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Comparison of sampling methods for estimation of nearest-neighbor index values

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Complete List of Authors:	Mauro Gutiérrez, Francisco; Oregon State University, College of Forestry. Forest Engineering, Resources and Management. Haxtema, Zane; Oregon State University Temesgen, Hailemariam; Oregon State University
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Abstract

Neighborhood-based indices such as mingling index and diameter differentiation are a set of diversity measures that are based on the relationship between a reference tree and a certain number of nearest neighbors (i.e. trees to which it has the lowest horizontal distance). Using stem-mapped data from eight headwater sites, we compared the relative bias and relative root mean square error (relative to the true mean of each site) of several different methods of choosing reference trees for calculation of diameter differentiation ($\bar{D}$) and species mingling ($\bar{M}$) index. Indexes were defined using 2, 3 and 4 neighbors and methods for selection of reference tree were: random selection of a tree in a fixed radius plot (*FI*), random selection of a tree in a variable radius plot (*VA*), azimuth selection method (*AZ*) and nearest tree selection (*NT*). In general, the relative bias was lower than $\pm 2.5\%$ for $\bar{D}$ and lower than $\pm 10\%$ for $\bar{M}$ regardless of the method. The *FI* method consistently had the lowest relative bias and relative root mean squared error. The *NT* and *AZ* methods were second in terms of relative root mean squared error for $\bar{D}$ and $\bar{M}$ respectively. Simplicity of these two methods might outweigh their slightly worse performance.

1 Introduction

According to Gadow et al. (2012) the term forest structure *“usually refers to the way in which the attributes of trees are distributed within a forest ecosystem”*. Tree growth and mortality shape the forest structure and can be influenced by multiple factors, ranging from human intervention to biotic and abiotic events and processes. But the forest structure itself, modifies the driving factors of tree growth, mortality and regeneration (Gadow et al. 2012). Silvicultural interventions (Franklin and Spies 1991) modify forest structure pursuing an enhancement in productivity and/or the ecological functions of the forest at hand. A proper quantification of forest structure is therefore necessary for a better understanding of forest history and dynamics and for guiding the forest management.

Different forest structures are better suited for different management objectives (i.e. production, recreation or conservation of ecological values). To obtain those forest structures that best suit specific objectives, management systems try to mimic the disturbance regimes that generate the desired structures. Certain forest management systems and their associated structures are therefore preferred to others depending on the management goals. On one end of the gradient of forest management systems, even-aged forestry using clear cuts, shade-intolerant species and short rotation periods, is usually the selected method for production objectives. This management system tries to imitate high intensity disturbances such as forest fires and has certain advantages for harvest operations, however, it does not completely imitate the disturbance regime it is meant to mimic (García-Abril et al. 2013 p. 289). For example, trees and snags remaining after a fire produce conditions that facilitate or accelerate the regeneration, and a complete tree removal fail at producing such conditions. In addition this system produce over-simplified forest structures with a highly homogeneous

composition, similar to those obtained in the first stages of the ecological succession. Such simplification in structure results in a larger susceptibility to biotic and abiotic damages and in a lower resilience.

Management systems known as “close-to-nature” silviculture or continuous cover forestry (CCF), advocate a closer adaptation to natural processes and lead to more complex uneven-aged forest structures, similar to those found in mature forests (Schütz et al. 2012). This type of management appeared in the ninetieth century as a response to the problems associated with intense even-aged management and had a revival in the last decades of the twentieth century. Uneven-aged management systems are better suited for scenarios where multiple objectives have to be considered. They result in larger diversity (structural and biological), are better suited for production of high quality wood and are able to outperform even-aged management systems in terms of economic balance (Howard and Temesgen 1997, Schütz 1997). A thorough review on the history of CCF and comparisons between even-aged and uneven-aged management systems can be found in García-Abril et al. (2013 pp. 289-319).

Forest structure, as mentioned before, is a broad concept that is not restricted to a single attribute or to a single scale. Forest structure is a multidimensional and multiscale property. Different descriptors have been proposed to characterize its different facets at different scales. We will restrict the scope of this manuscript to quantifying forest structure at stand level which is usually linked to the concept of α -diversity (i.e., fine scale diversity) proposed by Whittaker (1960).

To quantify stand level structure, standard aggregated measures of structure such as stand density, basal area or volume can provide the necessary information to characterize stands for even-aged forest management. However, they do not suffice to fully characterize forest structure (Pretzsch 1997) and contain no information on the spatial arrangement of live trees within a stand (Pommerening 2002), which are key features for uneven-aged management systems. Standard aggregated measures and even

more sophisticated presentations such as a stand table, can tell us “what is out there” but not “how what is out there is arranged”. Zenner and Hibbs (2000) present a hypothetical example where two different stands have identical tree densities, basal areas and diameter distributions, and yet have very different forest structures as a result of differing management regimes. Spatial functions, such as Ripley’s K (Ripley 1977) or the pair correlation function (Pommerening 2002), describe the spatial pattern of trees across a continuous range of inter-tree distances. However, they require knowledge of the coordinate positions of all trees within a plot, limiting their use in practical forest inventory applications. Furthermore, they can be difficult to explain to forest managers who may lack advanced statistical training.

In response to the need for a set of analytical tools to quantify forest structure at stand level, nearest-neighbor indices (NNI) have received much attention from the forest research community in recent years. By focusing on the relationship between a given tree (the “reference” tree) and a fixed number of its nearest neighbors (generally three or four trees), NNI are capable of quantifying structural complexity at a very fine scale (e.g. Haxtema et al. 2012). Designed as a framework for characterizing structure without the need for expensive stem mapping (Gadow and Pogoda 2000), NNI have been promoted for their potential use in operational inventory programs (Pommerening 2006) and have been widely used in descriptive studies to quantify the structure of stem-mapped plots (e.g. Aguirre et al. 2003, Saunders and Wagner 2008, Mason et al. 2007, Haxtema et al. 2012). Neighborhood-based indices can be seen as fine-scale measurements of structural diversity, while conventional indices such as stand table measure diversity at the stand level, and other diversity measures such as Shannon and Simpson’s indices require proportional data (i.e., number of individuals of each species and total number of individuals).

Tree-size variability, species composition and spatial distribution of trees have been typically considered as the main features that describe forest structure at stand level (Pommerening 2002, Aguirre et al. 2003) and different NNI have been proposed to measure those features. A comprehensive review of available indexes, not restricted to NNI, to analyze forest structure can be found in (Pommerening 2002). The two commonly used NNI indices are differentiation index D_t developed by Gadow (1993) and species mingling (M_t) developed by Földner (1995). Below we will briefly describe these indices and their uses.

The differentiation index (D_t) describes the degree of interspersion of trees of different sizes. While this index can describe the differentiation of any size-related variable (e.g. diameter at breast height (DBH), height, or volume), only diameter differentiation (the differentiation of DBH) will be considered here. Higher values imply higher differentiation (i.e. more fine-scale variability in size); lower values imply lower differentiation. For the i^{th} reference tree and its j^{th} nearest neighbor, diameter differentiation (D_t) is estimated as:

$$D_t = \frac{1}{n} \sum_{j=1}^n \left[1 - \frac{\min(dbh_i, dbh_j)}{\max(dbh_i, dbh_j)} \right] \quad [1]$$

where $\min(dbh_i, dbh_j)$ is the smaller DBH of the two trees, and $\max(dbh_i, dbh_j)$ is the larger.

The D_t index can be interpreted as follows (Pommerening 2002):

- 1) D_t index values from 0.0-0.3 are evidence of small differentiation. The tree with the smaller DBH is 70% or more of the neighboring tree's DBH.

- 2) D_t index values from 0.3-0.5 are evidence of “average” differentiation. The tree with the smaller DBH is 50-70% of the neighboring tree’s DBH.
- 3) D_t index values from 0.5-0.7 are evidence of big differentiation. The tree with the smaller DBH is 30-50% of the neighboring tree’s DBH.
- 4) D_t index values from 0.7-1.0 are evidence of very big differentiation. The tree with the smallest DBH is less than 30% of the neighboring tree’s size.

The species mingling (M_t) index developed by Gadow and Hui (1999) provides a quantitative assessment of the degree of interspersal between trees of different species. Higher mingling values imply greater intermixing of species throughout a stand; lower values imply a tendency towards species-specific clumping and segregation. For a given reference tree, mingling is calculated as:

$$M_t = \frac{1}{n} \sum_{j=1}^n v_j \tag{2}$$

where n is the number of neighbors considered and v_j is 0 if the j^{th} neighbor is of the same species as the reference tree, and 1 otherwise.

Previous research considered the distribution of the tree level NNI values as the fundamental unit of information for forest structure characterization (Pommerening 2002). However, for comparative studies analyzing different edge-bias-corrections methods, the arithmetic mean of all individual NNI values has been considered as the parameter of interest, and the performance of different methods has been evaluated using their accuracy in estimating NNI population means (Pommerening and Stoyan 2006). We aim at providing references about the best method to select reference trees for NNI calculation by considering a broad range of alternative sampling protocols, sites, and measuring option.

At the expense of losing interpretability in ecological terms, we will restrict our analysis to the estimation of mean NNI values because analyzing the effect of multiple factors in distributions of NNI would make results intractable.

Sampling all trees in relatively large plots of fixed radius is a common alternative in forest inventories, however, this system will be sub-optimal in terms of efficiency (precision) for NNI estimation. When relatively large plots (e.g. permanent plots) are installed, some similarity between trees within a plot can be expected. Because of similarities between tree attributes within permanent plots, difficulties to cover the range of different structural variations that might appear in one stand can be expected. Thus, large plots will show some statistical inefficiency to characterize forest structure. In many cases, temporary sample points are used if the cost of sample point establishment is small relative to the cost of travel. Neighborhood-based indices were specifically designed to be easy to measure in the field, so it may be more statistically efficient to distribute temporary sampling points and reference trees throughout a stand rather than selecting them in permanent plots. Even though this alternative seems to be the best for NNI estimation, minimal guidance exists for practitioners seeking to integrate these indices into sampling protocols, and little is known about the best method of selecting reference trees when commonly used systematic designs, where sampling points are located on the nodes of a regular grid, are used. Instead of substituting standard measures of structure like basal area, volume or dominant height, NNI are meant to complement those measures. Similarly, it is important to note that the sampling for NNI is not supposed to substitute standard sampling procedures. It aims at providing specific information about NNI indexes in a fast and reliable way. Aiming at providing references for future inventories where NNI are measured we consider four different methods for selection of reference trees.

Two alternative methods based on plots can be employed to select reference trees. These methods use either fixed radius (*FI*) or variable radius (*VA*) plots to select a relatively small group of candidate trees. Selected trees are listed and then, a number of candidates, ranging from one the total number of trees selected in the plot, are randomly drawn and considered as reference trees.

Gadow and Pogoda (2000) suggested that reference trees be selected with what we refer to as the “nearest-tree” (*NT*) selection method, whereby the nearest tree to a given sample point is selected as the reference tree. Under this method, trees are selected with probability proportional to the area in which they are the nearest tree. Thus, selection probabilities will be unequal in all but the most uniformly-spaced populations. While Iles (2009) describes an unbiased method for estimating inclusion areas from field measurements, the added effort required to unbiasedly implement this method may tempt the sampler to avoid it due to the high effort required for its implementation. Nonetheless, if the bias incurred by treating a nearest-tree sample as an equal-probability sample is demonstrated to be small in a given forest type, the nearest-tree selection method may be acceptable.

A method sometimes used in forest inventory is to subsample from a fixed plot by selecting the first tree whose center is encountered in a clockwise sweep from north. This has been termed the “azimuth” method (*AZ*) by Iles (1979 p. 23). As with the nearest-tree selection method, inclusion areas will not be equal in most cases, and a satisfactory method has not yet been devised for measuring or estimating inclusion areas in the field. However, it may be reasonable to ignore the bias incurred from this sampling method if it is demonstrated to be small.

2 Objective

The objective of this study is to compare the statistical performance of the *FI*, *VA*, *NT* and *AZ* methods of reference tree selection for estimation of different NNI in headwater riparian forests of western Oregon. We selected diameter differentiation index (Pommerening 2002 after Fuldner, 1995) and species mingling index (Aguirre et al. 2003 after Gadown, 1993) as descriptors of tree size and species composition variability.

3 Materials and methods

3.1 Description of the stem maps

Selected sampling methods were evaluated using data from eight sites located in stem-mapped research plots installed as part of the United States Bureau of Land Management Density Management Study. Methods used to collect data are described in detail by Marquardt et al. (2010) and Eskelson et al. (2011), and briefly summarized here. Plots were located in the Coast Range and foothills of the Cascade Range of western Oregon. Each 0.518 ha plot (72 m x 72 m) was located such that a headwater stream flowed through the approximate centerline of the plot. The coordinate position, diameter at breast height (DBH), and species of all trees greater than 6.9 m tall or 7.6 cm in DBH were recorded.

All stem maps were composed of second-growth forest. Species composition was conifer-dominated, with either Douglas-fir (*Pseudotsuga menziesii* (Mirb.) Franco) or western hemlock (*Tsuga heterophylla* (Raf.) Sarg.) comprising the majority of total stem density on any given site. Western red cedar (*Thuja plicata* Donn) was present on six stem maps and some stem maps contained yew (*Taxus brevifolia* Nutt.) or grand fir (*Abies grandis* (Douglas ex D. Don) Lindl.). The hardwood species red alder (*Alnus rubra* Bong.), bigleaf maple (*Acer macrophyllum* Pursh) and black cottonwood (*Populus balsamifera* L. ssp. *trichocarpa* (Torr. & A. Gray ex Hook.) Brayshaw) were a minor component of some

stem maps (Marquardt et al. 2012). Species composition and average values for the species mingling and diameter differentiation indexes computed with 2, 3 and 4 neighbors in each site are provided in Table1.

3.2 Parameter of interest

The parameters of interest were the average values of the diameter differentiation ($\bar{D}$) and species mingling index ($\bar{M}$) (Table1) for each stem map. Because trees near a plot edge may have immediate neighbors that are outside the plot, bias can result from the calculation of index values when only trees inside the plot are considered (Pommerening 2006). Considering Pommerening and Stoyan (2006) edge effect were accounted for by using a toroidal edge correction (Ripley 1979) on each site.

Both, the diameter differentiation index and the species mingling index depend on the number of neighbors (n_n) considered to compute each index. We considered three different number of neighbors $n_n=2, 3$ and 4 , as these are sensible values to use in operational forestry applications. If n_n changes, the index y_t , associated to each tree (t) and the site averages ($\bar{Y}$) change too. To assess the importance of the change in $\bar{Y}$, we tested by means of ANOVA analysis whether or not increasing the number of neighbors from 2 to 4 resulted in different values for the average values of both indexes. We accounted for the effect of multiple comparisons, and performed a Bonferroni correction (Dunn 1961) by dividing the significance level $\alpha = 0.05$ by the number of comparisons performed.

3.3 Reference tree selection methods

The four methods compared in this study result in different reference tree selection probabilities. Selection probabilities are fundamental to derive estimators for different sampling protocols. An

unbiased estimator of the population mean for general sample designs of fixed size n (Horvitz and Thompson 1952) is given by $\hat{Y}_{HT} = \frac{\sum_{t=1}^n w_t y_t}{N}$, where sub index HT stands for Horvitz and Thompson, and w_t is the reciprocal of the probability of selecting tree t . For equal probability sample designs this estimator becomes the sample mean. To make the methods comparable, and to take into account the particular characteristics of each selection method, several factors were considered and, when possible, approximated sampling weights were obtained for each tree.

First, to make the methods comparable, it was necessary to keep the number of measurements equal between selection methods. Since the *NT* and *AZ* methods only select one tree per plot, only one tree was selected from the *FI* and *VA* plots methods. Then, the selection protocol resulting for each of these methods can be described as follows. For the *FI* method, a tree was sub-sampled from a fixed plot by drawing a random number from 1 to F where F is the number of trees in fixed the plot. When using the *VA* method to capture trees, a tree was sub-sampled by randomly selecting one of V trees captured in the variable radius plot with probability proportional to its basal area. Weights were then $w_{t,FI} = F$ and $w_{t,VA} = V \frac{BAF}{BA_t}$, where the term BAF is the basal area factor used in the variable plot and BA_t was the basal area of the selected tree. It is important to note that both weights are approximations to the real weight of the trees for the described sampling protocols. For the *NT* and *AZ* methods it was impossible to obtain approximated weights for the selected reference trees and they were all equally weighted with a weight of 1 in subsequent estimations.

3.4 Simulation of alternatives methods for reference tree selection

A simulation algorithm was written in R (R Core Team 2016) to simulate the field measurement performed using each of the described methods. Four sampling points were simulated at each of 500

repetitions in each site. Since systematic sampling is far more common than random sampling in most forestry sampling applications, this method of sample point placement was simulated. The first point was randomly located within the lower-left quadrant of the stem map using the pseudo-random number generator function in R. Subsequent points were placed on a 36m x 36m grid so every quadrant of the stand map had a plot included. The fixed plot radius and variable plot BAF were scaled to capture an average of 3, 6 and 9 trees (n_t). Finally, the four methods for selection of reference trees were applied in each sampling point. This process was iterated 500 times, as we empirically observed that rate of change for the accuracy statistics described in next section was negligible after 500 replications.

Since the probability of selecting a tree as a reference varies with the number of trees captured at a sample point, it is necessary to factor the number of trees per sample point into the weighted sample estimate produced by each selection process (Iles 2003 p. 562). For each sampling method, each neighborhood-based index was estimated at iteration k as a weighted average [3] of the sampled values in an attempt to obtain estimators resembling the Horvitz and Thompson (1952) estimator.

$$\hat{Y}_{k,j,m,n_t,n_n} = \frac{\sum_{t=1}^4 w_{t,k,j,m,n_t} y_{t,k,j,n_n}}{\sum_{t=1}^4 w_{t,k,j,m,n_t}} \quad [3]$$

Note that for each method (m) and site (j), $\hat{Y}_{k,j,m,n_t,n_n}$ always depends on n_n , and the iteration k . For the *FI* and *VA* methods, the selected reference trees depend on n_t but not for the *NT* and *AZ* methods. For generality sub index n_t was left on $\hat{Y}_{k,j,m,n_t,n_n}$. Four reference trees are selected for each site, iteration, n_t and method. Trees are indicated with sub index t . The approximated weight for the selected t^{th} tree selected at iteration k in site j by the m^{th} method tree depend on n_t which results on reference tree weights indexed as w_{t,k,j,m,n_t} . Weights w_{t,k,j,m,n_t} were assigned as explained in 3.3.

226 Finally, the index value for the t^{th} tree selected at iteration k in site j by the m^{th} method depend on
 227 n_n . Therefore, reference tree values for the neighborhood-based indexes are indicated as y_{t,k,j,n_n} .

228 The sampling methods were evaluated for estimation of species-specific index values for Douglas-
 229 fir (DF), western hemlock (WH), western red cedar (RC) and, red alder (RA); the four species that
 230 occurred on at least six stem maps. Species specific estimates for both indexes were calculated by
 231 considering only reference trees of each species in equation [3].

232 3.5 Accuracy assessment

233 The sampling methods were compared using relative bias (RB) and relative root mean square error
 234 ($RRMSE$) (e.g., Temesgen 2003, Temesgen et al. 2011 and Poudel et al. 2015). For each site, sampling
 235 method, number of neighbors for the indexes definition and average number of trees in the fixed and
 236 variable radius plots, relative bias was computed as:

$$RB_{j,m,n_t,n_n}(\%) = 100 \frac{\sum_{k=1}^{500} [\hat{Y}_{k,j,m,n_t,n_n} - \bar{Y}_{j,n_n}]}{500 \bar{Y}_{j,n_n}} \quad [4]$$

237 where $\bar{Y}_{j,n_n}$ is the true arithmetic mean index value of the population for site j when neighborhood
 238 based indexes are calculated based on n_n neighbors. We tested by means of t-tests whether or not for
 239 each combination of: site, method, n_n and n_t , the average of the difference $\hat{Y}_{k,j,m,n_t,n_n} - \bar{Y}$ (i.e. the
 240 absolute bias), was significantly different than 0.

241 The RRMSE was computed as:

$$RRMSE_{j,m,n_t,n_n}(\%) = \frac{100}{\bar{Y}} \sqrt{\frac{\sum_{k=1}^{500} [\hat{Y}_{k,j,m,n_t,n_n} - \bar{Y}]^2}{500}} \tag{5}$$

The *RB* and the *RRMSE* for each stem map and species were computed similarly, but only considering those iterations where at least one reference trees of the considered species was selected. Then the denominator and the summation limits in equations [4] and [5] were changed to $N_{iter,sp}$. Where $N_{iter,sp}$ is the number of iterations for which at least one reference tree belonged to the species of interest. We did not tested for each species whether or not for each combination of: stem maps, method, n_n and n_t , *RB* was significantly different than 0 because the species compositions of the stem maps is relatively uneven. This would result in a very different number of observations for each species and therefore different values for the power of the t-test, making interpretations of further comparisons difficult. Finally, factorial analysis of variance (ANOVA) was used to assess if significant differences were present for *RB* and *RRMSE* across methods and across methods and species, when changing both n_n and n_t . We accounted for the effect of multiple hypothesis testing by using a Bonferroni correction and when factors were significant we performed a post hoc analysis by computing Tukey’s honest significant differences.

4 Results and discussion

The statistical scope of inference of this study is limited to forests adjoining headwater streams within the Density Management Study sites. However, the general principles underlying the sampling methods we examined may be applicable to a wide array of forest types.

Reducing the number of neighbors from 4 to 2 in the definition of both indexes had no significant effect on their average values (p-value=0.99 for the diameter differentiation index and p-value=0.94 for species mingling index). This result has important practical consequences for future inventories. By reducing the number of trees the mean value of the studied indexes is not affected, but less neighbors need to be measured for each reference tree. This result partially supports previous research from Sterba (2008) who measured one nearest neighbor for all trees selected with a variable plot sample in the Austrian Alps and concluded that estimates of the diameter differentiation index could be obtained with “only little additional field work”. Finally, stand level distribution of NNI indexes are more meaningful than the means studied here. The number of neighbors to use for the index computation was not a significant factor for the average NNI in a stand. Leaving this factor out of the analysis in further studies might be a good compromise solution to approach the more complex problem of estimating stand level distributions of NNI.

For the fixed radius plot method, the t-test for the average of the differences $\hat{Y}_{k,j,m,n_t,n_n} - \bar{Y}$ for the species mingling index were significantly different from 0 in only 3 of the 72 possible combinations of stem map and number of neighbors, n_n and n_t (Table 2). For the diameter differentiation index, the average difference was, in all cases, not significantly different from 0. This result supports the idea, that the approximated weights used for this method are not perfect but effective in order to prevent biased estimates of the two considered indexes. For the variable radius plot method the number of combinations of stem maps, n_n and n_t for which a significant bias was found were 6 and 14 out of 72 possible combinations for the species mingling and diameter differentiation index respectively. For the nearest tree and the azimuth method, the number of combinations of stem maps, n_n and n_t for which a significant bias was found were respectively 16 and 16 for the species mingling, and 8 and 6 for and

diameter differentiation index. Despite trying to correct for bias by incorporating approximated weights, the *VA* method provided biased results in a number of combinations of n_n and n_t , similar to the *NT* and *AZ* method (Table 2).

In general, *RB* was in the range of [-10%,10%] for the species mingling index and in the range of [-2.5%,2.5%] for the diameter differentiation index, however, for certain combinations of stem map, method, n_n and n_t , the absolute value of *RB* exceeded 10% and 5% for each index respectively (Figure 1 and Figure 2). The *RRMSE* was in general below 10% for the species mingling index and below 4% for the diameter differentiation index while for certain combinations of stem maps, methods, n_n and n_t , *RRMSE* exceeded 20% and 5% for each index respectively (Figure 1 and Figure 2). The analysis of variance revealed that differences in *RRMSE* and *RB* among methods were significant for both variables (Table 3). Pair wise comparisons among methods by means of Tukey's honest significant differences tests showed that *FI* method had significantly lower *RRMSE* than any other method, except when compared to the *AZ* method for species mingling estimation. The between-site variability in *RRMSE* and *RB* for the remaining methods was high for both indices, making it difficult to draw general conclusions about the performance of the sampling methods (Table 3). Neither n_n nor n_t had significant effect on *RRMSE* or *RB* and interaction terms were not significant either.

Species specific results were similar to those obtained for all species together. The factor species was significant for the *RB* and *RRMSE* of both indexes. The method was again a significant factor for both error measures and indexes, and pairwise comparisons among methods by means of Tukey's honest significant differences tests showed that fixed radius plots had significantly lower *RRMSE* than any other method (Table 4).

For the diameter differentiation index the following sequence displays the methods tested in this study sorted by increasing species-specific $RRMSE$, $FI < (AZ, NT) < VA$. The symbol $<$ indicates that a method on the left is superior in terms of $RRMSE$ (i.e. lower $RRMSE$) to the method or group of methods (grouped with a parenthesis) on the right. For the species mingling index, the sequence of methods sorted by their species specific $RRMSE$ similar to the previous, however, in this case the $RRMSE$ of the FI method was not significantly smaller than the $RRMSE$ of the AZ method. The variability of RB and $RRMSE$ by methods and species is shown in Figure 3 and Figure 5 respectively for the species mingling index. Variability of RB and $RRMSE$ for the diameter differentiation index estimates is shown in Figure 4 and Figure 6. The FI method was fairly stable in terms of $RRMSE$ and RB among sites for both indexes. The variability of $RRMSE$ and RB for the azimuth and the nearest tree methods was important for certain combinations of species-index. For example, when considering the species mingling index for Douglas fir, variability of RB and $RRMSE$ for the NT method was consistently larger than the variability for the FI and AZ method. Similarly, the variability of RB and $RRMSE$ for diameter differentiation of Western Red Cedar, was larger than that observed for the same species with the FI and NT method.

While all sampling methods examined had low $RRMSE$ and RB , fixed plot sampling performed consistently better than the other methods, which suggest that this method should be preferred for further applications when only precision is considered. This method is relatively simple and does not require an important amount of extra field measurements when compared to the nearest tree or azimuth method, and its implementation in the field is straightforward. All methods are designed to select a single reference tree in each sampling point, however, the AZ and NT methods, do not require a first step to determine what trees are included in a plot. Both, the NT and AZ method select trees with probability proportional to the area of an associated polygon, the size and shape of which is

dictated by the sampling system and positions of the trees. The selection bias inherent in the nearest-tree method has been a topic discussion in natural resources sampling but the azimuth method has been little studied. The simplicity of the *AZ* and *NT* selection protocols comes at the expense of 1) a tendency to select more isolated trees and 2) a difficult quantification of inclusion probabilities for each tree. However, for both methods the *RRMSE* and *RB*, while dependent on the site, were relatively low (Figure 1 and Figure 2). It is therefore reasonable to think that the simplicity of these methods might outweigh their worse performance when compared to the *FI* method. Unfortunately, precise information about the time and effort required to implement each method in the field was not available for this study. Therefore a proper evaluation of the operational implications of each method was impossible.

In the only other comparison of sampling methods for estimation of NNI published in English, Kint et al. (2004) evaluated two sampling methods, “distance sampling” and “plot sampling”. Distance sampling is the random selection of trees from a tree-list, while plot sampling is the selection of a given number of trees that are nearest to a sample point. Distance sampling is a design-unbiased sampling method, while plot sampling is not design-unbiased (for a treatment of the calculation of inclusion areas for this sampling design, see Kleinn and Vilčko (2006). Kint et al. (2004) found that plot sampling had substantially greater bias than distance sampling even with relatively large sample sizes. However, they concluded that plot sampling was a sometimes a better candidate for estimation of diameter differentiation, while distance sampling was always a better candidate for estimation of species mingling.

One assumption of this study has been that a sampler wishes to estimate the arithmetic mean index value for a population. However, Gadow and Pogoda (2000) defended the nearest-tree approach

by stating that “the structural attributes of the reference trees do not represent the relative share of the number of trees but proportions of the forest area”. Under this framework, the sampler would actually be interested in estimating the average values that is weighted by the area a_i where each tree would be the nearest tree (i.e. the area of the Thiessen polygon of each tree). This weighted average will obviously be different from the arithmetic average $\bar{Y}$ introduced in equation [3] in all but the most uniform of stands. Selection probabilities for the *NT* method are proportional to a_i , so the Horvitz-Thompson estimator can be computed because the terms a_i cancel out. In addition, a strong correlation of the selection probabilities (proportional to a_i) with the variable of interest, $a_i y_i$, are very likely, and would ensure that this method nearly optimal is nearly optimal. Other choices of weights may also be considered. If the index values of large trees are considered to be more meaningful in determining forest structure than those of small trees, weighting by basal area would be appropriate and variable plot sampling would probably be the most efficient system. Regardless of what definition of NNI is adopted by the scientific community, a consistent definition will be helpful in facilitating comparisons between different research studies and moving NNI from the world of academia to the world of operational forest inventory.

5 Conclusions

While NNI have attracted much attention from the forest research community, little work has been done to determine the most efficient (lowest *RRMSE*) sampling system for estimating index values. This study was performed to fill that gap by evaluating the performance of four sampling methods for estimating the species mingling and diameter differentiation methods in headwater riparian forests of western Oregon. Of the sampling methods considered, fixed plot sampling consistently had the lowest bias and *RRMSE*. Fixed plot sampling would likely produce low bias in any forest type. The bias of the

other sampling methods was unpredictable and may be substantial under some conditions, however, in most situations was moderately low.

The appropriate sampling method to use is dependent on the attribute to be estimated. This study assumed that the sampler is interested in estimating the arithmetic mean index value for a population. Results would differ if a weighted mean was to be estimated.

Finally, for further studies aiming at analyzing the performance of different methods for estimation of NNI distributions, keeping the number of neighbors constant seems to be a reasonably good starting point.

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7 Tables

Table1. Summary statistics for each stem map. DF, Douglas-fir; WH, western hemlock; WR, western red cedar; GF, grand fir; PY, Pacific yew; RA, red alder; BM, big-leaf maple; BC, black cottonwood , GC golden chinquapin, PD pacific dogwood, SX Salix sp. N is the total number of trees at each site; $\bar{M}$ and $\bar{D}$ are the average value for the species mingling and diameter differentiation indices respectively.

Site	n_n						Percentage of total density											N
	2		3		4		DF	WH	WR	GF	PY	RA	BM	BC	GC	PD	SX	
	$\bar{M}$	$\bar{D}$	$\bar{M}$	$\bar{D}$	$\bar{M}$	$\bar{D}$												
BL13	0.14	0.40	0.16	0.40	0.17	0.39	85.2	-	-	-	0.5	-	11.4	-	-	2.9	-	210
KM17	0.43	0.27	0.43	0.27	0.45	0.27	30.1	60.3	0.8	-	-	8.8	-	-	-	-	-	239
KM18	0.48	0.39	0.50	0.39	0.51	0.39	30.8	51.2	11.7	-	-	6.3	-	-	-	-	-	383
KM19	0.47	0.38	0.47	0.37	0.47	0.37	49.6	30.8	17.3	-	-	2.1	-	0.3	-	-	-	341
KM21	0.41	0.34	0.43	0.34	0.45	0.34	36.4	40.4	8.4	-	-	14.7	-	-	-	-	-	225
OM36	0.22	0.36	0.22	0.35	0.23	0.35	73.6	26.4	-	-	-	-	-	-	-	-	-	239
TH46	0.35	0.27	0.35	0.26	0.36	0.26	83.5	3.3	1.2	2.9	-	6.6	0.4	0.4	0.8	0.4	0.4	242
TH75	0.37	0.37	0.40	0.38	0.41	0.38	65.2	4.6	3.5	-	-	2.7	23.7	0.3	-	-	-	371

481 Table 2. T-test p-values for each index and combination of stem map, method, number of neighbors and
 482 number of trees per plot. Highlighted cells indicate significant differences after performing the
 483 Bonferroni correction.

Index		Species mingling									Diameter differentiation								
n_t		3			6			9			3			6			9		
Site	n_n	2	3	4	2	3	4	2	3	4	2	3	4	2	3	4	2	3	4
BL13	NT	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.81	0.55	0.03	0.81	0.55	0.03	0.81	0.55	0.03
	FI	0.31	0.77	0.48	0.74	0.97	0.77	0.48	0.52	0.43	0.82	0.52	0.60	0.50	0.64	0.99	0.48	0.45	0.93
	AZ	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.02	0.00	0.04	0.02	0.00	0.04	0.02	0.00
	VA	0.14	0.30	0.01	0.29	0.14	0.00	0.72	0.07	0.00	0.33	0.40	0.28	0.28	0.15	0.38	0.21	0.30	0.34
KM17	NT	0.43	0.05	0.06	0.43	0.05	0.06	0.43	0.05	0.06	0.20	0.10	0.09	0.20	0.10	0.09	0.20	0.10	0.09
	FI	0.07	0.04	0.01	0.26	0.22	0.10	0.31	0.24	0.29	0.77	0.86	0.94	0.33	0.61	0.72	0.62	0.96	0.91
	AZ	0.03	0.16	0.45	0.03	0.16	0.45	0.03	0.16	0.45	0.78	0.04	0.00	0.78	0.04	0.00	0.78	0.04	0.00
	VA	0.47	0.35	0.46	0.54	0.26	0.24	0.00	0.01	0.05	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
KM18	NT	0.04	0.05	0.09	0.04	0.05	0.09	0.04	0.05	0.09	0.01	0.06	0.36	0.01	0.06	0.36	0.01	0.06	0.36
	FI	0.53	0.11	0.50	0.77	0.71	0.70	0.39	0.12	0.21	0.36	0.38	0.58	0.67	0.40	0.33	0.76	0.97	0.93
	AZ	0.11	0.30	0.40	0.11	0.30	0.40	0.11	0.30	0.40	0.90	0.38	0.53	0.90	0.38	0.53	0.90	0.38	0.53
	VA	0.64	0.89	0.65	0.76	0.96	0.40	0.88	0.96	0.31	0.25	0.13	0.03	0.37	0.13	0.04	0.27	0.30	0.48
KM19	NT	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.02	0.00	0.00	0.02	0.00	0.00
	FI	0.00	0.00	0.00	0.33	0.13	0.03	0.00	0.00	0.00	0.18	0.23	0.16	0.92	0.48	0.39	0.50	0.92	0.98
	AZ	0.00	0.06	0.29	0.00	0.06	0.29	0.00	0.06	0.29	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	VA	0.02	0.02	0.05	0.00	0.02	0.11	0.00	0.00	0.01	0.08	0.11	0.28	0.06	0.02	0.09	0.11	0.04	0.08
KM21	NT	0.09	0.02	0.00	0.09	0.02	0.00	0.09	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	FI	0.29	0.61	0.82	0.86	0.04	0.01	0.32	0.40	0.70	0.90	0.52	0.67	0.97	0.62	0.12	0.93	0.41	0.77
	AZ	0.95	0.46	0.30	0.95	0.46	0.30	0.95	0.46	0.30	0.36	0.14	0.56	0.36	0.14	0.56	0.36	0.14	0.56
	VA	0.09	0.76	0.97	0.04	0.84	0.55	0.01	0.41	0.18	0.03	0.55	0.48	0.00	0.00	0.00	0.00	0.00	0.00
OM36	NT	0.00	0.25	0.90	0.00	0.25	0.90	0.00	0.25	0.90	0.75	0.88	0.67	0.75	0.88	0.67	0.75	0.88	0.67
	FI	0.55	0.48	0.28	0.29	0.51	0.33	0.83	0.94	0.66	0.38	0.24	0.09	0.06	0.15	0.10	0.91	0.99	0.68
	AZ	0.01	0.00	0.01	0.01	0.00	0.01	0.01	0.00	0.01	0.53	0.13	0.61	0.53	0.13	0.61	0.53	0.13	0.61
	VA	0.59	0.94	0.79	0.47	0.33	0.19	0.96	0.17	0.07	0.07	0.04	0.16	0.97	0.83	0.61	0.03	0.01	0.00
TH46	NT	0.00	0.02	0.00	0.00	0.02	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	FI	0.08	0.19	0.14	0.86	0.90	0.61	0.62	0.97	0.67	0.19	0.18	0.00	0.17	0.15	0.06	0.01	0.01	0.01
	AZ	0.82	0.90	0.39	0.82	0.90	0.39	0.82	0.90	0.39	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	VA	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.35	0.33	0.08	0.01	0.02	0.00	0.01	0.02	0.00
TH75	NT	0.37	0.88	0.77	0.37	0.88	0.77	0.37	0.88	0.77	0.81	0.29	0.01	0.81	0.29	0.01	0.81	0.29	0.01
	FI	0.84	0.57	0.79	0.12	0.17	0.22	0.24	0.29	0.23	0.90	0.57	0.67	0.26	0.08	0.18	0.75	0.15	0.10
	AZ	0.50	0.86	0.86	0.50	0.86	0.86	0.50	0.86	0.86	0.29	0.06	0.02	0.29	0.06	0.02	0.29	0.06	0.02
	VA	0.09	0.00	0.00	0.04	0.00	0.00	0.33	0.06	0.00	0.42	0.20	0.04	0.03	0.03	0.00	0.56	0.25	0.09

484

485 Table 3. Analysis of variance for RB and RRMSE for estimation of the overall diameter differentiation and
486 species mingling indexes. The factor method is indicated as m , n_n and n_t indicate the number of
487 neighbors used to compute the indexes and the average number of trees in the fixed and variable radius
488 plots.

Factor	RB diameter differentiation					RRMSE diameter differentiation				
	Df	Sum of Squares	Mean square	F value	Pr(F)	Df	Sum of Squares	Mean square	F value	Pr(F)
Factor n_n	2	3.0E-04	1.5E-04	1.8E-01	8.3E-01	2	2.0E-04	1.0E-04	3.2E-01	7.3E-01
Factor n_t	2	1.6E-03	7.9E-04	9.6E-01	3.8E-01	2	1.6E-04	7.8E-05	2.5E-01	7.8E-01
Factor $method (m)$	3	1.6E-02	5.4E-03	6.6E+00	*2.7E-04	3	3.1E-02	1.0E-02	3.2E+01	*<2E-16
Interaction $n_n \times n_t$	4	6.0E-05	1.5E-05	1.9E-02	1.0E+00	4	1.0E-05	2.0E-06	8.0E-03	1.0E+00
Interaction $n_n \times m$	6	4.7E-04	7.8E-05	9.5E-02	1.0E+00	6	9.4E-04	1.6E-04	5.0E-01	8.1E-01
Interaction $n_t \times m$	6	4.6E-03	7.7E-04	9.4E-01	4.7E-01	6	1.8E-04	3.0E-05	9.4E-02	1.0E+00
Interaction $n_t \times n_t \times m$	12	1.1E-04	9.0E-06	1.1E-02	1.0E+00	12	2.0E-05	2.0E-06	6.0E-03	1.0E+00
Residuals	252	2.1E-01	8.2E-04			252	7.9E-02	3.2E-04		

Factor	RB species mingling					RRMSE species mingling				
	Df	Sum of Squares	Mean square	F value	Pr(F)	Df	Sum of Squares	Mean square	F value	Pr(F)
Factor n_n	2	9.4E-03	4.7E-03	4.9E-01	6.1E-01	2	2.0E-03	9.9E-04	1.6E-01	8.6E-01
Factor n_t	2	6.0E-04	3.0E-04	3.2E-02	9.7E-01	2	2.4E-03	1.2E-03	1.9E-01	8.3E-01
Factor $method (m)$	3	3.1E-01	1.0E-01	1.1E+01	*1.1E-06	3	1.5E-01	4.8E-02	7.6E+00	*6.9E-05
Interaction $n_n \times n_t$	4	4.0E-04	1.0E-04	1.0E-02	1.0E+00	4	3.0E-04	9.0E-05	1.3E-02	1.0E+00
Interaction $n_n \times m$	6	2.1E-02	3.5E-03	3.7E-01	9.0E-01	6	5.8E-03	9.7E-04	1.5E-01	9.9E-01
Interaction $n_t \times m$	6	2.7E-03	4.6E-04	4.8E-02	1.0E+00	6	2.7E-03	4.4E-04	7.0E-02	1.0E+00
Interaction $n_t \times n_t \times m$	12	5.0E-04	4.0E-05	4.0E-03	1.0E+00	12	6.0E-04	5.0E-05	8.0E-03	1.0E+00
Residuals	252	2.4E+00	9.5E-03			252	1.6E+00	6.4E-03		

489

Table 4. Analysis of variance for RB and RRMSE when estimating diameter differentiation and species mingling indexes by species and method. The factor method is indicated as *m*, the factor species is denoted as *sp*, n_n and n_t indicate the number of neighbors used to compute the indexes and the average number of trees in the fixed and variable radius plots. Interactions are denoted as Int.

Factor	RB species mingling					RRMSE species mingling				
	Df	Sum of Squares	Mean square	F value	Pr(F)	Df	Sum of Squares	Mean square	F value	Pr(F)
Factor n_n	2	7.0E-03	3.6E-03	6.2E-01	5.4E-01	2	1.6E-02	8.0E-03	2.4E+00	8.9E-02
Factor n_t	2	1.5E-02	7.7E-03	1.3E+00	2.7E-01	2	7.4E-03	3.7E-03	1.1E+00	3.3E-01
Factor <i>method</i> (<i>m</i>)	3	3.4E-02	1.1E-02	1.9E+00	1.2E-01	3	6.6E-01	2.2E-01	6.6E+01	*2.0E-16
Factor <i>species</i> (<i>sp</i>)	3	2.7E-01	9.0E-02	1.5E+01	*1.2E-09	3	3.0E-01	9.8E-02	3.0E+01	*2.0E-16
Int $n_n * n_t$	4	0.0E+00	1.1E-04	1.8E-02	1.0E+00	4	2.0E-04	6.0E-05	1.9E-02	1.0E+00
Int $n_n * me$	6	4.0E-03	6.5E-04	1.1E-01	1.0E+00	6	3.5E-03	5.8E-04	1.7E-01	9.8E-01
Int $n_t * me$	6	1.8E-02	3.0E-03	5.1E-01	8.1E-01	6	1.6E-02	2.7E-03	8.1E-01	5.6E-01
Int $n_n * species$	6	5.0E-02	8.3E-03	1.4E+00	2.1E-01	6	3.3E-02	5.5E-03	1.7E+00	1.3E-01
Int $n_t * species$	6	2.3E-02	3.8E-03	6.5E-01	6.9E-01	6	1.9E-02	3.2E-03	9.7E-01	4.5E-01
Int <i>me</i> * <i>species</i>	9	1.5E+00	1.6E-01	2.7E+01	*2.0E-16	9	2.0E-01	2.2E-02	6.7E+00	*2.8E-09
Int $n_n * n_t * m$	12	1.0E-03	8.0E-05	1.3E-02	1.0E+00	12	8.0E-04	7.0E-05	2.1E-02	1.0E+00
Int $n_n * n_t * sp$	12	1.0E-03	1.0E-04	1.7E-02	1.0E+00	12	7.0E-04	6.0E-05	1.7E-02	1.0E+00
Int $n_n * me * sp$	18	6.0E-02	3.4E-03	5.7E-01	9.2E-01	18	5.2E-02	2.9E-03	8.8E-01	6.0E-01
Int $n_t * me * sp$	18	1.1E-01	6.1E-03	1.0E+00	4.2E-01	18	6.5E-02	3.6E-03	1.1E+00	3.5E-01
Int $n_t * n_t * me * sp$	36	3.0E-03	9.0E-05	1.6E-02	1.0E+00	36	3.7E-03	1.0E-04	3.1E-02	1.0E+00
Residuals	822	4.8E+00	5.9E-03			822	2.7E+00	3.3E-03		

Factor	RB diameter differentiation					RRMSE diameter differentiation				
	Df	Sum of Squares	Mean square	F value	Pr(F)	Df	Sum of Squares	Mean square	F value	Pr(F)
Factor n_n	2	1.7E-02	8.7E-03	7.4E-01	4.8E-01	2	7.0E-03	3.6E-03	6.2E-01	5.4E-01
Factor n_t	2	3.0E-03	1.6E-03	1.4E-01	8.7E-01	2	1.5E-02	7.7E-03	1.3E+00	2.7E-01
Factor <i>method</i> (<i>m</i>)	3	8.2E-01	2.7E-01	2.3E+01	*1.9E-14	3	3.4E-02	1.1E-02	1.9E+00	1.2E-01
Factor <i>species</i> (<i>sp</i>)	3	5.0E-01	1.7E-01	1.4E+01	*5.6E-09	3	2.7E-01	9.0E-02	1.5E+01	*1.2E-09
Int $n_n * n_t$	4	0.0E+00	1.0E-05	1.0E-03	1.0E+00	4	0.0E+00	1.1E-04	1.8E-02	1.0E+00
Int $n_n * m$	6	6.5E-02	1.1E-02	9.2E-01	4.8E-01	6	4.0E-03	6.5E-04	1.1E-01	1.0E+00
Int $n_t * m$	6	5.0E-03	7.5E-04	6.4E-02	1.0E+00	6	1.8E-02	3.0E-03	5.1E-01	8.1E-01
Int $n_n * species$	6	4.9E-02	8.1E-03	6.9E-01	6.6E-01	6	5.0E-02	8.3E-03	1.4E+00	2.1E-01
Int $n_t * species$	6	9.0E-03	1.5E-03	1.2E-01	9.9E-01	6	2.3E-02	3.8E-03	6.5E-01	6.9E-01
Int <i>me</i> * <i>species</i>	9	2.2E-01	2.4E-02	2.1E+00	3.1E-02	9	1.5E+00	1.6E-01	2.7E+01	*2.0E-16
Int $n_n * n_t * m$	12	1.0E-03	6.0E-05	5.0E-03	1.0E+00	12	1.0E-03	8.0E-05	1.3E-02	1.0E+00
Int $n_n * n_t * sp$	12	2.0E-03	2.1E-04	1.7E-02	1.0E+00	12	1.0E-03	1.0E-04	1.7E-02	1.0E+00
Int $n_n * m * sp$	18	7.5E-02	4.2E-03	3.5E-01	9.9E-01	18	6.0E-02	3.4E-03	5.7E-01	9.2E-01
Int $n_t * m * sp$	18	9.1E-02	5.0E-03	4.3E-01	9.8E-01	18	1.1E-01	6.1E-03	1.0E+00	4.2E-01
Int $n_t * n_t * m * sp$	36	7.0E-03	1.9E-04	1.6E-02	1.0E+00	36	3.0E-03	9.0E-05	1.6E-02	1.0E+00
Residuals	822	9.7E+00	1.2E-02			822	4.8E+00	5.9E-03		

8 Figure captions

Figure 1. Relative bias (RB in %) and RRMSE (%) for estimation of the overall species mingling index.

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516 Figure 2. Relative bias (RB in %) and RRMSE (%) for estimation of the overall diameter
517 differentiation index.

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Figure 3. Variability of relative bias (RB) across sites by species and methods for the species mingling index. Species are denoted as: DF, Douglas-fir; WH, western hemlock; WR, western red cedar and RA, red alder.

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548 Figure 4. Variability of relative bias (RB) across sites by species and methods for the diameter
549 differentiation index. Species are denoted as: DF, Douglas-fir; WH, western hemlock; WR, western red
550 cedar and RA, red alder.

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Figure 5. Variability of relative root mean squared error (RRMSE) across sites by species and methods for the species mingling index. Species are denoted as: DF, Douglas-fir; WH, western hemlock; WR, western red cedar and RA, red alder.

Figure 6. Variability of relative root mean squared error (RRMSE) across sites by species and methods for the diameter differentiation index. Species are denoted as: DF, Douglas-fir; WH, western hemlock; WR, western red cedar and RA, red alder.

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9 Figures

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