Forecasting Probability Distributions of Forest Yield Allowing for a Bayesian Approach to Management Planning

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Probability distributions of stand basal area were predicted and evaluated in young mixed stands of Scots pine (*Pinus sylvestris* L.), Norway spruce (*Picea abies* (L.) Karst.) and birch (*Betula pendula* Roth and *Betula pubescens* Ehrh.) in Sweden. Based on an extensive survey of young stands, individual tree basal area growth models were estimated using a mixed model approach to account for dependencies in data and derive the variance/covariance components needed. While most of the stands were reinventoried only once, a subset of the stands was revisited a second time. This subset was used to evaluate the accuracy of the predicted stand basal area distributions.

Predicting distributions of forest yield, rather than point estimates, allows for a Bayesian approach to planning and decisions can be made with due regard to the quality of the information.

Keywords basal area growth model, mixed-model, uncertainty of predictions, Monte Carlo simulation
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1 Introduction

Traditionally, forest planning has been carried out deterministically. Predicted parameters involved have been considered known with certainty and decisions derived accordingly. However, for some time the trend has been to actively account for risk since optimal decisions in a stochastic setting are often quite different from the corresponding decisions in a deterministic setting (e.g., Lohmander 1987, Haight 1990).

Studies on forest planning under risk have, to some extent, focused on economic parameters such as stochastic timber prices and harvesting costs. Studies on planning under risk in the growth process are not as common, although many articles treat the problem (e.g., Kao 1982, Hof et al. 1988, Gove and Fairweather 1992, Valsta 1992, Pukkala and Miina 1997, Kangas and Kangas 1999).

Closely related to the latter area is the field of growth and yield research in which substantial efforts have, lately, been put on the random variability. A basic assumption for many growth simulators used is that future growth conditions will remain similar to those of the past, and yield prediction becomes a forward projection of past patterns of growth (c.f., Kimmins 1990). If this 'historical bioassay' approach is correct, the errors in predictions of future states can be regarded as being the result of four major components (c.f., Gertner 1987, Ståhl and Holm 1994, Kangas 1996, 1997, 1999):

(i) Pure errors. In a perfect growth model, given a perfect initial state description, the inherent randomness of nature causes random errors by factors not possible to describe in the model, e.g. random weather conditions.

(ii) Incomplete model due to incomplete description of present state. A properly estimated although not complete growth model, i.e. lack of relevant variables, will increase the random error component. From a theoretical point of view, the precision of the growth function is determined by its capacity to distinguish growth from different initial forest conditions. A high spatial and structural resolution (i.e. models at the single tree level), should generally, if there is more information available for prediction, lead to more accurate estimates than growth models with only a few variables to characterise the initial state.

(iii) Errors in the description of initial state. Given a properly derived growth function, sampling and measurement errors in the state variables (as well as prediction errors when a model is used recursively) will decrease the accuracy of the predictions. When input data contain errors, a high-resolution model can sometimes yield worse predictions than a low-resolution model (c.f., Gertner 1986).

(iv) Errors in the estimation of parameters in the growth model due to uncertain data for model development.

The size of errors from (ii), (iii) and (iv) can be influenced by the choice of growth models and forest inventory strategies.

A number of studies have been conducted to determine the effect of uncertainty in input data and estimated parameters on the accuracy of the predictions (e.g., Smith and Burkhart 1984, Gertner and Dzialowy 1984, Gertner 1986, Kangas 1998). Gertner (1991) showed that random errors in input data cause bias in non-linear models and Kangas (1996) compared different methods for reducing this kind of bias in predictions of forest yield. Error propagation in forest growth simulations has been quantified empirically, using Monte Carlo simulations, and analytically, by variance functions derived from Taylor approximation (e.g., Mowrer and Frayer 1986, Gertner 1987, Mowrer 1990, Vanclay 1991, Green and Strawderman 1996, Kangas 1997).

An important part of the model building process is to characterise the error structure of the growth model. Gregoire (1987) and Gregoire et al. (1995) focus on how spatial and temporal correlations affect the precision of parameter estimates in stand level growth models. Stage and Wykoff (1993) extend this to models of individual trees and show that the stochastic components affect predicted stand dynamics. Mixed linear models methodology (Searle 1971, Harville 1977) has commonly been used in this connection, for developing functions from data with spatiotemporal correlations (e.g., Lappi 1986, Lappi and Bailey 1988, Penner et al. 1995).

Stochasticity in timber yield can, technically, be introduced to a planning problem in different ways. Hof et al. (1988) and Pickens and Dress (1988) introduced random components in an LP-formulation. A common approach for restricted problems is to use stochastic dynamic programming (e.g., Riiters et al. 1982, Kao 1982, Haight 1990), a technique which provides an opportunity for decisions to be made adaptively based on the outcome of the random process. A problem is, however, that the outcome must be observed. To control both the growth process and the observations of it, Ståhl et al. (1994) used dynamic programming in a Bayesian setting.

Bayesian decision-making is a common approach to handle risk in planning (e.g., Lindgren 1962). Rather than considering point estimates of the parameters involved, entire (joint) probability distributions of the parameters are used when the outcome of a decision is evaluated. Although there has been a great deal of debate on the element of subjectivity in Bayesian methods, Bayesian inferences tend to be accepted when

the subjectivity in assessing priors is restricted. Also, recent advances in computational statistics have made the methods more appealing, e.g. the Gibbs sampler, applied in forestry by Green and Strawderman (1992) and Green and Valentine (1998). Gertner et al. (1999) estimated the distribution of the parameters of a growth model by Bayesian estimation with rejection sampling.

A Bayesian approach to consider risk in future yield requires the prediction of joint probability distributions rather than point estimates. This can be made in different ways. One possibility is to assume a parametric setting with 'conjugate' prior distributions and growth processes. By convolution, the yield distribution after a certain period of growth is obtained. E.g., a normal prior distribution can be coupled with a linear normal growth process, resulting in a normally distributed predicted distribution of yield. However, this set-up imposes considerable restrictions on what kind of growth models can be used.

Another possibility is to leave the parametric setting and make use of simulation for determining the distributions. An advantage with this is that no assumption about the form of the distributions is needed. Any growth process can be used since any shape of the yield distribution is allowed. Also, it is possible to use a high spatial and structural resolution in the growth process, e.g. models at the single tree level. The drawback is the amount of computation needed.

The aim of this article is to describe and evaluate a straightforward technique for the prediction of within-stand probability distributions of forest yield based on growth models for single trees. A Monte-Carlo simulation approach is used in which the variance/covariance components of the random elements of growth, estimated from mixed model regression and other analyses, are added. The accuracy of the predictions is evaluated in terms of their ability to correctly forecast entire distributions of yield. Moreover, it is shown how extensive Monte-Carlo simulations are needed to obtain reliable estimates. Finally, it is outlined how the predicted yield distributions can be utilised in a Bayesian approach to forest management planning.

2 Material and Methods

2.1 Basic Approach

The study is limited to predictions of basal area in young stands, here defined as stands with mean height between 3–8 meters. Individual tree growth models for Scots pine (*Pinus sylvestris*, L.), Norway spruce (*Picea abies* (L.) Karst.) and birch (*Betula pendula* Roth and *Betula pubescens* Ehrh.) were developed using mixed linear regression on data from an extensive survey of young stands. Based on these functions for five year basal area growth, and the corresponding estimated variance/covariance components, predictions of future stand level basal area distributions were made using Monte-Carlo simulation.

Predictions were first made at the plot level, by summing the predictions for all trees on a plot. Stand-wise basal area probability distributions were then obtained by merging the plot-wise predictions within a stand. The following general recursive model structure was used for the predictions at the tree level:

$$Y_{ijk}^{t} = Y_{ijk}^{t-1} + f\left(Y_{ijk}^{t-1}, X_{ij}\right) + \varepsilon_{ijk}^{t} \qquad (1)$$

Here, Y_{ijk}^{t} is the predicted variable in time period t, for tree k on plot j in stand i; X_{ij} is a vector of stationary variables (e.g., site quality), and ε_{ijk}^{t} is the random error term. The growth function is indicated by $f(\cdot)$. Due to the hierarchical structure of data (trees on plots within stands), the random error terms were separated into the following components:

$$e_{ijk}^{t} = \varepsilon_{i}^{t} + \delta_{ij}^{t} + \gamma_{ijk}^{t} \qquad (2)$$

Three separate independent terms were considered: ε_{i}^{t} is the random effect due to stand i, δ_{ij}^{t} is the random effect due to plot j in stand i, and γ_{ijk}^{t} is the residual random error at the tree level. The distributional assumptions of the error terms were: $e_{ijk}^{t} \sim \mathrm{N}(0, \kappa^2)$, $\varepsilon_{i}^{t} \sim \mathrm{N}(0, \sigma^2)$, $\delta_{ij}^{t} \sim \mathrm{N}(0, \tau^2)$, $\gamma_{ijk}^{t} \sim \mathrm{N}(0, \theta^2)$, and tied $\kappa^2 = \sigma^2 + \tau^2 + \theta^2$.

In a single repetition of simulating the growth in a stand, the same random stand component was used for all trees, and the same plot component for all trees on a plot. Moreover, since the growth functions were developed for each species indi-

vidually, cross-correlations between the different species' random components at the stand and plot levels were estimated and considered in the simulations.

Ideally, the complete error structure of the prediction system should be known and accounted for in the simulations. It involves (c.f., Gertner 1987, Mowrer 1990, Gregoire 1995 et al., McRoberts 1996, Kangas 1997) the residual components embedded in e^t_{ijk}, their serial correlations (and cross-correlations over time), the correlations between random components of different species, the random errors in the estimated model parameters and their cross-correlations, and errors in input data.

The effect on growth of random errors in the estimated model parameters was considered to be small in relation to the effect of the residual random errors. Thus, to simplify the simulations, these errors were not accounted for (the models were considered to be exact). Moreover, since most of our data were available from a single five-year period only, serial correlations could not be estimated. The effect of varying degrees of serial correlation was, however, evaluated on a sensitivity basis. The magnitude of correlations to test was taken from Kangas (1997).

Distributions were predicted at the stand level. However, to keep the evaluations straightforward, we considered the plots within a stand to provide a perfect description of the initial state. After a ten years growth projection, the predicted distribution was compared with the actual state, obtained from a field inventory of the same plots.

In the following, the data set is first described. Secondly, the development of the growth functions, including the estimation of variance components of the random error terms, is presented. Thirdly, it is shown how the cross-correlations of the random error components for the different species were derived. Lastly, the evaluations made are described.

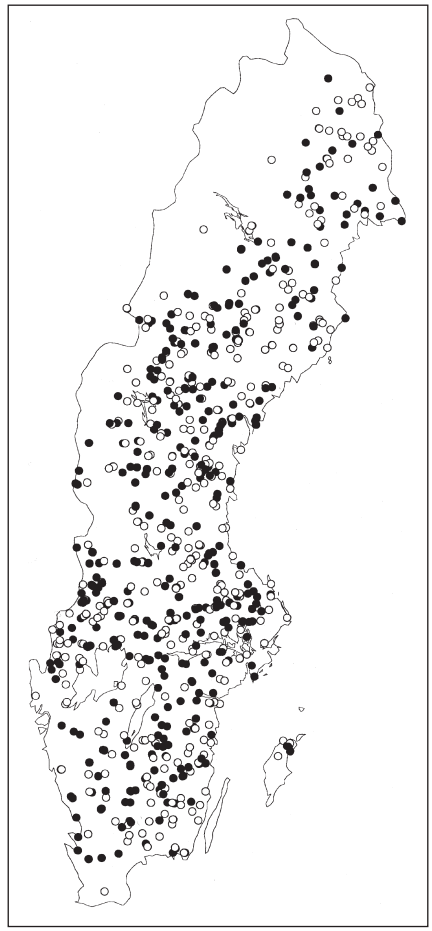

Fig. 1. Geographical distribution of the calibration (•) and validation (○) data.

2.2 The HUGIN Young Stand Survey

Data were obtained from the HUGIN survey of young stands (Elfving 1982). In the period 1976–79, permanent plots were established in 799 young stands in Sweden. In each stand, five circular sample plots of 100 m^2 size were randomly laid out.

Each plot was marked and the position of every tree mapped. Total height and diameter at breast height (1.3 m) were measured, and damage registered. Data describing site characteristics were also recorded.

After five years, in the period 1981–84, the plots were revisited. It was registered whether the trees remained or had been removed by pre-commercial thinning. On remaining trees, height and diameter were measured and damage assessed as light, moderate, severe, or fatal. In the period 1987–1990, 49 stands were re-inventoried

Table 1. Mean, standard deviation (SD), and range for some characteristics in the calibration and validation data sets, respectively. Stand level data at the point of time of the first inventory.

	Latitude (°N)	Altitude (m.a.s.l.)	A_{13}[a)] (yr)	N[b)] (no. ha^{-1})	H_L[c)] (dm)	Ba[d)] ($m^2 ha^{-1}$)	Dgw[e)] (cm)
Calibration data set (378 stands, 1750 plots)							
Mean	61.5	246	10.9	2003	54	5.4	7.8
SD	3.0	156	4.9	851	22	4.5	3.8
Range	55.6–68.1	10–800	2.0–39.4	300–4242	17–168	0.1–25.4	1.4–27.0
Validation data set (405 stands, 1879 plots)							
Mean	61.3	252	10.9	2094	57	5.9	8.2
SD	2.8	165	4.2	868	24	5.1	3.8
Range	56.1–68.2	0–710	2.0–33.3	200–5308	16–225	0.1–35.6	1.3–33.4

[a)] A_{13} = stand age, expressed as basal area weighted mean age at breast height
[b)] N = number of stems ha^{-1} with a height ≥ 1.3 m
[c)] H_L = mean height by Lorey; basal area weighted mean height, dm
[d)] Ba = basal area, m^2/ha
[e)] Dgw = basal area weighted mean diameter, cm

a second time. These stands were mainly located in northern Sweden.

In the present study, the data set was randomly split in two parts: calibration data (378 stands) and validation data (405 stands), located all over Sweden (Fig. 1). Plot data from the two data sets are presented in Table 1. Data for evaluating the predicted distributions consisted of the subset of 49 stands, re-measured twice.

2.3 Basal Area Growth Model

A mixed linear model approach (e.g., Penner et al. 1995, Hökkä et al. 1997, Hökkä and Groot 1999) was used to relate the five years basal area growth of individual trees (bai, cm^2/5 yr.) to a set of independent variables. Undamaged trees, only, were considered in the model development. Summary statistics for the trees in the calibration data set are shown in Table 2.

The selection of variables for the functions was based on experience from a previous study (Nyström and Kexi 1997) in which individual tree growth models for Norway spruce were constructed with ordinary least-squares regression. The variables of the models are characteristics related to tree size, stand attributes, site quality, and treatments. The measures of overall density and relative competition status were plot basal area (Ba) and relative diameter (R_d). R_d is expressed as the ratio between the tree diameter at breast height (d) and basal area weighted mean diameter of the plot (Dgw), defined as $\Sigma d^3 / \Sigma d^2$. Plot age (A_{13}) was expressed as basal area weighted mean age at breast height (1.3 m) on a plot. The climatic effect on growth was modelled with the temperature sum (TS_5), defined as the sum of all daily mean temperatures exceeding the threshold temperature 5 °C during the growing season (Odin et al. 1983). Site fertility was derived indirectly from the ground vegetation type. It was registered as 'Rich', 'Medium', or 'Poor' and included in the models using two indicator variables. The effects on growth due to pre-commercial thinning before the first measurement or between the measurements were also

Table 2. Summary statistics for the trees used for parameter estimation (the calibration data set).

	Scots pine		Norway spruce		Birch	
	Mean	SD	Mean	SD	Mean	SD
bai (cm^2/5 yr.)	31.0	24.2	27.6	29.0	16.6	21.1
Diameter (cm)	6.3	3.9	5.1	3.5	4.1	2.9
R_d[a)]	0.8	0.4	0.7	0.4	0.7	0.4
Number of stands	264		276		245	
Number of plots	790		822		609	
Number of trees	5620		7991		4036	

[a)] R_d = relative diameter, defined as d/Dgw; where d = breast height diameter (cm) and Dgw = basal area weighted mean diameter.

incorporated as indicator variables (Clbefore, Clbetween).

The independent variables were assumed to interact multiplicatively with the basal area increment. To make the model linear, a logarithmic transformation was made. Preliminary fits of the models and examination of scatter-plots of residuals versus predicted values indicated that the logarithmic transformation was appropriate with regard to desirable statistical properties of the random error term, i.e. normally distributed residuals with homogenous error variance. To overcome problems with zero and negative increment due to measurement errors, a small constant was added to the dependent variable for all observations.

The random variation in basal area growth was divided into: (i) random effects connected to stands, (ii) random effects connected to plots within stands, and (iii) residual effects at the tree level. All random effects were assumed to be normally and independently distributed with zero mean and constant variance. Consequently, the general model for 5-year basal area growth was:

Growth = fixed(tree and site characteristics) + random(stand, plot within stand, residual)

The fixed effects and the variance components of the random effects were estimated with PROC MIXED within the SAS® package version 6.10. The variance components were estimated using the restricted maximum likelihood (REML) procedure. The result is presented in Table 3.

2.4 Model Validation

The fixed parts of the models were evaluated

Table 3. Regression coefficients and their t-values for the basal area increment functions. Dependent variable: ln(bai + 1), cm^2.

Variable	Scots pine		Norway spruce		Birch	
	Coefficient	t-value	Coefficient	t-value	Coefficient	t-value
Constant	0.933574	-	–2.728978	-	–1.390751	-
d	–0.173599	–8.1	–0.163038	–8.9	–0.298734	–8.2
$\ln^2(1+d)$	0.542906	11.2	0.573185	14.2	0.872871	12.2
$\ln(1+A_{13})$	–0.322222	–6.4	–0.356603	–7.7	–0.299192	–4.9
Ba	–0.103558	–18.3	–0.079372	–18.7	–0.072119	–7.4
Dgw	0.061871	12.7	0.061814	11.3	0.051759	5.8
R_d	–1.887638	–10.4	–1.203774	–7.6	–2.077699	–8.4
$\ln(1+R_d)$	4.190010	11.0	2.723129	8.2	4.427092	9.3
$Ba \times R_d$	0.061928	12.4	0.059337	13.8	0.039920	3.8
$\ln(TS_5)$	0.158676	2.1	0.676821	8.4	0.369737	3.6
Rich[a)]	0.077991	2.2	0.144772	5.0	0.143448	3.2
Poor[b)]	–0.065451	2.0	–0.142958	–3.3	–0.157092	–3.1
Clbefore	0.098786	2.3	0.087956	2.1	0.164439	2.5
Clbetween	0.096635	2.6	0.154158	4.1	0.241963	4.2
n	5620		7991		4036	
Bias correction (λ)[c)]	1.066916		1.101679		1.197957	
Estimated variance components						
Stand, $\hat{\sigma}^2$	0.0472		0.0504		0.0730	
Plot(stand), $\hat{\tau}^2$	0.0462		0.0613		0.0643	
Tree, $\hat{\theta}^2$	0.1789		0.1777		0.2947	
Total, $\hat{\kappa}^2$	0.2723		0.2894		0.4320	

[a)] Rich = 1 if the ground vegetation type on the plot is herb types or broad grass type, otherwise Rich = 0.
[b)] Poor = 1 if the ground vegetation type on the plot is dwarf-shrub types (other types than *Vaccinium myrtillus*) and lichen-cover types, otherwise Poor = 0.
[c)] When the estimated dependent variable is retransformed to bai in a deterministic setting, it should be corrected for logarithmic bias. The correction factor is: $\lambda = \Sigma(y) / \Sigma \exp(\ln(\hat{y}))$ which gives $\hat{y} = [\exp(\ln(\hat{y})) - 1] \times \lambda$

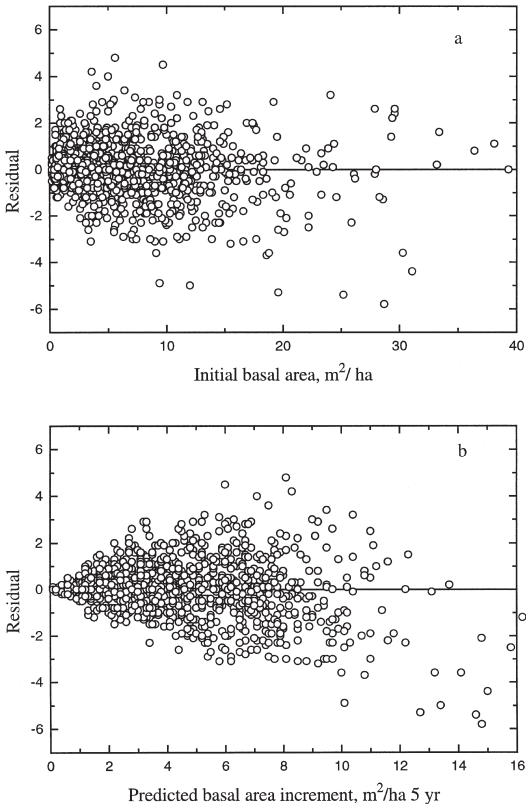

Fig. 2. Plot residuals, observed-predicted basal area increment (m^2/ha 5 yr.), as a function of initial basal area (a) and predicted basal area increment (b).

against the validation data set. No obvious bias or systematic patterns over the different independent variables were revealed in the residual analysis. The average bias in log scale was –0.02, 0.00, and –0.01 for Scots pine, Norway spruce and birch, respectively. After re-transforming the dependent variable to the natural scale (cm^2 per 5 yr.), a slight overestimation of the growth of trees in the test data was found. The average bias was –0.5, –1.7, and –3.8 percent for Scots pine, Norway spruce and birch, respectively.

When testing the functions at the plot level (aggregated tree increments for all undamaged and light damaged trees) under different conditions regarding the tree species composition, only very small and non-significant bias-terms were found. The average bias and standard deviation estimated, when the growth functions were used in a deterministic setting, were 0.0 and 1.2 m^2/ha 5 yr., respectively. The distribution of the plot level residuals (observed – predicted basal area increment), over initial plot basal area and predicted basal area increment are shown in Fig. 2.

2.5 Cross-Correlations between Tree Species

Within each projection period the estimated stochastic components corresponding to stand, plot and tree residual variation were added to the logarithmic growth prediction as normally distributed random variables with zero mean and variances ($\hat{\sigma}^2$, $\hat{\tau}^2$, $\hat{\theta}^2$) obtained from the model estimation, see Table 3.

The basal area growth models were developed for each tree species separately. It is, however, reasonable to believe that the random components of different species are correlated at the stand and plot levels. At the stand level, random weather conditions and/or macro site and stand conditions, not properly included in the model, can be the

Table 4. Correlations between the different species' random stand and plot components.

	Species		
	Scots pine/ Norway spruce	Scots pine/ Birch	Norway spruce/ Birch
Plot level, ($\hat{\rho}_p$)	0.50	0.10	0.36
Stand level, ($\hat{\rho}_s$)	0.32	0.62	0.51
Number of stands	205	165	236
Number of plots	867	702	1007
Number of trees	5557/5472	4590/3581	7841/5642

causes. At the plot level, micro stand and site conditions could lead to dependencies. To account for the cross-correlations in the simulations, their strengths had to be estimated.

The correlations (ρ) were estimated according to the definitions as shown in Eq. (3). Here, Scots pine, '*p*', and Norway spruce, '*s*', are taken as examples.

$$\text{(i) Stand level} \quad \hat{\rho}^{p,s}_{\text{stand}} = \frac{\hat{\text{cov}}\left(\varepsilon^p, \varepsilon^s\right)}{\hat{\sigma}^p \hat{\sigma}^s} \quad \text{and}$$
$$\text{(ii) Plot level} \quad \hat{\rho}^{p,s}_{\text{plot}} = \frac{\hat{\text{cov}}\left(\delta^p, \delta^s\right)}{\hat{\tau}^p \hat{\tau}^s} \tag{3}$$

The variance components were obtained from the output of the mixed linear regression (Table 3) and the covariances from a separate study of the residuals, according to what follows.

The covariances between the residuals of different species e.g., cov(ε^p, ε^s) and cov(δ^p, δ^s) were estimated using data from mixed stands. As previously described, the residual variation at tree level (e^{ts}_{ijk}) was divided into the following independent components:

$$e^{ts}_{ijk} = \varepsilon^{ts}_i + \delta^{ts}_{ij} + \gamma^{ts}_{ijk} \tag{4}$$

where
ts is an index for tree species, (Scots pine (*p*), Norway spruce (*s*), and birch spp. (*b*))
i is an index for stands, *j* an index for plots, and *k* an index for trees

From this, it follows that plot and stand level averages are obtained as:

Plot level:

$$e^{ts}_{ij.} = \varepsilon^{ts}_i + \delta^{ts}_{ij} + \frac{\sum_{k=1}^{m^{ts}_{ij}} \gamma^{ts}_{ijk}}{m^{ts}_{ij}} \tag{5}$$

Stand level:

$$e^{ts}_{i..} = \varepsilon^{ts}_i + \frac{\sum_{j=1}^{n_i} m^{ts}_{ij} \delta^{ts}_{ij}}{\sum_{j=1}^{n_i} m^{ts}_{ij}} + \frac{\sum_{j=1}^{n_i} m^{ts}_{ij} \sum_{k=1}^{m_{ij}} \gamma^{ts}_{ijk}}{\sum_{j=1}^{n_i} m^{ts}_{ij}} \tag{6}$$

where
n_i = number of plots within stand *i*
m^{ts}_{ij} = number of trees on plot *j* within stand *i*, for tree species *ts*

To obtain the covariances, the expectations

$$E\left[\sum_i \sum_j m^p_{ij} m^s_{ij} e^p_{ij.} e^s_{ij.}\right]$$

and

$$E\left[\sum_i n_i e^p_{i..} e^s_{i..}\right]$$

were developed using formulas (4–6), see Appendix 1. It follows that the covariances can be estimated as:

(i) Plot level:

$$\hat{\text{cov}}\left(\delta^p, \delta^s\right) = \frac{\sum_i n_i e^p_{i..} e^s_{i..} - \sum_i n_i \frac{\sum_i \sum_j m^p_{ij} m^s_{ij} e^p_{ij.} e^s_{ij.}}{\sum_i \sum_j m^p_{ij} m^s_{ij}}}{\sum_i n_i \frac{\sum_j m^p_{ij} m^s_{ij}}{\sum_j m^p_{ij} \sum_j m^s_{ij}} - \sum_i n_i} \tag{7}$$

(ii) Stand level:

$$\hat{\text{cov}}\left(\varepsilon^p, \varepsilon^s\right) = \frac{\sum_i \sum_j m^p_{ij} m^s_{ij} e^p_{ij.} e^s_{ij.}}{\sum_i \sum_j m^p_{ij} m^s_{ij}} - \hat{\text{cov}}\left(\delta^p, \delta^s\right) \tag{8}$$

The formulas obtained were validated using a simulation procedure in which correlated random numbers were generated and the formulas applied. The between species correlations, estimated from the real data using formulas 7 and 8, are presented in Table 4.

At the plot level, the correlation is higher between Scots pine and Norway spruce than between any of these two species and birch. At the stand level, the opposite is the case. Possibly, this could be the result of a competition between conifers and birch. A low plot correla-

tion indicates high competition and vice versa. At the stand level, the correlation can be high although the species compete, since they may grow on different plots.

2.6 Evaluations

Two main evaluations were made using the growth functions and the variance/covariance components estimated, together with the data set from the HUGIN young stand survey. Both are relevant for the case when prior distributions of timber yield are predicted within a Bayesian planning framework. First, the accuracy of the distributions was evaluated by comparing the predicted distributions with actual outcomes. Secondly, a study was made to evaluate the number of Monte-Carlo simulations needed for the estimated distributions to be reliable. The details are given below.

2.6.1 Evaluation of Predicted Distributions vs. Real Outcomes

The aim was to study how well the predicted distributions conformed to the actual outcomes of basal areas in the stands that were followed for 10 years (mainly between 1977–1987).

In each stand, the observed basal area at the end of the period was compared with the predicted distribution (obtained from 10^5 simulations). It was registered at what percentile the inventoried stand basal area was located within the distribution. If the predictions were adequate, the recorded percentiles should be uniformly distributed. This assumption was evaluated by a Chi-square test, using 10 classes of percentiles (each class covering 10% of the predicted distribution). If the predictive properties were adequate, the null hypothesis of an equal proportion of observations in each class should not be rejected.

Three different cases concerning the level of the serial correlation in the random components were tested. Although there may be reason to believe that the serial correlation varies between the different random components, no differentiation was made. The correlations tested were 0, 0.4, and 0.7.

2.6.2 Number of Monte-Carlo Simulations Needed

In applications, it is important to limit the number of simulations needed for predicting the distributions due to the time required for solving a large planning problem. Therefore, it is of interest to study the precision of the predicted distributions after varying numbers of simulations.

The continuous variable stand basal area was divided into classes of 0.1 m^2/ha width. The number of simulations when the basal area fell in each class was recorded (after 10 year forecasts). Letting the number of simulations tend towards infinity (10^6 in the study), the true distribution, f^*, according to the growth model parameters and the variance/covariance components estimated, was obtained. If a smaller number of simulations is used, the resulting distribution, $\hat{f}$, will deviate from f^*. The size of the deviation depends on where, on the true distribution, the focus is set and on what width of the classes is used.

A number of percentiles (5, 10, 25, 50, 75, 90, 95%, determined by the 0.1 m^2/ha class they belong to) of f^*, for 20 different stands, were selected for the study. At each percentile, the relative standard deviation of the proportion of observations in that particular class (0.1 m^2/ha width), given a certain number of simulations (n), was calculated as:

$$\mathrm{cvp}_{(i)} = \frac{1}{p_{(i)}}\sqrt{\frac{p_{(i)}\left(1-p_{(i)}\right)}{n-1}} \qquad (9)$$

where

$\mathrm{cvp}_{(i)}$ = relative standard error for basal area class i

$p_{(i)}$ = the true proportion in basal area class i

3 Results

3.1 Observed Basal Area vs. the Predicted Distributions

The observed and predicted basal area after 10 years growth in the 49 stands used for the evaluation was, on an average after 10^5 simulations in each stand, 9.0 and 9.2 m^2/ha, respectively. The

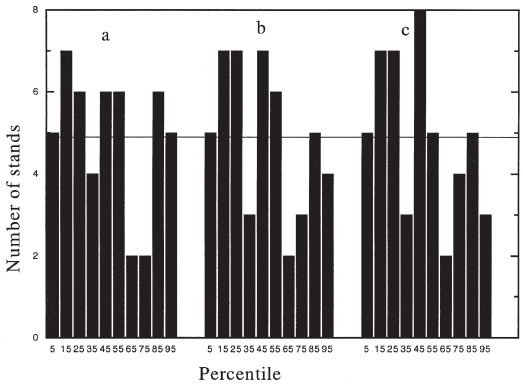

Fig. 3. Observed stand basal area within different classes of predicted percentiles of basal area distributions. (a) without serial correlation, (b) serial correlation (ρ=0.4) and (c) serial correlation (ρ=0.7).

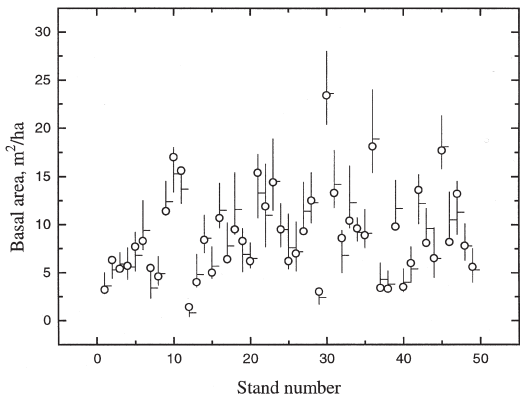

Fig. 4. Observed (○) basal area within the predicted basal area distribution, given by the 5th, 50th, and 95th percentiles.

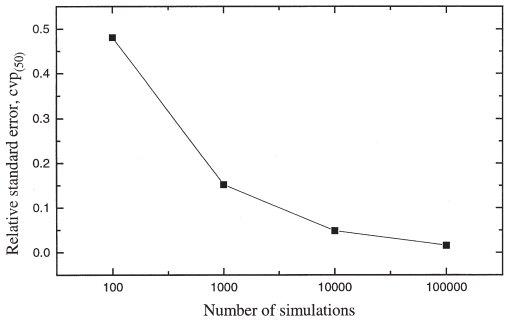

Fig. 5. Relative standard error after different numbers of simulations, for the proportion observations falling in the basal area class corresponding to the median, $cvp_{(50)}$, of the true distribution.

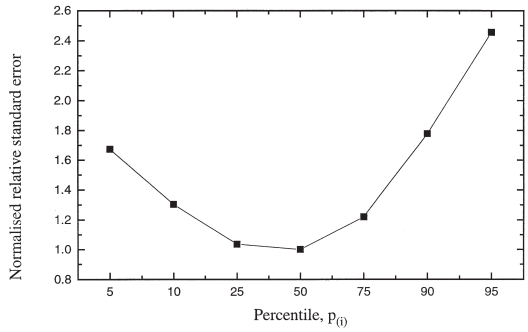

Fig. 6. Normalised relative standard error ($cvp_{(i)}$ / $cvp_{(50)}$) at different classes of percentiles of the basal area distribution. This relation does not depend of the number of simulations.

distribution of percentiles in which the observed basal area was registered should be uniform if the predictive properties of the functions were correct. Results concerning this, for the three different cases of serial correlation, are shown in Fig. 3.

According to the Chi-square test statistics, the null hypothesis of an equal proportion of observations in each class can not be rejected in any of the cases (the Chi-square test results in the p-values 0.79 (χ^2=5.5), 0.71 (χ^2=6.3) and 0.62 (χ^2=7.1) for the different levels of serial correlation 0, 0.4 and 0.7, respectively). Consequently, there is no evidence that the assumption about a uniform distribution should be rejected in any of the cases. According to Fig. 3, the case without serial correlation appears to provide the best fit.

Stand-wise results in terms of plots showing the observed basal area and the 5th, 50th, and 95th percentiles of the predicted distributions are given in Fig. 4 (for the case of no serial correlation).

3.2 Number of Monte-Carlo Simulations Needed

As expected, the results revealed major differences regarding the magnitude of the estimated relative standard errors, an average of 20 stands were used, when varying the number of simulations (Fig. 5) and also with regard to which part of the estimated distribution focus was set on (Fig. 6). The projected probability distributions were positively skewed which resulted in larger relative standard errors in the percentiles above the median as compared with those below. To achieve basal area distributions (decomposed in 0.1 m^2 classes) projected 10 years, with a relative standard error (cvp) less than 0.05 covering 90 percent of the distribution (5th–95th percentile) approximately 10^5 simulations were needed. As can be seen in Figs. 5 and 6, about 10 000 simulations lead to a corresponding precision of about 0.1.

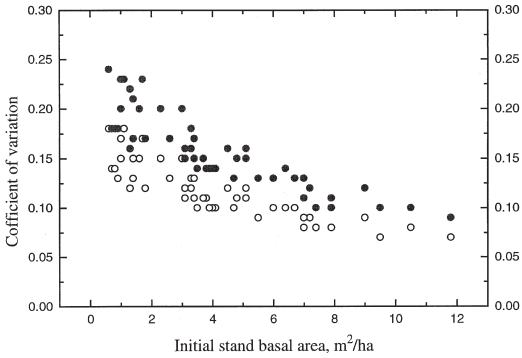

Fig. 7. Coefficient of variation (CV) for the estimated distributions, (○) without serial correlation and (●) with serial correlation $\rho = 0.7$ for all random components.

4 Discussion

The study focuses on how to estimate within-stand basal area distributions with single tree growth models, emphasising the spatial correlation in data. By using a mixed model approach, spatial dependencies in data were accounted for in the parameter estimation, and the sizes of the variance components of the random effects were estimated. The random effects were added to the fixed effects in Monte-Carlo simulations, and predicted distributions of stand basal area were obtained. In the evaluations, the distributions appeared to give a correct representation of the actual uncertainty in predicted data. However, the evaluation period was quite short (10 years) and the effects of possible serial correlation would increase over time. The sensitivity of the projections to serial correlation is illustrated in Fig. 7. In the figure, the coefficient of variation (CV; standard deviation/mean) of the predicted distributions after 20 years, based on 10^4 simulations, is presented for the cases with and without serial correlation. The serial correlation was assumed to be 0.7 for all components. On average the CV of estimated basal area distributions increased from 0.116 to 0.154 when serial correlation was introduced.

In all models, the random stand and plot effects were significant, indicating that growth varies randomly from stand to stand and from plot to plot within a stand. The estimated variance components (Table 3) for the stand and plot random effects accounted for about 35 percent of the total residual variance. The variance of the random parameters was greatest for birch and lowest for pine.

One drawback with the study was that measurement errors were not explicitly accounted for. Although the data collection was made for research purposes and, consequently, the survey was carefully carried out, there is no reason to believe that the data used were free from measurement errors. The result of such errors would be a too large variance component at the tree level, and to some extent reduced correlations between the random components of different species, mainly at the plot level, (see e.g., Stage and Wykoff 1993)

4.1 Bayesian Application

By predicting distributions of forest yield rather than point estimates, a Bayesian approach to management planning can be adopted. Since data about the state of forests are almost always uncer-

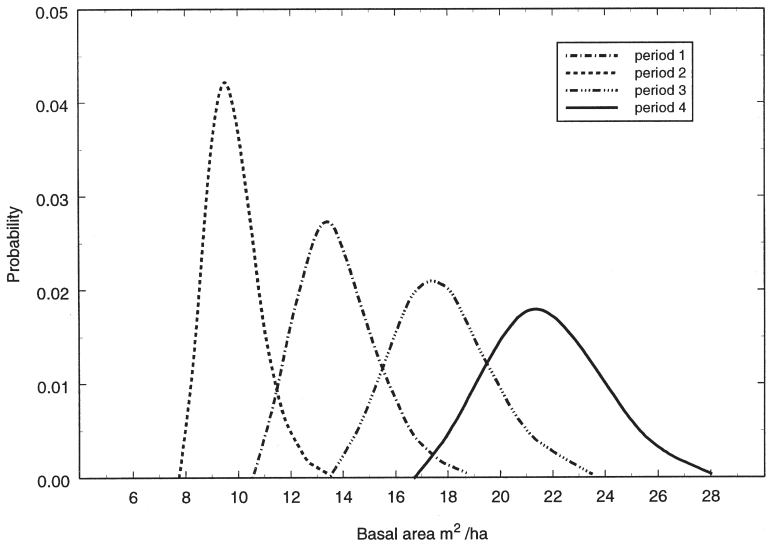

Fig. 8. An example of a 20 years projection (four periods, per 1–4) of within-stand basal area probability distributions. Initial basal area 6.4 m^2/ha.

tain, and since inventories are costly, it is wise to continuously update not only the data about the forest state, but also the precision of the state estimates. An example is shown in Fig. 8, in which a 20-year projection of the within-stand basal area distribution is made from a perfectly known initial state. It is quite clear that the usefulness of a mere point estimate can be questioned after only a few periods of growth. In practice, it would perhaps not be wise to present distributions to a manager, but rather some derived data quality measure.

By using probability distributions in forest management, decisions can be evaluated considering the whole range of possible states according to the standard methods of Bayesian decision theory. E.g., if $l(A_i \mid \theta)$ is the loss of a certain action, A_i, given that the true state is θ, and $p(\theta)$ is the probability density function of the forest state, the expected loss of the action is:

$$L(A_i) = \int l(A_i|\theta)p(\theta)d\theta \qquad (10)$$

When different actions are possible, the one that leads to a minimum expected loss, or perhaps a 'safe' outcome, can be selected. In case the distributions are wide, the optimal decision is often a compromise. Had the state been known with better accuracy, other decisions would have been more suitable. As an example consider Fig. 9, which illustrates the within-stand basal area probability distribution after a 20-year projection (cf., Fig. 8). Assume that optimal decisions about the stand management are dependent on the stand basal area as illustrated in Fig. 9.

To determine the optimal decision based on the available information, $p(\theta)$, one would typically apply (10) for each potential action (A_0, A_1 and A_2) to evaluate which one leads to the lowest expected loss.

By providing distributions rather than point estimates it can also be assessed whether or not a new inventory, to update the information about the state of the forest, would be worth the cost. If an inventory is carried out, a new probability distribution of basal area in the stand is obtained, by applying Bayes' theorem (e.g., Gamerman 1997). The prior (projected) distribution, $p(\theta)$, is then combined with the sampling distribution, $f(x \mid \theta)$, to obtain the new, posterior, distribution $p(\theta \mid x)$. Bayes' theorem can be written as:

$$p(\theta|x) = \frac{f(x|\theta)p(\theta)}{\int f(x|\theta)p(\theta)d\theta} \qquad (11)$$

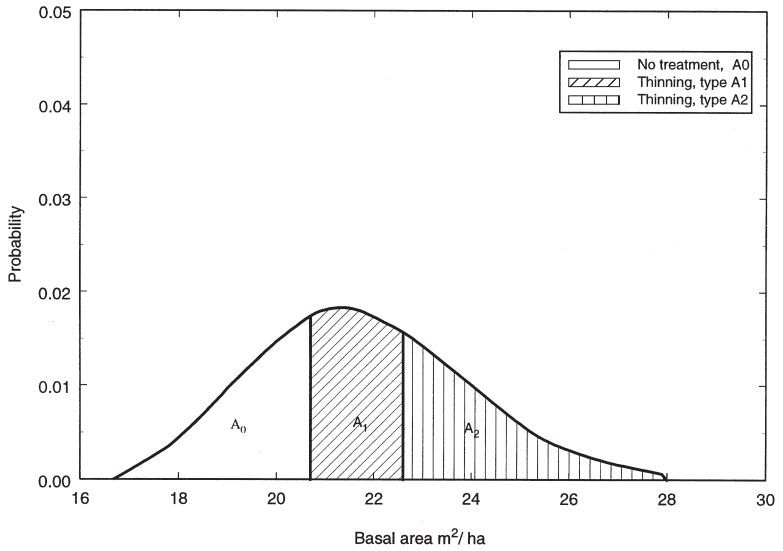

Fig. 9. An illustration of a fictitious optimal thinning decision, depending on the basal area in a stand

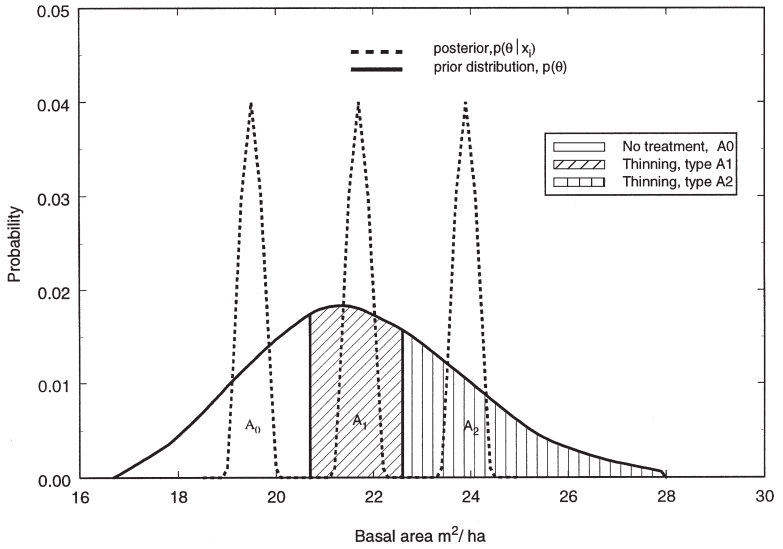

Fig. 10. An illustration of posterior distributions following three hypothetical outcomes of an inventory. For these particular distributions, the optimal decisions no longer need to be compromises.

The potential value added by an inventory stems from the benefits from better decisions due to the new information. Consider Fig. 10 as an example. Here, the posterior distributions following three different hypothetical outcomes of the inventory are depicted. The increased accuracy

of the posterior information is reflected in the narrow posterior distributions. The optimal decisions based on the posterior information no longer need to be compromises as was the case when the decision was based on the prior information. More details about this can be found in Ståhl et al. (1994).

Often, stand data are collected in large campaigns during which most old data are disposed of. Such campaigns are, at least in Sweden, made every 10–15 years. An alternative, for which the kind of predictions made in this paper should be very useful, would be to make stand-wise calculations to determine at what point in time a new inventory should be carried out.

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Appendix 1

Below, the details of the derivation of formulas (7) and (8) are shown (for abbreviations, see the main text). To arrive at the covariance estimators, the expectations

$$E\left[\sum_i \sum_j m_{ij}^p m_{ij}^s e_{ij.}^p e_{ij.}^s\right] \text{ and } E\left[\sum_i n_i e_{i..}^p e_{i..}^s\right]$$

were first developed using formulas (4–6). As in the main text, the tree species Scots pine ('*p*') and Norway spruce ('*s*') are used as examples. By deriving expectations of products of this kind, the covariances of interest will appear and the resulting equations can be solved for these covariances. The products were weighted by the number of plots and trees, in order to increase the influence of stands, where the components of interest are likely to show less random variation.

From the model specification, it is reasonable to assume that expectations of the kind

$$E\left[\varepsilon_i^p \delta_{ij}^s\right], E\left[\varepsilon_i^p \gamma_{ijk}^s\right], E\left[\delta_{ij}^p \varepsilon_i^s\right], E\left[\delta_{ij}^p \gamma_{ijk}^s\right], E\left[\varepsilon_i^s \gamma_{ijk}^p\right], E\left[\delta_{ij}^s \gamma_{ijk}^p\right], \text{ and } E\left[\gamma_{ijk}^p \gamma_{ijk}^s\right]$$

are all zero.

The first expectation is developed as:

$$E\left[\sum_i \sum_j m_{ij}^p m_{ij}^s e_{ij.}^p e_{ij.}^s\right] = E\left[\sum_i \sum_j m_{ij}^p m_{ij}^s (\varepsilon_i^p + \delta_{ij}^p + \frac{\sum_k \gamma_{ijk}^p}{m_{ij}^p})(\varepsilon_i^s + \delta_{ij}^s + \frac{\sum_k \gamma_{ijk}^s}{m_{ij}^s})\right] \tag{A1}$$

$$= \sum_i \sum_j m_{ij}^p m_{ij}^s (\text{cov}(\varepsilon^p, \varepsilon^s) + \text{cov}(\delta^p, \delta^s))$$

The second expectation is developed as:

$$E\left[\sum_i n_i e_{i..}^p e_{i..}^s\right] = E\left[\sum_i n_i (\varepsilon_i^p + \frac{\sum_j m_{ij}^p \delta_{ij}^p}{\sum_j m_{ij}^p} + \frac{\sum_j m_{ij}^p \sum_k \gamma_{ijk}^p}{\sum_j m_{ij}^p})(\varepsilon_i^s + \frac{\sum_j m_{ij}^s \delta_{ij}^s}{\sum_j m_{ij}^s} + \frac{\sum_j m_{ij}^s \sum_k \gamma_{ijk}^s}{\sum_j m_{ij}^s})\right] \tag{A2}$$

$$= \text{cov}(\varepsilon^p, \varepsilon^s) \sum_i n_i + \text{cov}(\delta^p, \delta^s) \sum_i n_i \frac{\sum_j m_{ij}^p m_{ij}^s}{\sum_j m_{ij}^p \sum_j m_{ij}^s}$$

The equation system (A1) and (A2) is then solved for the covariance terms, which gives:

$$\text{cov}(\varepsilon^p, \varepsilon^s) = \frac{E\left[\sum_i \sum_j m_{ij}^p m_{ij}^s e_{ij.}^p e_{ij.}^s\right]}{\sum_i \sum_j m_{ij}^p m_{ij}^s} - \text{cov}(\delta^p, \delta^s) \tag{A3}$$

Substituting $\mathrm{cov}(\varepsilon^p, \varepsilon^s)$ in Eq. (A2) with Eq. (A3) gives:

$$E\left[\sum_i n_i e^p_{i..} e^s_{i..}\right] = \left(\frac{E\left[\sum_i \sum_j m^p_{ij} m^s_{ij} e^p_{ij.} e^s_{ij.}\right]}{\sum_i \sum_j m^p_{ij} m^s_{ij}}\right) \sum_i n_i - \mathrm{cov}\left(\delta^p, \delta^s\right) \sum_i n_i + \mathrm{cov}\left(\delta^p, \delta^s\right) \sum_i n_i \frac{\sum_j m^p_{ij} m^s_{ij}}{\sum_j m^p_{ij} \sum_j m^s_{ij}}$$

which implies that:

$$\mathrm{cov}\left(\delta^p, \delta^s\right) = \frac{E\left[\sum_i n_i e^p_{i..} e^s_{i..}\right] - \sum_i n_i \frac{E\left[\sum_i \sum_j m^p_{ij} m^s_{ij} e^p_{ij.} e^s_{ij.}\right]}{\sum_i \sum_j m^p_{ij} m^s_{ij}}}{\sum_i n_i \frac{\sum_j m^p_{ij} m^s_{ij}}{\sum_j m^p_{ij} \sum_j m^s_{ij}} - \sum_i n_i} \qquad \text{(A4)}$$

This expression (A4) is inserted in (A3) to derive the covariance at the stand level. Then, using the plug-in estimates to replace the expected values in (A3) and (A4) leads to the covariance estimates (7) and (8), presented in the main text.