INDICES OF STAND STRUCTURAL DIVERSITY:
MIXING DISCRETE, CONTINUOUS, AND SPATIAL VARIABLES

VALERIE LEMAY[1] and CHRISTINA STAUDHAMMER[2]

[1]Associate Professor, Department of Forest Resources Management, University of British Columbia, 2045-2424 Main Mall, Vancouver, BC. Valerie.LeMay@ubc.ca, corresponding author
[2]Assistant Professor, University of Florida, Gainesville, Florida, USA Email: staudham@ifas.ufl.edu
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ABSTRACT. Stand structural diversity, defined as the diversity of trees in stands, can be indicative of overall biodiversity and habitat suitability, useful in forecasting stand growth, and provide within stand detail for forest inventories. A number of authors have suggested which tree variables to use to indicate structural diversity, and have combined these variables into structural indices. Other authors have suggested indices of spatial arrangement. A limited number of authors have tried to combine tree variables and spatial position into structural indices. Central issues in developing structural indices are 1) what is considered a most diverse stand in terms of vertical and horizontal diversity; 2) how can distributions of continuous variables (e.g., diameter and height) be mixed with species distribution as a discrete variable into a structural diversity index (indices); and 3) how should spatial heterogeneity be reflected in a structural index (indices). For this paper, a brief presentation of indices found in literature is given. The definition of most heterogeneous (most structurally diverse) stand is proposed as a uniform distribution over each continuous and each discrete stand variable, and a Poisson distribution of trees in clumps of varying sizes for the spatial distribution. A discussion of this definition and how a previously described structural index might be expanded to incorporate spatial arrangement is given.

Keywords: structural diversity indices; vertical and horizontal diversity; height and diameter distribution; species distribution; spatial heterogeneity

1   INTRODUCTION

Stand structure is an important element of stand biodiversity (MacArthur and MacArthur 1961; Willson 1974; Franzreb 1978; Temple et al. 1979; Aber 1979; Ambuel and Temple 1983; Freemark and Merriam 1986). High biodiversity is associated with stands where there are multiple tree species and sizes (Buongiorno et al. 1994). For forested ecosystems, structural diversity can indicate overall species diversity (Kimmins 1997), as shown in research on avian and insect diversity (Whittaker 1972; Franzreb 1978; Aber 1979; Temple et al. 1979; Recher et al. 1996; Moen and Gutierrez 1997). Managing forests for biodiversity may be accomplished by managing for structural diversity (Önal 1997). In addition to being useful as a possible proxy for measuring stand biodiversity, measures of stand structural diversity are also important for predicting future stand growth and development (Pretzsch 1997). Oliver and Larson (1996) indicated that a variety of patterns of growth are related to structural complexity. As a measure of horizontal complexity, spatial indices can be useful for comparing point patterns (Goreaud and Pélissier 1999) and for interpreting the ecology of species (Goreaud and Pélissier 1999; Davis et al. 2000).

Several indices of stand structure have been proposed based on tree attributes, particularly species and tree size. Indices of spatial arrangement have also been proposed. A limited number of authors have suggested ways to provide indices that represent a mixture of spatial diversity (arrangement) and tree attribute diversity into an overall structural index. Good reviews of indices are given by Pommerening (2002), who described indices without considering spatial arrangement as "distance-independent", versus those with spatial arrangement as "distance-dependent", and in Cressie (1993, Chapter 8) and Dale (1999, Chapter 7) for spatial and mixed spatial/variable indices.

Related to structural diversity indices is the development of competition indices used to modify tree growth. Weigelt and Jolliffe (2003) provided a review of competition indices, including the benefits and problems of

using indices to summarize information. For both types of indices, information on a number of attributes (e.g., tree sizes, spatial arrangements) are summarized and presented as an index. However, competition indices are often calculated for each tree and may be summarized for all trees in a stand, whereas structural indices are only given for a group of trees, typically a stand of trees. As with competition indices, desirable attributes of structural indices are that the indices should: 1) be clear, specific, and relevant to the intended uses; 2) have known mathematical properties; 3) be invariate to size differences (e.g., tree size for competition indices versus area size for structural indices); 4) be unaffected by the specifics of the data gathered (e.g., invariant to differences in plot size); 5) be invariate to differences in frequencies; and 6) be standardized relative to a useful and universal standard (adapted from Weigelt and Jolliffe 2003). In all cases, indices reduce the information, in an effort to provide clarity in interpretation and facilitate comparisons.

In this paper, a brief review of proposed indices for stand structure is given, including measures that have been developed following (or during) the review given in Pommerening (2002). A possible extension of an index by Staudhammer and LeMay (2001) for continuous and discrete tree attributes using the distribution of distances is presented for discussion.

2 BACKGROUND

2.1 Indices based on tree attributes. Species diversity indices, based on a distribution of individuals by species, have gained wide acceptance in forestry (e.g., Swindel et al. 1984; McMinn 1992; Silbaugh and Betters 1995; for a thorough review of biodiversity indices, see Magurran 1988). A very commonly used species diversity index is Shannon's index (Shannon and Weaver 1949; also called the Shannon-Weiner, or the Shannon-Weaver index), which is based on the probability that an individual picked at random from an infinitely large community will be a certain species. The more uncertainty one has about the species of an individual, the higher the diversity of the community. Shannon's index, H', is defined as follows:

[1]
$$H' = \sum_{i=1}^{S} p_i \ln p_i$$

where p_i is the proportion of individuals in the i th species, and S is the number of species. The proportion of a species has been based on a variety of variables to represent frequency, including: number of individuals (Franzreb 1978; Swindel et al. 1991; Niese and Strong 1992; Condit et al. 1996), basal area (McMinn 1992; Harrington and Edwards 1995; LeMay et al. 1997), stems per ha (McMinn 1992; Harrington and Edwards 1995); foliar cover (Swindel et al. 1984; Lewis et al. 1988; Qinghong 1994; Corona and Pignatti 1996), crown cover (Corona and Pignatti 1996), and biomass (Swindel et al. 1984; Swindel et al. 1991). The maximum value for Shannon's index occurs when the proportions are equal over all species (uniform distribution), resulting in a value of ln S.

Because of tree size variation, traditional diversity indices are not entirely suited to the measurement of structural diversity (Lähde et al. 1999). Modifications of indices have been proposed. MacArthur and MacArthur (1961) constructed foliage height profiles by measuring the amount of vegetation at different heights above ground. A foliage height diversity index, FHD, was calculated using Shannon's index (Equation [1]), where p_i was replaced by the proportion of total foliage in the ith layer, and S was replaced by the number of layers. Subsequent researchers into avian community structure have used MacArthur and MacArthur's approach to evaluate vertical diversity, with slight modifications to the calculation of p_i (e.g., Willson 1974; Aber 1979; Ambuel and Temple 1983; Erdelen 1984; Ferris-Kaan et al. 1998). For other studies, p_i was replaced by the proportion of individuals in the ith diameter class, and S was replaced by the number of diameter classes (e.g., Patil and Tallie 1982; Buongiomo et al. 1994; Buongiomo et al. 1995). Freemark and Merriam (1986) introduced heterogeneity over plots into their derivation of Shannon's index. Their habitat heterogeneity index (HH), patterned after research by Orloci (1970), was defined as:

[2]
$$HH = -\sum_{i=1}^{n} \sum_{j=1}^{c} X_{ij} \ln(X_{ij} / \overline{X}_i)$$

where n is the number of plots; c is the number of classes; and X_{ij} is the proportion of individuals in the ith class of the jth plot. Equation [2] differs from the Shannon index in that the denominator is the average rather than the total for the class. HH was computed separately for eight components: tree density, tree diameter class, canopy closure, foliar cover in vertical bands, average canopy height, herb height, percent litter, and percent bare ground.

Lähde et al. (1999) derived an index using seven variables: stems, basal area of growing stock, volume of standing dead trees, volume of fallen dead trees, undergrowth density, occurrence of "special trees", and volume of charred wood. For each species, all variables were grouped into classes (e.g., trees were classed into three diameter groups and two basal area groups). Stands were given diversity scores by species, which were then combined into a single index for the stand.

For all of these modifications of Shannon's index, continuous variables were grouped into classes in order to calculate proportions. Staudhammer and LeMay (2001) proposed an alternative to grouping continuous variables into classes by using sampling variance. For this index, termed Stand Variance Index (STVI), the variance of the basal area distribution for the target stand was compared to the variance of a theoretically maximally diverse stand. Maximal stand structural diversity was considered to be an even distribution of basal area per ha (uniform distribution) over a wide size range, based on a definition by Lähde et al. (1999) and following previous species diversity indices. Basal area per hectare was used instead of stems per ha to better represent resource use, with larger trees having more influence (as suggested by LeMay et al. (1997), and Solomon and Gove (1999)). Minimum diversity was similarly defined as one species and size, distributed as a spike at a single point. Diameter outside bark at breast height (diameter; 1.3 m above ground) and total tree height were used to indicate variety in tree size, since these are commonly available.

2.2 Indices of spatial heterogeneity. Indices of spatial heterogeneity of trees in a stand (or other objects) have been developed, and used to separate spatial patterns into a continuum from regular (also termed uniform), random (also called a Poisson distribution), and clumped (also called aggregated) distributions (Dale 1999). In regular distributions, individuals are evenly distributed over space, indicating avoidance (e.g., territoriality, or shading effects). In a random distribution, individuals are distributed in space in an unpredictable manner; there is equal probability of an organism occupying any point in space. Clumped distributions occur when resources in the environment are themselves distributed patchily, or if individuals tend to be behaviourally attracted to one another. Spatial indices, therefore, also give insights into species ecology. Goreaud et al. (1999 and 2002) discussed the use of stand level spatial indices, rather than tree level competition indices, in predicting plant survival and forest dynamics.

For many spatial indices, a random spatial distribution (homogeneous Poisson or complete spatial randomness (CSR) process) is used as the standard. Quadrat count data have been used in many studies to compare to a CSR process (e.g., Hanewinkel 2004; see descriptions of indices in Cressie (1993, Chapter 8) and in Dale (1999, Chapter 7). Samples can be more easily obtained over an area, but quadrat sizes are somewhat arbitrary and information is lost. As an alternative, event-to-event distances, for a sample of trees or for a complete enumeration of trees, or a sample of point-to-event distances could be used. The simplest approach is to use nearest neighbour (first) distances, where statistics are well defined for a CSR process with:

[3]
$$E[D] = \frac{1}{2\sqrt{\lambda}} \text{ and } Var[D] = \frac{4-\pi}{4\lambda\pi}$$

where λ is the average number of items per unit area. Clark and Evans (1954) suggested the average distance over the expected distance under a CSR process as a spatial index. However, this can fail to identify clumped distributions (Dale 1999, Chapter 7), statistics are not well defined for other processes (Cressie 1993, Chapter 8), and this also results in a loss of information as only small scale spatial patterns are examined. The distribution of all possible pair-wise distances was first proposed by Thompson (1956) with an expected value for the kth nearest neighbour of a CSR process given as:

[4]
$$E[D_k] = \frac{(2k)!k}{\sqrt{\lambda}\left(2^k k!\right)^2}$$

The Clark and Evans (1954) index could then be extended for all neighbours and plotted against k to examine clustering of objects (Cressie 1993, page 612). All possible plant-to-plant distances were used by Galiano (1982), by plotting frequencies by distances. Manly (1981) and Davis et al. (2000) also used all possible distances to examine processes across different scales. Other authors have tried to base comparisons on a primary neighbour, such as the 3rd nearest neighbour distances, but the choice of what is the primary neighbour is largely subjective. Ripley (1976; 1977) developed an index based on the number of items within a specified radius relative to a CSR process (commonly called Ripley's K), and graphed this against an increasing radius. This graph of Ripley's K has been widely used. Edge effect corrections have been proposed, including those discussed by Goreaud and Pélissier (1999). One other alternative is to calculate the linear distances produced by tessellations of points. For a distribution of even sized and evenly distributed clumps, tessellated distances would result in a bimodal distribution (Dale 1999). Tessellated distances might be advantageous in identifying primary neighbours that are influential to plant growth and survival.

2.3 Indices of stand structure combining tree attributes with spatial heterogeneity. For any stand, separate indices of tree size diversity and spatial arrangement could be reported. A multivariate index is difficult to develop (Dale 1999), and may mask important differences in each variable (Weigelt and Jolliffe 2003). However, a single index would allow for easier comparisons.

Marked point processes and indices have been used to combine spatial patterns with species (e.g., Pielou 1977; Galiano 1983; Shimatani 2001; Renshaw 2003). Zenner and Hibbs (2000) used a tessellation of distances via a triangulated area network (TIN) constructed with tree spatial positions and height as a vertical measure, resulting in weighted distances. They then took the sum of tessellated areas, and compared this to the sum of areas where all heights were equal. Pommerening (2002) discussed several ways of mixing stand attributes with spatial structure, including the Diameter Differentiation Index, which uses the sum of tree-level indices similar to competition indices. Hanewinkel (2004) examined spatial patterns over time, and separated trees by diameter class and species as a means to include tree attributes.

3 EXTENSION OF THE STVI TO INCLUDE SPATIAL HETEROGENEITY

3.1 Description of STVI. The STVI developed by Staudhammer and LeMay (2001), was based on the variance of basal area per ha for diameter and height relative to the variance for a maximally diverse stand with a uniform distribution of diameter (dbh; diameter outside bark at 1.3 m above ground) and height. Dbhs and heights are commonly measured and indicate both horizontal (diameter) and vertical (height) diversity. Basal area per ha was used to better reflect the impact of larger trees. One version of this index used a bivariate distribution of height and diameter. However, using the criterion of a bivariate uniform as the most diverse distribution of sizes, very small indices were obtained, since many combinations of diameter and height have a zero probability of occurring in natural populations (e.g., very small diameter with a very large height). For this reason and to incorporate species diversity, separate calculations for dbh and for height by species were recommended ($STVI_{dbh_i}$ and $STVI_{ht_i}$, from i =1 to S), with each index constrained to be between 0 (low diversity; i.e., nearly 0 when only one tree size is represented) to 1 (maximum diversity with a uniform distribution over a wide range). The variances for the target stand, the maximally diverse population (uniform distribution), and the bimodal distribution (maximum variance), were used to develop the index.

The developed diversity index, as shown for diameter ($STVI_{dbh_i}$ for a species i), was:

[5]
$$STVI_{dbh_i} = \begin{cases} 1 - \left(\dfrac{S^2_{dbh_U} - S^2_{dbh_i}}{S^2_{dbh_U}} \right)^{p1}, & \text{when } S^2_{dbh_i} \leq S^2_{dbh_U} \\[4mm] 1 - \left(\dfrac{S^2_{dbh_i} - S^2_{dbh_U}}{m \times S^2_{dbh\max} - S^2_{dbh_U}} \right)^{p2}, & \text{when } S^2_{dbh_i} \rangle\ S^2_{dbh_U} \end{cases}$$

where $S^2_{dbh_i}$ is the variance of diameter (dbh) for species i; $p1$ and $p2$ are constants > 0; and m is a constant ≥ 1.0. Sample variance was calculated by:

$$[6] \qquad S^2 = \frac{\sum_{i=1}^{n}\left[w_i \times (x_i - \bar{x})^2\right]}{\sum_{i=1}^{n} w_i}$$

where x_i is dbh_i or $height_i$; w_i is the basal area per ha represented by the ith tree in the sample plot; $\bar{x}$ is the average of dbh or height, weighted by basal area; and n is the number of trees in a sample plot. The variance of a uniform distribution is given by:

$$[7] \qquad S^2_U = \frac{(b-a)^2}{12}$$

where a and b define the range of the distribution, differing for dbh versus height. The maximum possible variance of a distribution occurs when the distribution is maximally bimodal, when half the basal area is at a and half the basal area is at b. For this basal area distribution, the variance is:

$$[8] \qquad S^2_{max} = \left[\frac{1}{2} \times \left(\frac{(a+b)}{2} - a\right)^2 + \frac{1}{2} \times \left(b - \frac{(a+b)}{2}\right)^2\right] = \frac{(b-a)^2}{4}$$

The constants $p1$ and $p2$ define the shape of the curve relating the value of the index to the sample variance: when $p1$ (or $p2$) < 1, the curve is concave upward; when $p1$ (or $p2$) $= 1$, the curve is segmented linear; when $p1$ (or $p2$) > 1, the curve is concave downward. If $p1 = p2 > 1$, then a smooth, continuous function results. The coefficient m controls the value of the index when the distribution is maximally bimodal. If $m = 1$, then the index will be zero for a maximally bimodal distribution; as m gets larger, the index value increases for the maximally bimodal case. The values for $p1$, $p2$, and m were chosen by placing three constraints on the index to yield certain index values under defined conditions. The index was constrained to equal 0.5 when: 1) the variance is equal to that of a uniform distribution over half the maximum possible range ($S^2_{0.5U}$); and 2) the variance is equal to that of a bimodal distribution, with half of the values uniformly distributed over the lower quartile, and the other half uniformly distributed over the upper quartile of the maximum possible range (S^2_B). The index was also constrained to equal 0.1 for the maximum variance (maximally bimodal stand). Again illustrating this using dbh, the three constraints were:

$$[9] \qquad 0.5 = STVI_{dbh_i} = 1 - \left(\frac{S^2_{dbh_U} - S^2_{dbh_{0.5U}}}{S^2_{dbh_U}}\right)^{p1}$$

$$[10] \qquad 0.5 = STVI_{dbh_i} = 1 - \left(\frac{S^2_{dbh_B} - S^2_{dbh_U}}{m \times S^2_{dbh_B} - S^2_{dbh_U}}\right)^{p2}$$

$$[11] \qquad 0.1 = STVI_{dbh_i} = 1 - \left(\frac{S^2_{dbh_{max}} - S^2_{dbh_U}}{m \times S^2_{dbh_{max}} - S^2_{dbh_U}}\right)^{p2}$$

Since the variances used in defining these constraints are all functions of the variance of a uniform distribution, $p1 \approx 2.4094$, $p2 \approx 0.5993$, and $m \approx 1.1281$, for any defined size ranges from a to b (see Appendix of Staudhammer and LeMay (2001) for details). To arrive at a measure of structural diversity for species i, $STVI_{dbh_i}$ and $STVI_{ht_i}$ were averaged, with a maximum value of 1 (uniform for both diameter and for height, equally weighted). These were summed over all species in the plot ($STVI_{d+h}$), for a maximum value equal to the number of species.

In terms of the properties of this structural index:

1. The separation by diameter and height distributions by species allowed for a more complete view of the stand structure, obtaining an overall index, indices by species, and indices for dbh and for height by species, making the index potentially more relevant;
2. The index is somewhat size invariant, as the constraints are the same regardless of the choice of (a,b); however, the same (a,b) must be used if comparisons over time or over stands are to be made; and
3. The index is standardized relative to a uniform distribution as a maximal distribution of basal area over size classes, which follows previous arguments regarding a standard for maximal diversity.

However:
1. Simulations and field data indicated that some different stand structures would yield the same overall STVI (Staudhammer and LeMay 2001);
2. If each species is a different size as may be the inclination for successional species, STVI would approach 0. STVI values for dbh and for height obtained by pooling all species might be more meaningful;
3. For a very large number of species, pooling dbh and height over all species, or over species guilds would be more meaningful than separating by species;
4. Mathematical properties, including sampling properties, are not known; and
5. The index would likely be affected by sample plot size, as a wider range of tree sizes would be found in larger sized plots up to the plot size where the maximum ranges present in the stand also occur in the samples.

Also, even though basal area per ha by dbh reflects horizontal distribution, spatial distribution of trees is not explicitly represented in the index.

3.2 Extensions and modifications to include spatial distributions. In order to retain the nature of STVI, a separate component of the index for distance could be developed. The main reasons for possibly developing and using this $STVI_{dist}$ rather than a well known spatial index are: 1) the standard for the index would be maximally diverse spacing, rather than Poisson spacing; 2) each component (dbh, height, distance) could be reported separately; and 3) the index could be easily combined with the separate dbh and height indices to report one measure of structural diversity. All three structural measures would then indicate a value near zero for low diversity, and a value near one for high diversity, resulting in some consistency of interpretation.

The issues in extending the STVI are:
1. What is the most spatially diverse arrangement? What standardization is meaningful, in terms of spatial diversity?
2. What type of distance metric would be useful?
3. How would the standard and distance metric be used to obtain an STVI component for distance? What other changes to STVI would need to be done?

3.2.1 Basis for spatial diversity index. Most spatial indices have been developed using a Poisson process as their basis. The indices then indicate aggregation and regularity of spacing, and could be used to indirectly indicate spatial diversity, relative to a random distribution. However, using the same principal for standardization as that used to develop STVI, what would the standard be if this was to be considered the maximally spatially diverse stand? One possibility for the maximal spatial diversity index is a Poisson distribution of different sized clumps. The Poisson distribution of clumps would result from microsite variability, inter-tree competition over different species and tree sizes, and/or disturbance events. This would likely produce a higher diversity in tree size, vigor, shape, and survival rates, and likely produce a wider variety in habitat than a Poisson or regular distribution of individual trees.

This basis is more subjective than the uniform distribution over a wide range of tree sizes used to develop the STVI index for dbh and height. A specific number of clumps and a distribution of clump sizes (number of trees and space occupied by the trees in the clump) would need to be specified. For a given number of trees per unit area, the distribution of trees would approach a Poisson as the number of clumps increases. For a given number of clumps, the distribution of trees would also approach a Poisson distribution, as the size of clumps increases and clumps overlap.

To maintain the constraint of 0 (low diversity) to 1 (high diversity), and using similar additional constraints used to develop the index, $STVI_{dist}$ should equal:

1. Nearly 0 for very regular (e.g. square) spacing of trees, where the number of clumps is equal to the number of trees;
2. A bit larger than the value for regular spacing for a Poisson distribution, where the number of clumps is less than or equal to the number of trees;
3. 1.0 for a very highly diverse stand, possibly a Poisson distribution of different sized clumps ("maximally diverse");
4. A value of 0.5 for a diverse stand with a Poisson distribution of different sized clumps, but half the diversity of maximal diversity; and
5. A value a bit larger than a Poisson distribution for two equal sized clumps, maximally dispersed in space (e.g., at diagonal corners in a square space).

These additional constraints are quite arbitrary, but result in known values for specific circumstances.

3.2.2 Distance metrics. As noted by Dale (1999), the use of first nearest neighbours does not differentiate a very clumped pattern from an even distribution of regularly sized clumps, and information is lost (Cressie 1993). Alternatives include using another neighbour that might better indicate primary neighbours, using all possible tree-to-tree distances, or using tessellated distances similar to Zenner and Hibbs (2000). The selection of primary neighbours that are more effective than the first nearest neighbour would be largely subjective, unless used for a specific objective such as growth modelling of a particular ecotype. The calculations involved for all possible tree-to-tree distances (neighbours) is computer intensive for large numbers of trees, but all information would be included. Also, tessellated distances are difficult to calculate, and differ depending on the algorithm used (Dale 1999).

Another alternative, following the development of STVI for dbh and for height, is to calculate STVI for the x-direction and for the y-direction separately, rather than combining these into a distance value. The advantage is that the expected distributions in each direction may be more predictable. For example, given:
1. A regular (square) spacing distribution, the frequencies will all be equal and spread widely over the ranges, but there will be discontinuities in distances, relating to regular gaps in x- and in y-directions;
2. Maximal separation of 2-clumps, even-sized, the frequencies would be equal and separated into two modes at the extremes of the two axes;
3. A Poisson distribution of trees, a uniform distribution over the ranges in x- and y-directions would be indicated;
4. Maximal separation of 2-clumps in the x-direction, but minimal separation in the y-direction, the difference between the x- and y-directions would be clearly indicated; and
5. A Poisson distribution of a number of unequal sized clumps, unequal frequencies would be shown, with gaps in both directions.

Although using two measures adds complication, there would be no issue about which distance measures to use. Also, developing the constraints for the STVI could be easier, since the expected variances of the regular, 2-clump, and Poisson distributions could be uniquely determined for x- and for y-directions. However, if the standard is a Poisson distribution of unequal sized clumps, the expected variances would still be difficult to determine. This might be considered a non-homogeneous Poisson; however, there would be no spatial trends in the number of items per unit area that could be modelled.

3.2.3 STVI component for distance. Using the standard and constraints described in 3.2.1, the spatial index for distance (dist) over all species would be:

[12]
$$STVI_{dist} = \begin{cases} 1 - \left(\dfrac{S^2_{dist_{MD}} - S^2_{dist}}{S^2_{dist_{MD}}} \right)^{p1}, \text{ when } S^2_{dist} \leq S^2_{dist_{MD}} \\ 1 - \left(\dfrac{S^2_{dist} - S^2_{dist_{MD}}}{m \times S^2_{dist_{2-C}} - S^2_{dist_{MD}}} \right)^{p2}, \text{ when } S^2_{dist} \rangle S^2_{dist_{MD}} \end{cases}$$

where S^2_{dist} is the target stand variance of distances for all species; $S^2_{dist_{MD}}$ is the variance for a most spatially diverse stand; $S^2_{dist_{2-C}}$ is the variance of a distribution of two maximally separated equal-sized clumps, with

Poisson spacing within clumps. Then, using a similar concept as for tree size variables, values for $p1$, $p2$, and m would be chosen by placing constraints on the index to yield certain index values under defined conditions.

Using the constraints defined in 3.2.1 to calculate the constants:

[13]
$$0.2 = STVI_{dist} = 1 - \left(\frac{S^2_{dist_{MD}} - S^2_{Poisson}}{S^2_{dist_{MD}}} \right)^{p1}$$

[14]
$$0.5 = STVI_{dist} = 1 - \left(\frac{S^2_{dist_{0.5MD}} - S^2_{dist_{MD}}}{m \times S^2_{dist_{2-C}} - S^2_{dist_{MD}}} \right)^{p2}$$

[15]
$$0.3 = STVI_{dist} = 1 - \left(\frac{S^2_{dist_{2-C}} - S^2_{dist_{MD}}}{m \times S^2_{dist_{2-C}} - S^2_{dist_{MD}}} \right)^{p2}$$

where $S^2_{dist_{0.5MD}}$ is the variance of a distribution with ½ the diversity of a most spatially diverse stand; values for $p1$, $p2$, and m could be calculated given expected values of the variances. Since expected values for the variances are not known for these distributions, regardless of which distance metric is selected, Monte Carlo simulations would be needed to obtain these variances. This procedure is not unusual, as Monte Carlo simulations are commonly used for testing spatial distributions (Dale 1999). This index could be calculated for any selected distance measurement, for x- and y-directions, separately, and pooled across or separated by species.

3.2.4 Combining STVI for distance with STVI for diameter and height by species. If the STVI were calculated by species, then STVI components for diameter, height, and distance for each species i, ($STVI_{dbh_i}$, $STVI_{ht_i}$, and $STVI_{dist_i}$) could be averaged (would be four values if x- and y-distance variances were separately calculated). This would result in a maximum value of 1 for a most diverse stand, if each component was given equal weight in averaging. This type of stand would have a wide range of tree sizes (height and dbh), and a diverse distribution of trees in clumps for the species. Combining these indices over a number of species, the maximum value for the combined index, $STVI_{d+h+dist}$ would have a maximum value of S, the number of species in the stand.

However, for successional species, or for many rare species, calculation of the components by species would result in very low values for each component, likely making comparisons over time and over stands difficult. Instead, groups of species (guilds or habitats) could be used in the place of species (maximum value equal to number of guilds), or all species could be combined (maximum value of 1).

3.3 Illustration of STVI spatial component using simulated patterns. Using 300 stems per ha (SPH), one realization of spatial pattern was generated over a 100m X 100m (1 ha) space for each of five spatial patterns[1], described as:
1. Regular (square) spacing, representing a plantation in rows (Figure 1);
2. Poisson spacing, with uniform distances in each of two directions (Figure 2);
3. 2-clumps, where ½ of the stems per ha are in each clump and the clumps are isolated over a very close distance at diagonal corners in space, with an average inter-tree distance of 1.0 m (Figure 3);
4. A Poisson distribution of 10 clump centres, and a uniform distribution of number of trees per clump (e.g., 300/10=30 trees per clump on average). Trees in each clump were located using a Poisson distribution around the clump centre, with the average inter-tree distance of 1 m (Figure 4); and
5. As item 4, but only five clump centres (Figure 5).

Since both the fourth and fifth patterns indicate changes in the number of items over the space, where areas with no trees have a parameter of zero, a non-homogeneous Poisson might describe the distribution. However, λ would not show a trend with spatial direction.

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[1] SAS Version 8.02, SAS Institute Inc., Cary, NC.

Square spacing results in as many clumps as the stems per ha, with one tree per clump. Poisson spacing results in a number of clumps less than the number of stems per ha, with one or a few trees per clump. Both of these were considered to have low diversity, as there would be low variety in habitat and in inter-tree competition across the area. Histograms of x- and y-distances indicate that the regular spacing has a uniform distribution of distances, with gaps in the distances (Figure 1b). The number of gaps depends upon the distance class width used in creating the histograms. The Poisson spacing should indicate a uniform distribution along each axis (Figure 2b); departures do appear as this is only one realization. Cressie (1993) used 200 realizations to obtain a confidence envelope for Ripley's K, for example. The regular and Poisson distributions show similar patterns over all neighbours (Figures 1c versus 2c, and 1d versus 2d), except for the first few neighbours, where square spacing has larger distances, and little variance.

The 2-clump spacing was set as having ½ of the stems per ha in each clump, for a bimodal distribution in both the x- and y-directions (Figure 3b), and a bimodal distribution of all possible distances (Figure 3, c and d). This would have the higher variances for both the x- and y-directions, and for distances using all neighbours. Again, this might be assigned a low diversity index, as there would be either the "no-tree" or the "treed" habitats represented over the area.

The number of clump centres that might be used to represent a most diverse stand is somewhat arbitrary, but bounded by regular spacing (number of clumps equals number of trees) and 1-clump spacing patterns. The fourth pattern was used to indicate "most-diverse", based on the number of clumps, the Poisson location of these clumps, and the variety of number of trees at each clump location. The 10-clump centres ("most diverse") and the 5-clump centres ("half-most diverse") indicate a great deal of spatial variety that appears as multi-modal distributions for the x- and y-directions (Figures 4b and 5b). These later spatial distributions would vary greatly among realizations, as some realizations would have clump centres in close proximity and others would be very far apart. Also, since the number of trees per clump was also allowed to vary, some realizations would have only one tree in one or more clumps, further increasing the variance of distances among realizations, particularly for first nearest neighbour distances. While the choice of 10-clumps was arbitrary, using many clumps would result in a nearly Poisson distribution. Using very few clumps would result in distributions with few modes, closer to the 2-clumps distribution.

Means and variances for each spatial pattern were calculated for the first nearest neighbour, the farthest nearest neighbour, all neighbours, and for x- and y-directions (Table 1). Since the variability among spatial patterns is very large for the "most diverse" and "half diverse" patterns, averages of 10 realizations are shown. To give some indication of the changes in these values due to differing stems per ha, values are also shown for 100 and 500 stems per ha. A greater number of realizations for all patterns (excepting the regular spacing) would be preferred. Cressie (1993) used 200 realizations for Poisson spacing, for example; more than 200 would be needed to obtain values close to the expected values for the means and variances for the more diverse patterns. However, Table 1 does indicate that

1. The use of 10-clumps and 5-clumps to indicate "most diverse" and "half most diverse" are not tractable. Using STVI, the variances would need to follow in order from regular, Poisson, most diverse, half diverse, and 2-clumped. The averages of 10 realizations indicates that this would not be the case using the 10- and 5-clumped patterns as the "standard";
2. The distributions for the x- and the y-directions, separately, might be useful. However, applications to actual data would likely require a rotation of the coordinates (see Figure 6). Also, the choice of which direction is x and which is y with actual field data could be selected for easier comparison. For example, the most diverse could always be set as the x-direction;
3. As noted by many authors, the first nearest neighbour is not very useful in defining patterns, except for defining the regular pattern versus other patterns; and
4. The use of all neighbours might be a better choice. Alternatively, selecting a set of neighbours of most influence might be preferred. The choice of which neighbours to use would vary with the use of the index, however.

Using Equations [13] – [15] and Table 1 values for all possible distances and 300 stems per ha:

$$0.2 = STVI_{dist} = 1 - \left(\frac{743.9 - 648.2}{743.9} \right)^{p1}$$

$$0.5 = STVI_{dist=} 1 - \left(\frac{871.0 - 743.9}{m \times 3459.0 - 743.9} \right)^{p2}$$

$$0.3 = STVI_{dist=} 1 - \left(\frac{3459.0 - 743.9}{m \times 3459.0 - 743.9} \right)^{p2}$$

Resulting in $p1 \approx 0.1088$, $p2 \approx 0.1099$, and $m \approx 20.3672$. Given the variance of all possible distances of a target 1-ha area, the STVI could then be calculated using Equation [12].

However, more examination and thought on what might be a useful standard for most diverse spatial arrangement, and what constraints (values for particular patterns) might be useful is needed. The average variances of more realizations would be needed in actual application, also.

3.4 Application to unevenaged Douglas-fir stands. Dbh, height, and spatial position values for each tree of stem-mapped permanent plots located in unevenaged Interior Douglas fir (IDF) stands stands growing in the interior of British Columbia, Canada, were obtained. The stem maps for the first time period for two of these plots (Figures 6 and 7), indicate that the patterns are near to the Poisson distribution, with some "clumpiness". The x- and y-coordinates were those given in the data, and represent East-West (x-direction) and North-South (y-direction). All trees were Douglas-fir (*Pseudotsuga menzeisii* (Mirb.) Franco) in these two plots. Plot 3 was 0.10 ha in size, placed in a stand that was selectively cut and had a light pre-commercial thinning over 20 years ago. Plot 6 was 0.05 ha in size, placed in a stand that had no history of being cut, but was lightly burned over 30 years ago.

For each plot, the variance of basal area per ha for dbh was calculated, and $STVI_{dbh_i}$ was then calculated using and interval of 0 to 100 cm. Similarly, $STVI_{ht_i}$ for each plot was calculated using an interval of 0 to 40 m. The resulting values were:
1. Plot 3: $STVI_{dbh} = 0.86$, and $STVI_{ht} = 0.74$; and
2. Plot 6: $STVI_{dbh} = 0.47$, and $STVI_{ht} = 0.68$.

Since the standard for most diversity was based on a uniform distribution of basal area per ha, only the interval values for dbh and for height were needed to calculate the indices. Using these index values, the height structural diversity would be greater for Plot 3 than Plot 6 (Figures 6d and 7d).

To calculate $STVI_{dist}$ for each plot, a series of steps would need to be followed:
1. The standard for most and half diverse would need to be set, and simulations (likely more than 500 replications), would be needed to obtain approximate expected values for the variances of all distances;
2. The approximate expected variance for the Poisson spacing (perhaps 200 replications would be sufficient) would also need to be obtained, along with the approximate expected variance for the 2-clump spacing;
3. The expected variances from the most, half diverse, Poisson, and 2-clump spacings would be used to calculate $p1$, $p2$, and m;
4. A rotation of the axis for the plot (e.g., Plot 3) might be considered, prior to calculating the variance of all possible inter-tree distances; and
5. STVI for distance would be calculated for the plot.

Since border trees were recorded for these plots, edge effects could be addressed by including them in calculating distances for trees within the plot boundary and a similar approach would be included in the simulations.

Unlike STVI for dbh and height, simulations would be needed to calculate the necessary variances and the parameters used in the STVI for space. Also, what should be the standard for the most and half diverse spatial patterns? Since the size of the distances affects the variances, the size of the area used in the simulations would need to be the same as the plot size, or some other way of standardizing the distances would need to be used.

4 CONCLUSIONS

Stand structural diversity affects key ecological processes. Understanding and quantifying these effects can aid in growth and yield modeling, as well as help forest managers make important conservation decisions. A variety of spatial and structural indices have been developed. Spatial indices commonly use a random spatial pattern as the standard for comparison, which may not be useful in reflecting spatial diversity. Furthermore, structural indices often require the separation of continuous variables into arbitrary classes, and there are few indices that combine aspects of tree size with spatial arrangement.

The STVI was originally introduced as an index of the variability in horizontal and vertical structure of a stand, relative to a maximally diverse stand defined as a uniform distribution of basal area per ha across wide size ranges. Using dbh and height separately, the structural diversity of each species was represented by $STVI_{dbh}$ and $STVI_{ht}$, by species. These were averaged for each species, and then summed over all species to obtain one value, as well as separate components. In order to add spatial diversity to the index, the possibility of a separate STVI for distance was discussed. The main reasons for developing $STVI_{dist}$ are that the standard for the index would be maximally diverse spacing, giving a value of 1 for a most diverse stand, and this could be combined with the components for dbh and for height for one measure of structural diversity. Each component index would indicate a value near zero for low diversity and a value near one for high diversity, resulting in some consistency of interpretation.

The illustration of a spatial STVI index was constrained to yield particular values for particular spatial arrangements: for regular (square) spacing, values of the index were nearly zero; for Poisson spacing, values were marginally larger than for square spacing; and for maximally diverse spacing, the index has a value of one. However, a 'maximally diverse' stand structure must be defined to use the index. The STVI for dbh and for height used the uniform distribution as the maximal diversity, resulting in a clear definition of expected variances, and one set of parameters for given values of the intervals (a,b) for dbh and for height. The definition of a maximally diverse spatial arrangement is somewhat arbitrary. Also, using all possible inter-tree distances, simulations to obtain variances of distances for a maximally diverse stand, a Poisson spatial arrangement, a ½ maximally diverse stand, and a 2-clumps (highest variance in distance) arrangement would be needed to calculate the STVI for distance in any situation.

The choice of distance metric was also briefly discussed, since a variety of measures have been used in spatial diversity indices. Using x- and y-distances separately might seem to be a clearer choice, since the diversity in the two directions is isolated, whereas this is somewhat masked in the conversion to Euclidean distances. However, rotations and consideration as to which direction to set as x versus y would be needed, as illustrated with two stem-mapped tree plots. Even if the two directions were isolated, the specific definition of maximum diversity is still arbitrary.

We set out to examine the possibility of using the same principals in developing the STVI for dbh and height to extend to distances. The extension would result in consistencies in the definitions of the three indices, and an overall index could be simply calculated. However, further thought is needed on what might be considered maximal spatial diversity to obtain meaningful and consistent index values.

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Table 1. Mean and variances for different distance metrics by stems per ha and by spatial pattern. Values for "1/2 diverse" and "diverse" were based on a average of 10 simulations; all other values were based on one simulation.

Stems/ha:	Nearest Neighbour			Farthest Neighbour			All Distances			x-Distances			y-Distances		
Type	mean	s^2	$s^2/$ mean	mean	s^2	$s^2/$ mean	mean	s^2	$s^2/$ mean	mean	s^2	$s^2/$ mean	mean	s^2	$s^2/$ mean
100SPH:															
Poisson	5.9	12.3	2.1	98.1	233.8	2.4	54.0	659.7	12.2	49.7	857.9	17.3	54.6	843.4	15.4
Regular	10.0	0.0	0.0	100.0	201.9	2.0	52.4	588.5	11.2	50.0	833.3	16.7	50.0	833.3	16.7
2-cluster	0.5	0.1	0.2	135.3	4.2	0.0	68.1	4068.2	59.7	50.3	2148.4	42.7	49.9	2207.2	44.2
1/2 diverse	0.6	3.3	5.2	69.9	86.0	1.2	35.1	676.8	19.3	49.3	429.3	8.7	53.2	563.3	10.6
diverse	0.8	5.2	6.6	89.0	163.6	1.8	48.3	815.0	16.9	50.8	771.0	15.2	45.3	821.6	18.1
300 SPH:															
Poisson	2.9	2.3	0.8	103.7	229.8	2.2	53.2	648.2	12.2	47.0	834.9	17.8	49.1	907.3	18.5
Regular	5.8	0.0	0.0	100.9	201.8	2.0	51.3	583.1	11.4	49.1	802.8	16.4	49.1	802.8	16.4
2-cluster	0.5	0.1	0.1	132.1	11.6	0.1	65.2	3459.0	53.1	50.4	1940.2	38.5	49.7	1913.4	38.5
1/2 diverse	0.5	0.7	1.3	78.7	123.8	1.6	39.5	871.0	22.0	53.5	421.3	7.9	48.4	841.2	17.4
diverse	0.5	0.7	1.4	89.9	183.9	2.0	46.8	743.9	15.9	49.6	884.8	17.8	52.9	619.9	11.7
500 SPH:															
Poisson	2.2	1.3	0.6	104.3	211.2	2.0	52.6	625.6	11.9	49.8	828.4	16.6	50.3	759.1	15.1
Regular	4.5	0.0	0.0	102.2	200.2	2.0	51.4	589.5	11.5	49.2	806.7	16.4	49.2	806.7	16.4
2-cluster	0.5	0.1	0.2	129.6	20.7	0.2	63.9	3100.9	48.5	49.8	1786.3	35.9	50.4	1803.6	35.8
1/2 diverse	0.5	0.1	0.2	80.9	135.5	1.7	42.5	775.8	18.3	49.3	621.5	12.6	51.9	703.8	13.6
diverse	0.5	0.1	0.2	88.1	143.8	1.6	45.3	761.0	16.8	52.8	664.5	12.6	51.6	754.4	14.6
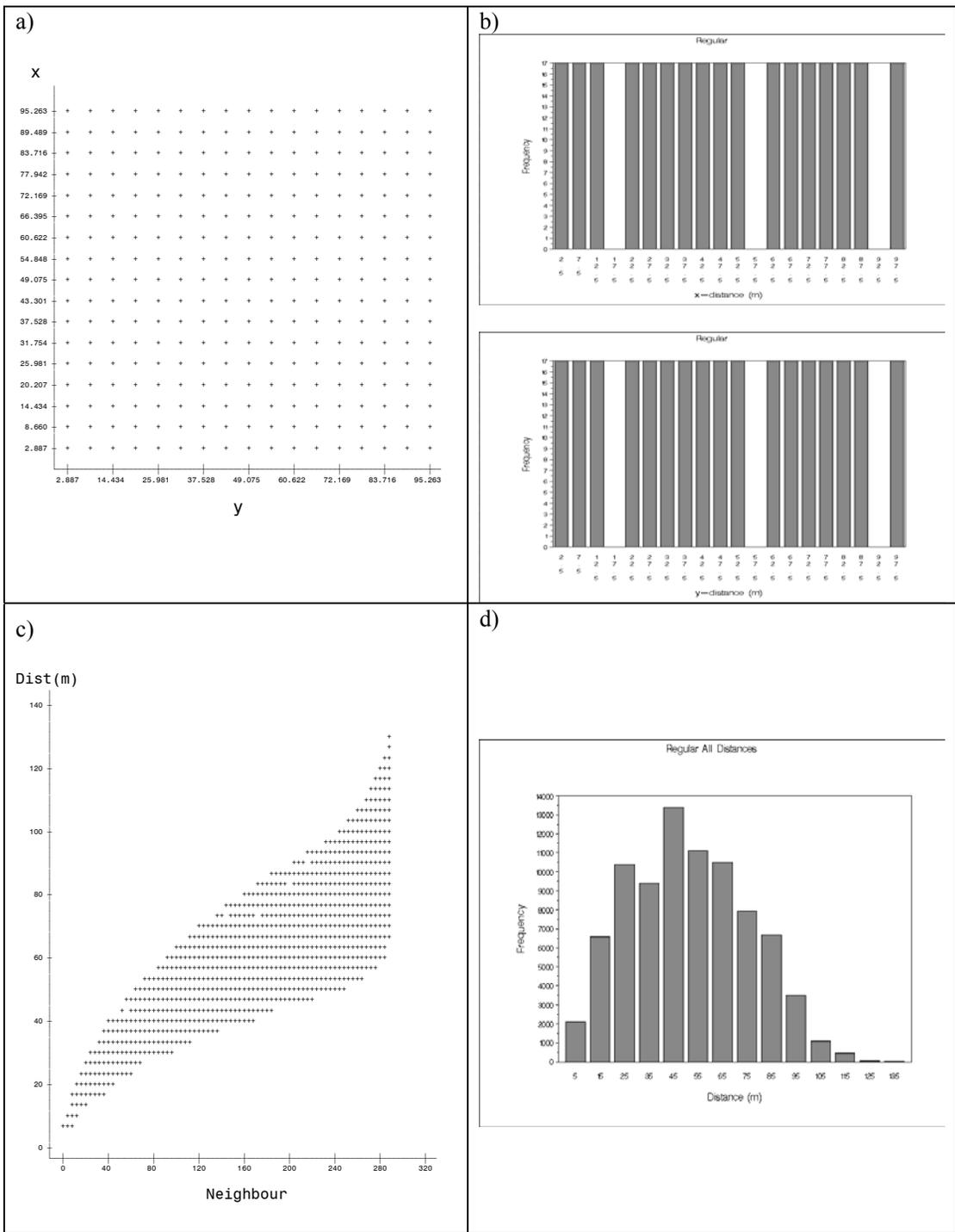
Figure 1. Regular (square spacing), 300 stems per ha: a) spatial map; b) histogram for x and for y directions; c) all possible distances by neighbour (i.e., nearest neighbour=1); d) histogram of all possible distances.
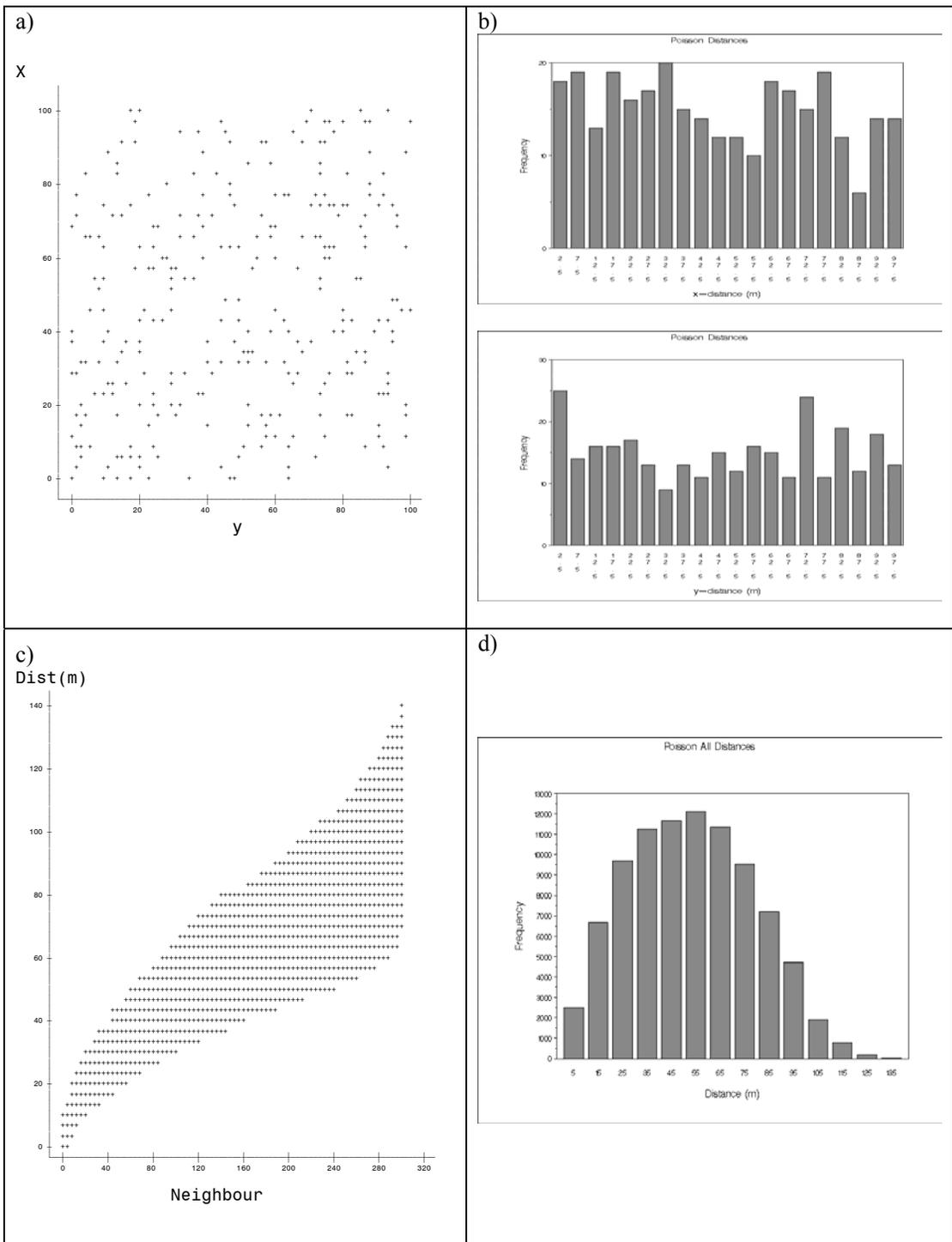
Figure 2. Poisson, 300 stems per ha: a) spatial map; b) histogram for x and for y directions; c) all possible distances by neighbour (i.e., nearest neighbour=1); d) histogram of all possible distances.
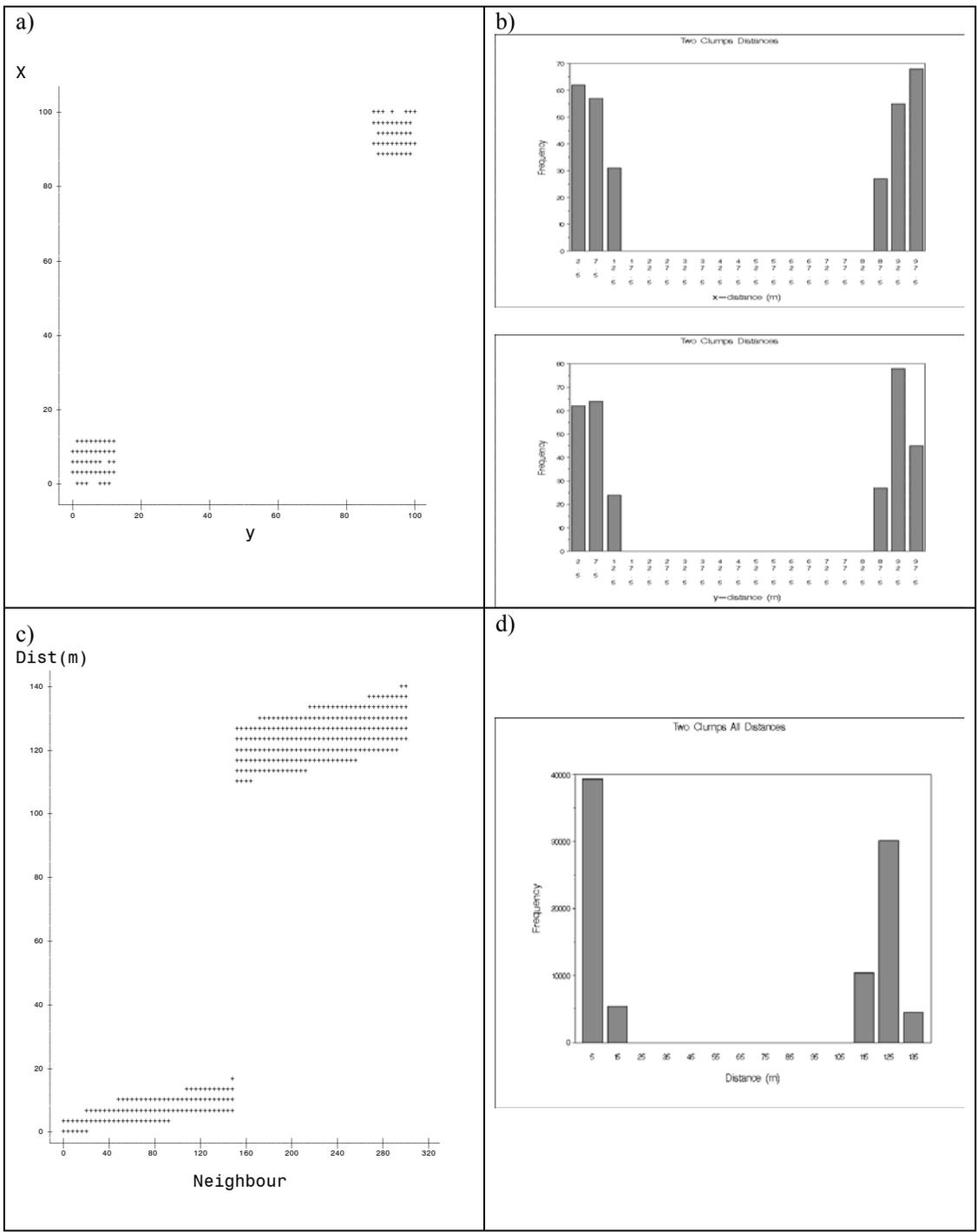
Figure 3. 2-clumps, 300 stems per ha: a) spatial map; b) histogram for x and for y directions; c) all possible distances by neighbour (i.e., nearest neighbour=1); d) histogram of all possible distances.
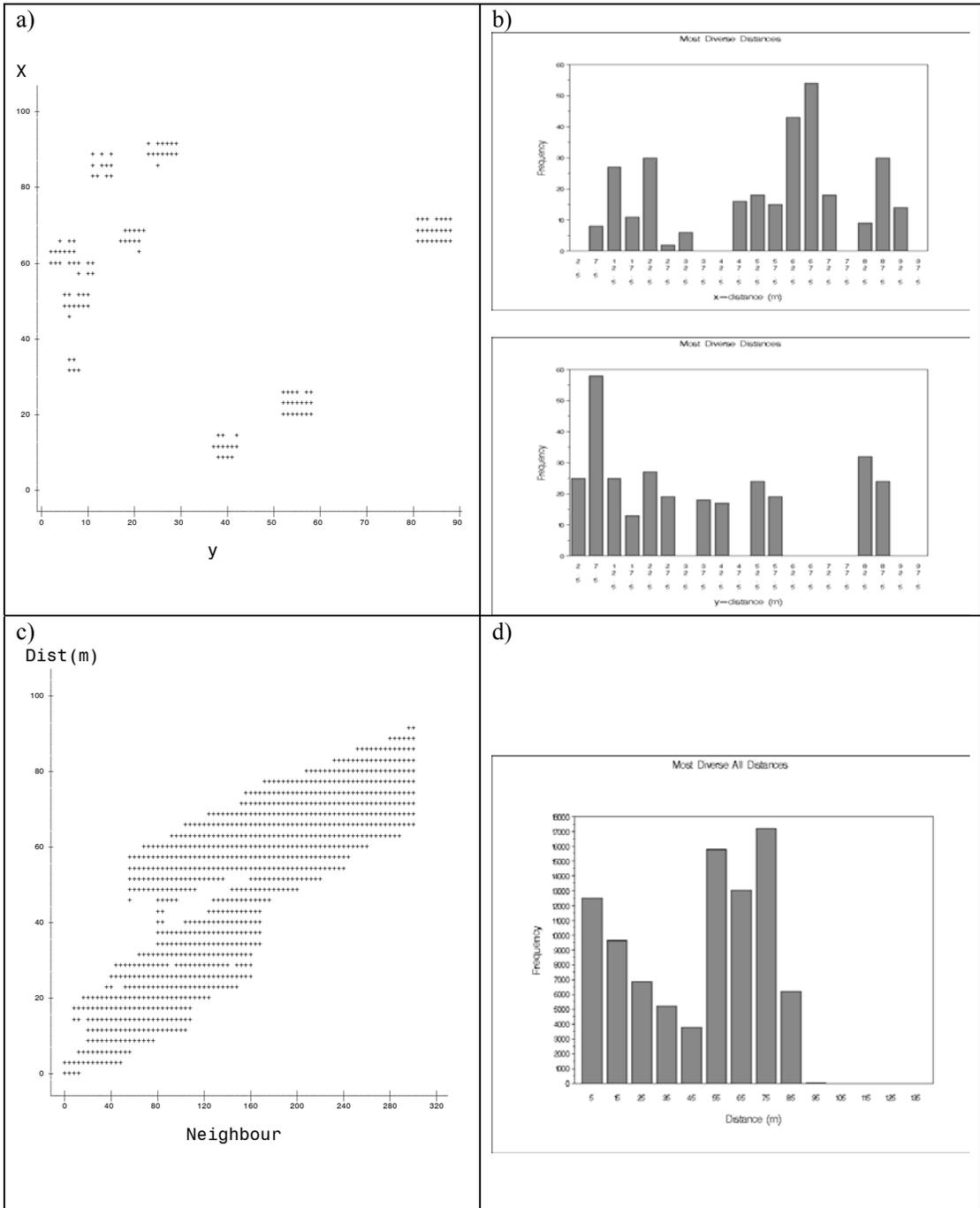
Figure 4. 10-clumps ("most diverse"), 300 stems per ha: a) spatial map; b) histogram for x and for y directions; c) all possible distances by neighbour (i.e., nearest neighbour=1); d) histogram of all possible distances.
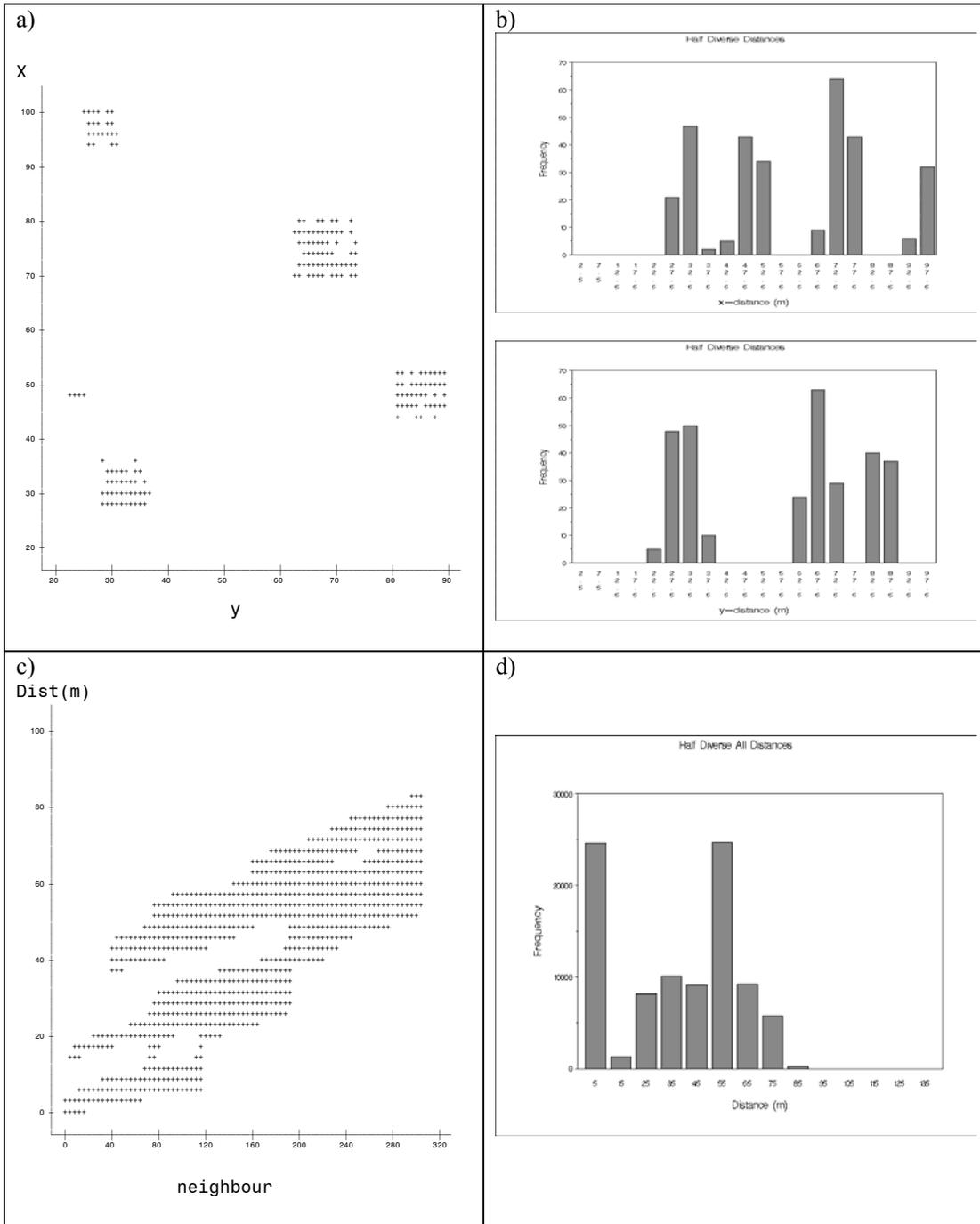
Figure 5. 5-clumps ("half-most diverse"), 300 stems per ha: a) spatial map; b) histogram for x and for y directions; c) all possible distances by neighbour (i.e., nearest neighbour=1); d) histogram of all possible distances.
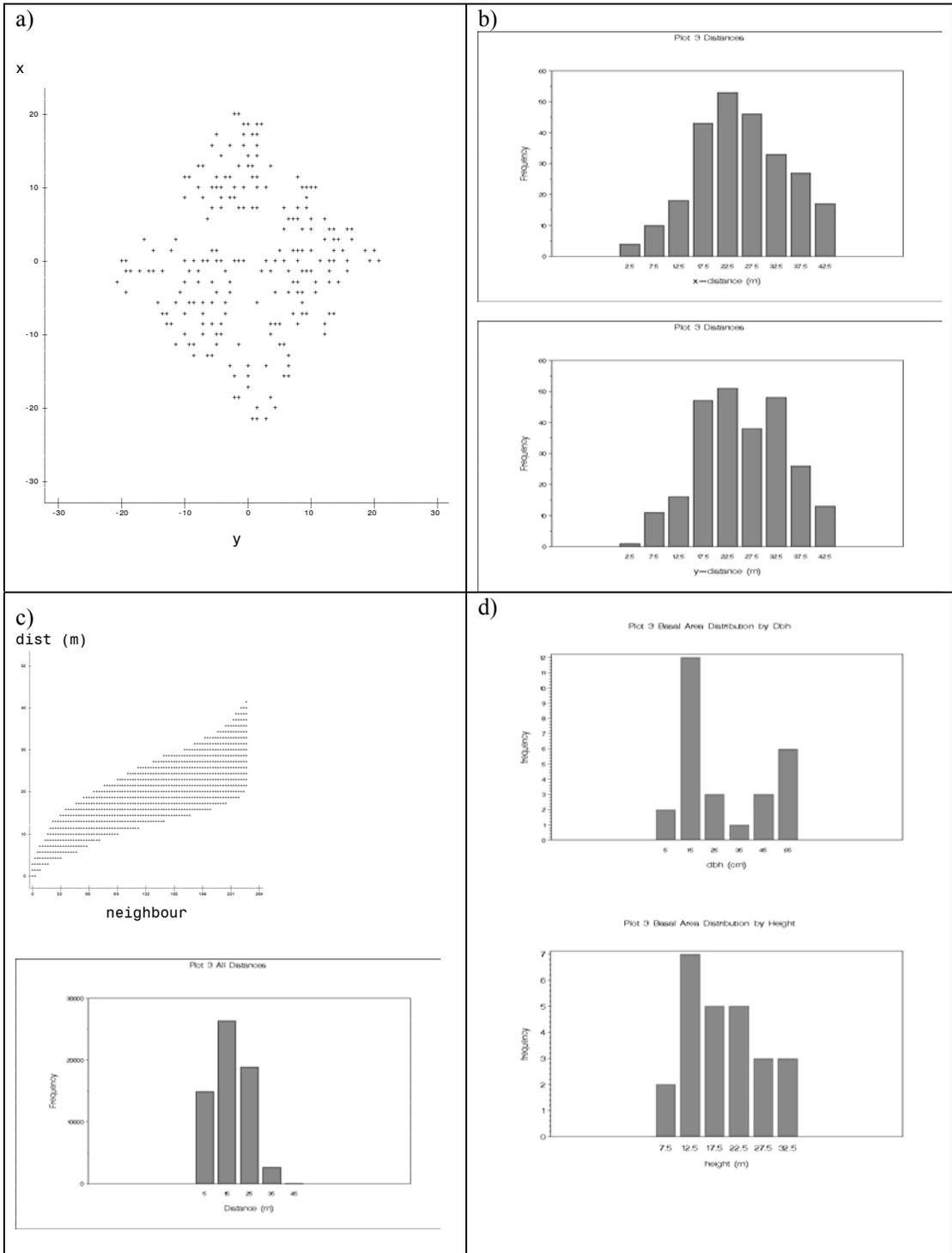
Figure 6. Plot 3, interior Douglas fir: a) spatial map; b) histogram for x and for y directions; c) all possible distances by neighbour (i.e., nearest neighbour=1) and histogram of all possible distances; and d) histogram of basal area per ha by dbh and by height class.
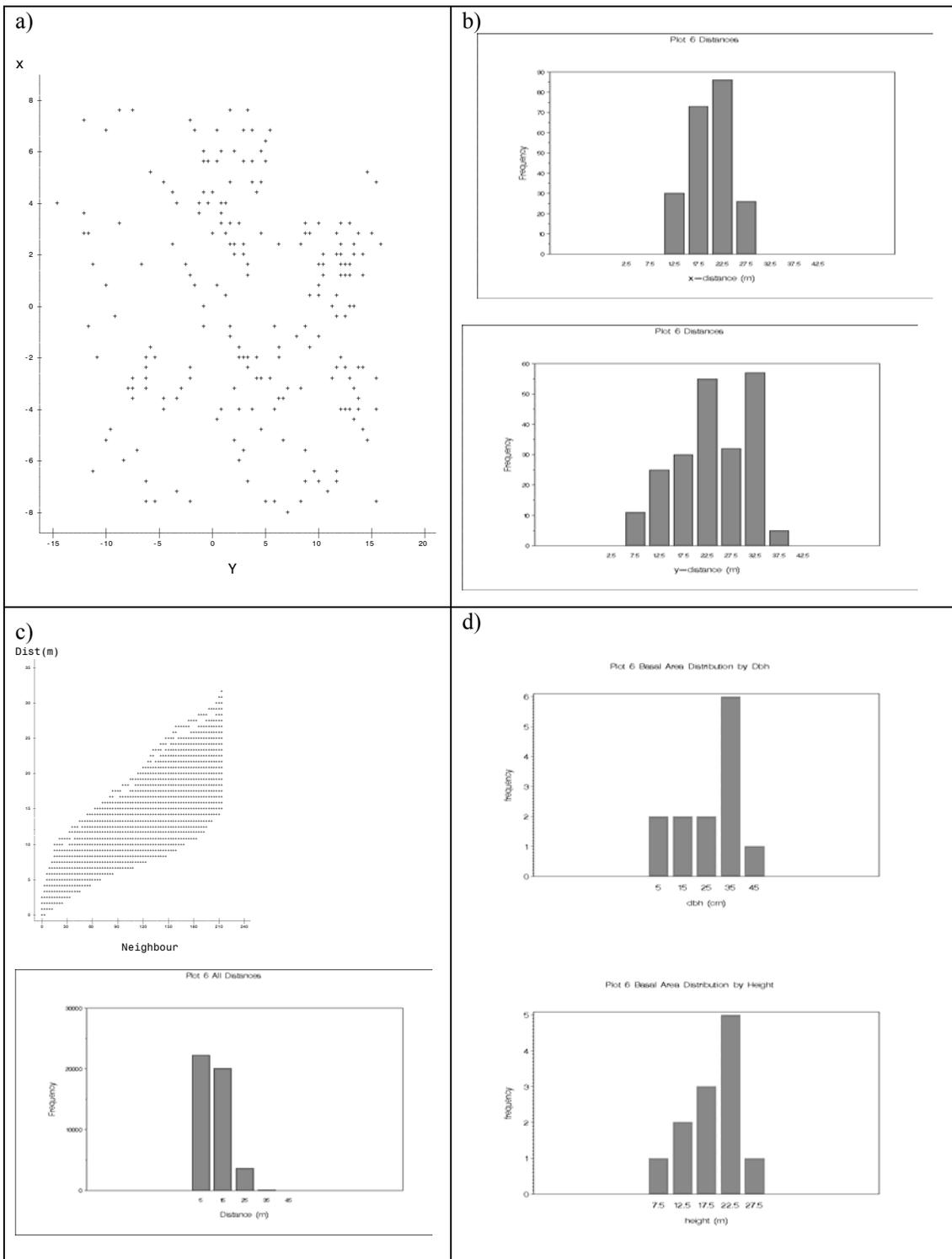
Figure 7. Plot 6, interior Douglas fir: a) spatial map; b) histogram for x and for y directions; c) all possible distances by neighbour (i.e., nearest neighbour=1) and histogram of all possible distances; and d) histogram of basal area per ha by dbh and by height class.