Spatially Correlated Stand Structures:
A Simulation Approach using Copulas

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ABSTRACT

In this paper, we propose a simple approach that is capable of generating multispecies stand structures. Based on the method of copulas (Genest and MacKay 1986, Am. Stat. 40:280-283), we utilize a normal copula to simulate spatially correlated stand structures. Species composition, diameter, height, and crown ratio distributions of each species, and their correlation with underlying spatial patterns are all controlled by user inputs. Example data sets are used to demonstrate how to estimate required parameters and to compare simulated spatial structures with observed spatial structures.

1 INTRODUCTION

Stand structure can be defined as the species composition, size and spatial distribution of trees and other vegetation within a forest stand (Husch et al. 2003). In addition to influencing growth of individual trees (Garcia 2006, Eerikäinen et al. 2007, Fox et al. 2007a, 2007b), stand structure has been shown to influence a number of biotic and abiotic processes within forest stands (Oliver and Larson 1996). Silviculture activities, such as thinning, impact stand structure (Bailey and Tappeiner 1998), and, as a result, influence wildlife populations (Harrington and Tappeiner 2007, Smith et al. 2008, Yamaura et al. 2008), stand dynamics (Saunders and Wagner 2008), tree regeneration dynamics (Getzin et al. 2008), and understory vegetation (Kembel and Dale 2006, Gilliam 2007).

The past decade has seen a rapid evolution in individual tree growth and yield models. It is generally acknowledged that spatial stand structure is one of the main driving forces behind growth processes, and that stand growth, in return, influences structural composition of

40 woodlands (Pommerening 2006). Several process based models and hybrid models have
41 emerged, and many of these models require spatial data including maps of individual tree
42 locations (e.g., Pretzsch 1992, Pacala et al. 1993, Courbaud 1995).

43 Initialization and testing projections of such models require adequate descriptions of
44 spatial distribution of trees in stands (Pukkala 1988). Collection of such data is generally time
45 consuming and expensive; therefore, very few datasets exists. As a result, several mechanisms
46 for generating spatial data have been proposed (e.g., Stoyan and Penttinen 2000, Valentine et al.
47 2000, Kokkila et al. 2002). Many growth models that require spatial data are highly sensitive to
48 initial stand structure (Valentine et al. 2000, Goreaud et al. 2004, 2006); therefore, it is
49 necessary to have stand structure generators capable of simulating realistic patterns of species
50 composition and spatial and size distribution patterns (Pretzsch 1997).

51 **2 EXISTING APPROACHES**

52 Most approaches, such as those of Valentine et al. (2000) and Kokkila et al. (2002), start
53 with a two-dimensional Poisson point process. Tree locations are generated using one of several
54 point process algorithms (e.g., Penridge 1986, Baddeley and Turner 2008). Depending on the
55 algorithm and parameter values, point patterns can vary from regular lattice processes
56 representing a single species, even-aged plantation to a highly clustered pattern as might be
57 found in a mixed species, uneven-aged stand. Some algorithms have the capability of
58 incorporating spatial inhomogeneity (Baddeley and Turner 2008).

59 Once tree locations (points in the point process) are determined, tree size and species
60 attributes are assigned. In some systems, this is done independently of the point pattern (e.g., Ek
61 and Monserud 1974). This approach ignores competitive interactions between individual trees
62 that greatly influence observed stand structure patterns (Valentine et al. 2000, Kokkila et al.

63 2002, Goreaud et al. 2004). Stand structures generated using such processes are often unrealistic
64 (Valentine et al. 2000, Kokkila et al. 2002), and can influence long-term growth projections
65 (Goreaud et al. 2006).

66 To avoid this problem, Valentine et al. (2000) utilized a multistep process to generate
67 initial stand structures used in the AMORPHYS model. In the first step, tree locations are
68 generated. Diameters are then sampled from a target distribution and assigned randomly to the
69 tree locations. The height of each model tree is then calculated from its assigned diameter and
70 distances to its neighbors. Next, crown length of each tree is calculated from its height and
71 distances to its neighbors. Finally, diameter is recalculated based on height and crown length.
72 While this resulting process produces realistic stand structures, the resulting diameter distribution
73 may deviate from the target distribution as a result of the recalculation step and require re-
74 simulation (Valentine et al. 2000).

75 An alternative approach is to use a marked point process model (Penttinen et al. 1992,
76 Mateu et al. 1998). In a marked point process model, points are tree locations in a Cartesian
77 coordinate system, and marks are qualitative characteristics such as tree species, or quantitative
78 characteristics such as stem diameter or height (Penttinen et al. 1992). Two correlation functions
79 characterize marked point processes (Penttinen et al. 1992): a pair correlation function which
80 characterizes variability within the system of tree locations; and a mark correlation function
81 which characterizes relationships between different sets of trees (marks) conditional on a
82 distance function.

83 Penttinen et al. (1992) provide excellent examples of the application of marked point
84 processes applied to modeling stand structure. Pommerening et al. (2000) and Mateu et al.
85 (1998) demonstrate the use of marked Gibbs processes to model forest stand structures and

discuss how these might be used to simulate forest stand structure. Kokkila et al. (2002) developed a stand structure simulator building upon Penttinen et al.'s (1992), Pommerening et al. (2000), Mateu et al.'s (1998), and others' work. Kokkila et al. (2002) combine marked Gibbs processes with Markov chain Monte Carlo simulation to produce a flexible stand structure simulator. In addition to the pair and mark correlation functions, they incorporate an additional site potential function which provides additional control on the spatial distribution of trees within simulated stands.

While these methods are able to generate structures that statistically resemble example data, no general methods for estimating the parameters required to initialize the simulators are presented (however, see Mateu et al. 1998 and Pommerening et al. 2000). In this paper we present a new approach based on the methods of copulas (Genest and MacKay 1986) and develop a simulation system in R (R Development Core Team 2009).

3 MODELLING APPROACH

Standard Normal copulas are utilized to transform random normal variables into correlated variables. Copulas, though widely utilized in several other fields (Accioly and Chiyoshi 2004, Yan 2007), are not very widely known, or at least not widely utilized, in forestry and natural resource management.

A copula is a multivariate distribution whose marginals are all uniform over (0, 1). For a p-dimensional random vector U on the unit cube, a copula C is:

$$\mathbf{C}(\mathbf{u}_1,\cdots,\mathbf{u_p}) = \Pr(\mathbf{U}_1 \le \mathbf{u}_1,\cdots,\mathbf{U_p} \le \mathbf{u_p}).$$

Because any continuous random variable can be transformed to be uniform over (0, 1) by its probability integral transformation, copulas can be used to provide multivariate dependence independent of marginal distributions (Genest and MacKay 1986, Nelsen 2006, Yan 2007). For

a complete treatment of the theory and basis of copulas see Nelsen (2006) and for a more descriptive treatment see Genest and MacKay(1986).

The basis of our approach assumes there is a correlation between a tree's characteristics (dbh, total height, and crown ratio) and the area available to the tree (Mitchell 1975, Ford and Diggle 1981, Nance et al. 1988, Valentine et al. 2000). A spatial point process (described below) is used to simulate **n** tree locations, and we use the polygon areas of a Voronoi tessellation based on point locations generated from a spatial process to define available polygon area (**apa**). Available polygon areas are standardized :

$$\mathbf{N_{apa}} = \left(\mathbf{apa} - \overline{\mathbf{apa}}\right) \Big/ \sqrt{\sum \left(\mathbf{apa} - \overline{\mathbf{apa}}\right)^2 \Big/ \left(\mathbf{n} - 1\right)},$$

and correlated with vectors of random Normal variables via Wang's (1998) standard Normal copula algorithm as follows:

1) Specify the matrix of partial correlations between available polygon area, diameter and height:

$$\Sigma = \begin{bmatrix} 1 & \rho_{\mathbf{apa},\mathbf{dbh}} & \rho_{\mathbf{apa},\mathbf{ht}} & \rho_{\mathbf{apa},\mathbf{cr}} \\ \rho_{\mathbf{dbh},\mathbf{apa}} & 1 & \rho_{\mathbf{dbh},\mathbf{ht}} & \rho_{\mathbf{dbh},\mathbf{cr}} \\ \rho_{\mathbf{ht},\mathbf{apa}} & \rho_{\mathbf{ht},\mathbf{dbh}} & 1 & \rho_{\mathbf{ht},\mathbf{cr}} \\ \rho_{\mathbf{cr},\mathbf{apa}} & \rho_{\mathbf{cr},\mathbf{dbh}} & \rho_{\mathbf{cr},\mathbf{ht}} & 1 \end{bmatrix}$$

2) Obtain the upper diagonal matrix [**A**] such that $\Sigma = \mathbf{A}'\mathbf{A}$. We obtain this using Choleski's decomposition (Andersen et al. 1999) in R.

3) Based on the number of points, **n**, generated with the spatial point process, generate three random standard Normal (**N**(0,1)) vectors ($\mathbf{N_{dbh}}, \mathbf{N_{ht}}, \mathbf{N_{cr}}$) of length **n**. The vectors are column bound with $\mathbf{N_{apa}}$ to form an augmented matrix, **M**:

$$\mathbf{M} = \left[\mathbf{N_{apa}} \quad \mathbf{N_{dbh}} \quad \mathbf{N_{ht}} \quad \mathbf{N_{cr}}\right].$$

4) The columns of **M** are then correlated using **A**, the upper diagonal decomposition of Σ:

$$\mathbf{Z} = |\mathbf{M}| \cdot |\mathbf{A}| .$$

Because of the structure of A, the first column of **M**, corresponding to $\mathbf{N_{apa}}$, remains unchanged, and $\mathbf{N_{dbh}}$, $\mathbf{N_{ht}}$, and $\mathbf{N_{cr}}$ are correlated both with the underlying spatial pattern and the dbh-height-crown ratio relationships.

5) The Normal margins are stripped by applying the inverse cumulative Normal probability distribution:

$$\mathbf{U} = \left[\Phi^{-1}(\mathbf{Z_{apa}}) \quad \Phi^{-1}(\mathbf{Z_{dbh}}) \quad \Phi^{-1}(\mathbf{Z_{ht}}) \right].$$

U is a standard Normal copula (Wang 1998).

6) The correlated size-spatial data are then obtained by applying the appropriate cumulative margin distribution functions, $\mathbf{F_i}(\mathbf{u_i})$, to the columns of **U**. For **apa**, the cumulative function is the inverse of the standardization formula, or simply the original Voronoi polygon areas. The marginal distribution functions for diameter, height and crown ratio are described below.

3.1 Spatial Models

We utilize two spatial processes: a Lattice Process and a Thomas Process. The lattice process is used to simulate plantation spacing and is implemented in a custom function in R (R Development Core Team 2009), *rlattice*. This function utilizes the *rlinegrid* function (Baddeley and Turner 2008). Angles for the x-oriented lines and y-oriented lines are specified. The **x-angle** and **y-angle** must be of opposite sign and between 0 and 90 degrees to insure that lines intersect. The desired **density** (number of trees within the stand) and the **xy-ratio** must also be specified. The stand area, **density** and **xy-ratio** define the spacing of the x and y lines. The **xy-**

ratio specifies the relative spacing of x lines versus y lines and if not equal to 1 will result in rectangular spacing. The *rlinegrid* function is used to generate a set of x-lines based on **x-angle** and **x-spacing** and a set of y-lines based on **y-angle** and **y-spacing**. The intersections of the two sets of lines define the lattice points. Random variation is added using the *jitter* function, with a **jitter-factor** parameter that defines how much random variation about the lattice intersection exists. Using a **jitter-factor** greater than 0 is the only method to add inhomogeneity into the lattice process. Examples of a lattice process with and without jittering are shown in figures 1A and 1B.

The Thomas process simulates clustering, and utilizes the *rThomas* function which implements a realization of a Thomas cluster process (Baddeley and Turner 2008). As with the lattice process, the desired **density** must be specified. **Density** is then used to calculate the **kappa** parameter (intensity of the parent process) for the *rThomas* function based on the stand area and expected number of points per cluster parent (**mu**). The expected number of points per parent (**mu**) and the standard deviation of displacement about parents (**sigma**) determine the number of points and spatial extent of each cluster. By controlling **mu** and **sigma**, the degree of clustering in the spatial process is controlled. Inhomogeneity can be simulated by specifying the name of an R pixel image (object class *im*) for **mu** rather than a numeric value (see the help pages for *rThomas* for examples of creating pixel images). Figures 1C and 1D illustrate a Thomas process with a low level of clustering and an inhomogeneous Thomas process with high density toward the center and decreasing density toward the edges.

After the point process is generated, the Voronoi functions provided in the tripack package (Gebhardt 2009) are utilized. The *voronoi.mosaic* function is run to generate the Voronoi polygons and the *voronoi.area* function is used to calculate the area of each Voronoi

polygon which is is used as our estimate of available polygon area (**apa**) for each tree. Boundary points are torused by default so that edge points have bounded Voronoi polygons. The Voronoi object returned by the *voronoi.mosaic* function forms the base of the data frame used to store tree characteristics.

3.2 Species – Size Distributions

Diameter and height distributions are specified using mixture Weibull distributions (Liu et al. 2002, Zhang and Liu 2006), and crown ratio is specified using a mixture four-parameter Beta distribution. A mixture distribution is defined as a frequency distribution made up of two or more component distributions. The distribution of the i^{th} individual component is described by a specific probability density function (pdf), $\mathbf{f_i(x)}$. Then the general pdf, $\mathbf{f(x)}$ for the mixture distribution is expressed as:

$$\mathbf{f(x)} = \sum_{\mathbf{i}=1}^{\mathbf{k}} \mathbf{p_i f_i(x)} = \mathbf{p_1 f_1(x)} + \mathbf{p_2 f_2(x)} + \cdots + \mathbf{p_k f_k(x)},$$

where $\mathbf{p_i}$ = the probability of belonging to component **i**. In this case, $\mathbf{p_i}$ is derived from species composition and $\mathbf{f_i(x)}$ are species-specific distributions.

Species composition can be specified in a number of ways including percentiles, quantiles, or actual densities of each species. During the structure simulation process, the specified composition is converted into a frequency distribution ($\mathbf{p_i}$) and used to randomly assign species to each tree (point).

For diameter, the inverse cumulative two-parameter Weibull distribution function is used to obtain values:

$$\mathbf{D_i} = \mathbf{b_i}\left[-\ln(1-\mathbf{u})\right]^{(1/\mathbf{c_i})},$$

where $\mathbf{D_i}$ is diameter of the i^{th} species corresponding to cumulative probability **u**; **u** is a cumulative probability obtained from a standard Normal copula; $\mathbf{b_i}$ is a species-specific Weibull scale parameter; and $\mathbf{c_i}$ is a species-specific Weibull shape parameter. Species-specific two-parameter Weibull distributions were used for simulating dbh because of the flexibility of the Weibull distribution, wide application in forestry, and readily available methods for estimating the parameters (Bailey and Dell 1973, Hyink and Moser 1983, Little 1983, Robinson 2004).

A modified three-parameter reverse Weibull distribution (Robinson 2004) was chosen for the species-specific height distributions. The cumulative three-parameter Weibull distribution is given by:

$$\mathbf{F_i(h \le H) = e^{-\left(\frac{a_i - H}{b_i^*}\right)^{c_i}}}$$

where, $\mathbf{a_i}$ is a species-specific maximum height $(\max(\mathbf{H}) - \mathbf{H_B})$; $\mathbf{b_i^*}$ is a species-specific scale parameter; and $\mathbf{c_i}$ is a species-specific shape parameter. The scale parameter, $\mathbf{b_i^*}$, is defined in reverse from the maximum, $\mathbf{a_i}$, and would be interpreted as distance below maximum height. $\mathbf{H_B}$ is the height at which diameter is measured, typically referred to as breast height (1.3 m in metric and 4.5 ft in Imperial). In order to make the scale parameter interpretable in terms of tree height, we use $\mathbf{b_i^* = a_i - b_i}$. The inverse cumulative distribution function for the modified reverse Weibull becomes:

$$\mathbf{H_i = H_B + a_i + (b_i - a_i)[-\ln(u)]^{(1/c_i)}}.$$

213 Inclusion of $\mathbf{H_B}$ insures that no tree is shorter than the height at which diameter is measured.
214 Like the two parameter Weibull distribution, parameter estimation for the three-parameter
215 reverse Weibull is relatively straightforward (Robinson 2004).

216 For crown ratio, **CR**, a 4-parameter Beta distribution (Johnson et al. 1995 pp. 210 - 275)
217 is used. The pdf for the four parameter Beta distribution is given by:

218 $$\mathbf{f(CR)} = \left(\frac{\Gamma(\alpha+\beta)}{\Gamma(\alpha)\Gamma(\beta)}\right)\left(\frac{\mathbf{CR}-\xi}{\lambda-\xi}\right)^{\alpha-1}\left(1-\frac{\mathbf{CR}-\xi}{\lambda-\xi}\right)^{\beta-1},$$

219 where α and β are the Beta shape parameters, ξ is the minimum crown ratio, λ is the maximum
220 crown ratio, $\Gamma(\bullet)$ is the gamma function, and **CR** is the observed crown ratio. Simulated crown
221 ratios are obtained using the *rbeta* function in R using the correlated **U**(0,1)'s from the Normal
222 copula. The *rbeta* function is a two parameter Beta distribution and returns a random variable, **Z**,
223 between 0 and 1. **Z** is transformed into crown ratio using:

224 $$\mathbf{CR} = \xi + \mathbf{Z}\cdot(\lambda-\xi).$$

225 The beta parameters are readily estimated using the method of moments or maximum likelihood
226 methods (Johnson et al. 1995 pp. 210 - 275).

227 The mixture distributions are simulated using the following algorithm:

228 1) For the **n** points generated in the spatial process, species is assigned randomly based on a
229 weighted probability as defined by species composition.
230 2) Once species are assigned, then the species-specific distribution parameters are used to
231 calculate diameter, height, and crown ratio using the correlated U(0,1)'s from the
232 standard Normal copula as cumulative probabilities .

233 The algorithm is implemented in a custom R function *q.mixed*.

234 **4 THE STAND GENERATOR**

The stand generator is developed in the R statistical package (R Development Core Team 2009) and is implemented in a custom R function *stand.generate*. We utilize three contributed packages: spatstat (Baddeley and Turner 2008); tripack (Gebhardt 2009); and tcltk (Dalgaard 2001). The required inputs, structure generation, and visualization are controlled through a series of input windows built using the tcl/tk interface within R version 2.10.1.

The stand generator starts with a main menu window (Figure 2A). The input is divided into three components: Spatial; Species; and Correlation. The Spatial window (Figs. 2B and 2C) allows users to specify spatial information such as dimensions of the stand, desired density, and underlying spatial models. Currently, only rectangular stand areas are supported. Points are torused around the bounding box so that tree locations near the edge will have complete Voronoi polygons. Torusing can be turned off; however, the functions used to calculate the Voronoi polygon areas delete edge points with unbounded Voronoi polygons.

Species composition, diameter, height and crown ratio distribution parameters are specified in the Species window (Fig. 2D). Currently the system allows up to 10 species to be specified. The Correlation window (Fig. 2E) allows the user to specify desired correlations between available tree area, diameter, height, and crown ratio.

When the Generate button is pressed, the required inputs are used to generate the spatial processes, the voronoi polygon areas, and the trees' species-size distributions. The output is stored in a temporary data frame named temp.Trees. Each time Generate is clicked, temp.Trees is over written; therefore, if a user wishes to save results, temp.Trees must be save to a new file before Generate is reclicked. The Visualization window (Fig. 2F) writes an external Stand Visualization System (McGaughey 1997) compatible file and runs SVS (SVS must be installed on the computer) which displays the generated stand structure (Fig. 2G).

The R code for the stand generator is available at http://ifmlab.for.unb.ca/People/Kershaw. The stand generator will run on all platforms supported by R; however, the visualization step only runs on Windows-based platforms since it utilizes the stand visualization system which is a Windows-based application.

5 EXAMPLES

Data from two different studies are used to demonstrate parameter estimation and test simulation results. The first data set is a 4 ha mapped longleaf pine (*Pinus palustris* Mill.) stand (Platt et al. 1988) consisting of 584 trees. Only diameter at breast height (DBH) and tree locations were measured in this dataset. Total height was predicted using the height – diameter equation found in Shaw and Long (2007). Random error, sampled from a Normal distribution and correlated with available polygon area was added to the predicted heights. Crown ratio was predicted using the crown ratio equation by Acharya (2006)and random error based on the root mean square error was added to the predicted crown ratios from Acharya (2006) so that the resulting predicted crown ratios were correlated with available polygon area. Random errors were added to predicted heights and crown ratios to both add a degree of spatial correlation to the predicted data and reduce correlations within tree parameters. The resulting individual tree summary statistics for this dataset are shown in table 1.

The second dataset is a 50 m by 50 m mapped plot located in a mixed species Acadian Forest stand in central New Brunswick. Wooden stakes were surveyed and placed in the ground on a 10 m by 10 m grid. Distance (nearest .01 m) from two adjacent stakes were measured to the face of each tree in each 10m by 10 m block and triangulation, based on side-side-side geometry, was used to determine the xy coordinates of each tree. Tree species was noted, and dbh (nearest 0.1 cm) was measured with a diameter tape, and height (nearest 0.1 m) and height to crown base

(nearest 0.1 m) were measured with an Optilogic 800LH hypsometer (Opti-Logic Corporation, Tullahoma, TN). There were nine different species in this example: balsam fir (*Abies balsamea* (L.) Mill.); spruce (mostly black spruce (*Picea mariana* (Mill.) Britton, Sterns & Poggenb.) with some red spruce (*Picea mariana* (Mill.) Britton, Sterns & Poggenb.); eastern cedar (*Thuja occidentalis* L.); eastern hemlock (*Tsuga canadensis* (L.) Carrière); red maple (*Acer rubrum* L.); white birch (*Betula papyrifera* Marsh.); yellow birch (*Betula alleghaniensis* Britton); white ash (*Fraxinus americana* L.); and American mountain-ash (*Sorbus americana* Marsh.).The individual tree summary statistics by species for this dataset are shown in table 1.

5.1 Parameter Estimation

Thomas spatial processes were used to model spatial locations for both example datasets. Parameters for the Thomas process were estimated using the procedure described by Møller and Waagepetersen (2003 pp. 192 - 197) and Waagepetersen (2008) and implemented in the R function *thomas.estK*. The current version of the stand structure generator only allows a single spatial process for the entire stand; therefore, only a single process was estimated for the mixed species Acadian Forest dataset. The estimated parameters for the Thomas process are shown in table 2.

Maximum likelihood estimates of the Weibull shape and scale parameters for the diameter and height distributions were estimated using a modification of Robinson's (2004) algorithm. The minimum measured diameter (2.0 cm dbh for the Longleaf Pine dataset and 8.0 cm dbh for the Acadian Forest dataset) were used as the truncation points for the two-parameter left-truncated Weibull distribution (Table 3) and the maximum observed height (plus 0.1 m) for each species was used as the location parameter in the three-parameter reverse Weibull distribution (Table 4). The minimum and maximum crown ratios were used as the bounds of the

four parameter Beta distribution. The mean and variance of crown ratio was calculated and moment-based parameter recovery used to estimate the two Beta shape parameters (Table 5). The longleaf pine data were distinctly bimodal in the dbh and height distributions; therefore, the data were divided into overstory trees (trees > 24 cm dbh) and understory trees (trees $\leq$ 24 cm dbh).

The correlation matrix used in the standard Normal copula is the matrix of partial correlations between available polygon area and the tree characteristics. Because the marginal distributions are neither Normal nor the same distribution, we used Spearman's rank correlation coefficient (Zar 1999 pp. 395-398) rather than Pearson's correction coefficient (Table 6).

5.2 Assessment of Simulated Stand Structures

Fifty simulated stand structures were generated using the estimated parameters from each example dataset. The simulation results were compared to the observed results using the mark correlation coefficient of Stoyan and Stoyan (1994 pp. 262 - 266) as implemented in the R function *markcorr*. Observed and simulated mark correlations versus neighborhood radius are shown in figure 3. While the average mark correlations from the simulated stand structures were smoother than observed correlations, individual simulations often produced local peaks at or near the same spatial scales as the observed data. With the exception of the shorter neighborhood radii, the range of correlations from the simulated data included the observed correlations. This was especially obvious in the Longleaf Pine dataset (Fig. 3A). The smaller range of simulated variability observed in the height (Fig. 3C) and crown ratio (Fig. 3E) in the Longleaf Pine dataset was the result of the high correlations with dbh (Table 6) resulting from the prediction of the these variables using dbh.

6 DISCUSSION AND CONCLUSIONS

The stand structure generator developed in this paper is a simple and efficient method to simulate realistic stand structures. The distributions used to simulate the tree attributes are distributions commonly used in forestry research. The parameters of these distributions are easily estimated from observed data via maximum likelihood methods or moment-based parameter recovery methods. Moment-based parameter recovery methods are especially useful when only stand-level summaries are available (Hyink and Moser 1983). Any distribution could be substituted for those we chose by modifying the input menus and inverse cumulative distribution functions.

The use of a Normal copula (Wang 1998) provides an intuitive and fast method for generating the desired spatial dependency. Copulae are applied in many different fields to model complex dependencies (Accioly and Chiyoshi 2004). The critical assumption in the application present in this paper is that available polygon area provides the basic measure of spatial dependency. The available polygon area was proposed by Nance et al. (1988). Here we use Voronoi polygons which are tessellations of the stand area based on perpendicular bisectors of a tree and its immediate neighbors (Bowyer 1981). Nance et al. (1988) proposed weighted polygons, where the division of area was based upon a weighted tree size such that the bisecting line is located further away from the larger tree. This concept is the basis for many distance-dependent measures of competition (Tomé and Burkhart 1989, Stage and Ledermann 2008). While we do not produce weighted polygon areas, the copula produces effects similar such that larger trees tend to be located in larger polygons (assuming the correlation coefficient is positive).

A limitation to the copula approach is that all species have the same spatial and intra-tree level correlation coefficients. The system proposed by Valentine et al. (2000) has similar

limitations; however, systems based on Gibbs processes can have “repulsive potentials” that vary by species producing spatial patterns that vary by species (Kokkila et al. 2002). The advantage of the copula approach over these other approaches is that trees do not have to be spatially shifted based on potentials (Kokkila et al. 2002, Goreaud et al. 2004) or have tree attributes re-simulated to achieve the desired tree and or spatial distributions (Valentine et al. 2000). Eliminating the need for shifting or re-simulating distributions greatly increases the computational efficiency of our system relative to other systems. Further, the use of the correlation structure to determine the tree attributes (ie, dbh, height, and crown ratio) enables simulation of greater levels of variability and more realistic stand structures than predictive systems that often result in lower variation and greater ordering of tree attributes (ie, largest dbh trees tend to be the tallest, etc.).

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510

511 Table 1. Mean individual tree characteristics by species for the Longleaf Pine and Acadian
512 Forest example datasets. Number of observations appear below species code, and range is shown
513 in parentheses. Height and crown ratio are simulated for the longleaf pine data.

Species[1]	Parameter							
	DBH (cm)		Height (m)		Crown Ratio		Tree Area (m^2)	
	Mean	Std. Dev.	Mean	Std. Dev.	Mean	Std. Dev.	Mean	Std. Dev.
-- Longleaf Pine Dataset --								
LP	26.8	18.33	18.5	9.66	0.53	0.025	68.49	61.446
n=584	(2.0, 75.9)		(1.3, 39.9)		(0.50, 0.73)		(0.52, 407.88)	
-- Acadian Forest Dataset --								
BF	12.4	3.53	11.5	3.39	0.66	0.181	10.59	4.667
n=42	(8.1, 23.3)		(6.4, 18.5)		(0.17, 0.92)		(3.57, 23.01)	
SP	22.7	8.49	17.2	4.63	0.66	0.137	10.43	4.610
n=60	(9.0, 43.9)		(4.7, 24.3)		(0.30, 0.98)		(1.94, 23.66)	
EC	26.1	6.66	15.8	2.88	0.60	0.141	8.14	4.282
n=61	(11.1, 44.4)		(9.3, 21.2)		(0.28, 0.91)		(1.50, 21.16)	
EH	25.4	5.72	13.8	3.40	0.63	0.118	9.52	5.930
n=13	(16.1, 35.3)		(6.8, 17.6)		(0.46, 0.84)		(3.10, 24.25)	
RM	18.5	6.00	17.1	3.29	0.68	0.114	7.69	5.338
n=64	(8.3, 37.2)		(9.1, 24.2)		(0.45, 0.85)		(0.90, 22.33)	
WB	23.7	7.23	19.4	2.85	0.68	0.115	11.75	6.457
n=13	(10.5, 33.1)		(11.9, 23.7)		(0.51, 0.82)		(5.27, 28.41)	
YB	19.8	7.400	16.1	3.95	0.56	0.106	10.02	4.087
n=18	(9.0, 32.9)		(6.4, 22.1)		(0.37, 0.76)		(5.74, 21.02)	
WA	23.9	11.870	18.1	2.98	0.76	0.082	11.17	5.218
n=6	(8.7, 38.0)		(14.0, 23.2)		(0.65, 0.84)		(2.74, 15.52)	
AM	13.7	--	13.7	--	0.71	--	4.15	--
n=1	(--)		(--)		(--)		(--)	

514 [1]LP = longleaf pine; BF = balsam fir; SP = spruce; EC = eastern cedar; EH = eastern hemlock;

515 RM = red maple; WB = white birch; YB = yellow birch; WA = white ash; and AM = American

516 mountain-ash.

517

518 Table 2. Estimated parameters for the Longleaf Pine and Acadian Forest datasets.

Parameter	Dataset	
	Longleaf Pine	Acadian Forest
mu	5.7964	0.3054
sigma	4.1094	0.3204
kappa	2.5188×10^{-3}	0.3378
density (trees in area)	584	258
x-range	{0, 200}	{0, 50}
y-range	{0, 200}	{0, 50}

519

520 Table 3. Maximum likelihood estimates of the two-parameter, left-truncated Weibull distribution
521 for modelling dbh distributions by species.

Species	Parameter		
	Truncation (min. dbh, cm)	scale (b)	shape (c)
longleaf pine			
understory trees	2.0	8.8774	1.1236
overstory trees	24.0	44.1230	3.5925
balsam fir	8.0	10.1321	2.0094
spruce	8.0	24.9090	2.6850
eastern cedar	8.0	28.6132	4.2684
eastern hemlock	8.0	27.5676	5.3549
red maple	8.0	19.6190	2.8448
white birch	8.0	26.5636	4.3360
yellow birch	8.0	21.1103	2.6357
white ash	8.0	24.5526	1.9063
American mountain-ash[1]	8.0	13.7000	3.6000

522 [1]American mountain-ash had only 1 observation, scale parameter set to the observed dbh and the
523 shape parameter to be a symmetric distribution.

524

525 Table 4. Maximum likelihood estimates of the three-parameter, reverse Weibull distribution for
526 modelling height distributions by species.

Species	Parameter		
	location (max. ht., m)	scale[1] (b)	shape (c)
longleaf pine			
understory trees	22.7	8.3569	2.6615
overstory trees	40.1	25.2362	3.5502
balsam fir	18.6	10.7582	2.0524
spruce	24.4	16.4588	1.5749
eastern cedar	21.3	15.1229	1.9645
eastern hemlock	17.7	13.6660	1.1269
red maple	24.3	16.3058	2.1941
white birch	23.8	19.0692	1.5600
yellow birch	22.2	17.4692	1.4917
white ash	23.3	17.8289	1.3122
American mountain-ash[2]	14.7	13.7	3.6

527 [1]scale parameter defined in terms of height above ground, true scale parameter is height below
528 maximum and is location – scale. [2]American mountain-ash only had 1 observation, location was
529 set 1 m above observed value, scale was set to the observed value, and the shape was set to a
530 symmetric distribution.

531

532 Table 5. Minimum, maximum, mean and variance of crown ratio by species. Values are used to

533 obtain parameter recovery estimates of the 4-parameter Beta distribution.

Species	Parameter			
	Minimum	Maximum	Mean	Variance
longleaf pine				
understory trees	0.50	0.56	0.51	0.0001
overstory trees	0.51	0.73	0.54	0.0006
balsam fir	0.16	0.92	0.66	0.03268
spruce	0.30	0.99	0.66	0.01865
eastern cedar	0.27	0.91	0.60	0.01992
eastern hemlock	0.46	0.85	0.63	0.01381
red maple	0.45	0.85	0.67	0.00916
white birch	0.51	0.83	0.68	0.01266
yellow birch	0.36	0.76	0.56	0.01066
white ash	0.65	0.85	0.76	0.00681
American mountain-ash[1]	0.66	0.76	0.71	0.00071

534 [1]American mountain-ash only had 1 observation, minimum and maximum set to .05 below and

535 above the observed value, and mean and variance set to make a uniform distribution.

536

Table 6. Partial correlations, based on Spearman's rank correlation, between available tree area, DBH, height and crown ratio for the Longleaf Pine and Acadian Forest datasets.

Correlation	Dataset	
	Longleaf Pine	Acadian Forest
area – DBH	0.5556	0.1639
area – Height	0.6196	0.1313
area – Crown Ratio	0.7042	-0.1764
DBH – Height	0.9808	0.7118
DBH – Crown Ratio	0.9540	-0.2664
Height – Crown Ratio	0.9849	-0.1564

Figure Titles

Figure 1. Examples of spatial patterns: A) lattice process with no variation; B) a lattice process with multiplicative jittering; C) a homogeneous Thomas process; and D) an inhomogeneous Thomas process.

Figure 2. Input windows for the stand structure generator:A) the main menu; B) the lattice spatial model input window; C) the Thomas spatial model input window; D) the species parameter input window; E) the correlation input window; F) the visualization input window; and G) and example Stand Visualization window.

Figure 3. Marked spatial correlations for the example datasets: A) longleaf pine dbh; B) Acadian Forest dbh; C) longleaf pine height; D) Acadian Forest height; E) longleaf pine crown ratio; and F) Acadian Forest crown ratio.

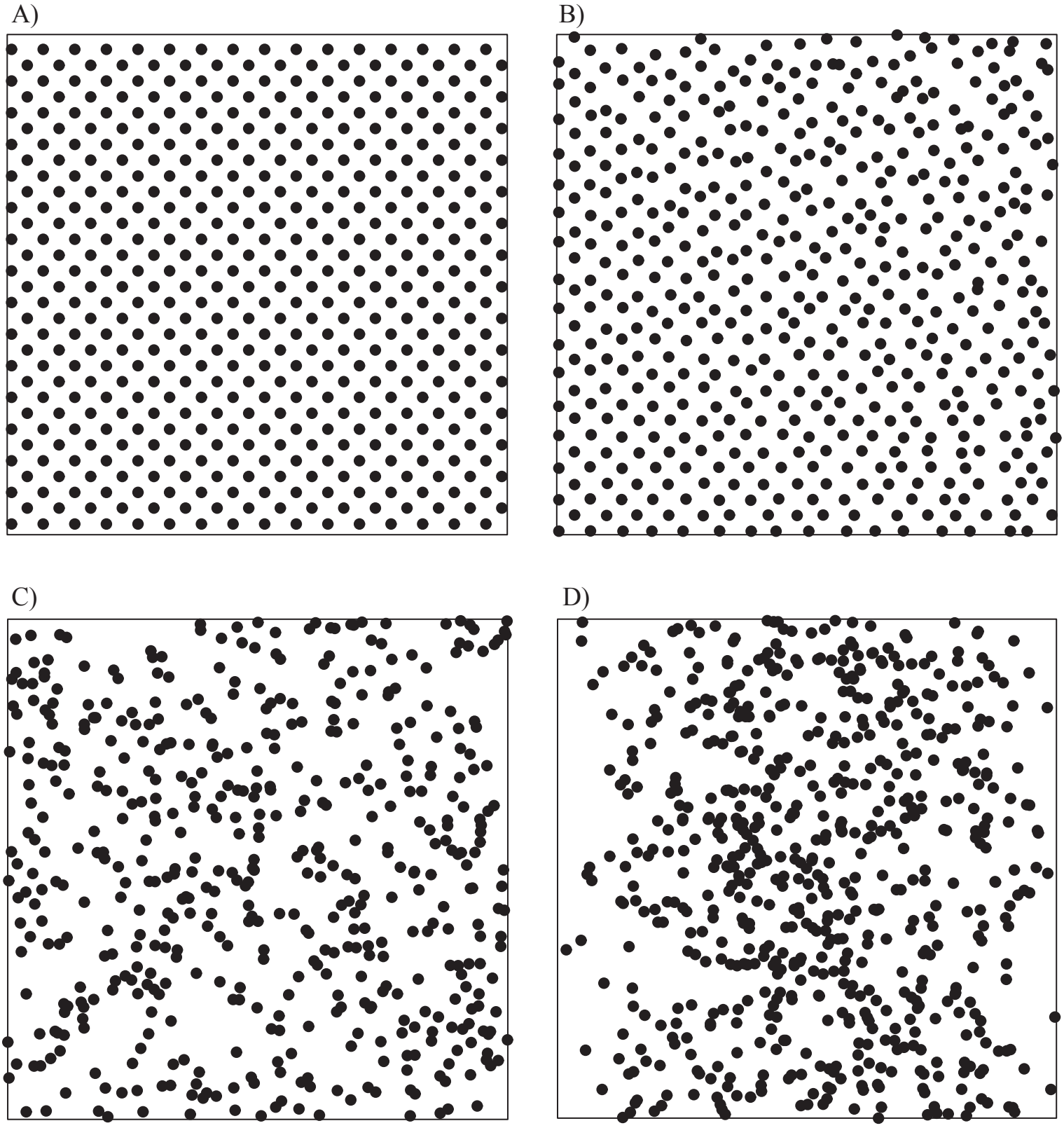
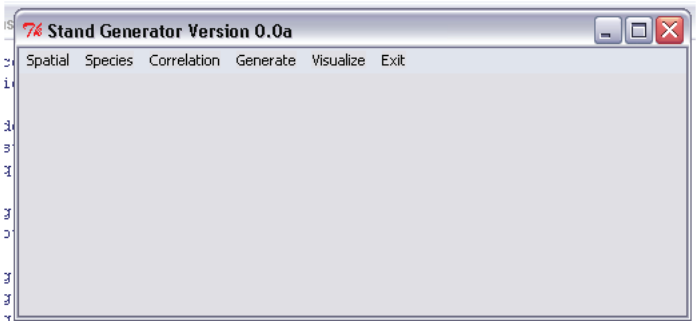
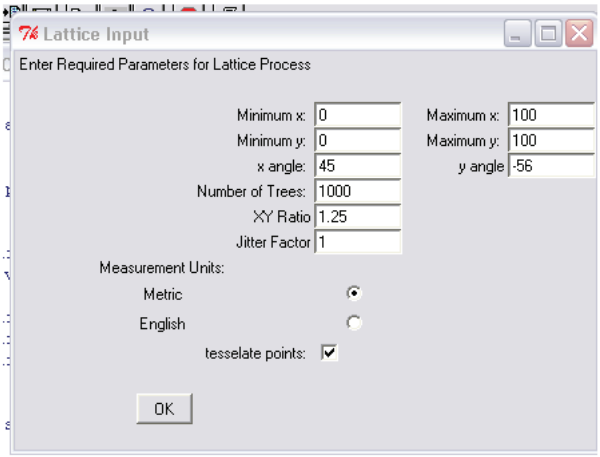


Figure 1

A)



B)



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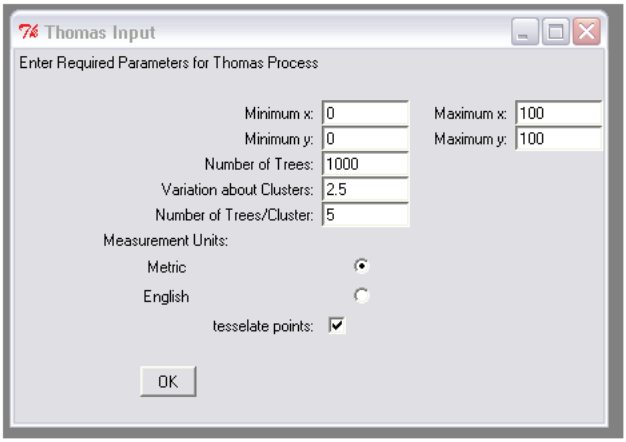
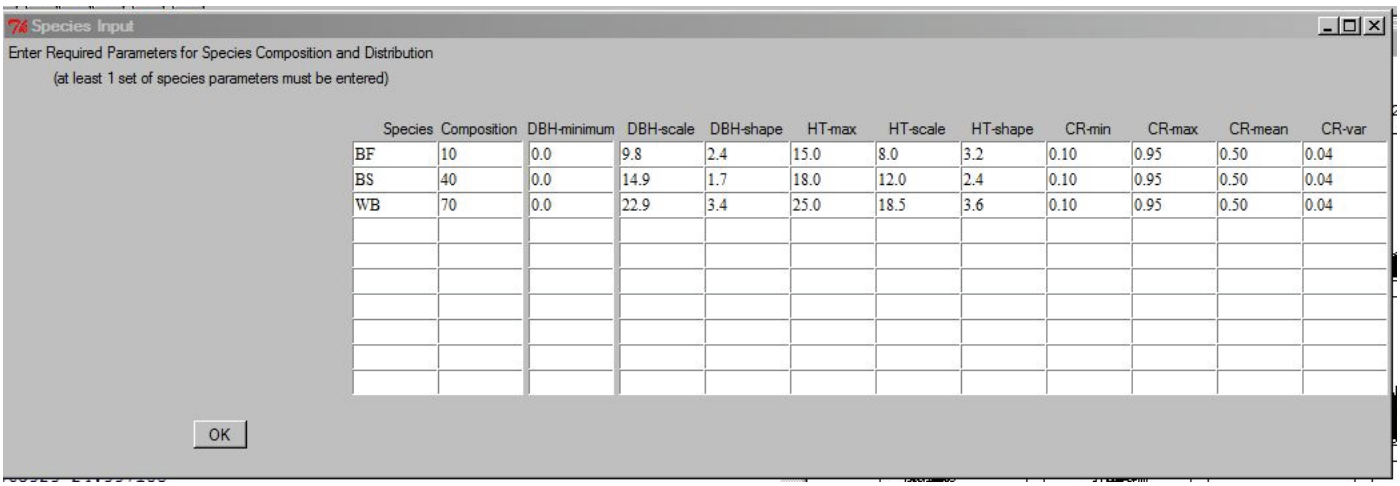
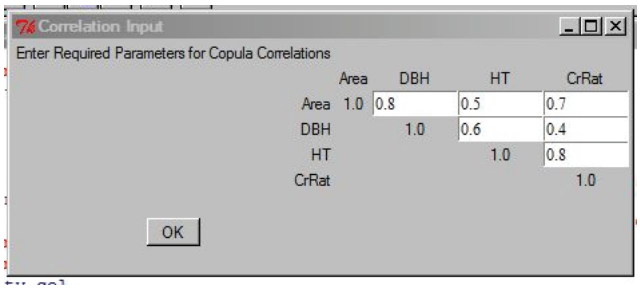


D)

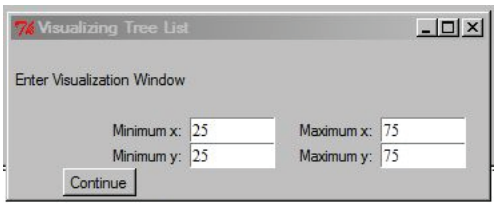


Species	Composition	DBH-minimum	DBH-scale	DBH-shape	HT-max	HT-scale	HT-shape	CR-min	CR-max	CR-mean	CR-var
BF	10	0.0	9.8	2.4	15.0	8.0	3.2	0.10	0.95	0.50	0.04
BS	40	0.0	14.9	1.7	18.0	12.0	2.4	0.10	0.95	0.50	0.04
WB	70	0.0	22.9	3.4	25.0	18.5	3.6	0.10	0.95	0.50	0.04

E)



F)



G)

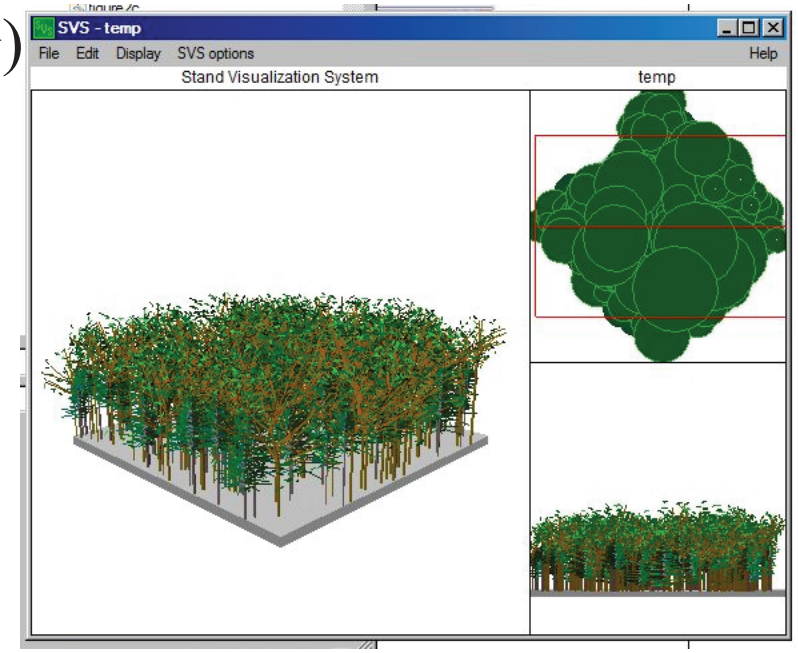


Figure 2

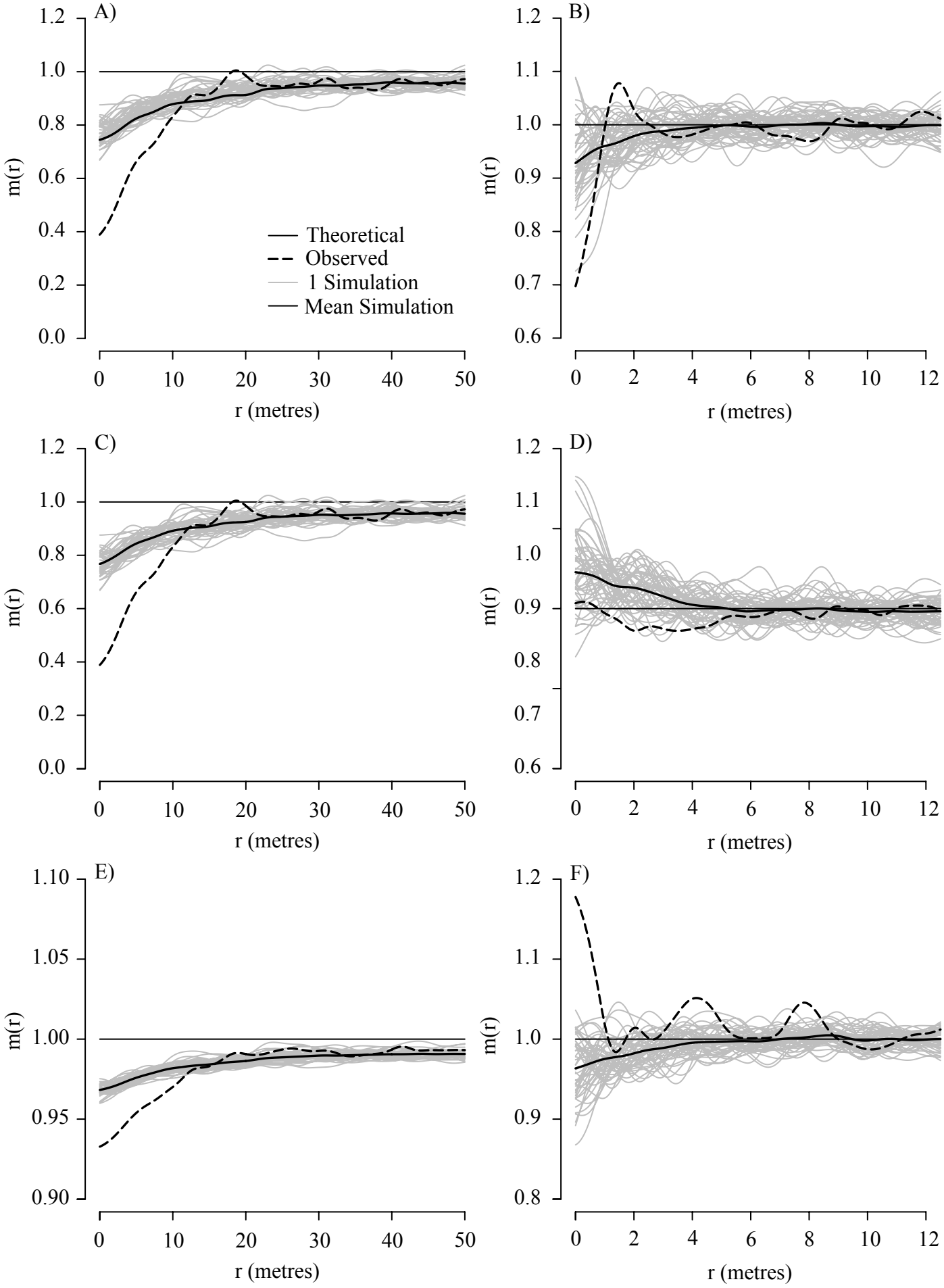

A)
B)
C)
D)
E)
F)
m(r)
r (metres)
Theoretical
Observed
1 Simulation
Mean Simulation

Figure 3