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Assessing Uncertainty: Sample Size Trade-Offs in the Development and Application of Carbon Stock Models

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Many parties to the United Nation's Framework Convention on Climate Change (UNFCCC) base their reporting of change in Land Use, Land-Use Change and Forestry (LULUCF) sector carbon pools on national forest inventories. A strong feature of sample-based inventories is that very detailed measurements can be made at the level of plots. Uncertainty regarding the results stems primarily from the fact that only a sample, and not the entire population, is measured. However, tree biomass on sample plots is not directly measured but rather estimated using regression models based on allometric features such as tree diameter and height. Estimators of model parameters are random variables that exhibit different values depending on which sample is used for estimating model parameters. Although sampling error is strongly influenced by the sample size when the model is applied, modeling error is strongly influenced by the sample size when the model is under development. Thus, there is a trade-off between which sample sizes to use when applying and developing models. This trade-off has not been studied before and is of specific interest for countries developing new national forest inventories and biomass models in the REDD+ context. This study considers a specific sample design and population. This fact should be considered when extrapolating results to other locations and populations.

Keywords: national forest inventory, model-dependent inference, model error, UN Framework Convention on Climate Change (UNFCCC), Land Use, Land-Use Change and Forestry (LULUCF)

In its early efforts at promoting climate change mitigation, the United Nation's Framework Convention on Climate Change (UNFCCC) placed considerable emphasis on forests (Ellison et al. 2014). Forests can play a role in removing greenhouse gases from the atmosphere by storing carbon in forests and forest products and by substituting fossil-based materials and energy. Deforestation, forest degradation, and natural disturbances in forests are linked to large emissions (e.g., Chazdon 2003). Following comprehensive guidelines developed by the Intergovernmental Panel on Climate Change (2006, 2014), parties to the UNFCCC must report changes in carbon pools to the secretariat of the UNFCCC each year.

Many parties base their reporting for the Land Use, Land-Use Change and Forestry (LULUCF) sector on existing or newly established national forest inventories (e.g., Tomppo et al. 2010). These inventories are typically sample based and often use permanent field plots or mixes of permanent and temporary plots. Provided that sample sizes are adequate, change in carbon stocks in several pools can be assessed within the range of degrees of accuracy appropriate for the purpose (e.g., Petersson et al. 2012). A strong feature of this type of sample-based inventory is that very detailed measurements can be made at the level of plots; thus, uncertainty in the results stems primarily from the fact that only a sample, and not the entire population, has been measured. Utilizing sampling theory, the level of uncertainty can be reduced to the specifically desired level by increasing sample size.

However, in forest inventories, total biomass on sample plots—and thus the corresponding carbon stocks—are not directly measured but rather estimated using models based on allometric features

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such as tree diameter and height. These allometric models are typically derived using data and regression analysis from a limited number of carefully measured sample trees. The biomass of these trees is obtained from destructive sampling, in which the weight of different tree components is carefully measured. In practice, models are scarce and existing models are often used in other populations as well. However, methodologically speaking, sample trees should originate from the same population to which the resulting models will be applied. Otherwise, the likely result is that carbon stock estimates will be biased. However, even when the models are derived from the same population to which they are applied, the use of models will still add uncertainty to the estimates (e.g., Cunia 1987). Estimators of model parameters are random variables that exhibit different values depending on which samples are used for estimating them. Model parameter uncertainties arising from allometric model development can be large with small sample sizes and vice versa for large sample sizes.

As illustrated in Ståhl et al. (2011, 2014), the total variance of an estimator in a sample survey in which plot level values are predicted using a model is the sum of the sampling error in the application stage and the modeling error due to uncertainty in the model parameter estimates. Although sampling error is strongly influenced by sample size when the model is applied, modeling error is strongly influenced by the sample size when the model is developed. Thus, there is a trade-off between what sample sizes to use when either applying or developing models. This trade-off is of specific interest for countries developing new national forest inventories and biomass models in the REDD+ context (e.g., UN-REDD Programme 2014). Moreover, such trade-offs have thus far not been studied. However, based on statistical theory, or Monte Carlo simulations in case studies, the potential combined modeling and sampling error has been investigated (e.g., Breidenbach et al. 2014 McRoberts et al. 2015, Ståhl et al. 2014).

In this study we address the trade-off problem between sampling and modeling errors. We provide results expressed in terms of the uncertainty of living tree biomass and carbon stock estimates, for different combinations of sample sizes, both for developing and for applying biomass models. We simulate the case of a country that plans to establish a new national forest inventory for estimating carbon stocks for above- and belowground tree biomass. The study is based on models derived by Marklund (1987, 1988) and data from the Swedish National Forest Inventory (Swedish NFI; Axelsson et al. 2010).

Materials and Methods

Uncertainties in the estimators of tree biomass in Sweden were estimated according to Ståhl et al. (2011, 2014, Appendix 1). Ståhl et al. (2011, 2014) divide the total variance of an estimator in a sample survey into (1) the sampling error at the application phase ($S1$) that arises from the fact that only a sample and not the whole population is observed and (2) the modeling error arising from modeling rather than physically measuring the biomass on the sample plots. Modeling error is linked to the precision of the estimated model parameters that were fitted to data from a separate and independent destructive sample ($S2$) from the same population as $S1$. The biomass of living trees is estimated using area-based sampling, in which one sample unit represents the biomass for a larger area and all sample units together represent the biomass of the total area. It is possible to reduce total variance in the biomass estimates by increasing sampling intensity either in the application phase ($S1$), or in the model development stage ($S2$), or both.

Different sampling intensities in $S1$ and $S2$ were used to address the trade-off problem between allocating resources to the two different surveys. In this study, $S1$ data were obtained from the Swedish NFI (Axelsson et al. 2010) and the regression functions were based on data from Marklund (1987, 1988). Biomass was estimated per region (31 counties) using a ratio estimator (Appendix 2). To obtain national-level estimates, the region-level estimates were summed.

Sampling Error—The Swedish NFI

The Swedish NFI is an annual, systematic, stratified, cluster-sample inventory of Sweden's forests and uses a periodic 5-year inventory cycle (Figure 1, A and B) . In 2013, 889 permanent survey sample clusters from 31 regions were reinventoried. The clusters are distributed all over the country in a pattern that is denser in the southern than in the northern part of the country (Fridman et al. 2014). The clusters (tracts) are square shaped, with sample plots along each side. Each cluster consists of four to eight sample plots with a radius of 10 m. The total sampled area per tract varies from $4 \times 314\ m^2$ to $8 \times 314\ m^2$. The distance between plots within tracts differs per geographic region (stratum) because of differing degrees of autocorrelation (Ranneby et al. 1987). On each circular sample plot, stem diameter is measured at breast height (dbh, 1.3 m above the ground) for all living trees. All trees with a dbh greater than 99 mm are recorded on the plots. Using the Swedish NFI, the sample variances of estimates depend on the sample design, the sample intensity, and the population of interest. The Swedish NFI is unique in the sense that it covers almost all land-use categories where trees occur. Urban trees and trees in the mountainous regions have historically been excluded either because they are typically limited in number or are located in areas characterized by sparse, marginal forest cover. Given this approach, it is possible to estimate the biomass stocks of trees in different land-use categories as well as the change in biomass stocks over time and across different land-use categories.

To simulate different sample intensities in $S1$, estimates were based on 889, 445, 224, and 123 sample units, respectively. Note that a tract (not a plot) designates the sample unit. The 445 tracts were obtained by systematically removing every second tract from the original 889 tracts with a minimum limit of at least three tracts per region (31 regions in total). This process was repeated twice until only 123 sample units remained. The tracts are (more or less) ordered by latitude (Figure 1A). The uncertainty arising from the sampling error associated with biomass estimates was estimated as mean squared error (MSE; $[Mt]^2$), denoted $\widehat{Var}(\hat{D}_1)$, where $\hat{D}1$ is an estimator of the difference between sample and population terms (Appendix 2, Equation 24). This is a standard variance estimator for a ratio estimator (e.g., Thompson 1992).

Model Error—Marklund's Data

Tree biomass was not measured on the sample units but modeled using regression functions. Marklund (1987, 1988) determined an appropriate model for estimating biomass in which the dependent variable was transformed using the natural logarithm. The same model was used in this study for developing regression functions based on different total numbers of derivation trees. Parameter estimates and summary statistics have been made available in Appendix 3. The species Norway spruce (*Picea abies*), Scots pine (*Pinus sylvestris*), and birch (*Betula pendula* and *Betula pubescens*) make up approximately 93% of the standing volume in Sweden (Sveriges Lantbruksuniversitet 2014). To independently predict above- and

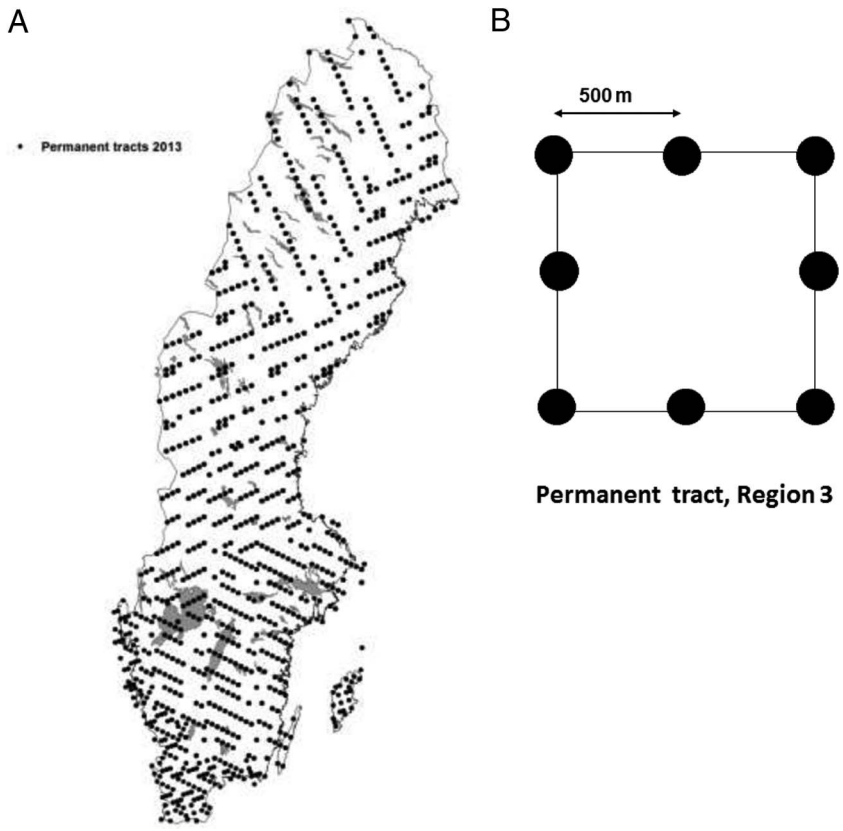

Figure 1. A. The position of the 889 permanent sample units that make up individual clusters of, normally, eight sample plots (four in southernmost Sweden) with a radius of 10 m, as surveyed by the 2013 Swedish National Forest Inventory. The sample plots cover almost all land measured in the field and may be divided into more than one land-use category. The position of sample units is not known to landowners. B. Example of sample unit (tract) consisting of a cluster of eight sample plots with radius 10 m. All trees on the plots are measured for dbh and the species is registered. The country is divided into five regions and both the distance between plots within tracts and the distance between tracts differs by region.

belowground biomass, regression functions were developed for Scots pine, Norway spruce, and birch using dbh and species as independent variables. At the application phase, the Scots pine functions were applied to all "pine-species," the Norway spruce functions to all "spruce-species," and the aboveground birch model was applied to all broadleaved species. Because of the lack of data, the belowground biomass model for spruce was applied to all broadleaved species.

The regression functions were derived based on data acquired by Marklund (1987, 1988). Marklund's single-tree allometric regression functions were developed for predicting aboveground biomass (branches, bark, stem, and needles, not leaves) for Scots pine, Norway spruce, and birch. Belowground biomass refers to stump and roots down to a root diameter of 5 cm (because of the method used for stump excavation, some smaller roots are included) and was only measured for Scots pine and Norway spruce. The stump height was defined as 1% of the tree height. The total fresh weight of each tree (in total, ~1,300 for aboveground measurements and ~660 for belowground measurements) and the fresh weight of samples from different fractions were measured in field. The dry weight of each sample, defined as the constant weight at 105° C, was determined in the laboratory. The calculation of dry weight per fraction was based on these measurements. The trees were selected from approximately 130 stands from different parts of Sweden, covering a wide variety of stand and site conditions. Where possible, Marklund sampled up to four trees per plot in the classes 0–9.9, 10.0–19.9, 20.0–29.9, and 30.0 cm in dbh.

To simulate different intensities in developing regression functions, 508 Scots pines, 546 Norway spruces, and 241 birches were used to develop aboveground biomass functions (Appendix 3). The trees were ordered by latitude, by plot within stand, and by dbh within plot. Approximately every second tree was systematically removed and new regression functions were fitted to data. The process of systematically removing trees continued until the final regression functions were based on only eight, nine, and four trees for Scots pine, Norway spruce, and birch, respectively.

Similarly, for belowground biomass, regression functions were fitted to data for 296 Scots pines and 311 Norway spruces. Every second tree was systematically removed until only nine Scots pines and nine Norway spruces remained. The aboveground regression functions were fitted to data using the "stem over bark" models based on Marklund (1988) whereas the belowground regression functions were fitted to data using the "stump and root system" models (based on Marklund 1988). We estimate the uncertainty arising from the model error as MSE ($[\mathrm{Mt}]^2$), denoted $\widehat{Var}(\hat{D}_2)$ (Appendix 2, Equation 29).

Results

Given an accepted level of uncertainty, Table 1 provides a hint of how to allocate resources between $S1$ and $S2$. The MSEs are used for comparing sample and model errors to total errors whereas the root

Table 1. Estimated MSE [(Mt)^2] and RMSE [Mt] within parentheses for aboveground dry matter biomass in Sweden in 2013.

Model intensity	Sample intensity			
	123	224	445	889
1,295				
Sample MSE	27,048	12,836	6,945	3,478
Model MSE	236	219	222	246
MSE (RMSE)	27,284 (165)	13,055 (114)	7,167 (84,7)	3,724 (61.0)
648				
Sample MSE	27,760	13,175	7,123	3,571
Model MSE	520	485	494	550
MSE (RMSE)	28,280 (168)	13,660 (117)	7,617 (87,3)	4,121 (64.2)
325				
Sample MSE	27,082	12,848	6,949	3,483
Model MSE	1,048	970	990	1,096
MSE (RMSE)	28,130 (168)	13,818 (118)	7,939 (89,1)	4,579 (67.7)
163				
Sample MSE	28,698	13,631	7,355	3,696
Model MSE	2,733	2,547	2,602	2,899
MSE (RMSE)	31,431 (177)	16,178 (127)	9,957 (99,8)	6,595 (81.2)
82				
Sample MSE	24,598	11,605	6,322	3,151
Model MSE	2,927	2,673	2,745	3,011
MSE (RMSE)	27,525 (166)	14,278 (119)	9,067 (95,2)	6,162 (78.5)
42				
Sample MSE	22,764	10,731	5,853	2,914
Model MSE	5,218	4,791	4,910	5,398
MSE (RMSE)	27,982 (167)	15,522 (125)	10,763 (104)	8,312 (91.2)
21				
Sample MSE	18,775	8,896	4,818	2,413
Model MSE	15,540	14,423	14,781	16,313
MSE (RMSE)	34,315 (185)	23,319 (153)	19,599 (140)	18,726 (137)

Sample intensity refers to the number of sampling units (tracts of sample plots; *S*1) and model intensity refers to the number of trees used (*S*2) for developing regression functions (e.g., the number 1,295 in the first row refers to the application of three different equations based on 508, 546, and 241 individual trees for Scots pine, Norway spruce, and birch, respectively; see Appendix 3).

mean squared error (RMSE) is used for relating errors to the estimates of biomass in comparable units. On the basis of the complete set of 889 sample units (*S*1) and using regression functions derived from all 1,295 trees (*S*2), the aboveground biomass estimated was 2,145 [Mt], with a corresponding RMSE of 3% or 61 [Mt] (Tables 1 and 3 and Figure 2).

Given the complete set of *S*1 sample units (889), the proportion of the total MSE due to the biomass model parameter uncertainty was estimated at 7, 13, 24, 44, 49, 65, and 87%, given 1,295, 648, 325, 163, 82, 42, and 21 trees for model development, respectively (Table 1). As expected, the MSE due to sampling decreases with increased sampling intensity. Given *S*1 sampling intensity, the true unknown sample MSE is expected to be independent of the number of trees (*S*2) used for developing biomass models.

However, if 82 or fewer trees are used for model development, then the estimated sample MSE decreases with the declining number of trees used for developing models (Table 1). This effect is due to the effect of random sample selection because the sample MSE is estimated from a sample and not measured. Given sampling intensity in *S*1, the true unknown model MSE is expected to increase with the decreasing number of trees used for model development. This was also what we found. However, there was no major difference between using either 82 or 163 trees (Table 1). This can also be explained by random sample selection because the model MSE is estimated from a sample and not measured. As expected, given model intensity in *S*2, the estimated model MSE was independent of sample intensity in *S*1.

On the basis of a complete set of sample units (*S*1) and using regression functions derived from all 607 trees (*S*2), the belowground biomass was estimated at 615 [Mt] and the RMSE was estimated at 3% or 17 [Mt]. Given all sample units (889), the model MSE of total MSE was estimated to 26, 42, 57, 71, 77, and 86% given 607, 303, 151, 75, 37, and 18 trees for model development, respectively (Table 2 and Figure 3). As expected, the estimated MSE due to sampling decreased as a function of increased sampling intensity. With respect to sample intensity, the true unknown sampling MSE was expected to be the same regardless of the number of trees used for model development. However, the estimated sampling MSE increased slightly with a decreasing number of trees for model development (Table 2). This effect is due to the effect of random sample selection. The estimated model MSE increased by decreasing the number of trees for model development. As expected, the model MSE indicated no major trend by sample intensity (Table 2).

Discussion

It should be emphasized that change in living tree biomass stocks is reported under the UNFCCC/Kyoto Protocol framework and not actual biomass stocks. Using the Swedish and Finnish National Forest Inventories as case studies, Ståhl et al. (2014) estimated the model uncertainty at approximately 10% for stocks and 1% for change in stock. However, both measures are important. Therefore, we have focused our study on the more "model-uncertain" estimate of stocks.

The interpretation of the results depends on the national situation for a country aiming at establishing a new survey for estimating living biomass (and probably also other forest measures) at a national scale. Countries should have a survey budget and the costs for developing models occur only once because models can be reused whereas sampling costs are long-term, ongoing, running

Table 2. Estimated MSE [(Mt)^2] and RMSE [Mt] within parentheses for belowground dry matter biomass in Sweden in 2013.

Model intensity	Sample intensity			
	123	224	445	889
607				
Sample MSE	1,632	825	426	216
Model MSE	78.3	73.2	71.7	77.8
MSE (RMSE)	1,710 (41.4)	898 (30,0)	498 (22.3)	294 (17.1)
303				
Sample MSE	1,783	900	466	236
Model MSE	171	159	156	169
MSE (RMSE)	1,954 (44.2)	1,059 (32.6)	622 (24.9)	405 (20.1)
151				
Sample MSE	1,940	980	507	256
Model MSE	342	319	313	338
MSE (RMSE)	2,282 (47.8)	1,299 (36.0)	820 (28.6)	594 (24.4)
75				
Sample MSE	1,979	1,000	516	262
Model MSE	651	609	596	646
MSE (RMSE)	2,630 (51.3)	1,609 (40.1)	1,112 (33.4)	908 (30.1)
37				
Sample MSE	2,896	1,462	756	383
Model MSE	1,274	1,195	1170	1,272
MSE (RMSE)	4,170 (64.6)	2,657 (51.6)	1,926 (43.9)	1,655 (40.7)
18				
Sample MSE	2,039	1,029	534	269
Model MSE	1,720	1,600	1562	1,678
MSE (RMSE)	3,759 (61.3)	2,629 (51.3)	2,096 (45.8)	1,947 (44.1)

Sample intensity refers to the number of sampling units (tracts of sample plots; *S*1) and model intensity refers to the number of trees used (*S*2) for developing regression functions (e.g., the number 607 in the first row refers to applying two different equations based on 296 and 311 individual tress for Scots pine and Norway spruce, respectively, see Appendix 3).

Table 3. Estimated stock of aboveground living biomass in Sweden in 2013 [Mt] given different sampling intensities at application and different numbers of trees for developing estimation functions.

Model intensity	Sampling intensity			
	889	445	224	123
1,295	2,145	2,024	2,017	2,076
648	2,163	2,039	2,030	2,089
325	2,128	2,006	1,996	2,054
163	2,185	2,057	2,046	2,102
82	1,935	1,827	1,816	1,877
42	1,849	1,747	1,736	1,796
21	1,747	1,647	1,638	1,686

costs. If the country can accept an RMSE of 100 [Mt] and, given a similar sampling design and population of interest as in the present study, then 450 sampling units and model development based on 160 trees for estimating aboveground living biomass may be sufficient. These numbers may need to be adjusted for larger or smaller populations.

However, we generally do not recommend fewer than 300 model trees and 900 sample units for estimating aboveground living biomass. If fewer than 300 trees are used, then unstable sample RMSEs and model RMSEs indicate that variances at a national scale can be biased (recall that Figure 3 and Table 1 suggest a total of 300 trees is required for developing three different models for the groups of species "pine," "spruce," and "broadleaved"; see also Appendix 3). On the basis of Table 1, some improvement seems to be gained in reduced model RMSE from increasing the *S*2 sample from 162 to 325 trees for developing models. It should also be noted that model RMSEs refer to variation in the estimation of model parameters and not to uncertainty arising from an incorrectly specified model.

An incorrectly specified model can introduce bias. Such bias is indicated in Table 3 based on sample intensity, especially for an *S*2 sample of fewer than 163 trees. Although we expect the model based on all trees (1,295) to predict the most accurately, estimates based on fewer than 163 trees seem to predict the most unreliably. This outcome may be the result of random sample selection, but it may also depend on how trees were removed (in each step every second *S*2 observation per species was removed). Carefully choosing model trees that represent a broad range across dependent and explanatory variables may reduce the risk of model specification error and decrease the variance of parameter estimators. The systematic methodology for selecting model trees was chosen to avoid dependence between trees (to avoid more than one sampled tree per plot) and to make the tree selection objective.

To study a wide range of combinations, we developed models based on an unrealistically low number of model trees. These models should not be used in practice. Furthermore, we note that there is uncertainty in estimating the uncertainty of estimates, and using fewer *S*1 trees may increase such uncertainty. Using too few *S*1 trees may also increase the risk of bias from incorrectly specified models. However, the analysis of residuals from the transformed model exhibits a rather constant homoscedastic residual variation given dbh.

Given 300 or more trees for developing regression functions, the RMSE that arises from sampling dominates the error budget (over the modeling RMSE). However, it seems promising to further reduce the sample RMSE by increasing the *S*1 sample beyond 889 units. In practice, estimates based on the Swedish NFI are based on a running average over five cycles. This has the explicit advantage of increasing the *S*1 sample from 889 (one cycle) to approximately

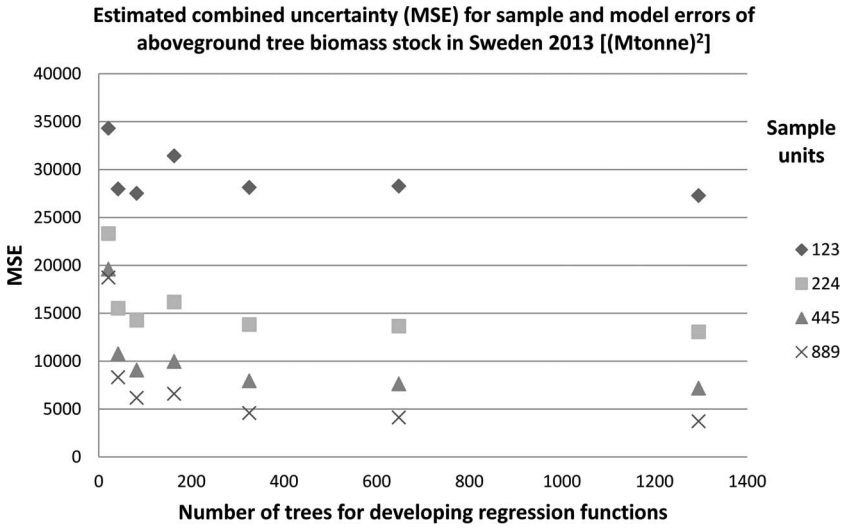

Figure 2. Estimated MSE ([Mt]^2) for aboveground tree biomass (dry matter) in Sweden in 2013. Sample intensity (123, ..., 889) refers to the number of sampling units (tracts of sample plots; *S*1), and model intensity (1,295, ..., 21) refers to the number of trees used (*S*2) for developing regression functions.

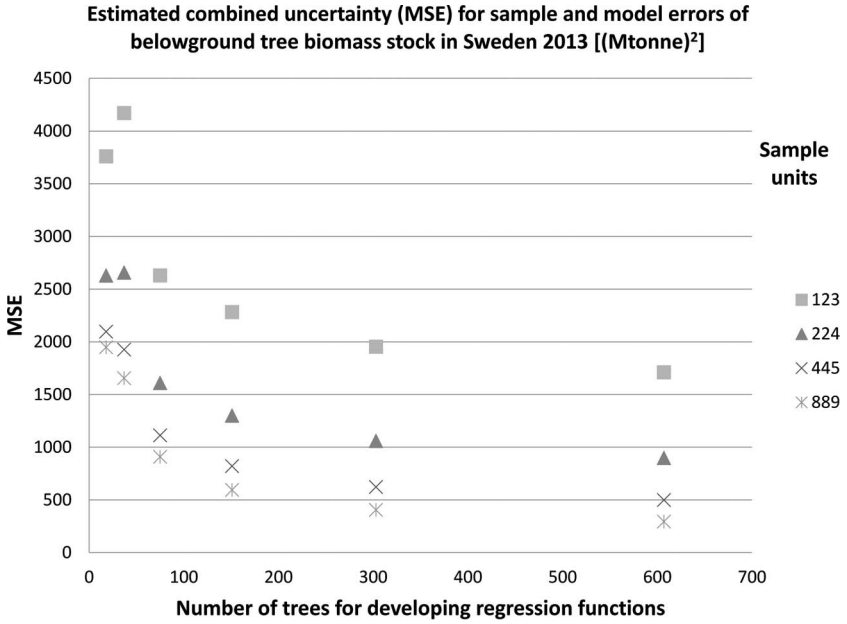

Figure 3. Estimated MSE ([Mt]^2) for belowground tree biomass (dry matter) in Sweden in 2013. Sample intensity (123, ..., 889) refers to the number of sampling units (tracts of sample plots; *S*1), and model intensity (607, ..., 18) refers to the number of trees used (*S*2) for developing regression functions.

4,400 (five cycles) units and may reduce the total RMSE from 60 to approximately 30 [Mt]. However, given an RMSE of 30 [Mt] or 1.4%, a further increase in sample intensity is not likely to improve accuracy very much. This assumption is based on the fact that the relative importance of an unknown bias should be significant when, because of sampling, the RMSE approaches zero. In other words, given a situation in which we expect a bias of $\pm 3\%$, we do not gain much by increasing sample intensity to further reduce RMSE. Increasing the sampling intensity from 445 to 889 units for estimates of aboveground living tree biomass reduces the sampling RMSE by only approximately 20 [Mt].

The proportion of belowground living biomass constitutes approximately 20–25% of the trees biomass in Sweden (given definitions of aboveground and belowground biomass that exclude finer roots). Compared with aboveground biomass, the goodness of fit in parameter estimates is less precise. However, in many situations, reliable estimates of belowground biomass are required. Aboveground and belowground biomass are simultaneously estimated in a national forest inventory survey, and we recommend using the same sampling intensity for both. To avoid similar problems as described for aboveground biomass, Tables 2 and 4 in combination suggest that models based on at least 300 trees may be appropriate for similar-sized populations.

Because the regression model is nonlinear, a Taylor expansion was used to derive an expression of $\widehat{Var}(D_2)$. A Taylor expansion series is an approximation and assumes that the model may be linearized close to a specific value. This may not always be the case, and

Table 4. Estimated stock of belowground living biomass in Sweden in 2013 [Mt] given different sampling intensities at application and number of trees for developing functions.

Model intensity	Sampling intensity			
	889	445	224	123
607	615	585	590	607
303	640	609	614	632
151	670	638	643	661
75	682	648	653	672
37	820	780	786	809
18	659	629	635	656

for small sample sizes it is likely that the Taylor expansion series yields a biased approximation. The risk of using a Taylor expansion series can be exemplified using the simplest possible model, in which the biomass is modeled using a constant: $b_{ij} = \alpha_1$. For large sample sizes in $S2$, the expected (average) value of $\hat{\alpha}_1$ should be close to the true average value of b_{ij} from the $S1$ population. This may not be the case for smaller sample sizes in $S2$. Given any model, the risk of heteroscedastic residual variation should be considered.

Measurement errors arising from the in-field measurement error of independent variables (dbh) and registration errors from double-counting or missing trees may influence the results at a local level (Holdaway et al. 2014). However, because these errors are assumed to be random, we do not think they should have a significant influence on estimates at the national scale. To study and reduce such errors, a control inventory team can be used.

Models were not developed for all species, and this may introduce bias, as for example when applying the birch models to all broadleaved species. In the Swedish case and without appropriate models, if for some reason such bias is approximately 10% for the least common species (~7% of the total population), the bias at a national scale should be less than 1%. This refers to estimates of biomass stock. However, as emphasized above, UNFCCC/Kyoto Protocol reporting requires estimates of change in stock. We assume that such potential bias can be ignored for estimates of change in stock because the bias at two consecutive inventory occasions is correlated and tends to average out. This conclusion is very promising, especially for tropical countries with many species, because it suggests that these countries can focus efforts on developing models for groups of the most important species.

Conclusion

We have studied the trade-offs that arise from using different sample sizes when applying and when developing models for predicting the carbon stock in living tree biomass at a national scale. Given a standard design of a national forest inventory and a population of similar size, our case study suggests that 300 modeling trees should be sampled for model development and 900 sampling units should be used for the application of estimation models to national forest inventories. This suggestion should establish a minimum ambition for improving accuracy and arriving at an acceptable cost-benefit compromise. For countries that are in the process of establishing national forest inventory procedures, investing additional (adequate) resources in (allometric) model development can have a positive impact on the overall reliability and robustness of estimated forest-based carbon stocks and carbon stock change. Furthermore, for the establishment of an appropriate and well-designed forest carbon assessment model, the establishment and use of an adequate number of sampling units for the regular measurement of change in forest carbon represents an important threshold for achieving reliable accounting measures. Finally, because the related costs occur only once, it may be preferable to invest more resources in model development than to invest additional resources in larger sampling sizes during model application.

Appendixes and Supporting Materials

Appendix 1: Deriving a Formula for Estimating Uncertainty Arising from Both Sampling and Model Errors

Ståhl et al. (2011) define a generic model of the population mean, μ_Y, as

$$\mu_Y = \frac{1}{M}\sum_{k=1}^{M} g(\mathbf{x}_k, \boldsymbol{\alpha}) \tag{1}$$

where $\mathbf{x}_k$ is a vector of regressor variables, $\boldsymbol{\alpha}$ is a vector of model parameters, and M is the population size. A model-based estimate of this estimator is provide by

$$\hat{\mu}_Y = \frac{1}{m}\sum_{i=1}^{m} g(\mathbf{x}_{iS1}, \hat{\boldsymbol{\alpha}}) \tag{2}$$

where m is the sample size, $\mathbf{x}_{iS1}$ are the regressors given sample $S1$, and $\hat{\boldsymbol{\alpha}}$ are the estimated model parameters. Ståhl et al. (2011) assume simple random sampling, and $S1$ refers to the national forest inventory sample. The model parameters are estimated from a separate sample ($S2$) from the same population as $S1$.

With the intention of estimating the uncertainty of the estimate, further steps are (Ståhl et al. 2011)

$$\hat{\mu}_Y - \mu_Y = \hat{\mu}_Y - \frac{1}{m}\sum_{i=1}^{m} g(\mathbf{x}_{iS1}, \boldsymbol{\alpha}) + \frac{1}{m}\sum_{i=1}^{m} g(\mathbf{x}_{iS1}, \boldsymbol{\alpha}) - \mu_Y = \tag{3}$$

$$= \frac{1}{m}\sum_{i=1}^{m} g(\mathbf{x}_{iS1}, \hat{\boldsymbol{\alpha}}) - \frac{1}{m}\sum_{i=1}^{m} g(\mathbf{x}_{iS1}, \boldsymbol{\alpha}) + \frac{1}{m}\sum_{i=1}^{m} g(\mathbf{x}_{iS1}, \boldsymbol{\alpha}) - \mu_Y \tag{4}$$

The term D_1 is the difference between sample and population terms and is used for deriving sample uncertainty:

$$D_1 = \frac{1}{m}\sum_{i=1}^{m} g(\mathbf{x}_{iS1}, \boldsymbol{\alpha}) - \mu_Y \tag{5}$$

The term D_2 is the difference within sample and is used for deriving model uncertainty:

$$D_2 = \frac{1}{m}\sum_{i=1}^{m} \{g(\mathbf{x}_{iS1}, \hat{\boldsymbol{\alpha}}) - g(\mathbf{x}_{iS1}, \boldsymbol{\alpha})\} \tag{6}$$

D_1 and D_2 are uncorrelated, thus

$$Var(\hat{\mu}_Y - \mu_Y) = Var(\hat{\mu}_Y) = Var(D_1 + D_2) = Var(D_1) + Var(D_2) \tag{7}$$

$$Var(D_1) = Var\left\{\frac{1}{m}\sum_{i=1}^{m} g(\mathbf{x}_{iS1}, \boldsymbol{\alpha}) - \mu_Y\right\} = Var\left\{\frac{1}{m}\sum_{i=1}^{m} g(\mathbf{x}_{iS1}, \boldsymbol{\alpha})\right\}$$

$$= \frac{1}{m^2} Var\left\{\sum_{i=1}^{m} g(\mathbf{x}_{iS1}, \boldsymbol{\alpha})\right\} \quad (8)$$

If all $g(\mathbf{x}_{iS1}, \boldsymbol{\alpha})$ are uncorrelated, then

$$Var\left\{\sum_{i=1}^{m} g(\mathbf{x}_{iS1}, \boldsymbol{\alpha})\right\} = \sum_{i=1}^{m} Var(g(\mathbf{x}_{iS1}, \boldsymbol{\alpha})) \quad (9)$$

If all $g(\mathbf{x}_{iS1}, \boldsymbol{\alpha})$ have the same variance σ_g^2, then

$$Var(D_1) = \frac{1}{m^2} m \cdot \sigma_g^2 = \frac{\sigma_g^2}{m} \quad (10)$$

$$Var(D_2) = Var\left\{\frac{1}{m}\sum_{i=1}^{m}\{g(\mathbf{x}_{iS1}, \hat{\boldsymbol{\alpha}}) - g(\mathbf{x}_{iS1}, \boldsymbol{\alpha})\}\right\}$$

$$= \frac{1}{m^2} Var\left\{\sum_{i=1}^{m}\{g(\mathbf{x}_{iS1}, \hat{\boldsymbol{\alpha}}) - g(\mathbf{x}_{iS1}, \boldsymbol{\alpha})\}\right\} \quad (11)$$

To simplify the expression in Equation 11, Ståhl et al. (2011) introduce a Taylor expansion series by linearization around $g(\mathbf{x}_{iS1}, \boldsymbol{\alpha})$. For large sample sizes, it is reasonable to use a Taylor expansion series, $E(\hat{\boldsymbol{\alpha}}) = \boldsymbol{\alpha}$, and noting that $\boldsymbol{\alpha} = (\alpha_1, \alpha_2, \cdots, \alpha_p)$, where p is the number of parameters in the model:

$$g(\mathbf{x}_{iS1}, \hat{\boldsymbol{\alpha}}) - g(\mathbf{x}_{iS1}, \boldsymbol{\alpha}) = \left\{\frac{\partial g}{\partial \alpha_1}(\mathbf{x}_{iS1}, \hat{\boldsymbol{\alpha}})\right\} \cdot (\hat{\alpha}_1 - \alpha_1)$$

$$+ \left\{\frac{\partial g}{\partial \alpha_2}(\mathbf{x}_{iS1}, \hat{\boldsymbol{\alpha}})\right\} \cdot (\hat{\alpha}_2 - \alpha_2) + \cdots$$

$$\cdots + \left\{\frac{\partial g}{\partial \alpha_p}(\mathbf{x}_{iS1}, \hat{\boldsymbol{\alpha}})\right\} \cdot (\hat{\alpha}_p - \alpha_p) + etc \ldots$$

If $\hat{\alpha}$ is close to α, then the following terms can be ignored:

$$\sum_{i=1}^{m}\{g(\mathbf{x}_{iS1}, \hat{\boldsymbol{\alpha}}) - g(\mathbf{x}_{iS1}, \hat{\boldsymbol{\alpha}})\} \approx \sum_{i=1}^{m}\left[\sum_{k=1}^{p}\frac{\partial g}{\partial \alpha_k}(\mathbf{x}_{iS1}, \hat{\boldsymbol{\alpha}}) \cdot (\hat{\alpha}_k - \alpha_k)\right]$$

$$= \sum_{k=1}^{p}(\hat{\alpha}_k - \alpha_k) \cdot \left[\sum_{i=1}^{m}\frac{\partial g}{\partial \alpha_k}(\mathbf{x}_{iS1}, \hat{\boldsymbol{\alpha}})\right]$$

Given $\overline{\frac{\partial g(\hat{\alpha})}{\partial \alpha_k}} = \frac{1}{m}\sum_{i=1}^{m}\frac{\partial g}{\partial \alpha_k}(\mathbf{x}_{i1}, \hat{\boldsymbol{\alpha}})$ then

$$\sum_{i=1}^{m}\{g(\mathbf{x}_{iS1}, \hat{\boldsymbol{\alpha}}) - g(\mathbf{x}_{iS1}, \hat{\boldsymbol{\alpha}})\} \approx \sum_{k=1}^{p}(\hat{\alpha}_k - \alpha_k) \cdot m \cdot \overline{\frac{\partial g(\hat{\alpha})}{\partial \alpha_k}}$$

$$= m \cdot \sum_{k=1}^{p}(\hat{\alpha}_k - \alpha_k) \cdot \overline{\frac{\partial g(\hat{\alpha})}{\partial \alpha_k}}$$

$$Var(D_2) \approx \frac{1}{m^2} Var\left\{m \cdot \sum_{k=1}^{p}(\hat{\alpha}_k - \alpha_k) \cdot \overline{\frac{\partial g(\hat{\alpha})}{\partial \alpha_k}}\right\}$$

$$= Var\left\{\sum_{k=1}^{p}(\hat{\alpha}_k - \alpha_k) \cdot \overline{\frac{\partial g(\hat{\alpha})}{\partial \alpha_k}}\right\}$$

$$Var(D_2) = Var\{E(D_2|S1)\} + E\{Var(D_2|S1)\} \quad (12)$$

Given $S1$, $\overline{\frac{\partial g(\hat{\alpha})}{\partial \alpha_k}}$ is a constant c_k for each k (but a different constant for different ks); thus,

$$Var(D_2|S1) \approx Var\left\{\sum_{k=1}^{p}(\hat{\alpha}_k - \alpha_k) \cdot c_k\right\} \quad (13)$$

$$Var(D_2|S1) = \sum_{k=1}^{p} Var(c_k \cdot (\hat{\alpha}_k - \alpha_k)) + 2\sum_{k=1}^{p}\sum_{t=k+1}^{p} Cov(c_k$$

$$\cdot (\hat{\alpha}_k - \alpha_k), c_t \cdot (\hat{\alpha}_t - \alpha_t)) = \quad (14)$$

$$= \sum_{k=1}^{p} c_k^2 Var(\hat{\alpha}_k - \alpha_k) + 2\sum_{k=1}^{p}\sum_{t=k+1}^{p} c_k c_t Cov(\hat{\alpha}_k - \alpha_k, \hat{\alpha}_t - \alpha_t)$$

(15)

Noting that $E(\hat{\boldsymbol{\alpha}}_k) = \boldsymbol{\alpha}_k$,

$$Cov(\hat{\alpha}_k - \alpha_k, \hat{\alpha}_t - \alpha_t) = E(\{[\hat{\alpha}_k - \alpha_k] - E[\hat{\alpha}_k - \alpha_k]\}$$

$$\cdot \{[\hat{\alpha}_t - \alpha_t] - E[\hat{\alpha}_t - \alpha_t]\}) =$$

$$= E([\hat{\alpha}_k - \alpha_k] \cdot [\hat{\alpha}_t - \alpha_t])$$

Thus, given $S1$,

$$Var(D_2|S1) = \sum_{k=1}^{p} c_k^2 Var(\hat{\alpha}_k - \alpha_k) + 2\sum_{k=1}^{p}\sum_{t=k+1}^{p} c_k c_t E([\hat{\alpha}_k$$

$$- \alpha_k] \cdot [\hat{\alpha}_t - \alpha_t]) \quad (16)$$

Noting that $E(\hat{\boldsymbol{\alpha}}_k) = \boldsymbol{\alpha}_k$ and $Var(\hat{\alpha}_k - \alpha_k) = (E[\hat{\alpha}_k - \alpha_k]^2)$,

$$E\{Var(D_2|S1)\} = E\left\{\sum_{k=1}^{p} c_k^2 E([\hat{\alpha}_k - \alpha_k]^2)\right.$$

$$\left. + 2\sum_{k=1}^{p}\sum_{t=k+1}^{p} c_k c_t E([\hat{\alpha}_k - \alpha_k] \cdot [\hat{\alpha}_t - \alpha_t])\right\} =$$

$$= \sum_{k=1}^{p} E(c_k^2) \cdot E([\hat{\alpha}_k - \alpha_k]^2) + 2\sum_{k=1}^{p}\sum_{t=k+1}^{p} E(c_k c_t) \cdot E([\hat{\alpha}_k$$

$$- \alpha_k] \cdot [\hat{\alpha}_t - \alpha_t])$$

Thus, $E(D_2|S1) = E(\sum_{k=1}^{p}(\hat{\alpha}_k - \alpha_k) \cdot (c_k)) = 0$. and $Var(D_2) = Var(E(D_2|S1)) + E(Var(D_2|S1)) = E(Var(D_2|S1))$

Unconditionally for $S1$

$$Var(D_2) = \sum_{k=1}^{p} E(c_k^2) \cdot E([\hat{\alpha}_k - \alpha_k]^2) + 2\sum_{k=1}^{p}\sum_{t=k+1}^{p} E(c_k c_t) \cdot E([\hat{\alpha}_k - \alpha_k] \cdot [\hat{\alpha}_t - \alpha_t]) \quad (17)$$

Finally (see Ståhl et al. 2011, Appendix a),

$$Var(D_2) = \sum_{k=1}^{p}\sum_{t=1}^{p} Cov_{S2}(\hat{\alpha}_k, \hat{\alpha}_t) \cdot E_{S1}\left(\overline{\frac{\partial g(\hat{\alpha})}{\partial \alpha_k}} \cdot \overline{\frac{\partial g(\hat{\alpha})}{\partial \alpha_t}}\right) \quad (18)$$

$$Var(\hat{\mu}_Y) = \frac{1}{m}\sigma_g^2 + \sum_{k=1}^{p}\sum_{t=1}^{p} Cov_{S2}(\hat{\alpha}_k, \hat{\alpha}_t) \cdot E_{S1}\left(\overline{\frac{\partial g(\hat{\alpha})}{\partial \alpha_k}} \cdot \overline{\frac{\partial g(\hat{\alpha})}{\partial \alpha_t}}\right) \quad (19)$$

Appendix 2: Estimating Uncertainty Arising from Both Sampling and Model Errors for a Ratio Estimator

In the present study, the estimated biomass of tree j within stratum (region) i is

$$b_{ij} = g(x_{ij}, \alpha_1, \alpha_2) = g(dbh_{ij}, \alpha_1, \alpha_2) \quad (20)$$

Tree biomass (b_{ij}) is not measured, but it is indirectly modeled using a general regression function (Marklund 1987, 1988):

$$b_{ij} = \exp\left(\alpha_1 + \alpha_2 \cdot \frac{dbh_{ij}}{(dbh_{ij} + l)}\right) \quad (21)$$

where α_1 and α_2 are regression parameters, dbh is stem diameter measured 1.3 m above the ground for a tree from $S2$, and l is a species-specific constant.

The stock of biomass ($\hat{B}_i$) is estimated using a ratio estimator:

$$\hat{B}_i = A_i \cdot \frac{\sum_{j=1}^{n_i} \hat{b}_{ij}}{\sum_{j=1}^{n_i} a_{ij}} = A_i \cdot \hat{R}_i \quad (22)$$

where A_i is the measured area of stratum i, $\hat{b}_{ij}$ is the biomass of sample unit j (in stratum i), a_{ij} is the area of the sample unit j, and n_i is the number of sampling units of stratum i. (Observe that the index j now refers to all trees on a sample unit but to a single tree in Equations 20 and 21.)

In line with Equations 5 and 6,

$$\hat{B}_i = A_i \cdot \frac{\sum_{j=1}^{n_i} b_{ij}}{\sum_{j=1}^{n_i} a_{ij}} + A_i \cdot \frac{\sum_{j=1}^{n_i} (\hat{b}_{ij} - b_{ij})}{\sum_{j=1}^{n_i} a_{ij}} = A_i \cdot R_i + A_i(\hat{R}_i - R_i) = D_1 + D_2 \quad (23)$$

The sample variance of the D_1 estimator is estimated by a standard variance estimator for a ratio estimate:

$$\widehat{Var}(\hat{D}_1) \approx \frac{A_i^2}{(\sum_{j=1}^{n_i} a_{ij})^2} \cdot n_i \cdot S^2_{\hat{b}_{ij} - \hat{R}_i \cdot a_{ij}} \quad (24)$$

where $S^2_{\hat{b}_{ij} - \hat{R}_i \cdot a_{ij}}$ is the standard deviation based on $\hat{b}_{ij} - \hat{R}_i \cdot a_{ij}$. We will need the following derivatives:

$$\frac{\partial g}{\partial \alpha_1} = \hat{b}'_{\alpha_1 ij} = \exp\left(\alpha_1 + \alpha_2 \frac{dbh}{dbh + l}\right) \quad (25)$$

$$\frac{\partial g}{\partial \alpha_2} = \hat{b}'_{\alpha_2 ij} = \frac{dbh}{dbh + l} \cdot \exp\left(\alpha_1 + \alpha_2 \frac{dbh}{dbh + l}\right) \quad (26)$$

$$D_2 = A_i \cdot \frac{\sum_{j=1}^{n_i} (\hat{b}_{ij} - b_{ij})}{\sum_{j=1}^{n_i} a_{ij}} \approx A_i \cdot \frac{\sum_{j=1}^{n_i} ([\hat{\alpha}_1 - \alpha_1] \cdot \hat{b}'_{\alpha_1 ij} + [\hat{\alpha}_2 - \alpha_2] \cdot \hat{b}'_{\alpha_2 ij}}{\sum_{j=1}^{n_i} a_{ij}} = \quad (27)$$

$$= [\hat{\alpha}_1 - \alpha_1] \cdot A_i \cdot \frac{\sum_{j=1}^{n_i} \hat{b}'_{\alpha_1 ij}}{\sum_{j=1}^{n_i} a_{ij}} + [\hat{\alpha}_2 - \alpha_2] \cdot A_i \cdot \frac{\sum_{j=1}^{n_i} \hat{b}'_{\alpha_2 ij}}{\sum_{j=1}^{n_i} a_{ij}} \quad (28)$$

where $[\hat{\alpha}_1 - \alpha_1]$ and $[\hat{\alpha}_2 - \alpha_2]$ are random variables, and given $S1$, $A_i \cdot \frac{\sum_{j=1}^{n_i} \hat{b}'_{\alpha_1 ij}}{\sum_{j=1}^{n_i} a_{ij}}$ and $A_i \cdot \frac{\sum_{j=1}^{n_i} \hat{b}'_{\alpha_2 ij}}{\sum_{j=1}^{n_i} a_{ij}}$ are constants:

$$\widehat{Var}(D_2) \approx Cov(\hat{\alpha}_1, \hat{\alpha}_1) \cdot \left(\sum_{i=1}^{31} A_i \cdot \frac{\sum_{j=1}^{n_i} \hat{b}'_{\alpha_1 ij}}{\sum_{j=1}^{n_i} a_{ij}}\right)^2 + Cov(\hat{\alpha}_2, \hat{\alpha}_2) \cdot \left(\sum_{i=1}^{31} A_i \cdot \frac{\sum_{j=1}^{n_i} \hat{b}'_{\alpha_2 ij}}{\sum_{j=1}^{n_i} a_{ij}}\right)^2 + \quad (29)$$

$$+ 2 \cdot Cov(\hat{\alpha}_1, \hat{\alpha}_2) \cdot \left(\sum_{i=1}^{31} A_i \cdot \frac{\sum_{j=1}^{n_i} \hat{b}'_{\alpha_1 ij}}{\sum_{j=1}^{n_i} a_{ij}}\right) \cdot \left(\sum_{i=1}^{31} A_i \cdot \frac{\sum_{j=1}^{n_i} \hat{b}'_{\alpha_2 ij}}{\sum_{j=1}^{n_i} a_{ij}}\right)$$

$$\widehat{Var}(D_2) \approx C_{11} \cdot (U_{11})^2 + C_{22} \cdot (U_{12})^2 + 2 \cdot C_{12} \cdot U_{11} \cdot U_{12} \quad (30)$$

However, Equation 29 should be made per stratum for the three species:

$$\widehat{Var}(D_2) \approx C_{11} \cdot (U_{11})^2 + 2 \cdot C_{12} \cdot U_{11} \cdot U_{12} + C_{22} \cdot (U_{12})^2 + \\ + C_{33} \cdot (U_{21})^2 + 2 \cdot C_{34} \cdot U_{21} \cdot U_{22} + C_{44} \cdot (U_{22})^2 + \\ + C_{55} \cdot (U_{31})^2 + 2 \cdot C_{56} \cdot U_{31} \cdot U_{32} + C_{66} \cdot (U_{32})^2 \quad (31)$$

The covariance matrix for $(\hat{\alpha}_1, \hat{\alpha}_2)$ is

		Scots pine		Norway spruce		Birch	
$\hat{\sigma}(\hat{\alpha}_1,\hat{\alpha}_1)$	$\hat{\sigma}(\hat{\alpha}_1,\hat{\alpha}_2)$	C_{11}	C_{12}	C_{33}	C_{34}	C_{55}	C_{56}
$\hat{\sigma}(\hat{\alpha}_2,\hat{\alpha}_1)$	$\hat{\sigma}(\hat{\alpha}_2,\hat{\alpha}_2)$	C_{21}	C_{22}	C_{43}	C_{44}	C_{65}	C_{66}

Appendix 3: Summary Statistics for the Sets of Equations

The covariance matrix of the parameter estimates is central when estimating the model errors (e.g., Equation 31). The absolute values of covariances (as well as the model errors) are expected to increase when the number of trees (n) used for developing the model equations decreases. Seven and six sets of equations were derived for aboveground and belowground biomass, respectively. Summary statistics for the sets of equations are presented, including parameter estimates and covariances. The following model was used (Marklund 1987, 1988):

$$\ln b_{ij} = \alpha_1 + \alpha_2 \cdot \frac{dbh_{ij}}{(dbh_{ij} + l)}$$

For aboveground individual tree biomass, the constant l was set to 122, 148, and 83 for Scots pine, Norway spruce, and birch, respectively. For belowground individual tree biomass, the constant l was set to 120 and 140 for Scots pine and Norway spruce, respectively (α is a model parameter, *dbh* [mm], and b is biomass [g]).

At retransformation, correction for log bias is made by $\phi^2/2$ (ϕ is the residual variation, Satoo and Madgwick 1982). R^2 is the coefficient of determination. The predicted biomass (dry weight) may be converted to CO_2 equivalents by multiplying with $0.50 \cdot 44/12$ (Sandström et al. 2007).

Summary statistics for seven model combinations: aboveground biomass:

	$\hat{\alpha}_1$	$\hat{\alpha}_2$	n = 1,295	ϕ	R^2	$\hat{\sigma}(\hat{\alpha}_1,\hat{\alpha}_1)$	$\hat{\sigma}(\hat{\alpha}_1,\hat{\alpha}_2)$	$\hat{\sigma}(\hat{\alpha}_2,\hat{\alpha}_2)$
Scots pine	5.09	10.69	508	0.228	0.98	0.00148	−0.00249	0.00448
Norway spruce	5.99	10.28	546	0.211	0.99	0.00059	−0.00113	0.00251
birch	4.32	10.70	241	0.294	0.98	0.00336	−0.00580	0.01122
	$\hat{\alpha}_1$	$\hat{\alpha}_2$	n = 648	ϕ	R^2	$\hat{\sigma}(\hat{\alpha}_1,\hat{\alpha}_1)$	$\hat{\sigma}(\hat{\alpha}_1,\hat{\alpha}_2)$	$\hat{\sigma}(\hat{\alpha}_2,\hat{\alpha}_2)$
Scots pine	5.13	10.61	254	0.264	0.97	0.00433	−0.00725	0.01298
Norway spruce	6.00	10.25	273	0.216	0.99	0.00119	−0.00230	0.00520
birch	4.18	10.96	121	0.233	0.98	0.00498	−0.00857	0.01622
	$\hat{\alpha}_1$	$\hat{\alpha}_2$	n = 325	ϕ	R^2	$\hat{\sigma}(\hat{\alpha}_1,\hat{\alpha}_1)$	$\hat{\sigma}(\hat{\alpha}_1,\hat{\alpha}_2)$	$\hat{\sigma}(\hat{\alpha}_2,\hat{\alpha}_2)$
Scots pine	5.12	10.60	127	0.241	0.97	0.00822	−0.01379	0.02447
Norway spruce	5.99	10.29	137	0.225	0.99	0.00237	−0.00452	0.01023
birch	4.11	11.12	61	0.248	0.99	0.00905	−0.01571	0.03074
	$\hat{\alpha}_1$	$\hat{\alpha}_2$	n = 163	ϕ	R^2	$\hat{\sigma}(\hat{\alpha}_1,\hat{\alpha}_1)$	$\hat{\sigma}(\hat{\alpha}_1,\hat{\alpha}_2)$	$\hat{\sigma}(\hat{\alpha}_2,\hat{\alpha}_2)$
Scots pine	5.20	10.46	64	0.294	0.96	0.02322	−0.03821	0.06677
Norway spruce	6.00	10.26	69	0.248	0.99	0.00554	−0.01060	0.02424
birch	3.88	11.58	30	0.212	0.99	0.01469	−0.02635	0.05260
	$\hat{\alpha}_1$	$\hat{\alpha}_2$	n = 82	ϕ	R^2	$\hat{\sigma}(\hat{\alpha}_1,\hat{\alpha}_1)$	$\hat{\sigma}(\hat{\alpha}_1,\hat{\alpha}_2)$	$\hat{\sigma}(\hat{\alpha}_2,\hat{\alpha}_2)$
Scots pine	4.90	10.92	32	0.168	0.99	0.01610	−0.02637	0.04567
Norway spruce	5.98	10.34	35	0.193	0.99	0.00768	−0.01532	0.03564
birch	3.71	11.90	15	0.184	0.99	0.02971	−0.05425	0.10720
	$\hat{\alpha}_1$	$\hat{\alpha}_2$	n = 42	ϕ	R^2	$\hat{\sigma}(\hat{\alpha}_1,\hat{\alpha}_1)$	$\hat{\sigma}(\hat{\alpha}_1,\hat{\alpha}_2)$	$\hat{\sigma}(\hat{\alpha}_2,\hat{\alpha}_2)$
Scots pine	4.81	11.03	16	0.194	0.99	0.03075	−0.05240	0.09669
Norway spruce	5.94	10.47	18	0.187	0.99	0.01369	−0.02779	0.06568
birch	3.67	11.97	8	0.233	0.99	0.06739	−0.13071	0.28196
	$\hat{\alpha}_1$	$\hat{\alpha}_2$	n = 21	ϕ	R^2	$\hat{\sigma}(\hat{\alpha}_1,\hat{\alpha}_1)$	$\hat{\sigma}(\hat{\alpha}_1,\hat{\alpha}_2)$	$\hat{\sigma}(\hat{\alpha}_2,\hat{\alpha}_2)$
Scots pine	4.92	10.66	8	0.238	0.99	0.06931	−0.12411	0.24756
Norway spruce	5.81	10.73	9	0.211	0.99	0.03570	−0.08156	0.21628
birch	3.72	12.17	4	0.194	0.98	0.33694	−0.67853	1.40554

Summary statistics for six model combinations: belowground biomass:

	$\hat{\alpha}_1$	$\hat{\alpha}_2$	n = 607	ϕ	R^2	$\hat{\sigma}(\hat{\alpha}_1,\hat{\alpha}_1)$	$\hat{\sigma}(\hat{\alpha}_1,\hat{\alpha}_2)$	$\hat{\sigma}(\hat{\alpha}_2,\hat{\alpha}_2)$
Scots pine	3.46	11.11	296	0.364	0.96	0.00580	−0.00985	0.01813
Norway sprucev	4.44	10.54	311	0.341	0.97	0.00265	−0.00507	0.01129
	$\hat{\alpha}_1$	$\hat{\alpha}_2$	n = 303	ϕ	R^2	$\hat{\sigma}(\hat{\alpha}_1,\hat{\alpha}_1)$	$\hat{\sigma}(\hat{\alpha}_1,\hat{\alpha}_2)$	$\hat{\sigma}(\hat{\alpha}_2,\hat{\alpha}_2)$
Scots pine	3.48	11.01	148	0.331	0.97	0.00921	−0.01555	0.02853
Norway spruce	4.49	10.45	155	0.341	0.97	0.00531	−0.01017	0.02267
	$\hat{\alpha}_1$	$\hat{\alpha}_2$	n = 151	ϕ	R^2	$\hat{\sigma}(\hat{\alpha}_1,\hat{\alpha}_1)$	$\hat{\sigma}(\hat{\alpha}_1,\hat{\alpha}_2)$	$\hat{\sigma}(\hat{\alpha}_2,\hat{\alpha}_2)$
Scots pine	3.56	10.88	74	0.325	0.97	0.01687	−0.02850	0.05260
Norway spruce	4.54	10.40	77	0.324	0.97	0.00974	−0.01874	0.04190
	$\hat{\alpha}_1$	$\hat{\alpha}_2$	n = 75	ϕ	R^2	$\hat{\sigma}(\hat{\alpha}_1,\hat{\alpha}_1)$	$\hat{\sigma}(\hat{\alpha}_1,\hat{\alpha}_2)$	$\hat{\sigma}(\hat{\alpha}_2,\hat{\alpha}_2)$
Scots pine	3.65	10.76	37	0.303	0.98	0.02635	−0.04473	0.08378
Norway spruce	4.54	10.48	38	0.307	0.97	0.01847	−0.03600	0.08107
	$\hat{\alpha}_1$	$\hat{\alpha}_2$	n = 37	ϕ	R^2	$\hat{\sigma}(\hat{\alpha}_1,\hat{\alpha}_1)$	$\hat{\sigma}(\hat{\alpha}_1,\hat{\alpha}_2)$	$\hat{\sigma}(\hat{\alpha}_2,\hat{\alpha}_2)$
Scots pine	3.79	10.47	18	0.299	0.97	0.06014	−0.10216	0.18911
Norway spruce	4.75	10.13	19	0.251	0.98	0.02441	−0.04703	0.10489
	$\hat{\alpha}_1$	$\hat{\alpha}_2$	n = 18	ϕ	R^2	$\hat{\sigma}(\hat{\alpha}_1,\hat{\alpha}_1)$	$\hat{\sigma}(\hat{\alpha}_1,\hat{\alpha}_2)$	$\hat{\sigma}(\hat{\alpha}_2,\hat{\alpha}_2)$
Scots pine	3.18	11.54	9	0.207	0.99	0.05480	−0.09539	0.18187
Norway spruce	4.62	10.53	9	0.228	0.99	0.05272	−0.10502	0.23494

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