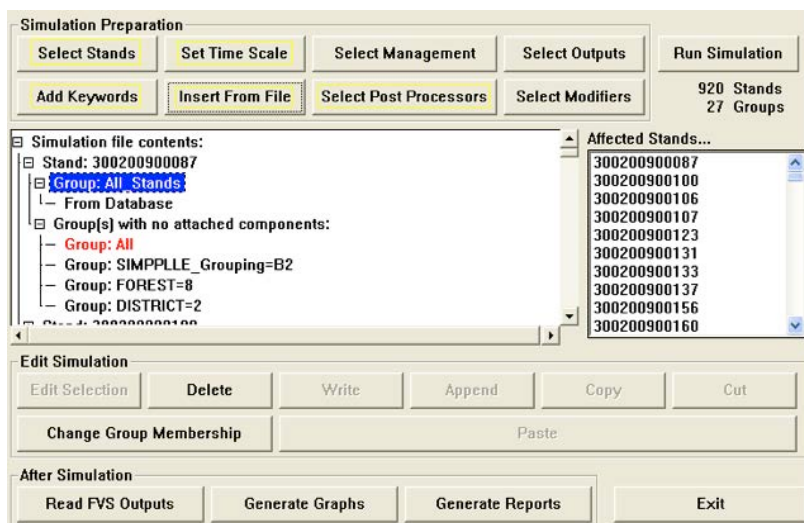


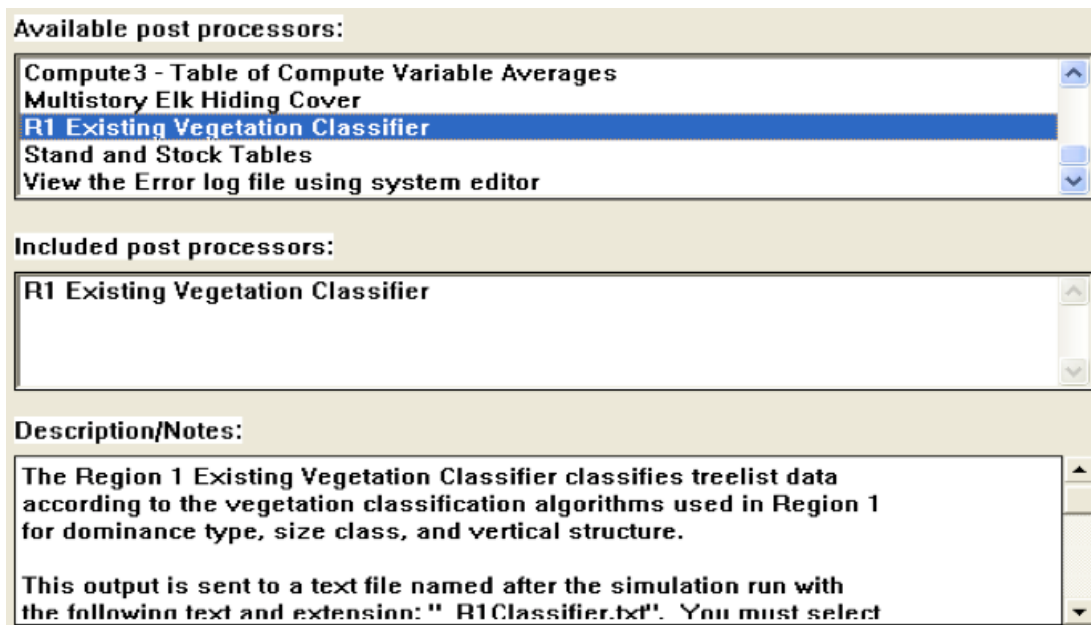
Figure 3.2 highlights the simulation preparations that were selected for this analysis. The first action taken was to adjust the time scale for the simulation. Given that the plots were measured over multiple of years, a common starting year needed to be selected. The last year of measurements was chosen as the common starting year. Since I was only concerned about current inventory at that point, the common ending year was chosen to be one year following the starting year. This allowed for the stands to be analyzed at a similar temporal scale.

Figure 3.2 - FVS Simulation Preparation- Highlighting the five simulation preparation toolboxes that were selected for the analysis



The final step in preparing the Suppose interface was to select the R1 Existing Vegetation Classifier in order to classify and attribute VMAP labels to the FIA plots. The classifier allowed us to maintain our MS Access Database while attaching VMAP attributes to the data table (Figure 3.3).

Figure 3.3 - R1 Existing Vegetation Classifier – Located in the Available post processors toolbox. Classifies treelist data according to the vegetation classification algorithm used in Region 1 for dominance type, size class, and vertical structure (Berglund et al. 2010)



Creating Cohort Classifications

Following the classification of the inventory data, I needed to create a method to disaggregate the stands into structural classes or cohorts. FVS was the predominant tool used in classifying and processing the inventory data to create species-size cohorts. To accomplish this, I developed a keyword file to input into FVS to separate the stand inventory data into unique size classes. These size classes were used as the basis for developing the cohorts within each stand. The size classes were in 5-inch increments thus defining a cohort as a unique species that fell within each particular size class.

Along with the MS Access database and the associated location file, two keyword (.kcp) files needed to be created. The first keyword file developed was named species_EM.kcp (Appendix A), allowed for the processed data to save directly to the original FIA database. After processing the plots, along with this keyword file, a new data table was created in

the MS Access database, which calculated the basal area (BA), volume (CFV), quadratic mean diameter (QMD), and trees per acre (TPA). The second keyword file created, named species_QMD.kcp (*Appendix B*), was used to develop individual cohorts by processing the data by size class within each present species. The size classes were delineated by 5-inch increments (i.e. 0.0"-4.9", 5.0"-9.9", 10.0"-14.9", etc). Following the FVS simulation of each FIA plot, output tables were created in the MS Access database to distinguish individual species cohorts for each stand. Once the database was complete and organized, I processed the stands through FVS Suppose in order to reclassify (cross walk) them with VMAP attributes. This was done using the Region One Existing Vegetation Classifier post-processing tool.

Database Construction to Allow for Analysis

In order to analyze the data in terms of each dominance type (DOM6040), a new database was created from the individual tree information. The Region One Classifier determines VMAP labels with the stand level data. However for this analysis, it must be attributed to the individual tree data. This was accomplished using lookup functions in MS Excel.

With the new database created from the tree list, I needed to combine certain attributes from both the stand level data, as well as the VMAP data. This was done using a lookup table (*Table 3.1*). From the stand table, I created a new table that includes the StandID, Forest, Region, Slope, Aspect, Elevation, DBH Group, and PVcode (Potential Vegetation). From the Region One Classifier table (from FVS output), a table was

created that included StandID, DOM6040, Size class, and Structure class. These 2 tables functioned as the lookup tables that attribute the Individual tree data (Tables 3.1 & 3.2).

Table 3.1 - Lookup Table for FIA and VMAP Attribution-Left table shows FIA stand data with SIMPPLLE habitat-type attribution (SMPL field). Right table show VMAP stand data with DOM_6040 groupings and calculated size class (5”).

STAND_ID_FIA	SMPL	ASPECT	SLOPE	ELEVFT	FOREST	DISTRICT	Stand_ID_Vmap	Dom_6040	Size_Class	Structure_Class
300400700002	B2	155	45	6044	12	01	300200900087	PICO	10.0-14.9	C
300400700049	F1	43	27	7773	12	01	300200900087	PICO	10.0-14.9	C
300400700052	G2	119	22	7460	12	01	300200900100	PIFL2-IMIX	10.0-14.9	C
300400700092	B2	353	44	5800	12	01	300200900100	PIFL2-IMIX	10.0-14.9	C
300404900159	B2	210	44	6045	12	04	300200900106	NONE	NONE	NONE
300404900202	F1	194	15	5596	12	04	300200900123	PICO	10.0-14.9	2
300404900250	A2	256	50	5791	12	04	300200900123	PICO	10.0-14.9	2
300404900266	D3	120	24	6108	12	04	300200900137	NONE	NONE	NONE
300404900271	G2	222	50	6950	12	04	300200900181	PIAL-IMIX	05.0-09.9	C
300404900282	A2	185	32	5746	12	02	300200900181	PIAL-TMIX	05.0-09.9	C
300404900337	A2	165	67	4376	12	02	300200900187	PICO	00.1-04.9	1
300404900350	B2	0	3	4756	12	02	300200900187	PICO	05.0-09.9	1
300404900362	A2	113	17	5105	12	02	300200900207	PICO-IMIX	10.0-14.9	C
300404903025	F1	65	41	5898	12	04	300200900207	PICO-IMIX	10.0-14.9	C
300405900087	B2	7	33	5814	12	01	300200900208	PIAL	10.0-14.9	2
300407700153	B2	130	17	6376	12	02	300200900208	PIAL	10.0-14.9	2
300407700231	G2	279	34	7599	12	02	300201100046	PIPO	10.0-14.9	1
300202700419	D3	15	50	6765	15	04	300201100046	PIPO	10.0-14.9	1
300203500297	G2	300	30	6862	15	01	300201100086	PIPO	10.0-14.9	C
300207300094	F1	88	8	6800	15	01	300201100086	PIPO	10.0-14.9	C
300209900028	G2	290	40	6067	15	01	300201100147	PIPO-HMIX	00.1-04.9	1
300209900102	G2	129	77	7383	15	01	300201100147	PIPO-HMIX	00.1-04.9	1
300209900190	F2	56	30	6488	15	01	300201100148	NONE	NONE	NONE

New columns were created in the tree output spreadsheet for Forest, Region, Slope, Aspect, Elevation, DBH Group, PVcode, SIMPPLLE habitat type, DOM6040, size class, and structure class. As shown in Table 3.1, the Slope, Aspect, Elevation, Forest, and District are attributes from the FIA plots. The dominance type, size class, and structure class are all derived from the R1 Existing Vegetation Classifier output for all VMAP attributes.

Table 3.2 - Lookup Table for SIMPPLLE Habitat Grouping – Table that allows SIMPPLLE forest habitat type groupings to crosswalk with FIA PV (potential vegetation) codes.

PV_CODE -- SIMPPLLE HABITAT														
91 A1		350 B1		510 B2		548 D1		660 D3		650 E2		770 F2		32 NF2
92 A1		370 B1		511 B2		555 D1		661 D3		651 E2		780 F2		33 NF2
93 A1		180 B2		512 B2		565 D1		662 D3		652 E2		790 F2		34 NF2
94 A1		181 B2		515 B2		570 D1		670 D3		653 E2		791 F2		35 NF2
95 A1		182 B2		523 B2		571 D1		671 D3		655 E2		792 F2		36 NF2
110 A1		190 B2		590 B2		572 D1		672 D3		675 E2		950 F2		37 NF2
380 A1		260 B2		591 B2		573 D1		673 D3		676 E2		810 G1		38 NF2
130 A2		261 B2		592 B2		574 D1		674 D3		677 E2		820 G1		39 NF2
140 A2		262 B2		516 B2		575 D1		680 D3		450 F1		830 G1		50 NF3
141 A2		263 B2		517 B2		578 D1		681 D3		640 F1		831 G1		60 NF4
142 A2		282 B2		518 B2		577 D1		682 D3		663 F1		832 G1		61 NF4
160 A2		310 B2		519 B2		578 D1		685 D3		690 F1		840 G1		65 NF4
161 A2		312 B2		520 B2		460 D2		686 D3		691 F1		841 G1		70 NF4
162 A2		313 B2		521 B2		461 D2		687 D3		692 F1		842 G1		71 NF4
210 A2		340 B2		522 B2		462 D2		733 D3		693 F1		850 G2		72 NF4
220 A2		430 B2		524 B2		420 D3		740 D3		694 F1		860 G2		73 NF4
230 A2		505 B2		525 B2		421 D3		540 E1		710 F1		870 G2		74 NF4
311 A2		506 B2		526 B2		422 D3		541 E1		711 F1		925 G2		78 NF4
321 A2		507 B2		529 C2		470 D3		542 E1		712 F1		940 G2		79 NF4
360 A2		508 B2		530 D1		480 D3		550 E1		713 F1		15 NF1		80 NF5
170 B1		250 B2		531 D1		579 D3		560 E1		720 F1		16 NF1		81 NF5
171 B1		580 B2		532 D1		620 D3		410 E2		730 F1		17 NF1		84 NF5
172 B1		281 B2		533 D1		621 D3		440 E2		731 F1		18 NF1		87 NF5
320 B1		283 B2		534 D1		622 D3		610 E2		732 F1		19 NF1		4 XX1
322 B1		292 B2		535 D1		623 D3		630 E2		910 F1		20 NF1		2 XX2
323 B1		290 B2		545 D1		624 D3		635 E2		920 F1		21 NF1		3 XX3
324 B1		291 B2		546 D1		625 D3		636 E2		930 F1		30 NF2		10 XX4
330 B1		293 B2		547 D1		654 D3		637 E2		750 F2		31 NF2		1 XX5

The DBH group label was used to categorize the stands into diameter classes. The DBH labeling corresponds to SIMPPLLE diameter naming (i.e. SS, Pole, Med, L, VLA, VLA).

Table 3.3 shows the function that I used to create the size classes and define the cohort classes. The function is an IF, THEN equation to classify the actual DBH of each tree into a SS (0"-4.9"), Pole (5.0"-9.9"), MED (10.0"-14.9"), L (15.0"-19.9"), VLA (20.0"-24.9"), or VLB (25.0" +) class.

Table 3.3 - DBH Grouping in SIMPPLLE Terms – Table used to classify size of individual tree DBH with SIMPPLLE DBH groupings (i.e. SS, Pole, Med, etc.).

StandID	DBH_GP	DOM6040	SIMPPLLE	SLOPE	ASPECT	ELEVATION	Forest	District
300200900087	SS	PICO	B2	29	93	6015	08	02
300200900087	SS	PICO	B2	29	93	6015	08	02
300200900087	SS	PICO	B2	29	93	6015	08	02
300200900087	Pole	PICO	B2	29	93	6015	08	02
300200900087	Pole	PICO	B2	29	93	6015	08	02
300200900087	Pole	PICO	B2	29	93	6015	08	02
300200900087	Pole	PICO	B2	29	93	6015	08	02
300200900087	MED	PICO	B2	29	93	6015	08	02
300200900087	MED	PICO	B2	29	93	6015	08	02
300200900087	Pole	PICO	B2	29	93	6015	08	02
300200900087	Pole	PICO	B2	29	93	6015	08	02

The newly created columns in the database were then populated from the lookup tables in order to attribute the stand level data to the individual tree data. Figure 3.4 illustrates a selection of the database with individual tree data along with the corresponding stand-level data.

Figure 3.4 - Crosswalk Database with VMAP Labels – DOM6040 column showing PSME-IMIX grouping. Column labels abbreviations as follows: TPA- Tree Per Acre; DBH- Diameter at Breast Height; Ht- Height; PrcCR- Percent Crown Cover; CrWidth- Crown Width; BAPctile- Basal Area Percentile; DOM6040- Dominance 6040 Grouping

A	B	C	D	E	F	G	H	I	J	K	L	M	N
Id	CaseID	StandID	Year	Treeld	TreeIndex	Species	TPA	DBH	Ht	PctCr	CrWidth	BAPctile	DOM6040
1	1	400101350011	2011	1	20	PSME	5.99224663	6.46357679	35.6282272	18	8.94003582	20.772007	PSME-IMIX
2	1	400101350011	2011	1	1	PSME	14.3813925	6.45731401	35.6282272	18	8.9357357	19.9992523	PSME-IMIX
3	1	400101350011	2011	1	21	PSME	3.59534812	6.45628119	35.6282272	18	8.93502617	18.1482353	PSME-IMIX
4	1	400101350011	2011	3	24	PSME	5.99237633	6.06277466	35.6566315	20	8.91445065	11.8896456	PSME-IMIX
5	1	400101350011	2011	3	3	PSME	14.3817034	6.05916929	35.6566315	20	8.91181946	11.2097416	PSME-IMIX
6	1	400101350011	2011	3	25	PSME	3.59542584	6.05557251	35.6566315	20	8.90919209	8.90095425	PSME-IMIX
7	1	400101350011	2011	6	30	PSME	5.99231195	6.26115704	35.6034851	15	8.37094593	17.6856308	PSME-IMIX
8	1	400101350011	2011	6	6	PSME	14.3815489	6.25876331	35.6034851	15	8.36935711	16.2355289	PSME-IMIX
9	1	400101350011	2011	6	31	PSME	3.59538722	6.25413847	35.6034851	15	8.36628723	12.7577658	PSME-IMIX
10	1	400101350011	2011	7	32	PSME	5.99231195	6.26056385	35.6019669	15	8.37052059	16.9605122	PSME-IMIX
11	1	400101350011	2011	7	7	PSME	14.3815489	6.25849867	35.6019669	15	8.36915016	14.4965744	PSME-IMIX
12	1	400101350011	2011	7	33	PSME	3.59538722	6.25361395	35.6019669	15	8.36590767	12.3236685	PSME-IMIX
13	1	400101350011	2011	8	34	PSME	5.99237633	6.05855703	35.5844574	15	8.23497295	9.57991219	PSME-IMIX
14	1	400101350011	2011	8	8	PSME	14.3817034	6.05552197	35.5844574	15	8.23292542	8.49397945	PSME-IMIX
15	1	400101350011	2011	8	35	PSME	3.59542584	6.05183697	35.5844574	15	8.23043728	6.86611176	PSME-IMIX
16	1	400101350011	2011	9	36	PSME	5.99198627	7.27308083	35.7481842	26	10.4865046	34.7873459	PSME-IMIX
17	1	400101350011	2011	9	9	PSME	14.3807678	7.26838017	35.7481842	26	10.4831371	33.8089561	PSME-IMIX
18	1	400101350011	2011	9	37	PSME	3.59519196	7.26469517	35.7481842	26	10.4804983	31.4638462	PSME-IMIX
19	1	400101350011	2011	10	38	PSME	5.99266577	5.15538692	35.5672073	15	7.60042906	1.96464825	PSME-IMIX
20	1	400101350011	2011	10	10	PSME	14.3823977	5.15278721	35.5672073	15	7.59852505	1.47300708	PSME-IMIX
21	1	400101350011	2011	10	39	PSME	3.59559941	5.14903355	35.5672073	15	7.59577703	0.294258088	PSME-IMIX
22	1	400101350011	2011	11	40	PSME	5.9920187	7.16716194	35.6681023	20	9.68695736	30.8781643	PSME-IMIX
23	1	400101350011	2011	11	11	PSME	14.380846	7.16081333	35.6681023	20	9.6826973	29.9280567	PSME-IMIX
24	1	400101350011	2011	11	41	PSME	3.59521151	7.15945244	35.6681023	20	9.68178272	27.6518345	PSME-IMIX
25	1	400101350011	2011	13	42	PSME	5.99098396	10.284174	43.9440193	36	13.8619385	54.2133522	PSMF-IMIX

Analysis of VMAP DOM6040 Groupings

The FIA/VMAP crosswalk database enabled a number of analyses to be conducted. I was interested in knowing the range of VMAP coverages that were assigned to the FIA data. This is important given the need to populate the vegetation coverage map with FIA constructed data. I was also interested in analyzing size class by species (cohorts) in each of the DOM6040 groupings that were present on Eastern Montana forests. Lastly, I wanted to know which species comprised each of the VMAP DOM6040 groupings. Much of this analysis was completed using Microsoft Excel pivot tables. Pivot tables were powerful tools in enabling the quantification of large amounts of data as well as the analysis of specific fields within a table.

This first step in analyzing the new database was to look at the number of occurrences of DOM6040 VMAP groupings and their species distributions. The plot distributions by DOM6040 types describe the range of plots within each size class for a particular DOM6040 grouping. Pivot tables were used to capture the plot distributions of DOM6040 size classes. In the PivotTable Field List, the DOM6040 and Size_Class fields were added to the Categories box and the StandID field was added to the Values box. The Plot Distributions charts illustrate the actual number of FIA plots within each DOM6040 group. These charts aided in identifying representative plots for the new SIMPPLLE pathways. The graphs in *Appendix C* describe the cohorts within each DOM6040 group, by species and size class.

Analyzing Species Cohorts

After determining the range of DOM6040 groups, I looked at species composition related to size class. Using the same steps as before, I created another pivot table for analyzing species cohorts. In the Pivot Table Field List, I selected the following fields to the report filter; StandID, Species, DBH_GP, DOM6040, TPA, Forest, and District.

By moving the DOM6040 and StandID fields into the Row Labels box, the DBH_GP in to the Column Labels box, and selecting the TPA (sum), I can begin to build a picture of stand composition in each DOM6040 grouping (*Figures 3.5*).

Figure 3.5 - Species Variability of TPA of Individual Stands – A selection of stands consisting of multiple cohort (species/size) groupings.

SPECIES VARIABILITY BY TPA OF INDIVIDUAL STANDS							
Sum of TPA	Column						
Row Labels	SS	Pole	MED	L	VLA	VLB	
200204351872							
ABLA	3777	32	8				
PICO		8	8				
PIEN	299	16	24				
200204951412							
ABLA	299	72	72				
PIEN		24	24	24			
200304352263							
ABLA	18463	143					
PIEN		48					
PSME			24				
200304953243							
ABLA	2073	166					
PIEN			48				
PIFL2		24	24				
200404953794							
ABLA	11938	70		23			
PIEN	873		47				
PSME		23		23			

By including the Forest and District in the Row Labels box, I can better analyze DOM6040 groupings with large numbers of plots, such as PICO and PSME groupings. With the Forest and District fields in the Report Filter, stands are narrowed to a particular National Forest and District (*Figure 3.6*). It is important to utilize local data to inform

species cohorts. By using FIA data from specific USFS Forests and Ranger districts, we can improve our prediction of cohort information within each vegetation unit.

Figure 3.6 - Species Variability by National Forest and Ranger District – Showing ABLA-TMIX grouping narrowed by forest and district plot locations.

Sum of TPA	Column					
Row Labels	SS	Pole	MED	L	VLA	VLB
ABLA-TMIX						
Forest 08						
District 02	3875	219	0			
301809500168						
ABLA	2979	76				
PIAL			0			
PIEN	897	143				
Forest 11						
District 01	11165	706	70			
300506700014						
ABLA	10652	295				
PIAL	292	123	6			
PIEN	221	288	64			
District 06	13894	781	296	72	12	
300503100093						
ABLA	1648	36	12			
PIAL	449	0	0	0		
PIEN	1199	36	24	0		
PSME	150	12				
300503100165						
ABLA	3133	170	62			
PICO		24	24	0		

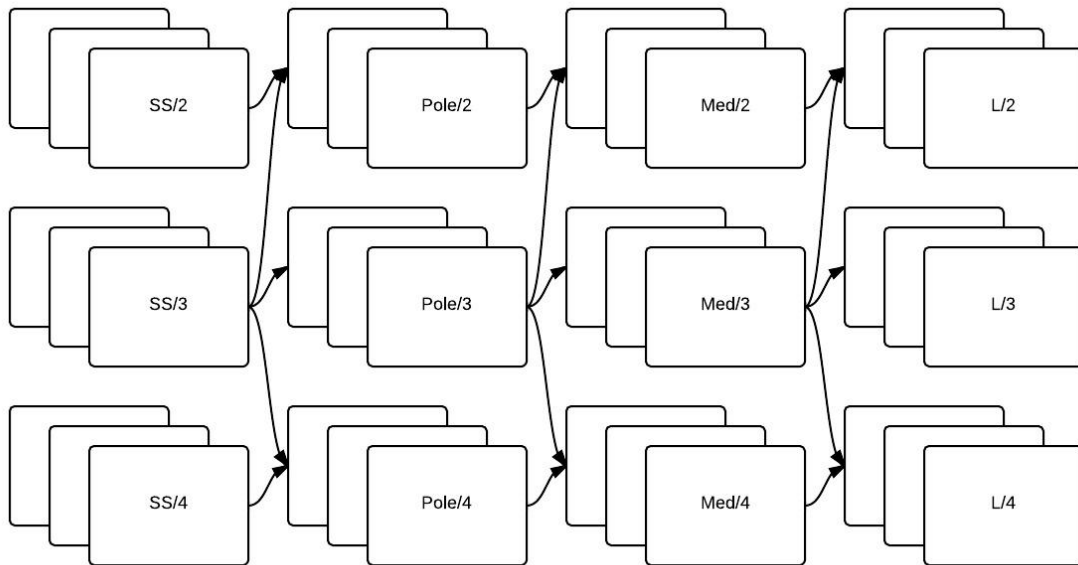
Figure 3.6 illustrates an example of how each of the FIA derived stands were disaggregated by VMAP type (e.g., ABLA-TMIX – *Abies lasiocarpa*, tolerant mix) showing a stand on National Forest 8 (USFS forest numbering), District 2. The figure also shows three stands on Forest 11. District 1 has one ABLA-TMIX stand and District 6 has two ABLA-TMIX stands. This figure shows the total TPA by size class for each stand representing a Forest, District, and DOM6040 grouping. This example shows how each of the stands were classified within a VMAP label (created in the R1 Existing Vegetation Classifier) while retaining attributes at both the stand level and individual tree level.

Modeling Species Cohorts in SIMPPLLE

This project allowed for the creation of individual species cohorts in the SIMPPLLE forest landscape model (FLM). Previous versions of SIMPPLLE have modeled an aggregate of species combinations based on size class and density (canopy coverage;

Figure 3.7

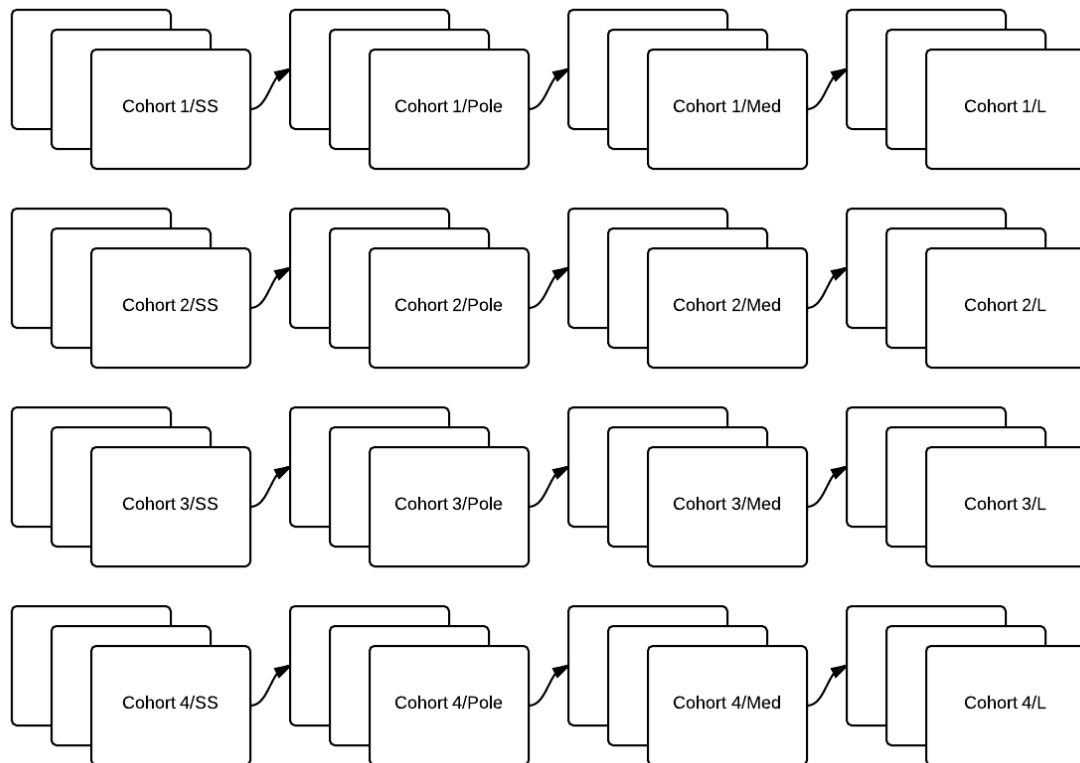
Figure 3.7 – Example of Interface showing Model Pathway Structure in SIMPPLLE 2.5 and earlier versions-. Pathways consisted of size class (SS, POLE, MED, L, VLA, VLB) and density levels (“1” - <10%, “2” – 10%-40%, “3” – 40%-70%, & “4” - >70%). Each state is a discrete 10 yr period.



In Figure 3.7, you can see a number of pathway options as each state transitions into larger states, as illustrated by the arrows. In succession, the state may increase or decrease in density as it ages. These transitions, in their current state, do not have the ability to react to species-level processes. Each state is defined by an ecological grouping which contains multiple species. These groupings respond to succession and disturbance as a singular unit, not allowing species to create unique responses to these processes.

A significant change in SIMPPLLE 3.0 is the transition from tracking these changes in density levels, to tracking the succession of individual cohorts over decadal time steps. The total stand density is the aggregate of each individual cohort's contribution to the total canopy coverage. Figure 3.8 illustrates the basic design of SIMPPLLE 3.0's user interface. In this example, you can see a collection of four cohorts, each with unique attributes describing species and abundance. The newly developed cohorts, from the example in Figure 3.8, can be imported into the new SIMPPLLE framework and be modeled for each habitat grouping and geographic region (i.e. Forest and District).

Figure 3.8 – SIMPPLLE 3.0 Pathways Structure through Succession – Pathways consist of multiple cohort pathways, each increasing in size in 10 yr periods, as characterized by individual states. Density is calculated within each states metadata, as opposed to shifting location in the user interface (i.e. top to bottom increasing in density as previous SIMPPLLE versions have done).



Each stand, as classified by habitat grouping, was created through the initialization and imputation of FIA data. The FIA plots were used to create these representative stands, which were processed through FVS in order to disaggregate the stands and allow for species-size cohort interactions, through succession and disturbance processes.

Chapter 4 - Results

The first objective in analyzing the newly created database was looking at the number of VMAP occurrences in each DOM6040 groupings. A total of 1527 forested plots were processed and assigned a VMAP label, using the vegetation classifier tool. There were 9 different tree species present among all plots, including a mix of both tolerant and intolerant species. A total of 26 different VMAP dominance groupings were identified in this Eastern Montana dataset (Table 4.1). Table 4.1 illustrates the number of plots in eastern Montana and their associated DOM6040 groupings.

As Figure 4.1 illustrates, a majority of the plots classified as VMAP DOM6040 groupings are either PICO (*Pinus contorta*) or PSME (*Psuedostuga menziesii*). Nearly half of all trees found on FIA plots are PICO or PSME.

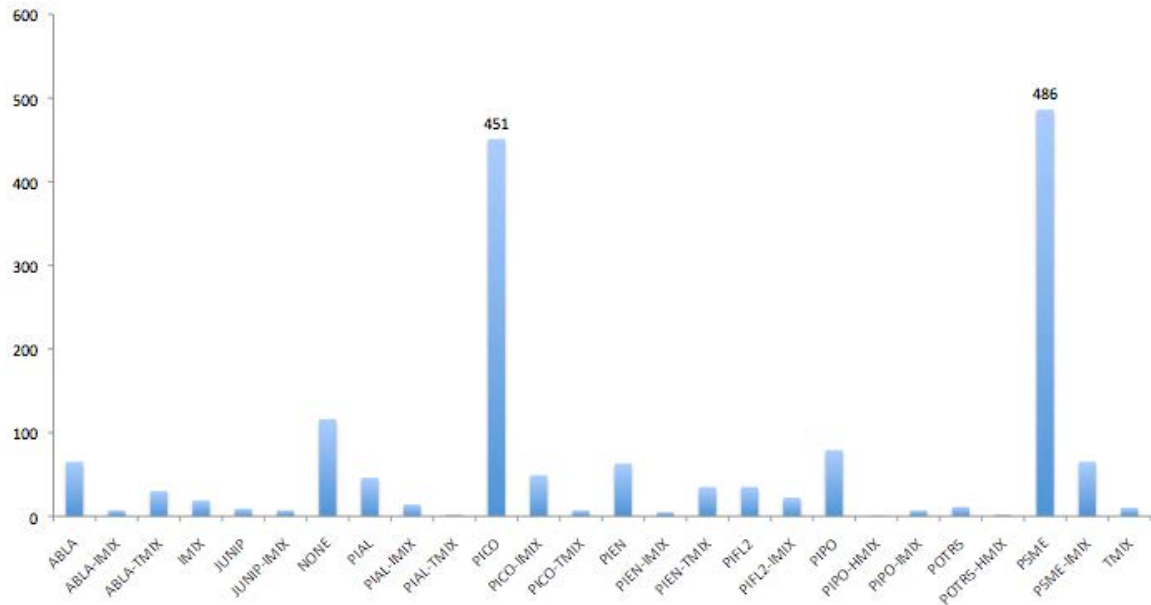
Table 4.1 - Number of FIA Plots in Each VMAP DOM6040 Groupings – Shown by each DOM6040 grouping within each species and the breakdown for tolerant and intolerant mixes.

Number of FIA Plots in Each VMAP DOM6040 Grouping									
ABLA	65	IMIX	19	PIAL	46	PICO	451	PIEN	63
ABLA-IMIX	7	TMIX	10	PIAL-IMIX	14	PICO-IMIX	49	PIEN-IMIX	5
ABLA-TMIX	30	NONE	116	PIAL-TMIX	2	PICO-TMIX	7	PIEN-TMIX	35
JUNIP	9	PIFL2	35	PIPO	79	POTR5	11	PSME	486
JUNIP-IMIX	7	PIFL2-IMIX	22	PIPO-HMIX	1	POTR5-HMIX	2	PSME-IMIX	65
				PIPO-IMIX	7				

The second part of this analysis was examining individual species cohorts within each of these newly created VMAP groupings. As previously mentioned, these species size cohorts were separated by 5-inch incremental size classes into individual species groupings. From this analysis, I was able to gather stand lists within each VMAP DOM6040 grouping as well as the species breakdown within each stand. Appendix C

shows a series of tables of VMAP DOM6040 groupings and the total number of stands that were given each respective label classified by size class.

Figure 4.1 – VMAP DOM6040 Groupings of FIA Plots within Eastern Montana – Plots showing dominance of DOM6040 groups PICO and PSME. (IMIX- intolerant mix; TMIX- tolerant mix; HMIX- hardwood mix)



The final part of this analysis was examining species cohort variability within a stand. For this analysis, I looked at individual cohorts within each National Forest, Ranger District, and VMAP DOM6040 grouping. The cohort variability analysis produced a dataset of each VMAP DOM6040 grouping containing the FIA stands that were given each respective label. Table 4.2 illustrates an example of the species variability exercise. The table shows a single stand from the PICO_TMIX VMAP grouping and the National Forest and Ranger District with the stands in that VMAP label. In this example, you can see Stand 300200900207 in Forest 11, District 03. This lodgepole pine, tolerant mixed stand contains twelve individual cohorts defined by species and size groupings. In this

stand PICO comprises 40%-60% of the total species canopy cover. The rest is a mix of shade tolerant species; ABLA (*Abies lasiocarpa*), PIAL (*Pinus albicaulis*), and PIEN (*Picea engelmannii*). Although PIAL and PIEN are present in the larger size class, a majority of the biomass in this stand is PICO.

Table 4.2 – Example Stand From Species Variability Analysis – Table shows individual cohorts (by size class and species) characterized by TPA within each respective cohort.

PICO-TMIX	SS	POLE	MED	L	VLA	VLB
<i>Forest 11</i>						
<i>District 03</i>						
<u>300200900207</u>						
ABLA	1944	24	24	0	0	0
PIAL	1344	48	60	36	0	0
PICO	0	72	83	24	0	0
PIEN	150	12	0	0	0	0

From the species variability analysis, we can begin to gather an idea of species cohort found in each VMAP grouping as well as the geographic arrangements of stands and their respective species cohorts (Appendix D). From here, representative stands can be selected based on these classifications. These cohort specified stands can then be imported into the SIMMPPLE interface to enable modeling species level processes.

As you can see in Table 4.2, there may be a wide range of species in each DOM6040 grouping. However, we can often see patterns or similarities of species in the stands. In the table, which is in the PICO TMIX DOM6040 grouping, ABLA and PIAL (*Pinus albicaulis*) are the two predominant species that are found along with PICO (*Pinus*

contorta). In this example, there are actually more PIAL individuals in the largest size grouping. However, there is a higher total percentage of PICO, which must make up at least 40% of total biomass canopy coverage to be given the DOM6040 title.

To further examine species present in each DOM6040 grouping, I created tables for each groups with each associated stand and species composition. Figure 4.2, which is labeled as a PSME DOM6040 group, has PSME primarily found with JUSC (*Juniperus scopulorum*) and PICO as sub-species. Further, National Forest and District fields can be added to narrow your analysis in geographic locations to calibrate at more local levels and gain specific species combinations within VMAP groupings. I wanted to analyze the variability of species present under each DOM6040 VMAP grouping. To accomplish this, a pivot table was created to see the species of each unique plot under each of the DOM6040 labels. Since this part of the analysis is not concerned with the actual trees per acre of each species, the Sum of the StandID (which will equal zero) is used to simply highlight which species are present. This example shows a list of stands with PSME (*Psuedotsuga menziesii*) VMAP labels. As you would expect, each stand has the presence of PSME (as represented by a “0” in the column. Since this VMAP grouping does not have a suffix attached, each stand in this example has at least 60% PSME comprising the stand.

Figure 4.2 - Species Presence in PSME DOM6040 VMAP Grouping – Table used to create species variability analysis. The pivot table shows “0” for the species occurrences within the DOM6040 grouping. This partial table displays each species present for all stands classified as Douglas-fir (PSME DOM6040). In this example, PSME (*Psuedotsuag menziesii*) is commonly associated with JUSC2 (*Juniperus scopulorum*) and PICO (*Pinus contorta*)

Row Labels	ABLA	JUSC2	PIAL	PICO	PIEN	PIFL2	PIPO	POBAT	POTR5	PSME
PSME										
200100750031						0				0
200100750061		0								0
200100750081		0								0
200100750101										0
200100750141				0						0
200100750151				0						0
200100750161		0								0
200100750171									0	0
200100750361		0								0
200100759031				0						0
200100759051										0
200104350151										0
200104350171										0
200104350211				0						0
200104950011				0						0
200104950111										0
200104950221										0
200104950231										0
200104950241		0								0
200104950271		0					0			0
200104950281		0								0
200104950311		0								0

Succession Data

One important part of this project was to utilize successional data from FVS simulation to inform the SIMPPLLE processes. The actual implementation of this data is beyond the scope of the paper, however, I will discuss what processes I used to create the succession data. First, I was able to utilize the growth and yield modeling function of FVS to grow the stands into the future. I processed the stands, derived from FIA data, in FVS this time growing them into the future to look at successional trajectories.

One important step in the process of creating successional data was to calibrate the initial starting point of the FIA inventory data. Each of the plots used in this analysis were grown in FVS to a common start year with the regeneration function turned on. The year chosen was the last year that measurements were taken. All previously measured plots were grown to this common starting point. Once all of the plots were calibrated, they were grown out in FVS to the greatest allowable year, which is 300 years.

I was able to utilize keywords to segregate stands into the newly developed cohorts and process those cohorts through the growth and yield function of FVS. I was then able to identify time in size-class for each individual cohort within a particular stand. The cohorts were grown collectively within the stand, but expressed individually. Each of the cohorts was allowed to act as one structural class unit in a multi-sized and mixed-species stand.

Chapter 5 – Discussion

There are inherent limitations anytime you are using inventory data. This is especially true when you are attempting to create representative stands from FIA data. While trying to capture species assemblages across large areas, it is difficult to replicate all existing forest conditions through inventory data. There will likely be forested stands that contain unique species compositions and unique structures due to management and disturbance history. While it was very beneficial to acquire the intensified grid data for Eastern Montana forests, it still only left us with roughly 1500 stands. Although it was a substantial amount of inventory data, much of it fell into two main VMAP DOM6040 groups (Douglas-fir and lodgepole pine groupings, PSME & PICO).

I have discovered that it is important to have flexibility when creating representative stands for use in modeling at large, landscape-level analyses. SIMPPLLE users must accept and be comfortable with a certain amount of uncertainty. Certain stands may need to be created in the absence of representative FIA plots to maintain coverage for all of the actual stands included within a large landscape. Vegetation maps often include large numbers of stand types that inventory data may not be able to provide full representation. In this analysis, we were able to assign representative stands to each VMAP label, but some DOM6040 groupings had very few stands. Many of the mixed stands (i.e. IMIX and TMIX) had very few representative stands to assign to VMAP groupings.

A stochastic method of randomly assigning representative stands from FIA data to match vegetation map coverage may be utilized, as described in Wang et al (2013). Further, FIA

derived stands can be randomly selected within a particular National Forest and Ranger District, with the benefit of using local data to classify the vegetation cover map. This is certainly the case with commonly observed species groupings, but may not be for unique groupings. For coverages that do not align with locally derived inventory data, users may expand their scope of plots to include plots found on other forests that resemble vegetation communities found on VMAP layers. Through this project, I created a method that allows plots to be distributed and assigned at local scales in order to better inform the model with the option to expand to larger regions to find a representative stand.

This project allowed for changes to be made to the SIMPPLLE model, from simulating a representation of an aggregate of mixed species over time to simulating the dynamics of individual species cohorts that make up each plant community. The changes in SIMPPLLE include the way in which individual species are modeled in each ecological grouping. This project also allowed for succession and disturbance processes to align with those within FVS, which the USFS relies heavily on for stand level projects. By processing the FIA data through FVS to project stand succession into the future, SIMPPLLE pathway succession of cohorts are able to calibrate with stand level analysis performed by FVS. Forest planners and analysis using FVS to measure stand level responses will find SIMPPLLE's succession alignment to be beneficial in merging landscape level planning with stand level management.

This project has allowed for a means to utilize cohort information to assign vegetation dominance groupings, not just in the starting vegetative state, but at each future simulated time-step similar to how the rules are used to process inventory data or FVS projection data. The species-specific information that is needed to determine disturbance process

probabilities derive from the cohort data that is associated with the broader dominance group assigned to the overall SIMPPLLE species value for an individual existing vegetation unit.

Assignment of cohort data will always have some problems in that there will most likely never be enough plot data to have the desired statistical confidence in the values assigned. Thus the users of this simulated stands will have to be willing to accept that the cohort values are to be thought of as being “representative” of plant communities assigned to the dominance group class. There is a benefit to modeling in a spatially interactive fashion. Concepts dealing with the linkage between disturbance processes can be tested, and management alternatives can be designed and evaluated without having a high level of statistical confidence in all the attributes assigned to the plant communities.

The future of this project could involve careful evaluation of use of FIA inventory data to develop representative stands from cohort data. For plot data that may represent significant variability in some species combination, users have to decide what part of the “range” of species combinations to use, or how to assign different combination using other attributes such as aspect, elevation, parent material, etc.

The choices that are used to select subsets of inventory plots to identify which cohorts to assign must also identify the inventory data to be projected with FVS and later embedded into SIMPPLLE. These choices vary for different analyses and different geographic portions. This project addressed the question of how to generate an individualistic community to model and make future predictions on how they function and interact with other plant communities.

This approach of utilizing inventory data to inform stand-level processes has proven to be a beneficial addition to other landscape models framework. Frasier et al. (2013) utilized Landis Pro in order to simulate stand-level prescriptions across landscape-scales. They were able to show that modeling inventory-derived species cohorts provided more accurate outputs from partial treatment of individual age class. They also concluded that through this method, they were better able to link landscape-level processes with stand-level management.

We know that individual species respond uniquely and separately to forest processes. Whether we are modeling succession, disturbance, or human interaction, species and size groupings (cohorts) will need to be free to change within the bounds of a forest stand. This will be increasing important as climate changes and species are seen responding differently to local climate and shifting to their preferred niche (Cushman 2010).

This project has taken the initial steps toward developing SIMPPLLE 3.0 to incorporate stand-level processes at landscape-scales. I developed a unique method to input FIA data and process it through FVS to create individual species cohorts. I also processed these data through FVS in order to attribute VMAP labels and develop tree-level and stand-level relationships within the datasets. I produced representative stands that can be used to inform the model on individual species cohort development.

Through developing this framework for inventory data utilization, it will be relatively straightforward to incorporate similar methods on other regions and modeling areas. The FIA data is a reliable source of inventory data that spans the entire United States. These data sets, along with a vegetation map for forest landscape modeling, can be set up

quickly and imputed into the SIMPPLLE modeling interface. Although this paper only details the initial process of developing species cohort modeling at landscape-levels, it is nevertheless an important process that can easily be replicated and will produce more realistic modeling outputs.

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Appendix A – Keyword File for Computing TPA, BA, CFV, and QMD

Computes species summarization data for EM Variant - 8 Species
TPA, BA, CFV, QMD by Species
Includes database connectivity (make empty database and specify the path to
your database)
For Permanent Growth plot summarization, created 10/13/12 by Jacob Muller
END

TreeList 0 3. 0 0 0
0

COMPUTE 0
WB_TPA = SPMCDBH(1, WB, 0)
WB_BA = SPMCDBH(2, WB, 0)
WB_CFV = SPMCDBH(3, WB, 0)
WB_QMD = SPMCDBH(5, WB, 0)

L_TPA = SPMCDBH(1, WL, 0)
L_BA = SPMCDBH(2, WL, 0)
L_CFV = SPMCDBH(3, WL, 0)
L_QMD = SPMCDBH(5, WL, 0)

DF_TPA = SPMCDBH(1, DF, 0)
DF_BA = SPMCDBH(2, DF, 0)
DF_CFV = SPMCDBH(3, DF, 0)
DF_QMD = SPMCDBH(5, DF, 0)

LP_TPA = SPMCDBH(1, LP, 0)
LP_BA = SPMCDBH(2, LP, 0)
LP_CFV = SPMCDBH(3, LP, 0)
LP_QMD = SPMCDBH(5, LP, 0)

S_TPA = SPMCDBH(1, ES, 0)
S_BA = SPMCDBH(2, ES, 0)
S_CFV = SPMCDBH(3, ES, 0)
S_QMD = SPMCDBH(5, ES, 0)

AF_TPA = SPMCDBH(1, AF, 0)
AF_BA = SPMCDBH(2, AF, 0)
AF_CFV = SPMCDBH(3, AF, 0)
AF_QMD = SPMCDBH(5, AF, 0)

PP_TPA = SPMCDBH(1, PP, 0)
PP_BA = SPMCDBH(2, PP, 0)
PP_CFV = SPMCDBH(3, PP, 0)
PP_QMD = SPMCDBH(5, PP, 0)

OT_TPA = SPMCDBH(1, OT, 0)
OT_BA = SPMCDBH(2, OT, 0)
OT_CFV = SPMCDBH(3, OT, 0)
OT_QMD = SPMCDBH(5, OT, 0)
END

DataBase
DSNOut
C:\FVSData\SMPL_HAB_GP\FVS_Data.mdb
CARBRPTS
Compute
Treelist
Summary

Appendix B – Keyword File for Computing QMD by Species

COMMENT
Compute TPA, BA, CFV, QMD by Species in 5" NTG diameter classes
EM variant
Includes database connectivity (make empty database and specify the path to
your database)
For Permanent Growth plot summarization, created 10/13/12 by Jacob Muller
END

TreeList 0 3. 0 0 0
0

COMPUTE
WB_QMD0 = SPMCDDBH(5,WB,0,0,5)
WB_QMD5 = SPMCDDBH(5,WB,0,5,10)
WB_QMD10 = SPMCDDBH(5,WB,0,10,15)
WB_QMD15 = SPMCDDBH(5,WB,0,15,20)
WB_QMD20 = SPMCDDBH(5,WB,0,20,25)
WB_QMD25 = SPMCDDBH(5,WB,0,25,99)

WL_QMD0 = SPMCDDBH(5,WL,0,0,5)
WL_QMD5 = SPMCDDBH(5,WL,0,5,10)
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WL_QMD15 = SPMCDDBH(5,WL,0,15,20)
WL_QMD20 = SPMCDDBH(5,WL,0,20,25)
WL_QMD25 = SPMCDDBH(5,WL,0,25,99)

DF_QMD0 = SPMCDDBH(5,DF,0,0,5)
DF_QMD5 = SPMCDDBH(5,DF,0,5,10)
DF_QMD10 = SPMCDDBH(5,DF,0,10,15)
DF_QMD15 = SPMCDDBH(5,DF,0,15,20)
DF_QMD20 = SPMCDDBH(5,DF,0,20,25)
DF_QMD25 = SPMCDDBH(5,DF,0,25,99)

LP_QMD0 = SPMCDDBH(5,LP,0,0,5)
LP_QMD5 = SPMCDDBH(5,LP,0,5,10)
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LP_QMD15 = SPMCDDBH(5,LP,0,15,20)
LP_QMD20 = SPMCDDBH(5,LP,0,20,25)
LP_QMD25 = SPMCDDBH(5,LP,0,25,99)

ES_QMD0 = SPMCDDBH(5,ES,0,0,5)
ES_QMD5 = SPMCDDBH(5,ES,0,5,10)
ES_QMD10 = SPMCDDBH(5,ES,0,10,15)
ES_QMD15 = SPMCDDBH(5,ES,0,15,20)
ES_QMD20 = SPMCDDBH(5,ES,0,20,25)
ES_QMD25 = SPMCDDBH(5,ES,0,25,99)

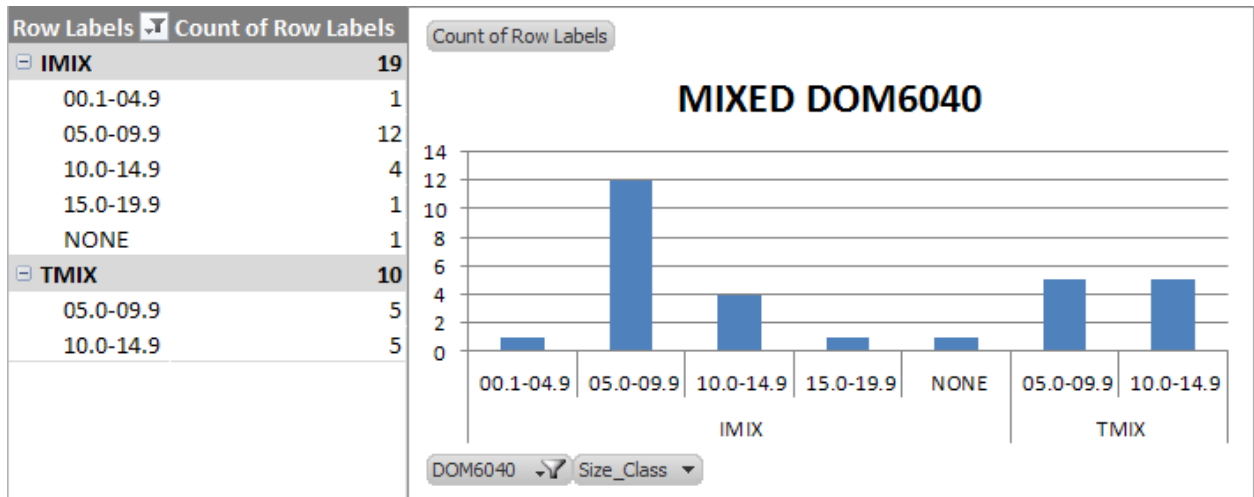
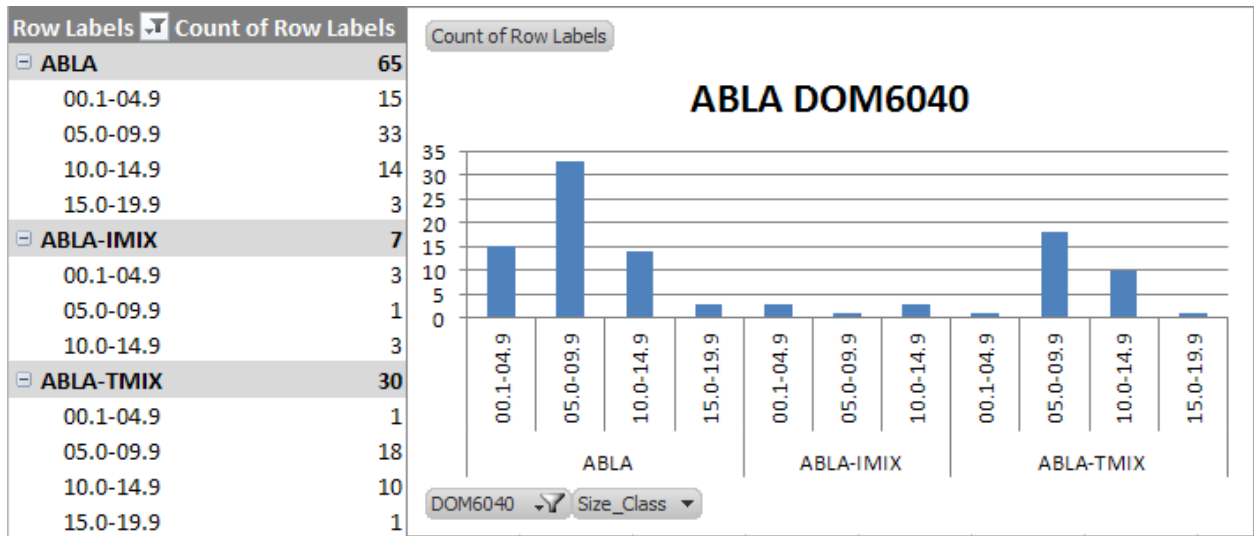
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AF_QMD10 = SPMCDDBH(5,AF,0,10,15)
AF_QMD15 = SPMCDDBH(5,AF,0,15,20)
AF_QMD20 = SPMCDDBH(5,AF,0,20,25)
AF_QMD25 = SPMCDDBH(5,AF,0,25,99)

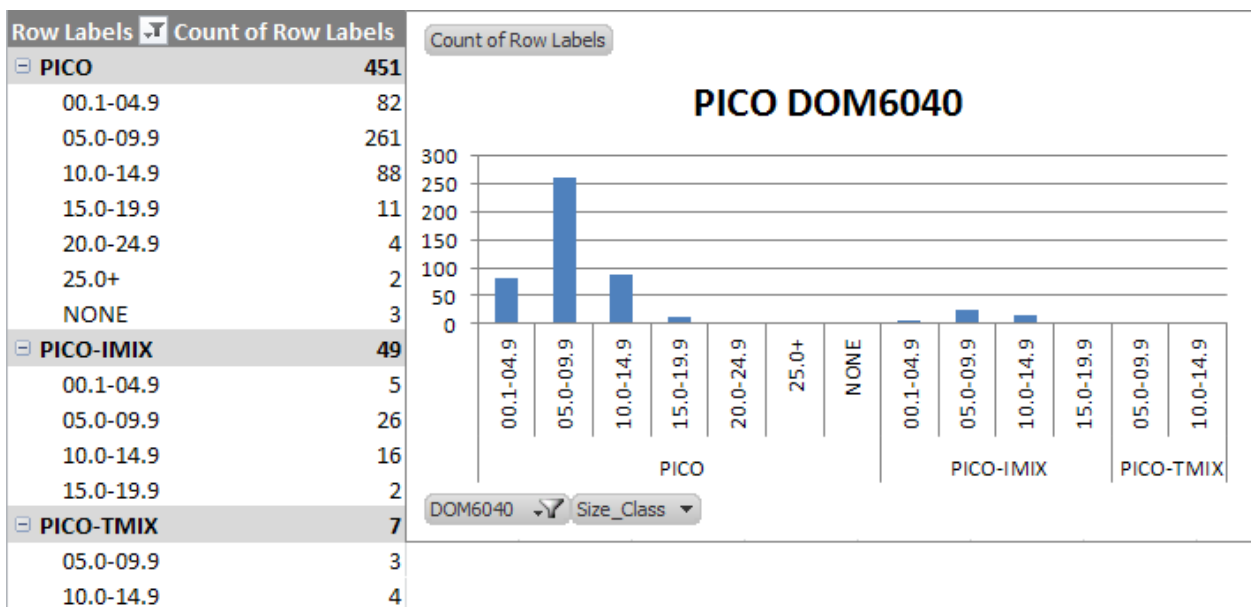
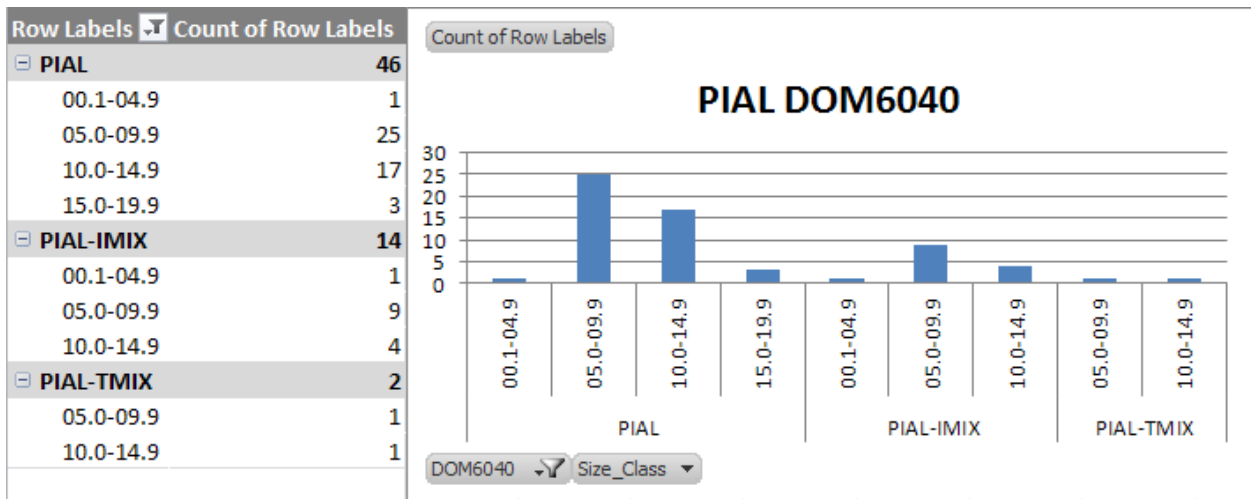
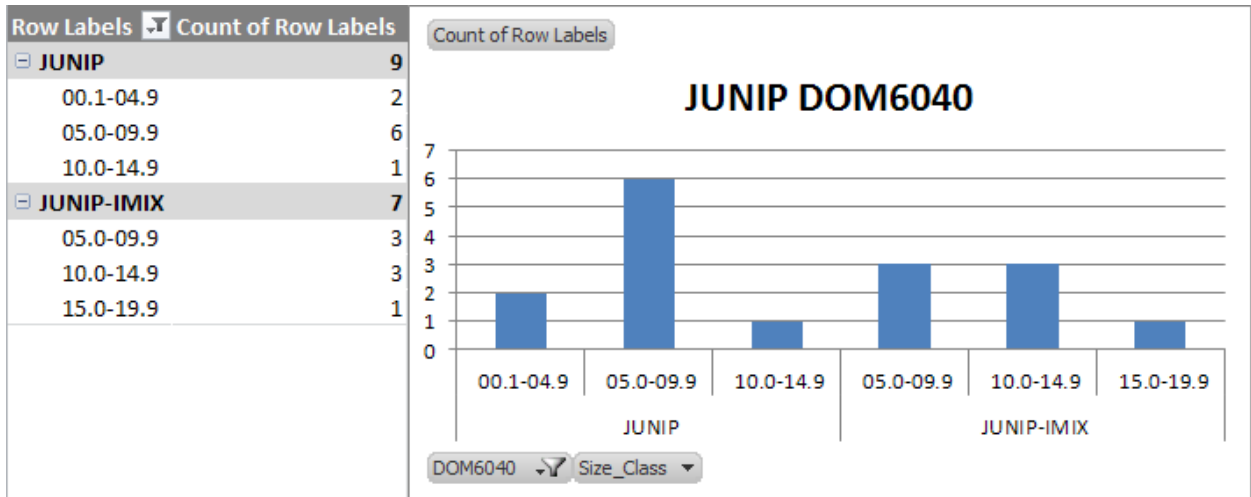
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PP_QMD5 = SPMCDDBH(5,PP,0,5,10)
PP_QMD10 = SPMCDDBH(5,PP,0,10,15)
PP_QMD15 = SPMCDDBH(5,PP,0,15,20)
PP_QMD20 = SPMCDDBH(5,PP,0,20,25)
PP_QMD25 = SPMCDDBH(5,PP,0,25,99)

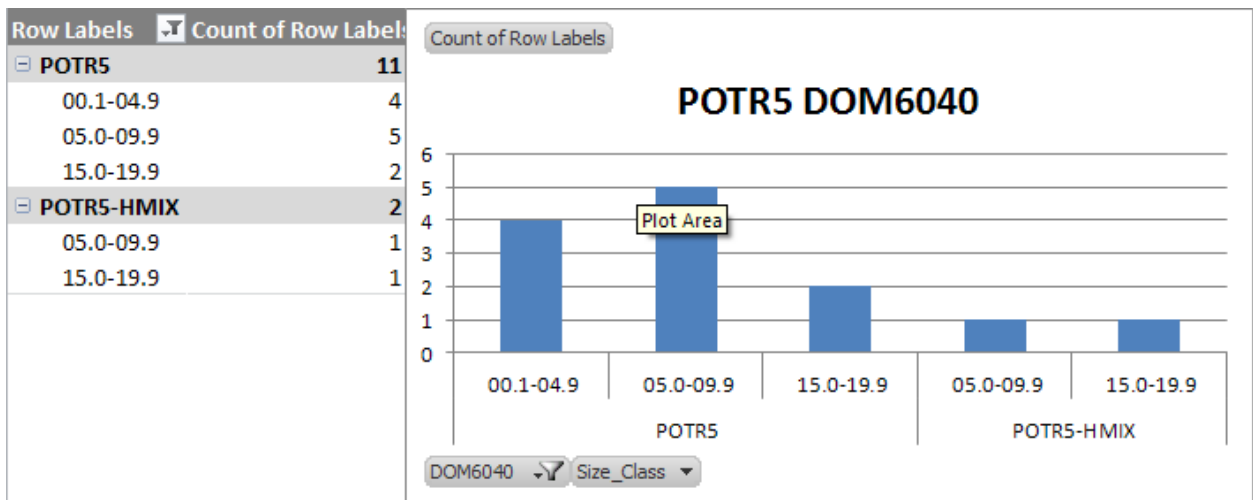
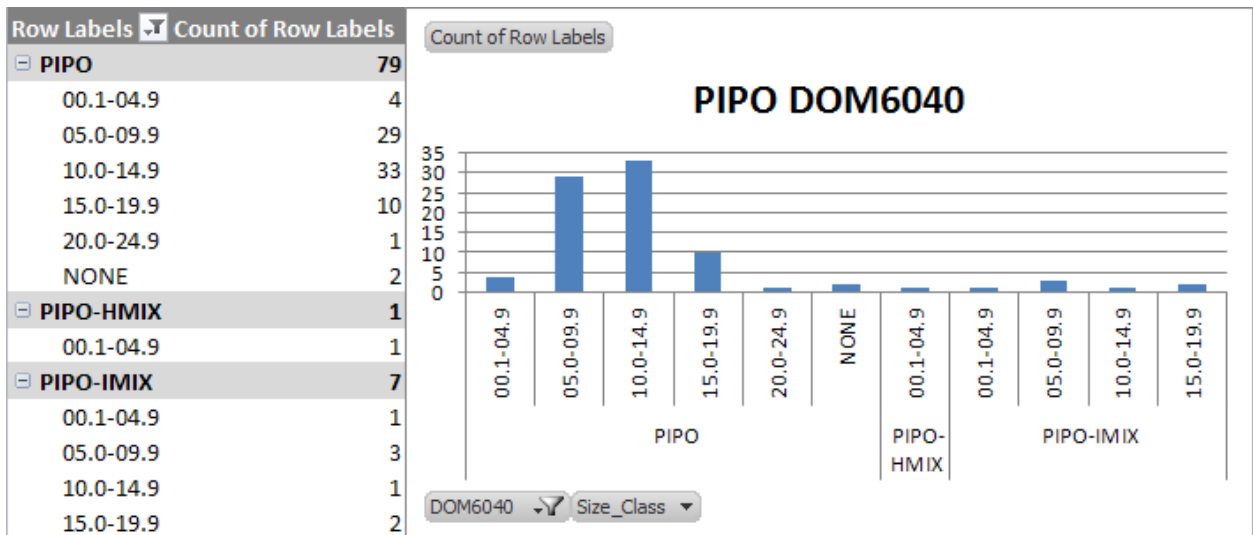
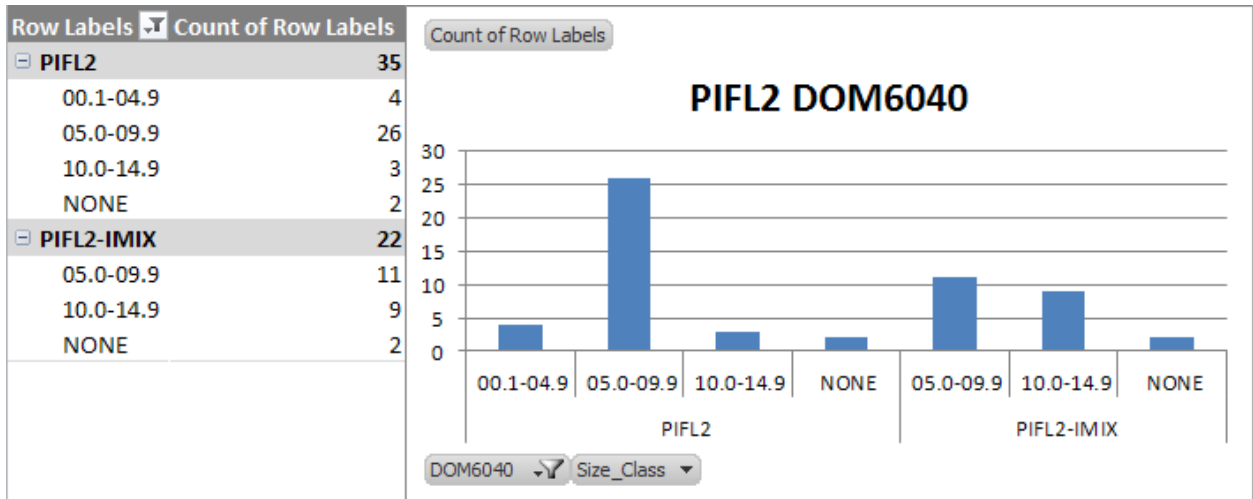
```
OT_QMD0    = SPMCDBH(5,OT,0,0,5)
OT_QMD5    = SPMCDBH(5,OT,0,5,10)
OT_QMD10   = SPMCDBH(5,OT,0,10,15)
OT_QMD15   = SPMCDBH(5,OT,0,15,20)
OT_QMD20   = SPMCDBH(5,OT,0,20,25)
OT_QMD25   = SPMCDBH(5,OT,0,25,99)
END
```

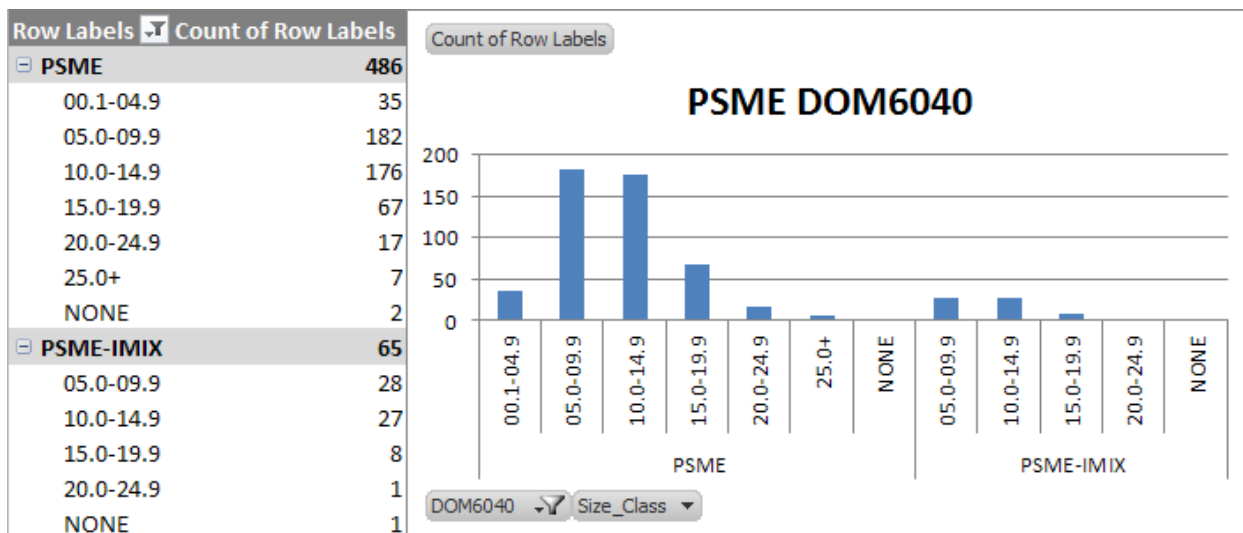
```
DataBase
DSNOut
C:\FVSDData\Jacob_Simpplle\out.mdb
CARBRPTS
Compute
Treelist
Summary
End
```

Appendix C- Plot Distribution Charts within VMAP Groupings









Appendix D – Species Variability within Each DOM6040 Grouping

DOM6040	Species	SS	Pole	MED	L	VLA	VLB
ABLA	ABLA	62463	1642	307	30	0	0
	PIAL	4334	233	0	0	2	0
	PICO	155	89	48	0	0	0
	PIEN	2308	525	61	23	24	0
	PIFL2	599	34	26	0	0	0
ABLA-TMIX	ABLA	67303	2823	443	49	0	0
	PIAL	1041	159	113	59	0	0
	PICO	143	389	209	24	0	0
	PIEN	9478	653	262	155	16	12
	PIFL2	0	36	24	0	0	0
	POTR5	149	0	0	0	0	0
	PSME	13296	114	113	12	12	0
IMIX	ABLA	16614	308	42	12	0	0
	JUSC2	59	58	0	0	0	0
	PIAL	5493	555	148	12	0	0
	PICO	1657	673	134	24	0	0
	PIEN	1352	400	77	12	5	0
	PIFL2	420	59	0	0	0	0
	PIPO	0	0	12	0	0	12
	POTR5	3925	78	42	0	0	0
	PSME	7099	513	117	74	24	0
JUNIP	JUSC2	2733	189	126	6	0	0
	PIPO	299	12	12	0	0	0
	PSME	0	12	0	0	0	0
JUNIP-IMIX	JUSC2	12146	620	67	12	0	0
	PICO	148	12	0	0	0	0
	PIFL2	0	36	0	0	0	0
	PIPO	832	213	102	6	8	0
	PSME	2246	162	12	12	2	2
NONE	ABLA	0	0	0	0	0	0
	JUSC2	150	24	24	0	0	0
	PIAL	155	36	18	0	0	0
	PICO	0	30	6	0	0	0
	PIEN	150	0	0	0	0	0
	PIFL2	257	36	0	0	0	0
	PIPO	273	126	71	39	0	0
	POTR5	0	48	0	0	0	0
	PSME	447	66	42	0	0	2
PIAL	ABLA	51442	1032	114	35	0	0
	PIAL	34124	6861	2060	479	79	2
	PICO	632	88	109	0	12	0
	PIEN	2293	427	203	42	0	0
	PSME	1197	12	0	0	0	0
PIAL-IMIX	ABLA	62768	857	183	2	0	0
	PIAL	11720	1792	403	100	14	6
	PICO	385	82	42	48	0	0
	PIEN	4623	332	206	50	18	4
	PIFL2	149	96	12	0	0	0
	PSME	162	48	22	1	0	0

DOM6040	Species	SS	Pole	MED	L	VLA	VLB
PIAL-TMIX	ABLA	13759	168	48	0	0	0
	PIAL	4319	174	90	0	12	0
	PICO	0	0	0	0	0	0
	PIEN	1948	102	24	12	0	0
PICO	ABLA	162736	1826	176	30	0	0
	JUSC2	149	0	0	0	0	0
	LAOC	149	0	0	0	0	0
	PIAL	11114	120	0	0	0	0
	PICO	123598	34171	5122	322	11	0
	PIEN	22831	623	127	24	0	0
	PIFL2	12123	72	18	12	0	12
	PIPO	0	12	0	0	0	0
	POTR5	10598	54	24	0	0	0
	PSME	38430	1186	191	111	23	5
PICO-IMIX	ABLA	46845	1100	249	0	0	0
	PIAL	2397	306	84	36	0	0
	PICO	19219	3288	807	128	0	0
	PIEN	9396	324	92	25	24	0
	PIFL2	1872	0	0	0	0	0
	PSME	5094	412	109	72	18	0
PICO-TMIX	ABLA	30633	310	36	12	0	0
	PIAL	1332	12	0	0	0	0
	PICO	2445	596	323	84	0	0
	PIEN	9245	502	260	53	12	0
	PSME	0	18	6	0	0	0
PIEN	ABLA	45902	1224	264	12	2	0
	JUSC2	0	24	0	0	0	0
	PIAL	3900	173	114	0	2	0
	PICO	446	263	143	0	0	0
	PIEN	35189	3029	1505	654	169	83
	PIFL2	2157	72	24	0	0	0
	PSME	2235	145	131	36	0	12
PIEN-IMIX	ABLA	299	0	0	0	0	0
	JUSC2	299	0	0	0	0	0
	PICO	0	96	0	0	0	0
	PIEN	1049	120	72	12	2	0
	PODEM	0	0	0	0	2	0
	POTR5	0	144	24	0	0	0
	PSME	1496	24	36	0	0	0
PIEN-TMIX	ABLA	70837	1618	332	51	0	0
	PIAL	4513	534	267	48	13	0
	PICO	1039	150	180	6	2	0
	PIEN	21259	1512	883	288	82	29
	PIFL2	149	0	0	0	0	0
	PIPO	0	0	0	12	0	0
	PSME	6715	109	118	24	14	2
PIFL2	ABLA	893	24	0	0	0	0
	JUSC2	0	12	0	0	0	0
	PIEN	449	12	0	0	0	0
	PIFL2	19459	1447	141	1	0	0
	PIPO	743	0	0	0	0	0
	PSME	7886	36	0	12	0	0

DOM6040	Species	SS	Pole	MED	L	VLA	VLB
PIFL2-IMIX	ABLA	29502	346	19	0	0	0
	PIAL	0	0	0	0	0	0
	PICO	0	66	107	18	0	0
	PIEN	449	108	54	18	0	0
	PIFL2	1339	413	272	24	0	0
	PIPO	0	24	12	0	0	0
	POTR5	1043	48	12	0	0	0
PIPO	PSME	2537	150	36	12	0	0
	FRPE	0	24	0	0	0	0
	JUSC2	5036	993	111	22	0	0
	PIFL2	296	60	36	0	0	0
	PIPO	99590	5919	2190	602	125	35
PIPO-HMIX	PSME	4029	258	12	18	0	12
	PIPO	898	0	0	0	0	0
PIPO-IMIX	POTR5	887	0	0	0	0	0
	JUSC2	0	12	12	0	0	0
	PIFL2	0	147	18	0	0	0
	PIPO	300	185	136	24	0	0
POTR5	PSME	2814	131	84	11	0	0
	ABLA	150	0	0	0	0	0
	PIAL	150	0	0	0	0	0
	PICO	14410	0	0	0	0	0
	PIEN	449	0	0	0	0	0
	POBAT	0	0	0	22	0	0
	POTR5	10577	618	26	7	0	0
POTR5-HMIX	PSME	449	0	0	0	0	0
	ABLA	148	0	0	0	0	0
	PICO	0	119	24	0	0	0
	PIEN	295	172	53	0	0	0
PSME	POTR5	7646	90	0	0	0	0
	ABLA	38835	363	84	12	12	0
	JUSC2	2232	378	30	0	0	0
	PIAL	454	90	24	0	0	0
	PICO	12192	1214	394	117	0	0
	PIEN	14715	956	257	88	0	0
	PIFL2	5180	353	65	0	0	0
	PIPO	897	193	153	12	14	0
	POAN3	0	0	0	0	0	0
	POBAT	0	6	6	0	0	2
	POTR5	5397	96	12	0	0	0
	PSME	133196	17152	7048	2284	775	191
PSME-IMIX	ABLA	25351	535	0	0	0	0
	JUSC2	0	12	0	0	0	0
	PIAL	469	48	0	0	0	0
	PICO	5897	392	238	0	0	0
	PIEN	3593	210	77	0	0	0
	PIFL2	4841	264	12	0	0	0
	PIPO	1799	294	60	72	0	0
	POTR5	145	0	0	0	0	0
TMIX	PSME	30162	885	536	186	28	24
	ABLA	53510	1211	181	10	0	0
	LAOC	0	24	12	0	0	0
	PIAL	2932	193	214	28	0	4
	PICO	593	403	210	24	0	0
	PIEN	10351	430	404	93	20	12
	PIFL2	0	0	0	0	0	0
	PSME	4775	72	90	120	20	0