# How many plots are needed to estimate sapling density and stocking in temperate forests?

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## ABSTRACT

Performing a complete silvicultural diagnosis before a silvicultural treatment generally requires assessing the state of regeneration with the help of an inventory by sampling, particularly for stands dominated by sugar maple (*Acer saccharum* Marsh.) or yellow birch (*Betula alleghaniensis* Britt.), in which partial cuts are recommended. This inventory may then be compared to the standard or used in a growth model for saplings (trees for which the diameter measured at 1.3 m above the ground (DBH) varies from 1.1 cm to 9.0 cm). Some of these tools are based on sapling density, while others are based on the stocking of the saplings or on the stocking of total regeneration (combining saplings and seedlings with a DBH  $\leq$  1.0 cm). We assessed the number of plots required to estimate the density and the stocking of saplings with a given margin of error in 28 stands. The results show that more plots are required than usual in practice to inventory sapling density. The stocking is much easier to estimate precisely.

Key words: sample plot, regeneration, inventory, sampling, northern hardwoods, yellow birch-balsam fir stand

## résumé

Réaliser un diagnostic sylvicole complet en vue d'un traitement sylvicole requiert généralement que l'état de la régénération soit évalué à l'aide d'un inventaire par échantillonnage, particulièrement pour les peuplements dominés par l'érable à sucre (*Acer saccharum* Marsh.) ou le bouleau jaune (*Betula alleghaniensis* Britt.), dans lesquels les coupes partielles sont préconisées. Cet inventaire peut ensuite être comparé à une norme ou être utilisé dans un modèle de croissance des gaules (arbres dont le diamètre mesuré à 1,3 m du sol (DHP) varie de 1,1 à 9,0 cm). Certains de ces outils utilisent la densité des gaules, tandis que d'autres s'appuient sur leur coefficient de distribution ou sur celui de toute la régénération (ce qui regroupe les gaules et les semis dont le DHP est  $\leq$  1,0 cm). Nous avons évalué le nombre de placettes requises afin d'estimer la densité et le coefficient de distribution des gaules avec une marge d'erreur donnée dans 28 peuplements. Les résultats démontrent qu'il faut plus de placettes que ce qui est habituellement rencontré dans la pratique pour inventorier la densité des gaules. Par contre, le coefficient de distribution est beaucoup plus facile à estimer avec précision.

Mots-clés : placette-échantillon, régénération, inventaire, échantillonnage, érablière, bétulaie jaune à sapin



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#### Introduction

Common silvicultural practices recommend protection of advanced regeneration when it is composed of desired species (e.g., MRN 2013; McGrath 2018). In temperate forests, sugar maple (*Acer saccharum* Marsh.), yellow birch (*Betula alleghaniensis* Britt.), red spruce (*Picea rubens* Sarg.) and white spruce (*Picea glauca* (Moench) Voss) are the species most in demand as advanced regeneration, unlike the American beech (*Fagus grandifolia* Ehrh.) and red maple (*Acer rubrum* L.) (e.g., MFFP 2018). Here, regeneration includes both seedlings (immature trees for which the diameter at breast height [DBH measured at a height of 1.3 m] is no more than 1.0 cm) and saplings (trees with a DBH of 1.1 cm to 9.0 cm; MRN 2013).

To perform a complete silvicultural diagnosis in such stands in preparation for partial cutting such as selection cutting and regular or irregular shelterwood cutting, the state of regeneration must be assessed (MRN 2013). This may also be necessary after a partial cut, in order to confirm the need to apply complementary understory treatments, such as regeneration enrichment planting, site preparation or clearing of certain species in the understory. Because the presence of a partial canopy sometimes prevents the use of aerial imaging techniques to assess the state of regeneration, a forest inventory by sampling at ground level represents the best option.

Determining what information is required for the regeneration inventory represents the next challenge. The ideal would be to know with certainty which variables have the most influence on the stand's long-term yield. However, this type of information is rarely available, due to the very longtime horizon necessary to obtain the results (Brand et al. 1991; Farnden 2009; Walters et al. 2022). Several authors have proposed standards to determine the desirable regeneration threshold, but they are often arbitrary (Farnden 2009). In most cases, these standards are based on the use of a stocking of regeneration (e.g., McGrath 2018), which measures the percentage occupancy rate by a species or a group of species (MRN 2013). For example, Leak et al. (2014) assess that regeneration of a maple stand is acceptable when 40% to 50% of the 4-m<sup>2</sup> plots are dominated by a desired species. For Great Lakes maple stands, Arbogast (1957) proposed to target densities of 465, 275, 160 and 95 saplings ha<sup>-1</sup> for DBH classes of 2, 4, 6 and 8 cm, respectively, for a total of nearly 1000 saplings ha<sup>-1</sup>.

Over the 1980s and 1990s, studies were initiated for longterm monitoring of natural stands or stands treated by partial cutting in Québec's temperate forest (e.g., Gagnon et al. 1994; Majcen et al. 2005; Prévost and Charette 2015). Their results could allow the establishment of connections between regeneration at the sapling stage and recruitment of merchantable size trees (DBH > 9.0 cm). When the trees have reached merchantable size, it is possible to assess the longer-term yield with an individual tree growth model, such as Artémis (Power 2021) or SaMARE (Fortin et al. 2009). Two other models are currently in development to predict recruitement of merchantable trees from saplings: one for northern hardwoods (Rijal et al. 2023) and one for yellow-birch-conifer stands (Power et al. 2022). However, these two models require data of saplings density per species and DBH class, rather than a stocking per species. This choice results both from the nature of the data collected in the field studies and

an intention to calibrate more precisely the models. In the case of northern hardwood stands, such a model would allow verification of the diameter structure proposed by Arbogast (1957) for saplings. However, the operational use of these new models requires a knowledge of sapling density by species and by DBH class, information that is not always available in the inventories associated with interventions in an operational context. Moreover, we question the statistical precision of the regeneration data from such inventories, when they come from a small number of plots.

Lynch (2017) reviewed the most recent work seeking to optimize plot sampling. Studies mainly focused on stand density, basal area, and volume, and included examples from other environmental sciences. Some studies sought to optimize the sampling plan (e.g., plot size and number) in terms of cost to obtain a given precision, while others rather tried to maximize precision for a given cost. We did not find any studies specific to regeneration that would apply in our conditions.

The purpose of this study is to assess the sampling effort required to estimate the density and the stocking of saplings within a given margin of error, under partial canopy (after cutting) or closed canopy (before cutting) conditions in hardwood and mixedwood stands with a predominance of shadetolerant hardwoods. This information is useful for forest practitioners who wish to have a better knowledge of the limits of the information they can derive from sapling inventory by sampling, particularly if they wish to use such data as inputs in a growth model. Statistical formulas exist to calculate the number of plots required when the variance is known, but this data is generally unknown by foresters. We present our method and the results intended to assess the order of magnitude of the sapling density variance, while briefly recalling the statistical variance calculation method in the case of a stocking.

#### Method

The assessment of the sample size (n, number of plots) required to obtain estimates within a given margin of error (E) necessitates an estimate of the variance ( $s^2$ ) or the standard deviation (s) of the target population and the use of the following formula for a simple random sampling (Eq.1; Cochran 1977; Avery and Burkhart 2002):

Eq. 1 
$$n = \left(\frac{t_{\alpha/2, n-1}s}{E}\right)^2$$

wh $\ell^{t}\alpha/2,n-1$  denotes the higher quantity of order  $\alpha/2$  of Student's *t*-distribution with n - 1 degrees of freedom,  $\alpha$  being the error threshold. Preliminary observations allowed us to confirm previous reports that the sapling density variance could be influenced by the plot size, the density of the population and, to a lesser degree, by the spatial distribution of the plots (Gregoire and Valentine 2007). We wanted to assess how the variance changed under these conditions. We assumed that plot shape had no effect, especially in our simulation context (see Gregoire and Valentine 2007).

## Study areas to determine the sapling density variance

From 1986 to 2004, permanent sample plots (PSP) were established in northern hardwood stands and in hardwood-dominated mixedwood stands in southern Québec (Fig. 1).



48

-78°

Ontario

50

100

km

-76

Ottawa

-74°

Montréal

United States

-72

**Trois-Rivières** 

Sherbrooke

-70°

Saguenay

Québec

-68°

Rimouski

New-

Brunswick

The PSPs of the RESEF had a rectangular shape (50 m  $\times$ 100 m, or 0.5 ha) and represented stands not treated by partial cutting; these plots served to assess a silvicultural diagnostic situation before intervention. The PSPs of the Armagh I, Armagh II and Duchesnay sites had a square shape 30 m or 40 m on a side (which corresponds to an area of 0.09 ha or 0.16 ha, respectively). Each of these three sites contained 16 PSPs in which four treatments were distributed according to a randomised complete block design. Each PSP was surrounded by a buffer strip 20 m wide in the same stand type. Thus, the edge of the PSP did not correspond to the edge of forest stand. One of the treatments was a control with no intervention, which was also used to represent a silvicultural diagnostic situation before intervention. The other three treatments of the Armagh I and Duchesnay sites were uniform partial cuts with harvesting of 40%, 50% or 60% of the

merchantable basal area (Prévost 2008). For the Armagh II site, three variants of selection cutting systems were tested: 1) single-tree selection cutting of 40% to 45% of the basal area; 2) small group and single-tree selection cutting of 35% of the basal area; and 3) patch-selection cutting harvesting 40% of the basal area distributed both to form 30 m gaps (diameter) and harvest single trees in the residual matrix. In all these partial cuts, we used post-cut data. This data can serve as input for a growth model that aims at quantifying tree recruitment at the DBH threshold of 9.1 cm from saplings. The saplings were numbered in each PSP after cutting or during the measurement after cutting. After noting the species and the DBH of each sapling, we grouped them by 2 cm DBH class and mapped them in the PSP. This data served to define the population in the analyses.

#### Analyses

To increase the area of the PSPs to represent the forest stands better, we first grouped the PSPs of the same treatment located in the same experimental stand. Thus, the 48 PSPs of the three experimental sites form 12 groups, one per treatment and per site. Subsequently, the PSPs of the RESEF and the PSP groups of the experimental sites were enlarged to a size of 5 ha by resampling and random juxtaposition. Because the population size, or area, had no influence on the required number of plots, only the population variance counted in the equation. This variance is independent of population size, except if it is small (Lohr 2010), which was not the case. Our choice to simulate an area of 5 ha to locate the plots was made for strictly practical reasons: this area allowed insertion of the desired number of plots to simulate.

We used an analysis method adapted from Guillemette et al. (2012) to assess the sample size required to obtain margins of error of 10%, 20% and 30%, according to the sampling plan used in the 28 stands of 5 ha thus created (Table 1). Thus, we simulated 120 sampling plans, varying the size, number and spatial distribution of the sapling inventory plots. Each sampling plan was repeated 1000 times. The simulated plots (always circular) had an area of 4.00 m<sup>2</sup>, 6.25 m<sup>2</sup>, 8.97 m<sup>2</sup>, 16.00 m<sup>2</sup>, and 25.00 m<sup>2</sup> to cover the range of sizes used in practice. We simulated four spatial distributions of plots: random, in linear clusters of 5 or 10 plots spaced 6-m apart on the same axis, and in clusters of five plots spaced 6 m apart but distributed in a cross-shaped pattern (Fig. 2). The starting point of the plot clusters was positioned at random, and the indicator of dispersion (e.g., the variance) was calculated at the cluster level in these cases, rather than at the plot level. Simulations were performed with 10, 50, 100, 150, 200 and 300 plots for each of the spatial distributions. We used the edge correction as a mirage effect to ensure that the sampling probability was the same for all trees (Gregoire 1982; Ducey et al. 2001).

The sapling density can be examined overall (total density), by species, or by species and DBH class (2 cm, 4 cm, 6 cm, or 8 cm). Preliminary analyses allowed us to determine

Table 1. Summary description of the 28 study stands: total sapling density, name and density of the three main species

Stand (system, 1 treatment) sa	Total number o plings∙h	of a <sup>-1</sup> (num	Main species* (number of saplings-ha <sup>-1</sup> )				
Armagh I, control	1392	RS (781)	YB (266)	BF (144)			
Armagh I, 40%	789	RS (595)	YB (101)	RM (41)			
Armagh I, 50%	629	RS (397)	YB (116)	RM (56)			
Armagh I, 60%	855	RS (632)	YB (122)	BF (48)			
Armagh II, control	2102	RS (982)	BF (799)	YB (239)			
Armagh II, 40%-45%	% 832	RS (498)	BF (236)	YB (51)			
Armagh II, 35%	802	RS (538)	BF (189)	YB (40)			
Armagh II, 45%	604	RS (298)	BF (185)	YB (87)			
Duchesnay, control	1868	RS (768)	OTH (340)	BF (336)			
Duchesnay, 40%	565	RS (244)	OTH (124)	RM (80)			
Duchesnay, 50%	550	RS (168)	BF (134)	OTH (110)			
Duchesnay, 60%	856	BF (313)	RS (249)	OTH (144)			
RESEF, 101	473	SM (378)	AB (95)	_			
RESEF, 102	529	SM (506)	YB (13)	OTH (9)			
RESEF, 103	733	SM (706)	OTH (18)	BF (7)			
RESEF, 105	598	BF (491)	SM (84)	AB (23)			
RESEF, 1201	374	SM (310)	AB (32)	YB (23)			
RESEF, 1205	352	SM (172)	OTH (128)	AB (44)			
RESEF, 1501	1560	AB (1024)	SM (483)	YB (38)			
RESEF, 1502	272	SM (242)	BF (11)	AB (10)			
RESEF, 301	1598	AB (1325)	SM (138)	YB (113)			
RESEF, 401	1315	SM (529)	AB (397)	OTH (229)			
RESEF, 402	1139	SM (580)	AB (386)	OTH (78)			
RESEF, 501	860	AB (494)	SM (277)	YB (47)			
RESEF, 701	325	SM (295)	OTH (18)	AB (12)			
RESEF, 703	827	SM (385)	OTH (258)	AB (130)			
RESEF, 802	3681	SM (3508)	OTH (167)	YB (6)			
RESEF, mixed	1427	BF (881)	YB (450)	OTH (95)			
Mean	997						

\*YB = yellow birch; RS = red spruce; RM = red maple; SM = sugar maple;

AB = American beech; BF = balsam fir; OTH = other, mainly paper birch, eastern hop-hornbeam and basswood.



Fig. 2 Spatial distribution of the plots tested during simulations: a) random, b) linear clusters of five plots, c) linear clusters of 10 plots, d) cross patterns of five plots.

that the density variance study by species provided a good coverage of the range of the total density by species and DBH class, ranging from 1 to 3508 saplings ha-1. Thus, we calculated the statistics on the distribution of the mean density obtained by species for the 1000 repetitions of each sampling plan simulated in the stands of the study. Let us remember that in this case, the standard deviation of 1000 means corresponds to the standard error (s/ $\sqrt{n}$ , Fan *et al.* 2002). The species studied in the hardwood stands were sugar maple, American beech, yellow birch, balsam fir and a group including the other species (primarily paper birch, Betula papyrifera Marsh., eastern hop-hornbeam (Ostrya virginiana (Mill.) K. Koch.) and basswood (Tilia americana L.)). Those studied in the mixedwood stands were balsam fir, red maple, yellow birch, spruces, and a group including the other species. We then modelled the variance for the plots distributed completely at random, or the variance of clusters of five or 10 plots and in cross pattern of five plots. The two explanatory variables were the sapling density of the species in the population and the sampled sapling plot size. We accounted for the correlation between the measurements coming from species of the same population. Smith (1938), cited in Gregoire and Valentine (2007), found a power function relating plot size to sample variance. We linearized the function with a logarithmic transformation that standardize the residues and stabilize their variance and then used a linear regression. The bias due to this logarithmic conversion can be corrected upon returning to the original scale (Calama and Montero 2005). Note the absence of zero values, since only the data for a species present in a group of PSPs were retained. The statistical analyses were produced with the MIXED procedure of SAS 9.4 (Stroup et al. 2018). We used the results of these models with Equation 1 to calculate the number of plots required to obtain a relative margin of error (E) of 10%, 20% or 30% with an error threshold ( $\alpha$ ) of 5%. In the case of clusters, we calculated the number of clusters required, then we multiplied it by the number of plots in a cluster.

The stocking is a discrete random variable, distributed according to the Bernoulli distribution, which takes the value of 1 when the species is present with probability p, and then a value of 0 in the absence of the species, with probability 1-p. For a random sample, the variance is calculated by multiplying the observed stocking by its complement  $[s^2=p(1-p)]$ . As a result, this variance reaches its maximum at a stocking of 50% and its minimum values at the two extremes, namely at stockings of 0% and 100%. Moreover, this variance is independent of plot size, for a given value of p. However, within the same population, larger plots will have a larger value of p than smaller plots. Therefore, the variance is indirectly

related to plot size, which is chosen according to the silvicultural objectives (Farnden 2009). We also checked how this variance calculation method could apply to the stockings observed by species in the sampling simulations with structured distributions in clusters or cross patterns. For these species, the variance increased very little compared to the random distribution (results not presented).

#### Results

The sapling density variance models explains a large part of the observed variation (coefficients of determination  $[R^2]$  from 77% to 87%; appendix).

The spatial distribution of the plots is the factor that least influences the sample size variation. For example, if we accept a margin of error of 200 saplings ha-1 (or 20%) to sample a population of 1000 saplings ha<sup>-1</sup> with 4 m<sup>2</sup> plots, the number of plots required varies from 349 (for a random distribution) to 430 (for a distribution in linear clusters of 10 plots; Fig. 3). With plots of 25 m<sup>2</sup> this number varies from 105 to 160 for these same two distributions, respectively. Note that the variation is lower among the three cluster distributions than between the cluster distributions and the random distribution, for which the number of plots required is always the lowest. For the next series of results, we will present only the distribution in linear clusters of 10 plots for parsimony and because this is a commonly used spatial distribution in forest inventories.

The sample size required for the estimates to fall within a given margin of error decreases as the plot size increases, but this reduction is not linear (Fig. 4). Consequently, the area that must be sampled is bigger if larger pots are used. For example, the same margin of error is obtained with 430 plots of 4 m<sup>2</sup> (cumulatively 1720 m<sup>2</sup>) as with 160 plots of 25 m<sup>2</sup> (cumulatively 4000 m<sup>2</sup>).

The sapling density of the target population and the accepted margin of error are the variables that most influence the sampling effort required to obtain estimates for a given margin of error (Fig. 5). For example, to sample a population with linear clusters of 10 plots of 4 m<sup>2</sup> while respecting a 20% margin of error, the number of plots required varies from 430 (for a population of 1000 saplings  $ha^{-1}$ ) to 3480 (for a population of 100 saplings ha<sup>-1</sup>, Fig. 5a). In this example, the attempt to sample for a population 10 times smaller (100 saplings ha<sup>-1</sup> instead of 1000 saplings ha<sup>-1</sup>) necessitates to sample 8 times more plots. Regarding the effect of the margin of error, with the same example of population (1000 saplings  $ha^{-1}$ ), it would take 190, 430 and 1710 plots to obtain estimates with margins of error of 30%, 20% and 10%, respectively. Thus, it would require nine times more plots to get a margin of error of 10% rather than 30%.

#### Discussion

We assessed the sapling density variances in northern hardwood and yellow-birch-conifer mixedwood stands, with the goal of estimating the number of plots required to obtain a given margin of error in the inventory. To our knowledge, this type of information is unavailable in the scientific literature for these northern temperate stands. Out of a population of 1000 saplings-ha<sup>-1</sup>, by using one of the three structured spatial distribution under study (clusters of 10, clusters of 5 or cross-shaped pattern of 5 plots), a 20% margin of error (19 times out of 20) can be obtained by sampling about 150 to







**Fig. 4** Number of plots required to obtain a 20% margin of error 19 times out of 20, in a population of 1000 saplings ha<sup>-1</sup> according to plot size, when the plots are distributed in linear clusters of 10.



Fig. 5 Number of plots a) of 4 m<sup>2</sup> and b) of 25 m<sup>2</sup> required to obtain sapling density estimates with a margin of error (E) of 10%, 20% and 30%, according to the targeted sapling population density if the plots are distributed in linear clusters of 10.

400 plots with a size of  $25 \text{ m}^2$  to  $4 \text{ m}^2$ , respectively (Fig. 3). According to our knowledge of the common practices in effect in northern hardwood and yellow birch–conifer stands in Québec, counting saplings in so many plots before producing a silvicultural prescription is rather unusual. The highest sampling intensities for saplings are those applied under specific conditions in the Outaouais region (S. Meunier, pers. comm., 2022), and they amount to nearly 200 plots of  $25 \text{ m}^2$ . Moreover, in experimental context, the total rarely exceeds 144 plots per treatment (e.g., Bédard *et al.* 2014, Raymond and Bédard 2017, Bilodeau-Gauthier *et al.* 2020, Raymond *et* 

*al.* 2020). In a recent study of regeneration before partial cutting of 141 northern hardwood stands in Michigan, Walters *et al.* (2022) used 25 plots of 12.57 m<sup>2</sup> per stand to count the saplings with a DBH of 0.1 cm to 5.1 cm. Consequently, the situations can rarely permit to attain a margin of error as small as 20% with estimated densities as low as 200 or 50 saplings-ha<sup>-1</sup>. Nevertheless, this level of precision should be the target for one to capture the density of companion species or the density in a specific DBH class. For example, to use the concepts related to the diameter distribution proposed by Arbogast (1957) for Great Lakes northern hardwoods, foresters must consider whether they observe as few as 95 saplings-ha<sup>-1</sup> with a DBH of 8 cm. To answer this question with an inventory, it would be necessary to sample from 1000 to a few thousand plots, as the case may be (Fig. 5). Another possibility, used in certain experiments such as those of the present study, involves conducting a complete inventory of the saplings instead of a sampling survey. However, this method can only be applied when the experimental units under study are already divided into small areas generally covering from 900 m<sup>2</sup> to 5000 m<sup>2</sup>.

The relationship between the number of plots to be inventoried and their size (Fig. 4) shows that small plots could be more efficient than large plots to attain a given level of precision in the estimates. Indeed, among the plot sizes tested, the 4 m<sup>2</sup> plot is the one that necessitates the smallest total sampling area. This advantage could be attributed to the fact that the small plots are more dispersed over the territory. The inventory of a larger number of small plots would be more advantageous than that of a few larger plots. The travel time between the more numerous clusters of small plots should also be considered to optimize the inventory and obtain the best level of precision with limited resources. In fact, there may be a sampling range where several sampling plans give similar results in terms of cost and variance (Lynch 2017). Work can be continued in the direction of optimizing the design, but it would be necessary to integrate a constraint related to the fact that the regeneration plots are often carried out simultaneously with plots for merchantable trees.

The stocking of saplings can be also very useful for the silvicultural diagnosis (e.g., McGrath 2018), especially that it can be estimated within a given margin of error with much fewer plots. Indeed, the number of plots required is maximum for a stocking of 50% and, at this level, only 25 to 30 plots are needed, regardless of their size, to obtain a margin of error of no more than 20% (19 times out of 20, Fig. 6). The margin of error is also smaller when the stockings are located closer to the two extremes.

#### Implications for forest management

These results show that a very large number of plots is required to inventory sapling density precisely by sampling. Such a high number of plots is rarely available, whether in research. monitoring or operational contexts. The precise estimate of sapling density nonetheless may be useful on a tactical scale. In this case, many small samples could be grouped on a regional scale. The sapling density estimated in experiments may also serve to provide better assessment of the study conditions of silvicultural treatments. However, to achieve this, it would be more efficient to perform counts over the entire study surface (experimental units of 0.1 to 2 ha, for example). In addition, these experiments should also assess the stocking. This would facilitate the transfer of research results into operational recommendations. Moreover, in this context, it would be preferable to use the stocking as a sapling inventory measurement. However, this method would have to be defined properly. For example, must the tallest species among the saplings of a plot be identified? Moreover, our results indicate that using smaller plots (e.g., 4 m<sup>2</sup>) would be preferable. Indeed, a stocking can be converted into a well-distributed number of stems per hectare, up to a maximum density per plot size. Thus, a stocking of 100% measured with plots of 4 m<sup>2</sup> or 25 m<sup>2</sup> indicates the presence of 2500 or 400 well-distributed stems per hectare, respectively. This way of using the small plots could thus allows a better estimation of the population density than by using large plots.



Fig. 6 Number of plots required to obtain stocking estimates with a margin of error (E) of 5%, 10% and 20%, according to the stocking of the target population.

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## Appendix

Estimated variance equation( $\hat{s^2}$ ):

 $\hat{s^2} = exp\{a_o + a_{ln(d)} * ln(d) + a_{ln(t)} * ln(t) + a_{ln(d)*ln(t)} * ln(d) * ln(t) + (\sigma_{subject}^2 + \sigma^2)/2\}$ 

where *a* are the coefficients of the equation; ln is the natural logarithm; *o* is the ordinate at the origin; *d* is the sapling density per hectare and *t* is the plot size (m<sup>2</sup>).

The bias due to the logarithmic conversion is corrected with the term  $(\sigma_{subject}^2 + \sigma^2)/2$  in the equation.

Estimated values and standard errors of the coefficients of the effects of the 4 models (random, in linear clusters of 5 or 10 plots, and in a cross pattern of 5 plots). The coefficient of determination ( $R^2$ ) of each model is also presented.

Source of variation*		Random		Linear clusters of 5 plots		Linear clusters of 10 plots		Cross pattern of 5 plots	
Effect type	Coefficients	Estimated value	Standard error	Estimated value	Standard error	Estimated value	Standard error	Estimated value	Standard error
Fixed	$a_o$	9.3454	0.07167	9.3957	0.09305	9.3303	0.09727	9.3782	0.09287
	$a_{ln(d)}$	0.9606	0.01524	0.9525	0.01978	0.9704	0.02068	0.9516	0.01975
	$a_{ln(t)}$	-1.0922	0.01185	-1.187	0.01893	-1.1597	0.01954	-1.1753	0.01939
	$a_{ln(d)*ln(t)}$	0.06301	0.002521	0.08762	0.004025	0.08582	0.004154	0.08923	0.004123
Random	$\sigma^2_{subject}$	0.06218	0.007877	0.09927	0.0126	0.1093	0.01386	0.0973	0.01237
	$\sigma^2$	0.007946	0.000438	0.01141	0.000704	0.01215	0.000749	0.01197	0.000738
R <sup>2</sup>		0.874		0.770		0.794		0.824	

\*All the coefficients were significant at the threshold  $\alpha=0.05$