Forestry An International Journal of Forest Research

Institute of Chartered Foresters

Forestry, Vol. 84, No. 2, 2011. doi:10.1093/forestry/cpq049
Advance Access publication date: 21 February 2011

On fixed-area plot sampling for downed coarse woody debris

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Summary

The use of fixed-area plots for sampling down coarse woody debris is reviewed. A set of clearly defined protocols for two previously described methods is established and a new method, which we call the 'sausage' method, is developed. All methods (protocols) are shown to be unbiased for volume estimation, but not necessarily for estimation of population density in terms of number of down pieces. The new sausage method performs best overall in terms of minimum variance criteria. This review should also help establish a description of the major fixed-area plot sampling methods that will allow unambiguous application and description in future studies.

Introduction

Recent research has advanced a number of new methods for sampling down coarse woody debris (CWD), roughly paralleling the rise in interest of this component of the forest ecosystem. Methods that are extensions of angle-gauge sampling such as transect and point relascope sampling (Ståhl, 1998; Gove *et al.*, 1999), distance-based methods such as perpendicular distance sampling (Williams and Gove, 2003) and the closely related line intersect distance sampling method (Affleck, 2008), have all been developed in the last dozen years along with some refinements and extensions (Williams *et al.*, 2005a, 2005b; Ducey *et al.*, 2008). Other methods, which employ a prism directly (Bebber and Thomas, 2003; Ståhl *et al.*, 2010), have also been put forth. These new techniques are of interest because they are all methods that allow sampling with probability proportional to various quantities of interest such as length, length square, volume and surface area. In addition to these methods, the well-known and well-tested line intersect method (Warren and Olsen, 1964) also samples pieces with probability proportional to length. If some quantity such as volume or carbon content is the main quantity to be estimated, then all of these methods will perform well because each of the variables that form the basis for the inclusion probabilities (length, length square and volume) are related to these quantities (Valentine *et al.*, 2008).

Given these new methods, which may generally be more optimal for estimation of carbon, surface area or volume, it may seem a rather odd subject at first glance to be reviewing methods that are seemingly as simple as circular fixed-area plots for sampling down CWD (hereafter simply logs). After all, it is generally accepted that fixed-area plots sample pieces with probability proportional to piece frequency, so unless the density of CWD is of prime interest, why not use one of the methods more tailored to the prime forest attribute of interest? In addition, one might wonder what could justify a review of this subject, upon considering the simplicity of sampling logs when some portion of them falls within a fixed area? As we shall see, often when one dusts off the surface on a 'trivial' subject, some interesting hidden treasures are uncovered in the process. We note that the very act of sampling a log in such methods is bound to the selection protocol chosen, and the given protocol determines the form of the resultant estimators in terms of the inclusion probabilities. Neglecting the protocol specifications can lead to biases in the estimates. In addition, as we will show, not all protocols for fixed-area plots are created equal when it comes to efficiency in terms of the resultant variance estimates. So perhaps a revisit of what might be thought a rather mundane and settled subject is actually worth another look.

A survey of the current textbooks in forest inventory yields some fruitful information on sampling with fixed-area plots for standing trees, but yields only limited results with regard to sampling down logs. For example, Husch *et al.* (2003) mention only that fixed-area plots can be used, while Gregoire and Valentine (2008, p. 215) discuss the

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importance of the protocol for fixed-area plots in general, but provide only one example for downed logs. Others either do not mention this method or only list it as an option. In addition, the oft-cited manual for sampling down deadwood, Harmon and Sexton (1996), mentions only the use of rectangular quadrats. Other studies are more helpful. For example, in a summary of existing methods, Ståhl *et al.* (2001) (and Newton, 2007, p. 288, summarizing these authors) present two protocols along with their respective estimators and discuss some of nuances of each. Their first method samples logs whose butt section lies within the circular plot. A second method samples only that portion of a log that lies within the circular sample plot, normally the sample is with regard to volume. We will refer to these as the 'stand-up' and 'chainsaw' methods, respectively, for reasons that will become obvious soon. These two methods have been used in studies on down CWD, though the former seems to be the more often used of the two. For example, Pesonen *et al.* (2009) used the stand-up method in a comparative study of several different methods for sampling downed CWD, and Jordan *et al.* (2004) used the stand-up method in a comparison to the line-intersect and point relascope methods. The chainsaw method was used by McCarthy and Bailey (1994), while Fraver *et al.* (2002) used what appears to be a hybrid of the stand-up and chainsaw methods. Other studies (e.g. Spies *et al.*, 1988; Fridman and Walheim, 2000; Vanderwel *et al.*, 2008) used fixed-area plot methods that are not clearly defined with respect to either of the above two protocols. Often the details of the protocols are neglected in the study methods descriptions in such papers, making it difficult to discern what was actually done.

Our treatment of fixed-area plot methods for down CWD is not exhaustive. Rather our purpose is to formalize three methods that evolve from clearly defined protocols. The procedure we use to distinguish these methods and show their sampling properties can be applied to other similar protocols. The exposition is restricted to fixed-area plots that are circular in shape. However, the principles involved are the same for other commonly used shapes such as square or rectangular plots. A related, but no less important purpose of this paper, is to clarify the use of the major fixed-area plot methods so that ambiguities do not arise in the future as they have in some of the explanations of methods encountered in the literature described here. We hope to establish a clear set of protocols that can be unambiguously cited in future studies where fixed-area plots have been used to sample the downed wood component.

Fixed-area plot sampling methods

Each of the three methods presented are based on sampling logs using a circular fixed-area plot. The difference between the methods arises from the protocols established to determine how a log (or portion of a log) is to be included into the sample plot. In addition, even within methods, such as the chainsaw, there are many 'sub-protocols' that might be envisioned. Indeed, there are undoubtedly infinitely many ways to set up the inclusion protocol in general under plot sampling. Here we confine the discussion to the most obvious protocols for the stand-up and chainsaw methods, and show how the latter leads directly to a new protocol with good properties.

The methods can be distinguished based on the sampling properties that their protocols impart. This comes about through the notion of the 'inclusion zone' of a log, which is denoted a m^2. Quite simply, this is the area or zone where a plot centre (point) can fall that selects the log (or some predefined portion thereof) under the given protocol. The inclusion zone leads immediately to the inclusion probability for the ith log in a probability sample:

$$\pi_i = \frac{a_i}{A}, \tag{1}$$

where $A = 100^2 A_h$ is the tract area in m^2 that we are conducting the inventory within, and A_h is the tract area in ha.

Each of the three methods discussed can be set in terms of varying probability sampling, even though the plot radius, and thus the plot size, is fixed. The general estimator for variable probability sampling is the Horvitz–Thompson estimator, which is defined for some quantity y on the jth sample plot as (Gregoire and Valentine, 2008, p. 215, Thompson, 1992, p. 49):

$$\hat{y} = \sum_{i=1}^{n_j} \frac{y_i}{\pi_i}, \tag{2}$$

and, if we sample m plots, the mean is given as:

$$\hat{\bar{y}} = \frac{1}{m}\sum_{j=1}^{m} \hat{y}_j, \tag{3}$$

where n_j is the number of logs sampled on the jth plot.

The stand-up method

With this first method, a log is judged to be selected on the plot if the centre of its butt end lies within the plot. The centre in this case is defined with respect to the longitudinal axis of a straight 'needle' traversing the butt to the tip; i.e. the pith on a straight, intact piece. Its name derives from the fact that the method can be envisioned quite simply as standing the log up in place, directly over where its butt lies (not where it might have actually fallen from), and performing measurements on it as we would standing trees on a fixed-area plot.

The plot area is determined by the plot radius, R m, and leads immediately to the inclusion zone for stand-up $a_u = \pi R^2$ m^2 where π (un-subscripted) is the universal constant. The inclusion probability follows directly from (1).

The chainsaw method

Under the chainsaw method, all of the down wood that falls within the plot is sampled. Wood on pieces that may fall across the plot boundary is truncated at the boundary. This method's name derives from the fact that one could use a chainsaw to slice through all of the down wood along the perimeter of a sample plot, including only those portions (which could be slivers depending upon the protocol) that lie within the plot.

There is no one protocol for the chainsaw method, in fact there may be many. However, as we discuss in more detail later, one must be careful in defining the protocols so that no effective bias is introduced. Here we admit just three protocols that differ with regard to how portions of the log are selected. In all three cases, any intersection from the ends of the log will sample the intersected portion, what differs is the selection rule when the plot intersects the log radially. In each case, when the plot intersects a given log, the 'sliver' resulting from the intersection of the two is unique: that exact sliver will only occur when the plot centre is at the current point in the tract. Therefore, in a very real sense, the inclusion zone for that exact sliver is the point defining the plot centre and is devoid of area. However, the selection of that sliver does depend upon the fixed-area plot radius and so the inclusion probability for the sliver is the same as under the stand-up method. In order to get to this point, we have to play a little loose with the concept of inclusion zone and assign area $a_c = \pi R^2$ m^2 to the plot (centre) at any point within the tract that selects a portion of the log.

Now, in view of the above, each point within the tract that is situated such that the plot perimeter for given radius R intersects the log will be part of the entire log's inclusion zone. This concept is illustrated in Figure 1 for each of the three chainsaw protocols. Again we emphasize that the protocols differ in the rules for radial intersections of plot and log. In protocol 1, an intersection producing a sliver will only be sampled if the plot perimeter is at least tangent to the 'needle' defining the longitudinal axis of the log. This is shown in the figure by the plot–log intersections defining the slivers that would be sampled on each plot (shaded darker in the figure). The whole-log inclusion zone is proportional to the log length for a fixed plot radius and is straightforward to calculate as we show below. In protocol 2, any size or shaped sliver can be selected by a log–plot intersection. This can be traced by locating sample plots whose perimeters are exactly tangent to the log perimeter. The whole-log inclusion zone in this case is more difficult to compute because it depends on the log taper as well as the log length for a fixed plot radius. Finally, protocol 3 admits only full log–diameter intersections with the plot. It can again be traced out by plots that lie tangent to the opposite side of the log from the plot centre. Again, this area is more difficult to compute for the same reasons as protocol 2.

One might inquire at this point as to why the whole-log inclusion zone is important, since we use the plot area to form the inclusion probability for the intersected piece, and ultimately for the estimate of volume via (2)? As will be shown in the simulations, an operationally unbiased estimate of the volume does accrue from this procedure. However, under the chainsaw protocol, it is the exact sliver determined by the log–plot intersection that is selected, not the log itself, so that making inferences beyond the sliver (i.e. to the entire log) is not possible without undertaking extra measurements. Therefore, other quantities even as simple as piece frequency will be biased if one uses the plot inclusion zone, a_c, in (1). Any attributes pertaining to the log as a whole that are to be estimated must use the whole-log inclusion zone in (1) rather than a_c. This was first pointed out with respect to frequency by Ståhl *et al.* (2001), who made the implicit assumption of protocol 1, and will be further demonstrated in the simulations section. Now, because the whole-log inclusion zones for chainsaw protocols 2 and 3 depend upon the log taper, it is impractical in general to try to compute them; therefore, we will concentrate on protocol 1.

The whole-log inclusion zone for the first protocol is defined by the longitudinal needle for the log and is symmetric with no need to know anything other than the log length and plot radius. It is given as:

$$a_s = 2RL + \pi R^2, \tag{4}$$

where L is the length of the log. This inclusion zone, a_s, and not a_c should therefore be used to estimate any quantity inferred to the entire log under the chainsaw method, protocol 1. But the use of two inclusion zones, one for expanding the volume or other attributes associated with the intersection sliver, and one for attributes associated with the entire log, seems fraught with possible misapplication. Therefore, we include the 'sausage' method in the next section, which is simpler and has better sampling properties in general.

Finally, it must be noted that protocol 2 is the only theoretically unbiased protocol of the three presented. This is because the adoption of rules that exclude some slivers from ever being sampled, as in protocols 1 and 3, will theoretically introduce some degree of bias into the estimate. Whether that bias is significant operationally is another question. As we will show later in the simulations, the bias is negligible in practical application for protocol 1. However, it may not be for protocol 3, but this cannot be known without undertaking more simulations. Since determination of the overall log inclusion zone for calculating whole-log quantities is problematic for protocols 2 and 3, they will not be considered further here except to note that protocol 2 would be the more desirable of the three to use when quantities easily measured on the individual slivers are of interest.

The sausage method

To our knowledge, the sausage method is new. It derives its name from the shape of the whole-log inclusion zone defined for protocol 1 of the chainsaw method, which resembles a sausage (see also Ducey *et al.* 2002 for a similar sausage method for standing snags). Quite simply, the entire log is selected by the plot if the plot perimeter intersects the log's longitudinal needle from any direction. This is the same selection protocol as that for protocol 1 of the chainsaw method, with the exception that the intersection selects the entire log, not just the sliver. Consequently, the method is unbiased for any attribute such as volume or frequency that can be measured for the entire log.

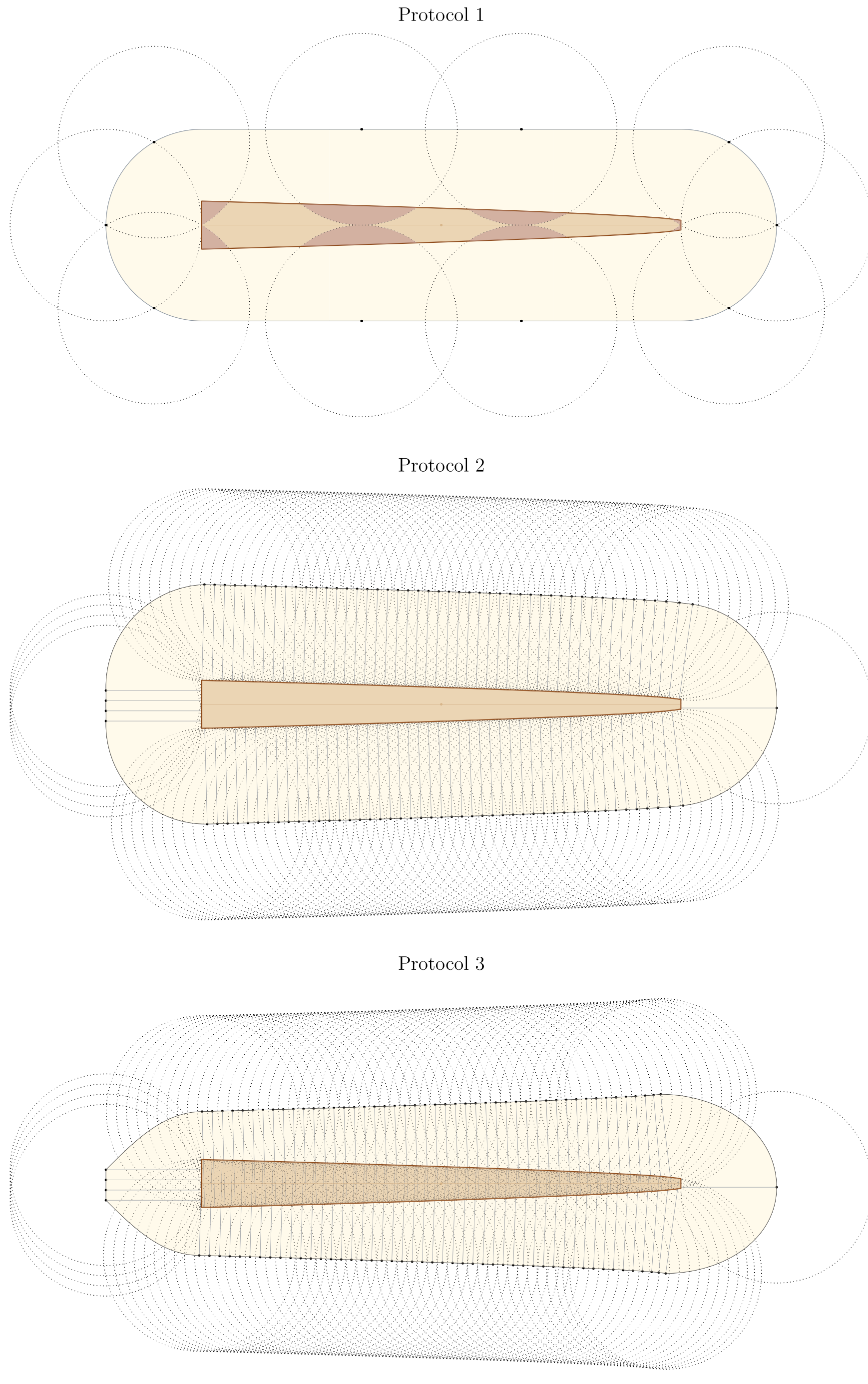

Figure 1. Three possible protocols under the chainsaw method. The curvature in the log inclusion zone at the ends for protocol 3 is close, but approximate.

As with the stand-up, whether a log is included in the sample is based on a fixed-area plot. However, the inclusion zone, and thus the inclusion probability, are different from that used in stand-up, i.e. one does not use the plot inclusion zone, a_u, for estimation, but rather one uses the zone mapping the locus of all fixed-area plot centres of radius R that will select the log, as given by a_s in (4). The sausage method could also be interpreted as a distance sampling method, since really all one requires is the plot radius, R, to determine the selection of a log from a given sample point. An alternative development for the inclusion zone is presented in Figure 2, where it can also be seen when compared with the log in Figure 1, that the zone is independent of log form. Now, if R is held fixed, then it follows directly from (4) that the sausage method is a probability proportional to length method. In addition, the plot

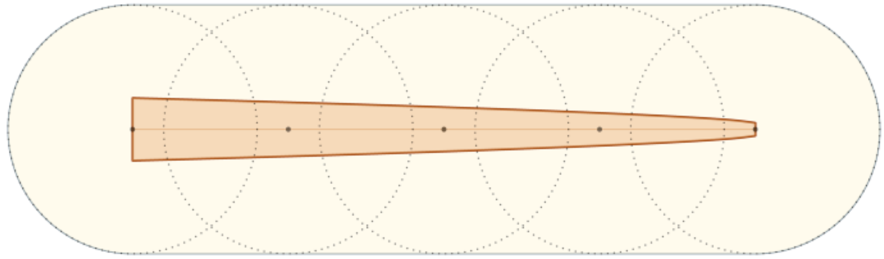

Figure 2. Alternative view of the whole-log inclusion zone under the sausage method.

radius, or limiting distance, plays an important role in the shape of the inclusion zone and the final inclusion probability. If R is large relative to L, the zone will be more nearly circular in shape; as L becomes larger relative to R, the zone becomes more elongated. As will be shown in the simulations, because the sausage method spreads the selection probability for a piece out over a larger area, the variance for the method will be smaller than that for either stand-up or chainsaw.

Sampling simulations and results

In the presentation in the previous section, we suggested some results that should follow from the geometrical development of the three methods. It is, however, useful to more fully establish the bias and variance properties using simulation. For example, though we can state that protocol 1 of the chainsaw method has a bias in the case we described, one has no idea of what magnitude the bias is, or whether it can be safely ignored. Similarly, we conjectured that the sausage method should have the best variance properties of the three, but again, it is useful to know the relative magnitudes of the variances for each method.

Williams (2001a) (also Williams, 2001b) presented a method to explore the properties of sampling estimators by simulation. He called his method sampling surface simulation because it results in a three-dimensional depiction of the attribute of interest under the proposed sampling method. Under this method, a tract of area A is divided into grid cells of equal size, with the centre of each cell being the position of a sampling point (i.e. representing the centre of a fixed-area plot). In this way, all possible sample points are defined for a given grid cell resolution. For any given sampling method or protocol, the inclusion zone for each log is determined and mapped. Then, for all grid cell centres falling within this zone, an estimate in terms of the variable of interest (e.g. volume, biomass, etc.) is determined using (2) and assigned to a given cell by summation with any values that might have been recorded from other logs whose inclusion zone overlaps that cell. Background cells outside the inclusion zones of any logs are always assigned zero. The technique is elegant in its simplicity, and allows one to get as refined an estimate as desired by changing the grid cell resolution: smaller cell sizes imply better estimates. In practice, grid cell sizes on the order of one-quarter of a meter have proven reasonable, while not placing an undue burden on computing (e.g. Williams and Gove, 2003; Gove *et al.*, 2005; Ståhl *et al.*, 2010). Finally, in addition to these features, the visual component allows for more intuitive understanding of the sampling comparisons made. For example, the sampling variance is directly related to the unevenness of the surface: the more uneven the surface, the higher the variance. More information on the sampling surface implementation used here, which is available as a package for the R statistical language (R Development Core Team, 2010), is given in Gove (2010).

In our definition of the sampling surface simulation, the grid cell centre is synonymous with a plot centre point for a fixed-area sample plot. Therefore, the application of (2) is direct and we regard n_j, the number of logs that were sampled at the point, synonymous with the number of overlapping log inclusion zones for the jth grid cell under the appropriate protocol. An unbiased estimate of the sampling surface variance from the simulations is given as:

$$\mathrm{Var}(\hat{y}) = \frac{1}{(m-1)} \sum_{j=1}^{m} \left(\hat{y}_j - \bar{\hat{y}}\right)^2, \tag{5}$$

where the summation over all m plots equates to summation over all m cells in the rectangular grid. Likewise an estimate of the surface standard deviation is simply $\mathrm{SD}(\hat{y}) = \sqrt{\mathrm{var}(\hat{y})}$.

The simulations require a population of logs, which were randomly generated from the following taper equation (Van Deusen, 1990):

$$d(l) = D_u + (D_b - D_u)\left(\frac{L-l}{L}\right)^{\frac{2}{r}},$$

with associated volume equation:

$$v(l) = \frac{\pi}{4}\left[D_u^2 l + L(D_b - D_u)^2 \frac{r}{r+4}\left(1 - \left(1 - \frac{l}{L}\right)^{\frac{r+4}{r}}\right)\right.$$
$$\left. + 2LD_u(D_b - D_u)\frac{r}{r+2}\left(1 - \left(1 - \frac{l}{L}\right)^{\frac{r+2}{r}}\right)\right],$$

where D_b is the large-end or butt diameter, with upper small-end diameter D_u, $0 \le l \le L$ is the intermediate log length for volume or diameter estimates and r is a parameter such that $0 \le r \le 2$ generates a neiloid, $r = 2$ generates a cone and $r > 2$ generates a paraboloid. Random uniform values for the each quantity were drawn from the following ranges: $D_b \in [0.2,1]$ m, $D_u \in [0,0.9] \times D_b$ m, $L \in [1,10]$ m and $r \in [1,10]$ m. Note that all diameters are in metres.

The same populations of sample logs were used to test each method. In each simulation, a population of $N = 50$ logs was generated with random placement inside the tract, which was minimally buffered so that the largest inclusion zone could completely fit within the grid, alleviating any potential boundary problems. In all simulations, the tract size was $A_b = 1$ ha. Each log was also given a random orientation angle $\phi_i \in [0,2\pi], i = 1,\ldots,N$ in addition to the specifications above. The whole simulation was repeated $M = 10$ times with different log populations in each independent simulation in order to minimize any possible anomalies that might occur conditioned on a given log population draw.

For both the stand-up and sausage methods, the height of the sampling surface within an inclusion zone for a given log is constant. For example, if y_i is volume of the ith log, then under the stand-up method, all grid cells within the inclusion zone get assigned a height Ay_i / a_{u_i} on a sub-grid before being added to the tract grid. This is illustrated in Figures 3 and 4 for the stand-up and sausage methods, respectively. These figures show a two-dimensional representation of the surface for volume with the same population of 50 random logs. The inclusion zones are shown shaded proportional to the expanded volume of the associated log. Overlapping zones are accumulated as described above. The surface, of course, could also be represented three dimensionally.

The chainsaw method presents somewhat of an enigma because each grid cell within the sausage-shaped inclusion zone will intersect the log in a different manner, generating a different sliver as described earlier. This is illustrated in Figure 5 for one grid cell. To determine the volume associated with each grid cell, we developed a simple approximation method that appears to work reasonably well. Each intersection polygon is encapsulated within a minimal bounding bolt, defined as the smallest section of the log that fully encloses the polygon sliver. The proportion of polygon sliver area to minimal bounding bolt area is subsequently used to apportion the bounding bolt

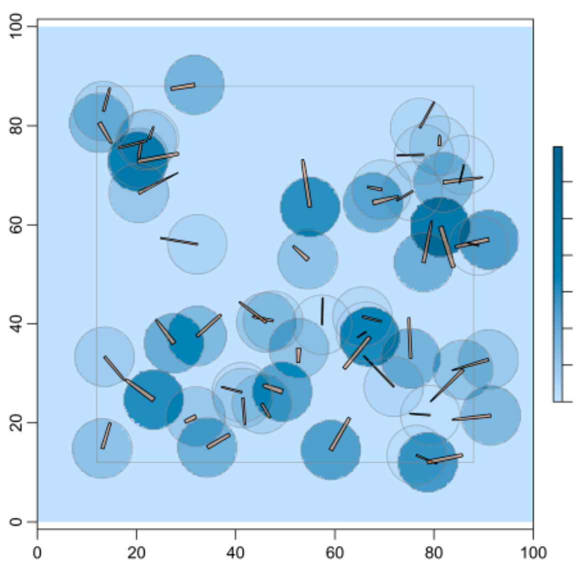

Figure 3. Two-dimensional representation of a volume sampling surface simulation for the stand-up method with N = 50 logs and 0.25-m grid-cell resolution with R = 6 m.

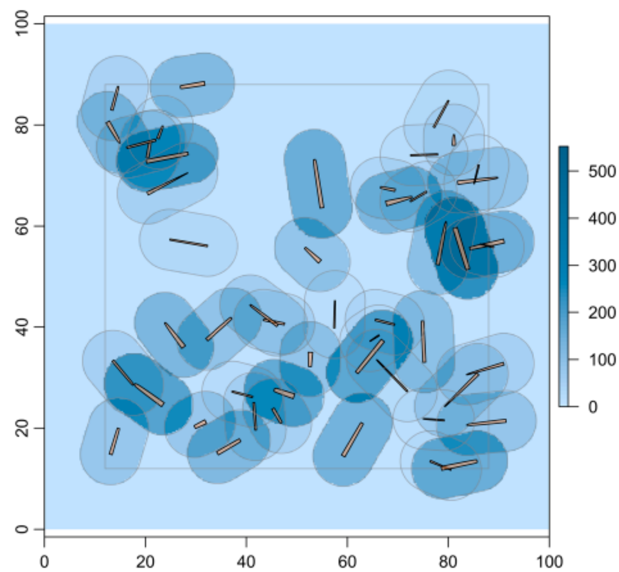

Figure 4. Two-dimensional representation of a volume sampling surface simulation for the sausage method with N = 50 logs and 0.25-m grid-cell resolution with R = 6 m.

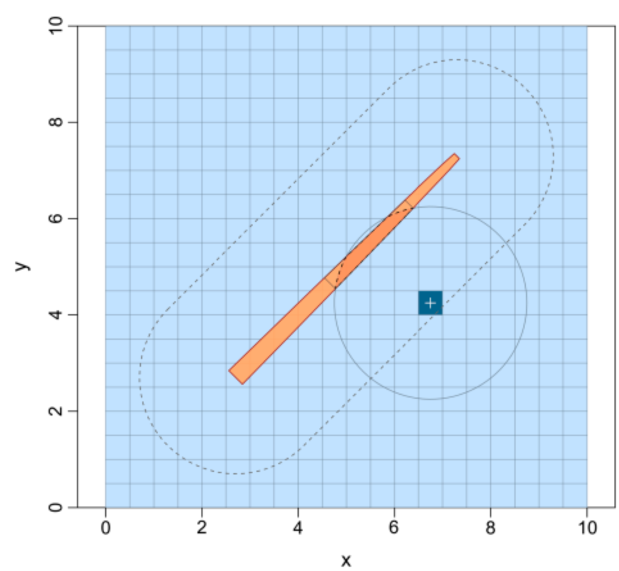

Figure 5. An example of the chain saw method for an individual grid point on a 0.5-m grid showing the fixed-area circular plot perimeter, log and whole-log inclusion zone (dashed) under chainsaw protocol 1. The intersection is shaded, with encompassing minimal bounding bolt delineated.

volume, which is then assigned to y_i for the ith grid cell. Because each cell within the whole-log inclusion zone will have a different estimate, the surface varies within each log's inclusion zone, rather than being constant as in the stand-up and sausage methods. However, because the surface trend is gradual, and is spread over a large area (that of the sausage inclusion zone under protocol 1), the variance properties are better than one might initially suppose. Figure 6 presents the volume sampling surface under the chainsaw method for the same populations of logs as Figures 3 and 4. The most obvious difference in the chainsaw surface is the non-uniform surface height within each log's inclusion zone. The zones can be directly contrasted with the constant within-log surface for the sausage method in Figure 4. In addition, note that the scale for the volume surface is different under each of the three methods, reflecting how the accumulation of estimates at each grid cell varies based on the method.

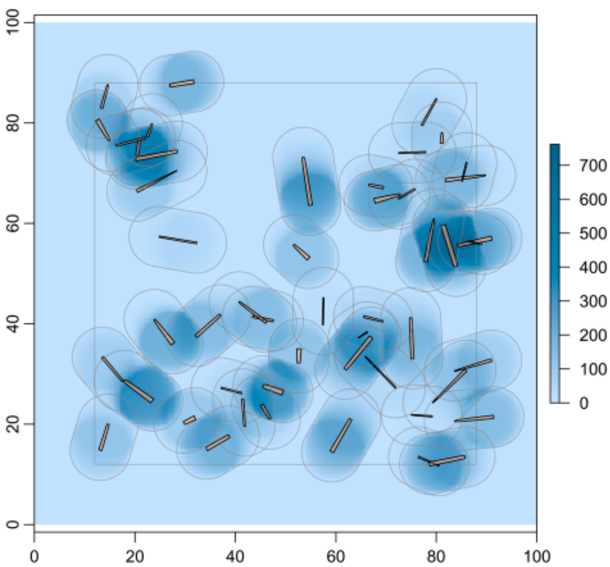

Figure 6. Two-dimensional representation of a volume sampling surface simulation for the chainsaw method with $N = 50$ logs and 0.25-m grid-cell resolution with $R = 6$ m.

Table 1 presents the results of the replicated sampling surface simulations. The results for both volume and frequency concur with our expectations. All three methods are unbiased for volume estimation. The slight negative value for bias that is shown for the sausage method derives from the grid cell resolution. Stand-up has slightly larger value, but this is also attributable to the resolution, combined with the circular inclusion zone intersection with the grid cells. The slightly larger still value for chainsaw is undoubtedly due to our approximation method for volume computation and should not be attributed to the possible theoretical bias that can accompany this method as mentioned earlier. The sausage method performs the best with respect to variance. It is superior to the stand-up method because it spreads the estimate over a larger area (inclusion zone) than the simple fixed-area plot. It is superior to chainsaw because even though they share the same inclusion zone (the whole-log inclusion zone for chainsaw), the surface within a zone is fixed for sausage, while it can vary markedly for chainsaw.

The results are very much the same for the estimation of log frequency under both the sausage and stand-up methods. However, with regard to the chainsaw method, a significant bias has been registered in accordance with theory. This result for the chainsaw method demonstrates the potential problems associated with its use on whole-log quantities when the plot inflation factor (a_c) rather than the proper inflation factor (a_s) has been used. Again, this could have been avoided in the simulations by using the appropriate factor, but the point here is to illustrate the potential for severe bias when the method is applied to whole-log quantities in a manner consistent with the sampled sliver, rather than the entire log.

In the replicated simulations, the plot radius was held constant at $R = 6$ m just as in the examples of Figures 3, 4 and 6, which is equivalent to a fixed-area plot of ~0.01 ha. One might argue that that the use of constant R (rather than enlarging R under the stand-up method for more equal area comparison) gives the sausage and chainsaw methods an advantage over the stand-up method because it does allow the spreading of the estimates over larger inclusion zone areas (thereby sampling the log more often). The answer to this is: that is exactly the point. For a given unit of sampling effort expressed in terms of plot radius, we are

Table 1: Comparison of mean sampling surface estimates for the estimator protocols averaged over $M = 10$ replications of populations containing $N = 50$ logs each

Protocol	Population mean	Sampling surface mean				
		Estimate	Standard deviation	Bias	Per cent bias*	Max
Volume (m^3)						
Stand-up	72.37	72.22	135.48	−0.14	−0.21	868.7
Chainsaw	72.37	72.10	120.18	−0.26	−0.37	748.1
Sausage	72.37	72.32	105.52	−0.04	−0.06	593.6
Frequency						
Stand-up	50	49.88	76.19	−0.11	−0.24	459.8
Chainsaw	50	81.59	104.06	31.59	63.20	574.7
Sausage	50	49.97	64.44	−0.03	−0.06	365.9

A plot radius of $R = 6$ m and a grid cell size of 0.25 m were used in all simulations.
*Per cent bias was calculated directly from the table averages.

looking for the method that is most efficient with regard to variance. Each of the methods uses the same fixed-area plot at each sampling point, so the plot-level effort is the same; the difference comes with how the methods apportion the estimates throughout the tract. The sausage and chainsaw (for volume) methods perform better in terms of variance than the stand-up exactly because they decrease the variance by spreading the estimates out more evenly over the tract. Williams (2001a) gives other examples of this phenomenon. The point is, this mechanism can be used to design more efficient sampling methods. Of course, it is not possible to compare actual within-log sampling times between chainsaw and the other two methods (which should be identical) because the estimation of volume under chainsaw varies and is not straightforward for many of the shapes that can occur. Therefore, the plot radius effort metric is a reasonable standard for comparison.

Discussion and conclusions

As stated earlier, upon further reflection, the application of fixed-area plot sampling to the estimation of attributes of down CWD is not as straightforward as it might seem at first. Different protocols are available, and each method has its advantages. The sausage method will result in the lowest variance for a given fixed-area plot size. However, this is at the expense of having to measure more logs. If the standing trees are measured on the same fixed-area plot as the downed wood, the stand-up method will lead to a downed wood sample that is more compatible with the standing tree sample. This is because the sausage method includes trees that were off the plot when they were standing, but happened to fall into the plot. The chainsaw method is not suitable for estimation of piece sizes per unit area; however, it frees the field crew from having to decide what constitutes a single piece. When logs fall to the ground, they often break. Field crews need to decide how to measure downed logs and component pieces for either the sausage or stand-up methods. This is irrelevant for the chainsaw method, since the field crew simply measures all downed wood that is inside the plot boundary. The chainsaw and stand-up methods work without modification for any fixed-area plot shape, while the sausage method may not generalize as easily.

Methods for estimation of log volume for stand-up and sausage include the usual model-based methods (Smalian's, etc.), taper equations, sub-sampling and the like. For the chainsaw method, however, calculating sliver volumes like those found in Figure 1 becomes problematic. One could adopt an approximation similar to what we did in the simulations, but then another layer of error is introduced into the procedure. Clearly, this is another reason to prefer the stand-up or sausage methods because the properties of the approximation methods used for volume computation on logs have been well studied (e.g. Fraver *et al.*, 2007). The bias in volume approximation under chainsaw, which is not estimable, will dwarf any theoretical bias in the method mentioned earlier. This later bias only shows up when the plot diameter shrinks to approximately the diameter of the large end of the log; in this case, the bias can be shown through simulation to be on the order of 20 per cent, and falls off rapidly to zero as the plot radius increases relative to the log diameter. Because using plot sizes this small is unlikely in practice, it should not be an issue in field surveys.

In a recent survey of national forest inventories by Woodall *et al.* (2009), some 63 per cent of respondent countries utilized fixed-radius plot sampling for the down deadwood component of the inventory. Unfortunately, as reported by these authors, the actual protocols for each country were evidently not made available. The authors also note that in many cases, the estimates of CWD had not been compiled or reported yet. The use of fixed-area plots on some national inventories coupled with the apparent lack of clarity in public availability of the protocols used reinforces the importance of the results derived here. In addition, if a country using fixed-area plots wants to continue doing so, a simple change of protocol could accrue some gains in precision for similar effort on the plot level.

In our reading of the literature, it was noted that many studies describing the use of fixed-area plot sampling for down CWD are ambiguous at best, while some implementations we have come across, if understood correctly, are clearly biased. For example, one method that appears to be a cross between the stand-up and chainsaw methods selects logs if their butt falls within the plot, the same as the stand-up. However, the authors state that the logs so selected were truncated at the plot edge as in the chainsaw method, so that only that portion falling within the plot was measured for volume. In this case, one does not even require any simulation to rationalize the bias in such a protocol. If the log length is $L < 2R$, then the length of the log is shorter than the fixed plot diameter, so that the entire log has full probability of being selected. In this case, the method is not biased. However, for logs whose length is greater than the plot diameter ($L > 2R$), the top portion of the log $L - 2R$ will never be selected on any plot because it will always be discarded. Therefore, the method produces a clear bias because those top sections, while part of the population of total log volume in the tract, will never be sampled under this protocol. The only way a method such as this could be unbiased is if the desire were to estimate the volume of all log sections whose length was less than the plot diameter.

Fixed-area plots, when applied correctly, can be a useful method for sampling downed CWD. In addition, they can form the basis for estimation in other methods, such as spoked line intersect sampling designs (Van Deusen and Gove, 2011). We have set forth a clear framework for the establishment and comparison of different protocols under fixed-area plot sampling that can be extended as other possibilities present themselves. This framework leads not only to a clear understanding of the application of each method but also to its resulting estimators so that no ambiguity remains. It should be apparent by now that simply stating that 'fixed-area plot sampling was used' in a particular study is not an adequate description of the field methods. In the future, studies involving the use of these methods require definition to the protocol level, either using our nomenclature for the methods or something similarly descriptive.

Acknowledgements

The authors would like to thank Dr Mark J. Ducey and an anonymous reviewer for their helpful comments on the manuscript. In addition, we thank Dr David L. R. Affleck for pointing out the potential for a theoretical bias associated with chainsaw protocol 1 and for other insightful comments on the manuscript.

Conflict of interest statement

None declared.

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Received 10 August 2010