

METHODS FOR SAMPLING DENSITY AND BASAL AREA OF MULTI-TRUNKED TREES: *JUNIPERUS OSTEOSPERMA* IN PINYON-JUNIPER VEGETATION

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ABSTRACT.—Sampling the density and basal area of trees is fundamental to quantitatively characterizing forests and woodlands. Commonly used sampling methods are well-suited for trees with single trunks, but are these methods also suitable for sampling multi-trunked trees? This question is especially important where multi-trunked trees are common, as is the case for Utah juniper (*Juniperus osteosperma*, JUOS), a codominant of large areas of pinyon-juniper vegetation in western North America. This study addresses the question of suitability by comparing 3 methods for sampling JUOS. The Dbase Method has been commonly used, and it focuses on the bases of trees for both identifying individuals and measuring tree diameters. The Dbh Method, which parallels the standard for sampling single-trunked tree species, also has been used for multi-trunked trees, and it focuses on breast height (i.e., 1.4 m above ground) for both identifying individuals and measuring diameters. The third method, the Base-Dbh Method, is proposed as a possible improvement. It focuses on the bases of trees for identifying individuals and on breast height for measuring diameters. Application of these 3 methods to the same JUOS trees produced statistically significant differences in values of density and basal area and thereby also produced differences in relative values (when JUOS was compared to the codominant two-needle pinyon, *Pinus edulis*). Comparison of the 3 methods determined that the proposed Base-Dbh Method is superior in terms of (1) biological validity, (2) comparability to data from single-trunked tree species, and (3) consistent application by field personnel.

RESUMEN.—El muestreo de la densidad y del área basal de los árboles es fundamental para caracterizar cuantitativamente bosques y bosques. Los métodos de muestreo comúnmente utilizados son adecuados para árboles con troncos simples, pero son estos métodos también adecuados para el muestreo de árboles de múltiples troncos? Esta cuestión es especialmente importante cuando los árboles de múltiples troncos son comunes, como es el caso del junípero de Utah (*Juniperus osteosperma*, JUOS), una co-dominante de grandes áreas de vegetación de enebro pinyon en el oeste de América del Norte. Este estudio aborda la cuestión de la idoneidad comparando tres métodos de muestreo JUOS. El Método Dbase se ha utilizado comúnmente, y se centra en las bases de los árboles para identificar a los individuos y medir los diámetros de los árboles. El Método Dbh, que es paralelo al estándar para el muestreo de especies arbóreas de un solo tronco, también se ha utilizado para árboles de múltiples troncos, y se centra en la altura del pecho (es decir, 1.4 m sobre el suelo) tanto para identificar individuos como para medir diámetros. El tercer método, el Método Base-Dbh, se propone como una posible mejora. Se centra en las bases de los árboles para identificar a los individuos y en la altura del pecho para medir los diámetros. La aplicación de estos tres métodos a los mismos árboles JUOS produjo diferencias estadísticamente significativas en los valores de densidad y área basal y por lo tanto también produjo diferencias en valores relativos (cuando JUOS se compara con el piñón codunante de dos agujas, *Pinus edulis*). La comparación de los tres métodos determinó que el Método Base-Dbh propuesto es superior en términos de (1) validez biológica, (2) comparabilidad con datos sobre especies de un solo tronco, y (3) aplicación consistente por el personal de campo.

Sampling the density and basal area of trees is fundamental to quantitatively characterizing forests and woodlands. The sampling methods commonly used (cf. Avery and Burkhart 2002, Husch et al. 2003, Köhl et al. 2006) are well-suited for trees with single trunks, but are these methods also suitable for sampling multi-trunked trees? Accurate sampling of trees with multiple trunks is especially important where such trees are common, as in pinyon-juniper vegetation (PJ). PJ is extensive

in western North America, covering more upland area in the southwestern United States than all other vegetation types combined (Vankat 2013). Although pinyon (*Pinus* spp.) individuals are usually single-trunked, many juniper (*Juniperus* spp.) individuals are multi-trunked. Therefore, PJ is an ideal vegetation type for addressing the question of sampling multi-trunked trees.

Previous studies have examined structural parameters of trees in PJ, but they focused on

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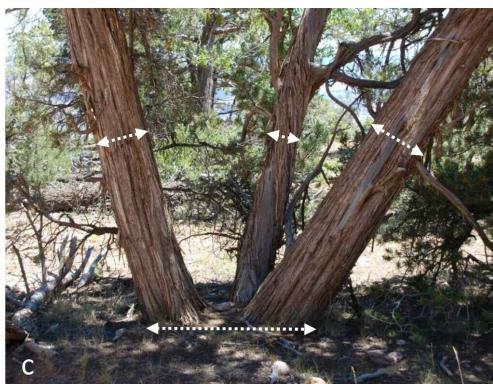
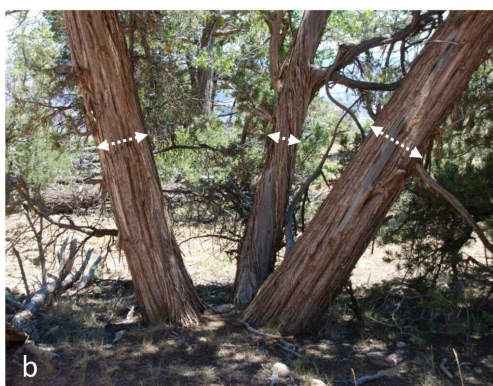


Fig. 1. A tri-trunked *Juniperus osteosperma* (with trunks presumably joined below the soil surface) as sampled by each of the 3 methods. Fig. 1a illustrates the Dbase Method with the dashed white line at the base of the tree indicating where the number of individuals is determined (1) and the diameter is measured. Fig. 1b illustrates the Dbh Method with the dashed white line on each trunk indicating where the number of individuals is determined (3) and each diameter is measured. Fig. 1c illustrates the Base-Dbh Method with the dashed white line at the base of the tree indicating where the number of individuals is determined (1) and the dashed white line on each trunk indicating where trunk diameters (3) are measured.

determining quantitative relationships between easily measured dimensions, such as diameter, and properties not easily measured, such as biomass (e.g., Miller et al. 1981, Grier et al. 1992, Chojnacky 1994, and Jenkins et al. 2004).

Numerous other studies of trees in PJ have reported data on the core attributes of tree density and basal area in describing vegetation. Such studies have sampled multi-trunked junipers in various ways, including measuring tree diameter at different positions, such as at the base or at breast height (i.e., 1.4 m). Such divergent approaches presumably produce divergent values for juniper density and basal area and therefore also affect comparisons with co-occurring tree species that are mostly single-trunked, such as pinyons. Chojnacky and Rogers (1999) described some of the issues with studies that use different positions to sample diameter and concluded that “ecosystem assessments need . . . a common measurement point for all tree diameters, regardless of species, to properly evaluate relationships between species and diameter classes.”

Here I examine 3 methods for sampling multi-trunked Utah juniper (*Juniperus osteosperma*, JUOS) and the effects of these methods on calculated values of tree density and basal area. Details of these methods are described in the following section. My objectives are to (1) document similarities and differences in results produced by the 3 sampling methods and (2) evaluate each method based on 3 criteria: biological validity, comparability to data on single-trunked tree species, and consistent application by field personnel.

METHODS

The 3 methods considered for sampling multi-trunked JUOS are herein referred to as the Dbase, Dbh, and Base-Dbh methods.

The Dbase Method is widely used for sampling multi-trunked trees (e.g., Chojnacky 1987, 1996, Miller et al. 1987, Grier et al. 1992, DeCoster et al. 2012). It focuses on the bases of trees for both identifying individuals and measuring tree diameters. As illustrated in Figure 1a, the Dbase Method treats each multi-trunked JUOS as a single individual if the trunks are likely to come from the same base, even when the trunks are separated at the ground surface. Diameter is sampled at ground level around the multiple trunks (diameter of

the root crown, drc) and is used to calculate basal area. Single-trunked JUOS are sampled similarly. A minimum drc of 10 cm was used for sampling in this study.

Use of the Dbh Method for sampling multi-trunked trees is historical. This method has not been widely used and to my knowledge has not been described in the literature on sampling. It was used in Grand Canyon National Park (GCNP) in 1935 to sample PJ and was later repeated on the South Rim of GCNP to determine changes in PJ since 1935 (Vankat 2017). The method focuses on the diameter at breast height (dbh) for both identifying individuals and measuring tree diameters. As illustrated in Figure 1b, each trunk with a dbh equal to or greater than a minimum value is treated as a separate individual in calculating density (even if trunks are joined below 1.4 m). Dbh is used to calculate basal area. A minimum dbh of 10 cm was used for sampling in this study.

The Base-Dbh Method is a hybrid of the above 2 methods. It was designed to include apparent positive features and avoid apparent negative features of those methods. It was also designed to parallel the standard method for sampling single-trunked tree species and thereby treat single- and multi-trunked trees equitably. As illustrated in Figure 1c, multi-trunked trees are identified as individuals at the base (as with the Dbase Method), and the diameter of each trunk exceeding a minimum value is measured at 1.4 m (as with the Dbh Method). The basal areas of the trunks are summed to calculate the basal area of the individual. Single-trunked trees are sampled identically, which matches the standard approach used for sampling such trees. A minimum dbh of 10 cm was used for sampling in this study.

An additional aspect of the hybrid Base-Dbh Method is that a single equivalent dbh can be calculated for multi-trunked individuals (cf. Meeuwig and Budy 1979):

$$\text{Equivalent dbh} = \sqrt{\sum_{i=1}^n \text{dbh}_i^2}$$

This equivalent dbh is the dbh required to produce a value of basal area equal to the summed cross-sectional areas of the multiple trunks (and the equivalent dbh of a single-trunked tree is the same as its standard dbh). An equivalent dbh for multi-trunked trees is

useful in studies of diameter distributions. In this study, calculated values for equivalent dbh were rounded to the nearest 0.1 cm to match field sampling.

Using the Dbase, Dbh, and Base-Dbh methods, I sampled live JUOS in 49 plots of 20 × 50 m dimensions (the number of plots matches that of historical plots first sampled in 1935 in GCNP, which were relocated and resampled recently; cf. Vankat [2017] for details). Analysis of variance was used to compare values of JUOS tree density and basal area produced by the 3 methods, with method of sampling as a fixed factor and plot as a random factor. Significance was determined at a Bonferroni-adjusted 0.05 level.

STUDY AREA

This study was conducted on the South Rim of the Grand Canyon in northern Arizona, nearly entirely within the boundaries of GCNP. The South Rim is part of the northern portion of the Coconino Plateau, which in turn is part of the Colorado Plateau. The regional climate is characterized by a bimodal precipitation regime, with elevations of PJ receiving mostly snow from November through March, little precipitation from April into June, and monsoonal rainfall from June or July into September. The Grand Canyon NP2 Weather Station, which is located at 2070 m on the South Rim near an ecotone between PJ and ponderosa pine (*Pinus ponderosa*) forest, received an annual average of 40.8 cm precipitation, including 115.3 cm snowfall, in 1976–2012 (Western Regional Climate Center 2017).

PJ is the most common type of vegetation on the South Rim and is codominated by JUOS and two-needle pinyon (*Pinus edulis*, PIED). PJ occurs mostly on flat terrain and gentle slopes. Study sites ranged from 1820 to 2280 m in elevation, and limestone was the most common soil parent material. Stands often form a mosaic with ponderosa pine forest in upper elevations and intergrade with sagebrush (*Artemisia tridentata*) shrubland at lower elevations.

RESULTS

Effects on Density Values

Sampling method significantly affected density values of JUOS (Fig. 2a). The proposed

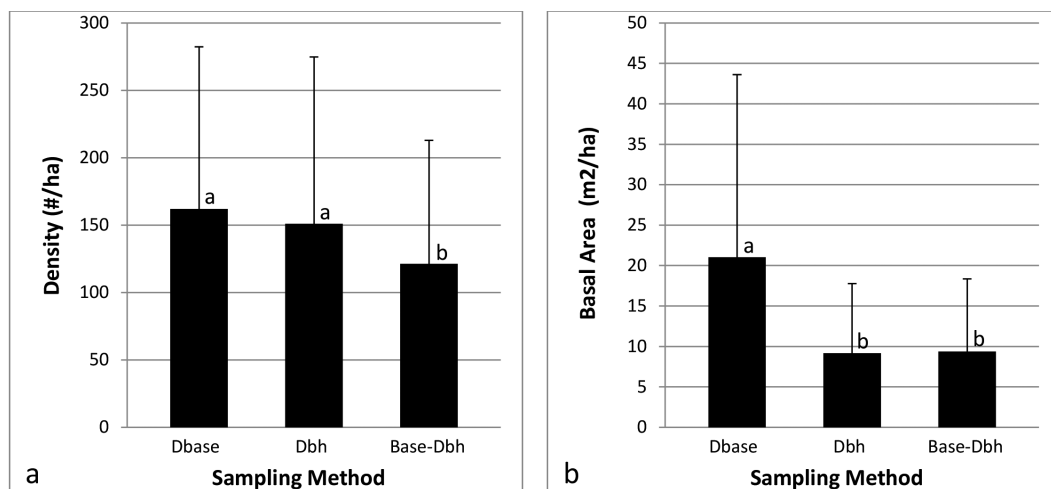


Fig. 2. Absolute density (a) and basal area (b) of *Juniperus osteosperma* produced by the Dbase, Dbh, and Base-Dbh sampling methods. Error bars are one standard deviation above the mean. Bars without shared letters differ at the Bonferroni-adjusted 0.05 level of significance.

Base-Dbh Method produced a density significantly lower than the historical Dbh Method (by 20%). The lower density resulted from individuals being defined at the base with the Base-Dbh Method, as opposed to being defined at 1.4 m with the Dbh Method (where every trunk ≥ 10 cm dbh was counted as a separate individual).

The density value produced by the proposed Base-Dbh Method was also significantly lower than that of the widely used Dbase Method (by 25%). The lower density resulted from individuals being required to have at least one trunk with a dbh ≥ 10 cm with the Base-Dbh Method, which is a more restrictive standard than the Dbase Method requiring a drc ≥ 10 cm.

The Dbase Method and the Dbh Method produced statistically similar values of JUOS density. Apparently, the inclusion of smaller trees in the Dbase Method (i.e., trees with a dbase ≥ 10 cm but dbh < 10 cm) was statistically offset by counting each trunk ≥ 10 cm dbh as a separate individual in the Dbh Method.

Findings for density also differed among diameter classes (Fig. 3). The historical Dbh Method produced the highest density values for 4 of the 5 smallest diameter classes (range 10–34.9 cm), and the lower density values produced by the other 2 methods tended to be similar to each other. In diameter classes ≥ 35 cm, the Dbh Method and Base-Dbh

Method produced declines in density to maximum diameters in the 85–89.9 cm diameter class, and the Dbase Method produced a more gradual decline to a maximum diameter ≥ 100 cm. In summary, compared to the proposed Base-Dbh Method, the Dbh Method biased diameter distributions toward smaller trees (10–24.9 cm diameter) and the Dbase Method biased diameter distributions toward larger trees (≥ 35 cm diameter).

Effects on Basal Area Values

Sampling method also significantly affected basal area values of JUOS (Fig. 2b). The proposed Base-Dbh and historical Dbh Methods produced statistically similar values of basal area, because both include the basal area of each trunk ≥ 10 cm dbh (the minor difference in basal area resulted from inclusion of dead trunks on live trees with the Base-Dbh Method). Both methods produced basal area values significantly lower (by 55%–56%) than the widely used Dbase Method did. Two factors account for these differences: (1) the Dbase Method uses drc measurements that exceed dbh measurements on the same tree and (2) arithmetic differences in diameter measurements produce exponential differences in basal area (because the measurement is squared in the calculation). For perspective, a single JUOS with a drc of 50 cm has the same basal area as 25 trunks, each with a dbh of 10 cm.

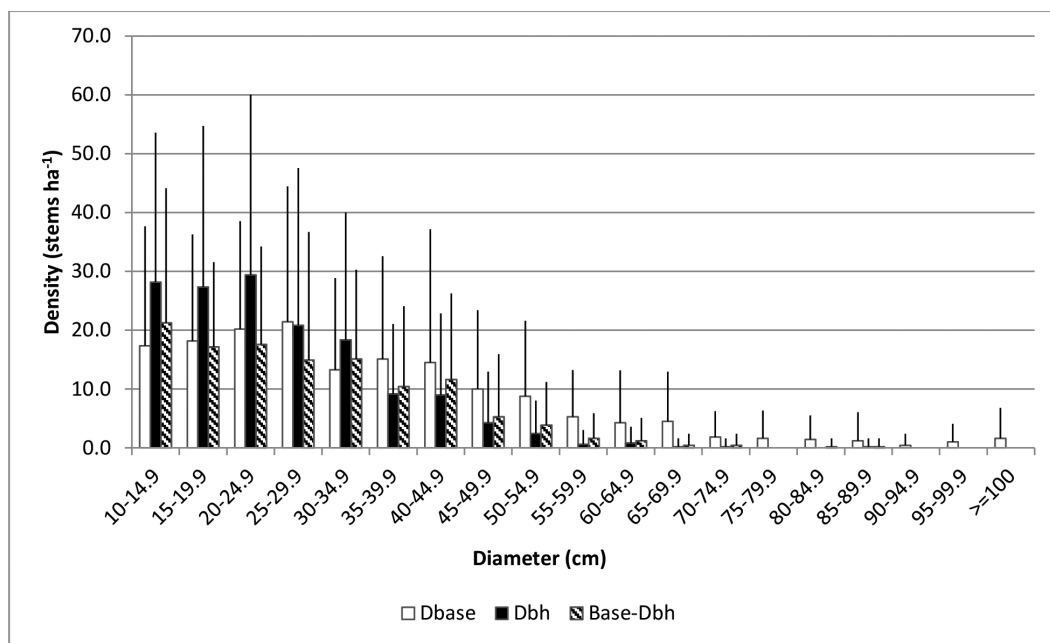


Fig. 3. Diameter distributions of *Juniperus osteosperma* produced by the Dbase, Dbh, and Base-Dbh sampling methods. Error bars are one standard deviation above the mean.

Effects on Relative Abundances of Species

Sampling method also influenced relative values of JUOS and its associated species, such as the codominant PIED. For example, relative density of JUOS in this study ranged from 42% with the widely used Dbase Method to 41% with the historical Dbh Method to 35% with the proposed Base-Dbh Method (Fig. 4a; based on data for PIED and other tree species in Vankat 2017). This result parallels the above-mentioned finding that the Dbase and Dbh methods inherently bias results toward higher overall densities of JUOS. As would be expected, the relative densities of associated species exhibit the opposite pattern, with calculated density of PIED increasing from 51% to 52% to 57% with the Dbase, Dbh, and Base-Dbh methods, respectively.

Differences among sampling methods for relative basal area are much larger. Values for JUOS ranged from 73% with the Dbase Method to 54% and 55% with the Dbh and Base-Dbh methods, respectively (Fig. 4b). This result parallels the above-mentioned finding that the Dbase Method inherently biases results toward higher basal area of JUOS. Again, relative basal area of PIED exhibits the opposite pattern,

increasing from 21% with the Dbase Method to 36% with both the Dbh and Base-Dbh methods. These differences are substantial, as the highest relative basal area value for JUOS is 35% greater than its lowest relative value and the highest relative basal area for PIED is 69% greater than its lowest relative value.

DISCUSSION

The above results demonstrate that the widely used Dbase Method, historical Dbh Method, and proposed Base-Dbh Method produced different results for the JUOS variables examined in this study, and thereby also influenced relative values calculated for JUOS and its major associated species, PIED. This raises the critical question: which method of sampling is superior? I address this question using 3 criteria: (1) biological validity, (2) comparability to data collected for single-trunked species (such as PIED), and (3) consistent application by field personnel (resulting in high comparability of measurements). Findings are compiled in Table 1. A possible fourth criterion, time required for sampling by field personnel, is not considered because the 3 methods are similar in this regard.

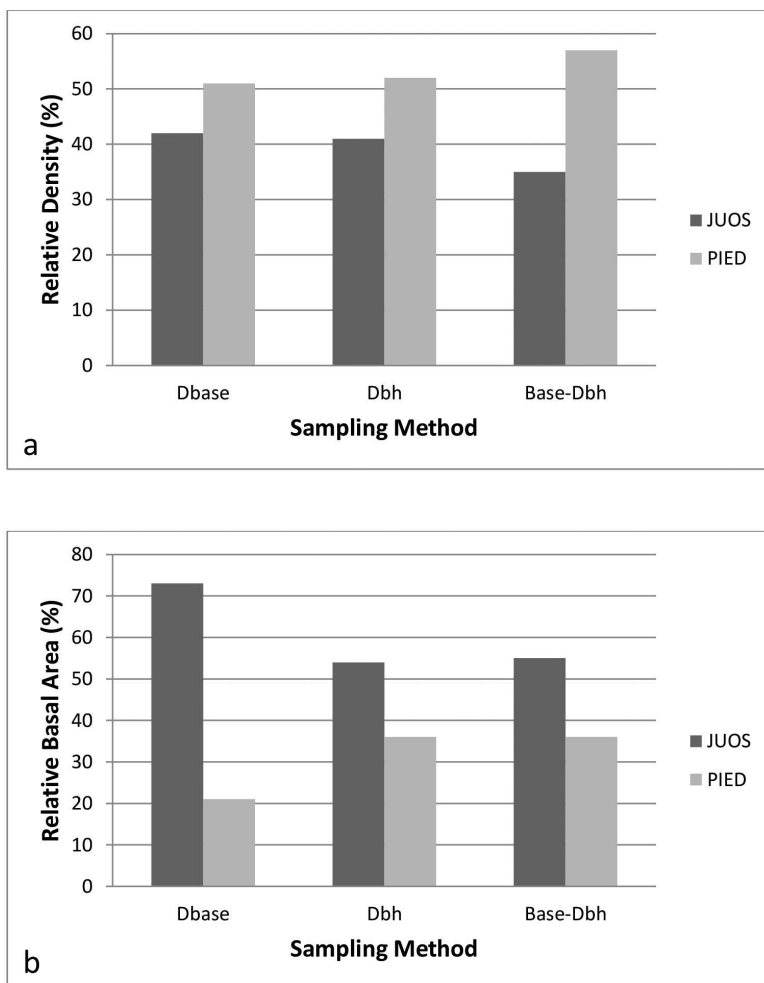


Fig. 4. Relative density (a) and basal area (b) of *Juniperus osteosperma* (JUOS) and *Pinus edulis* (PIED) produced by the Dbase, Dbh, and Base-Dbh sampling methods.

Dbase Method

The widely used Dbase Method of sampling is intended to determine density in a biologically valid manner, because field personnel attempt to identify individual JUOS even when trunks are separated at the ground surface. However, identifying individuals in the case of multi-trunked trees is challenging without excavating root systems or analyzing the genetics of the trunks, procedures that are currently impractical, especially for extensive sampling projects. Therefore, biological validity of density values can be compromised when multi-trunked individuals have trunks separated at the ground surface. Also, biological validity of basal area values is substantially

reduced by using drc when butt swell is present, especially when trunks are separated at the ground surface (Fig. 1a), which incongruously results in open spaces between trunks being included in basal area values.

Comparability to density data collected for single-trunked tree species (such as PIED) is facilitated by similar intent to identify biological individuals. However, comparability is reduced by the above-mentioned challenge of identifying JUOS individuals with separate trunks. Comparability to basal-area data of single-trunked species is very low because of differences in values based on drc measurements versus values based on the dbh measurements used for single-trunked trees. Comparability of

TABLE 1. Comparison of 3 alternative methods for sampling multi-trunked tree species (here applied to Utah juniper [*Juniperus osteosperma*]).

Criteria	Dbase Method	Dbh Method	Base-Dbh Method
Biological validity	Moderate for density Very low for basal area	Very low for density High for basal area	Moderate for density High for basal area
Comparability to data collected for single-trunked species	Moderate for density Very low for basal area Low for diameter distribution	Very low for density High for basal area Low for diameter distribution	Moderate for density High for basal area High for diameter distribution
Consistent application by field personnel	Moderate for density Moderate for basal area	High for density High for basal area	Moderate for density High for basal area

diameter distributions is low because the use of drc skews diameter distributions toward large diameter classes.

Consistent application of the Dbase Method is challenging. Given the seemingly infinite variation among multi-trunked trees, field personnel are likely to be inconsistent in identifying JUOS individuals and measuring drc if trunks are separated at the ground surface. Therefore, both density and basal area values are likely to be inconsistent. However, consistency in both can be improved by use of criteria for defining individuals, including maximum distance between bases of trunks, angle of lean of trunks from the center, and degree of similarity of dbh values of trunks (such criteria need to be tested for biological validity). Nevertheless, inconsistency is unlikely to be negated. Moreover, inconsistency accentuates the comparability issues described in the previous paragraph.

Dbh Method

The Dbh Method of sampling was used in the past to sample multi-trunked trees and has been used to repeat historical sampling (cf. Vankat 2017). A primary shortcoming of the Dbh Method is that it treats each trunk of a multi-trunked JUOS tree as a separate individual, which does not reflect biological validity for density. In contrast, the method does reflect biological validity for basal area, because dbh measurements generally avoid butt swell and open spaces between trunks.

The treatment of each trunk of a multi-trunked tree as an individual in the Dbh Method results in very low comparability to density data collected for single-trunked tree species (such as PIED). In contrast, this method's comparability to basal-area data collected for single-trunked tree species is high because dbh data are used in both sets of cal-

culations. Its comparability to diameter distributions of single-trunked trees is low because the sampling of individual trunks on multi-trunked trees skews diameter distributions toward small diameter classes.

The Dbh Method is generally consistently applied by field personnel, because both density and basal area are determined by dbh values and there are relatively few challenges to consistent measurement of dbh.

Base-Dbh Method

The proposed Base-Dbh Method of sampling, like the Dbase Method, attempts to identify JUOS individuals even when trunks are separated at the ground surface. As discussed for the Dbase Method, doing this task accurately is challenging, and biological validity of density is reflected to the degree that individuals are identified accurately. The Base-Dbh Method accurately reflects biological validity for basal area because dbh measurements are used, and these measurements generally avoid butt swell and open spaces between trunks.

Comparability to density data collected for single-trunked tree species such as PIED depends on the degree to which JUOS individuals are correctly identified, as with the Dbase Method. Comparability of basal-area data is high because dbh data are used in both sets of calculations. Comparability of diameter distributions is high, because the Base-Dbh Method avoids the skewed distributions produced by the other 2 methods for measuring multi-trunked trees.

Consistent application by field personnel is challenging for density because personnel are likely to differ on identification of JUOS individuals with trunks separated at the ground surface. As with the widely used Dbase Method, consistency can be improved by use

of criteria for defining individuals (see above). This consistency issue accentuates the comparability issues described in the previous paragraph. Consistency by field personnel is high for basal area because of the simplicity of sampling dbh.

Conclusion

This study found that the widely used Dbase Method for sampling multi-trunked trees has no strong points in terms of the 3 criteria considered. Moreover, its weak points are incongruent with this method's wide use: very low biological validity for basal area, very low comparability to basal area data collected for single-trunked tree species, and low comparability to diameter distributions of single-trunked tree species.

The Dbh Method for sampling multi-trunked trees, which was used historically but is rarely used today, has several strong points: high biological validity of basal area, high comparability to basal-area values collected for single-trunked tree species, and high consistency of application by field personnel in sampling both density and basal area. However, the Dbh Method also has several weak points: very low biological validity of density values and very low comparability to density data and to diameter-distribution data collected for single-trunked tree species.

The proposed Base-Dbh Method also has several strong points: high biological validity of basal area, high comparability to density values and diameter distributions of single-trunked tree species, and high consistency of application by field personnel in sampling basal area. Also important is the absence of any weak points, which is in sharp contrast to the other 2 methods.

In conclusion, this evaluation shows a clear ranking of the 3 methods of sampling multi-trunked trees. The widely used Dbase Method is the least effective. Intermediate in effectiveness is the historical Dbh Method with several strong points but also weak points. The proposed Base-Dbh Method is superior to both in reflecting biological validity, which is an essential standard for any sampling method. It is also superior in terms of comparability of data from multi- and single-trunked species, which is essential for equitable comparisons. Furthermore, it is superior to the Dbase Method and nearly matches the Dbh Method in terms of

consistent application by field personnel, which is essential for accurate research and monitoring efforts.

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