Estimating model- and sampling-related uncertainty in large-area growth predictions

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Abstract

Estimating uncertainty in forest growth predictions is essential to support large-area policies and decisions. The aim of this study was to estimate model and sampling uncertainties at a regional level. To do this, we generated forest growth predictions for three ecotypes in the Bas-Saint-Laurent region of Quebec, Canada. Predictions were generated using the ARTEMIS growth model that allows for stochasticity in some of the sub-models. We used a bootstrap hybrid estimator to estimate the variances arising from the model and the sampling. Moreover, the variance due to the model was further decomposed to determine which dynamic sub-model induced the greatest share of variance. Results revealed that sampling accounted for most of the variance in short-term predictions. In long-term predictions, the model contribution turned out to be as important as that of the sampling. The variance decomposition per sub-model indicated that the mortality sub-model induced the highest variability in the predictions. These results were consistent for the three ecotypes. We recommend that efforts in variance reduction focus on increasing the sample size in short-term predictions and on improving the mortality sub-model in long-term predictions.

Hybrid inference, regional level, variance decomposition, stochastic models, Monte Carlo techniques.

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1 Introduction

Knowledge of forest growth is important for assessing sustainable forest management (Peng, 2000), understanding the effects of climate change on forest dynamics (Ameztegui et al., 2015) and establishing changes in ecosystem productivity and biomass accumulation (Vanclay, 1994; Paré et al., 2016). Given those needs, it is not surprising that forest growth models have become indispensable tools for forest managers and policy makers. Models are a simplification of complex phenomena and as such they are subject to prediction errors. Model evaluation is then required to ensure user confidence. A thorough evaluation involves examinations of model design, fitting and implementation (Vanclay and Skovsgaard, 1997).

Since the mid-20th century, forest growth models have increased in complexity in order to meet stakeholder demands, including not only economical aspects but ecological and social issues as well (Porté and Bartelink, 2002). Multi-objective models have been developed. Nevertheless, this increasing complexity has non-negligible consequences (Pretzsch, 2009). A greater number of model parameters, random effects and interactions will increase prediction uncertainty (Walker et al., 2003).

Uncertainty is described as the lack of knowledge and random variation that arises from multiple sources of errors (Aven et al., 2014). Error propagation provides insights into uncertainties in predictions. It computes how much of output predictions are uncertain due to error propagation from the input model (Berger et al., 2014; Sexton et al., 2015). Previous studies about uncertainties in forest growth models have already highlighted the fact that sufficient information is frequently missing or incomplete, especially when it comes to propagating the errors from the tree to stand, regional or national levels (Phillips et al., 2000).

Over the last two decades, there has been an increasing demand for large-area predictions at the regional and national levels mainly due to international agreements concerning climate change (Ciais et al., 2008; Groen et al., 2013). Uncertainty estimation of large-area predictions is not straightforward for several reasons. Two major sources of uncertainty can be identified: the model and the sampling. Model uncertainty arises from model misspecification, the estimation of model coefficients and the residual variation (Kangas, 1999). Sampling uncertainty is due to the fact that the initial forest conditions are usually unknown. Instead, they are estimated from a forest inventory, leading to the propagation of sampling errors when large-area predictions are carried out (Breidenbach et al., 2014).

The aforementioned context is one of hybrid inference. The term hybrid was coined by Corona et al. (2014) and refers to the fact that the inferential process relies on both a model and a probability design (McRoberts et al., 2016). It arises when the variable of interest is not measured or not measurable, such as future forest growth, and when the explanatory variables are only available from samples and not for the whole population (Fortin et al., 2016). Some authors have already applied hybrid estimators in the context of large-area estimation of volume, biomass and carbon (e.g., Stahl et al., 2011; Healey et al., 2012; Saarela et al., 2015; Stahl et al., 2016; McRoberts et al., 2016). When working with complex models such as tree-level growth models, current analytic hybrid estimators, i.e., those based on algebra (e.g., Stahl et al., 2011), can rarely be applied. An alternative consists in using bootstrap hybrid estimators (Fortin et al., 2018).

Quantifying sampling and model errors of large-area growth predictions is essential since it can help us identify which issues need to be addressed in order to reduce the uncertainty of

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the predictions. Previous studies on large-area estimates of volume and biomass have shown that the major source of uncertainty originated from the sampling (Breidenbach et al., 2014; Stahl et al., 2014; McRoberts and Westfall, 2014). However, the use of growth models in the context of hybrid inference adds a temporal variability. Kangas (1999) reported that uncertainty increased along with projection length. Thus, the contribution of both sampling and models to prediction uncertainty may also change along the projection length. To the best of our knowledge, this temporal variability has not been addressed, with the notable exception of Condés and McRoberts (2017) who worked on short-term predictions. Moreover, tree-level growth models are complex when compared to stand-level models since they include many sub-models. This system of sub-models follows the dynamic of individual tree development through a temporal and spatial frame (Pretzch et al., 2008). Because mortality and recruitment are highly stochastic (Sheil and May, 1996), it could be anticipated that they would contribute more to the total uncertainty. Identifying which one of the sub-models contributes more uncertainty could help to improve models, understand forest dynamics and reduce prediction uncertainty. As far as we know, this has not been addressed yet.

The aim of this study was to estimate uncertainty in growth predictions at the level of a large area. To do this, we worked on two hypotheses: (i) over long simulation periods, i.e., a 100-year prediction, model uncertainty becomes greater than sampling uncertainty; (ii) among the model components, mortality is the major contributor to prediction uncertainty, then followed by recruitment. To confirm or invalidate these two hypotheses, we aimed at decomposing the total prediction variance into a model and sampling component that was made possible by using a bootstrap hybrid estimator. Secondly, through a variance decomposition approach, the prediction uncertainty was also decomposed into sub-models (i.e., growth, mortality and recruitment) in order to assess which one contributed the most to the variance of large-area growth predictions. We worked with the ARTEMIS tree-level growth model (Fortin and Langevin, 2012), which was used to generate large-area predictions for the Bas-Saint-Laurent region in Quebec, Canada.

2 Material and methods

2.1 Growth model

The 2009 version of the ARTEMIS distance-independent tree-level growth model was built, fitted and evaluated using data from the network of permanent plots of Quebec's provincial forest inventory. This network consists of 12,570 randomly located sample plots that were established in Quebec's commercial forests and that has been measured since the 1970s. ARTEMIS takes the vast majority of the forest types in Quebec into account (Fortin and Langevin, 2010, 2012).

The model consists of four dynamic and two static sub-models (Fig. 1). The dynamic parts are those typical of population dynamic models: a mortality sub-model, a diameter increment sub-model for survivor trees, and two sub-models that predict the number and the diameter at breast height (DBH, 1.3 m in height) of the recruits, respectively. The static sub-models predict tree height and commercial volume. All sub-models are of the linear or generalized linear type. The model is based on 10-year growth intervals. Longer predictions are obtained through an iterative procedure, the result of the previous interval being reinserted in the model. Readers are referred to Fortin and Langevin (2010, 2012) for further details on the model.

ARTEMIS growth predictions are based on a wide range of explanatory variables that can be retrieved from the compilation of forest inventories in Quebec: tree species, harvest occurrence (yes/no), spruce budworm defoliation (yes/no), stem density (tree ha^{-1}), basal area (m^{2}ha^{-1}) and forest type. ARTEMIS also makes use of climatic variables, such as the 1971-2000 mean annual precipitation (mm) and mean annual temperature (°C). These climate variables can be estimated using the BioSIM application (Régnière et al., 2010).

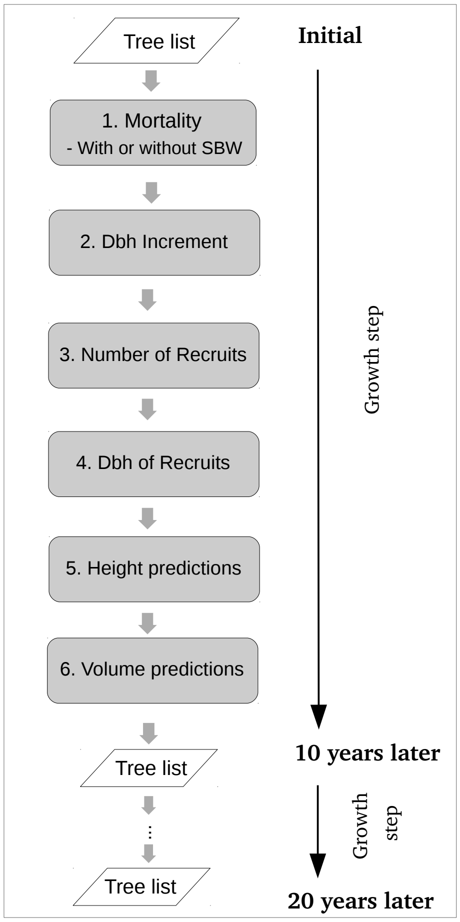

Figure 1: Structure of ARTEMIS-2009 simulation system considering an iterative process. Rectangles are for models.

ARTEMIS can predict forest growth either in a deterministic or stochastic fashion (Fortin and Langevin, 2010), depending on the user's decision. Stochastic predictions rely on the Monte Carlo technique (Rubinstein and Kroese, 2007) and they can be either fully or partially stochastic. The full stochastic mode assumes that all the sub-models are stochastic. In contrast, the partial stochastic mode makes it possible to disable the stochasticity in the selected sub-models. Predictions are generated at tree level, and the plot-level outcome can be obtained by aggregating tree-level predictions. The model was also designed to handle many plots at the same time since the usual input data were expected to come from forest inventories. ARTEMIS has been used for different applications, from simple productivity assessment to the comparison of different silviculture options (e.g., Fortin and Langevin, 2012; Fortin, 2014; Laliberté et al., 2016).

2.2 Input dataset

The input data we used to make large-area predictions also came from the provincial network of permanent plots of Quebec's Ministry of Forests, Wildlife and Parks (MFWP). Since our focus was to generate regional-level growth predictions, we kept only the measurements from the Bas-Saint-Laurent region, which covers an area of 28,401 km^2 and two vegetations zones: the northern temperate and the boreal zones (Poirier et al., 2013). The forest composition of the Bas-Saint-Laurent region made it possible to perform predictions for different forest types, since it encompasses broadleaved, mixed and coniferous stands. Broadleaved and mixed forests are mainly composed of sugar maple (*Acer saccharum* Marsh.), yellow birch (*Betula alleghaniensis* Britton), balsam fir (*Abies balsamea* Mill.) and white spruce (*Picea glauca* Voss). Coniferous stands are dominated by balsam fir, white and black spruce (*Picea mariana* Britton) with a minor component of white birch (*Betula papyrifera* Marsh.) and trembling aspen (*Populus tremuloides* Michx.) (Poirier et al., 2013). Moreover, this region has been exploited for timber since the beginning of the 19th century, and for this reason, it is of historical importance for forestry in Quebec Boucher et al. (2009). This first region-based screening resulted in 1,572 plot measurements that covered the period from 1975 to 2012. We chose the year for which we had the largest sample size, 2003, with a total of 393 plots.

The subsequent screening took the ecotype into account. We used the current ecological classification system used by the MFWP, which is based on the physical characteristics of the site, forest dynamics and its structural elements (Saucier et al., 2009, p. 186-205). Since there were too many ecotypes, we decided to keep three ecotypes that represented the diversity of forest stand composition and for which we had the largest sample sizes. We therefore worked on the following three ecotypes: sugar maple-yellow birch, balsam fir-white birch and balsam fir-white cedar. For convenience, we will refer to these three ecotypes as the broadleaved, mixed and coniferous ecotypes, respectively. The final dataset contained 188 plots.

In each of these 400-m^2 plots, all trees with DBH equal to or greater than 9.1 cm were tagged for individual monitoring. All explanatory variables required by ARTEMIS were available from the compilation of the inventory data. A summary of the dataset and the study area is provided in Table 1. The spatial distribution of the plots is shown in Fig. 2.

Table 1: Summary of study area and sample plots. Area is the total area occupied for each one of the three ecotypes in the Bas-Saint-Laurent region. The values in parentheses show the range of the variable.

Ecotype	Attribute	Values
Broadleaved	Number of plots	70
	Area ($\times 10^6$ ha)	5.524
	Basal area ($m^2 ha^{-1}$)	19.7 (1.0-38.9)
	Stem density (tree ha^{-1})	451 (125-1350)
Mixed	Number of plots	96
	Area ($\times 10^6$ ha)	39.735
	Basal area ($m^2 ha^{-1}$)	28.2 (0.2-47.0)
	Stem density (tree ha^{-1})	994 (35-2600)
Coniferous	Number of plots	22
	Area ($\times 10^6$ ha)	6.045
	Basal area ($m^2 ha^{-1}$)	30.6 (0.6-46.0)
	Stem density (tree ha^{-1})	800 (66 - 1691)

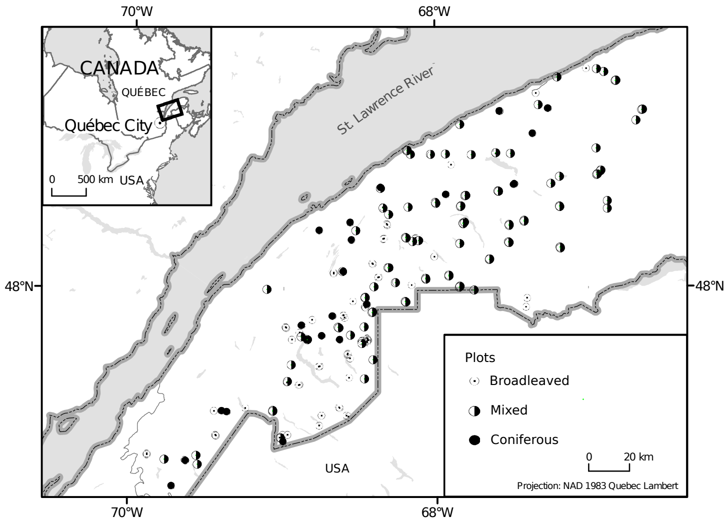

Figure 2: Distribution of the permanent plots that compose the input dataset we used in Bas-Saint-Laurent.

2.3 Simulation framework

We chose to quantify the variance of large-area growth predictions in terms of basal area. The simulation framework consisted of 100-year growth predictions running from 2003 to 2103 based on 10,000 Monte Carlo realizations. These predictions were generated for each one of the three aforementioned ecotypes and excluded all exogenous disturbances such as harvesting, pest outbreaks and fires. Additionally, we considered that the mean temperature and the mean precipitation would increase by 2°C and 5%, respectively, over the 21^{st} century. This climate change scenario is in line with the representative concentration pathway (RCP) 2.6 of the IPCC (IPCC, 2013, p. 40).

First, a large-area prediction was generated for each ecotype using the full stochastic mode, i.e., by considering the stochasticity of all ARTEMIS sub-models. The bootstrap variance estimator that is described in the next section made it possible to split the total variance of large-area predictions into a sampling- and a model-related component.

We then generated a series of large-area predictions using the partial stochastic mode, with the aim of decomposing the total variance. Using the above framework, we alternately disabled the stochasticity of the mortality, diameter increment and recruitment sub-models, while keeping the other sub-models in a stochastic mode. The same bootstrap variance estimator was used.

Basal area predictions at the plot level were obtained by aggregating the tree-level predicted basal areas since they were produced by ARTEMIS. The predictions were run on the CAPSIS platform (Dufour-Kowalski et al., 2012).

2.4 Hybrid estimator

Fortin et al. (2018) proposed a bootstrap variance estimator that can be used in the context of hybrid inference with complex models, such as tree-level growth models. This variance estimator is the one we used and it is briefly described in the next paragraphs.

Under the assumption of a simple random sampling design without replacement with equal inclusion probabilities, the sample mean is an unbiased estimator of the mean of the population (μ):

$$\hat{\mu} = \frac{1}{n} \sum_{i \in s} y_i \tag{1}$$

where s is the sample, y_i is the basal area in plot i, and n is the sample size. The design variance of this estimator is:

$$\hat{\mathbb{V}}_d(\hat{\mu}) = \left(1 - \frac{n}{N}\right) \frac{\sum_{i \in s}(y_i - \hat{\mu})^2}{n(n-1)} \tag{2}$$

where N is the number of units in the population.

Because future basal areas are unknown by definition, we relied on ARTEMIS to obtain basal area predictions ($\hat{y}_i$). Propagating the errors in the parameter estimates, the random effects and the residual errors in the two previous estimators is not straightforward and must be done using the Monte Carlo technique. For a particular realization b, random deviates are generated to account for these different sources of model-related uncertainty and realized plot basal areas are obtained. An estimate of the mean and its variance can then be obtained from Eqs. 1 and 2. After generating a large number of realizations, the bootstrap estimator of the mean is:

$$\hat{\mu}_{\mathrm{BS}} = \frac{1}{B} \sum_{b=1}^{B} \hat{\mu}_b \tag{3}$$

where $\hat{\mu}_b$ is the sample mean obtained from realization b, and B is the total number of realizations.

Consistent with Fortin et al. (2018), an unbiased bootstrap variance estimator is:

$$\hat{\mathbb{V}}(\hat{\mu}_{\mathrm{BS}}) = \frac{\sum_{b=1}^{B} (\hat{\mu}_b - \hat{\mu}_{\mathrm{BS}})^2}{B} + 2\hat{\mathbb{V}}_d(\hat{\mu}_{\bar{y}}) - \frac{\sum_{b=1}^{B} \hat{\mathbb{V}}_d(\hat{\mu}_b)}{B} \tag{4}$$

where $\hat{\mathbb{V}}_d(\hat{\mu}_{\bar{y}})$ can be obtained by substituting $\bar{y}_i = \sum_{b=1}^{B} \frac{y_{i,b}}{B}$ and $\hat{\mu}_{\mathrm{BS}}$ for y_i and $\hat{\mu}$, respectively, in the variance estimator found in Eq. 2. The term $\hat{\mathbb{V}}_d(\hat{\mu}_{\bar{y}})$ represents the contribution of the sampling to the total variance. The model contribution can be calculated as $\hat{\mathbb{V}}(\hat{\mu}_{\mathrm{BS}}) - \hat{\mathbb{V}}_d(\hat{\mu}_{\bar{y}})$. Equations 3 and 4 were used to obtain the model- and sampling-related variance components of our large-area growth predictions.

3 Results & Discussion

This study focused on estimating uncertainties arising from large-area growth predictions based on tree-level growth models. First, the predicted basal areas are shown in Fig. 3 considering the full and partial stochastic modes for the three ecotypes. For all ecotypes, the basal area predictions revealed differences depending on whether they were fully or partially stochastic. These differences were only perceptible after 2050 and slightly increased until 2103.

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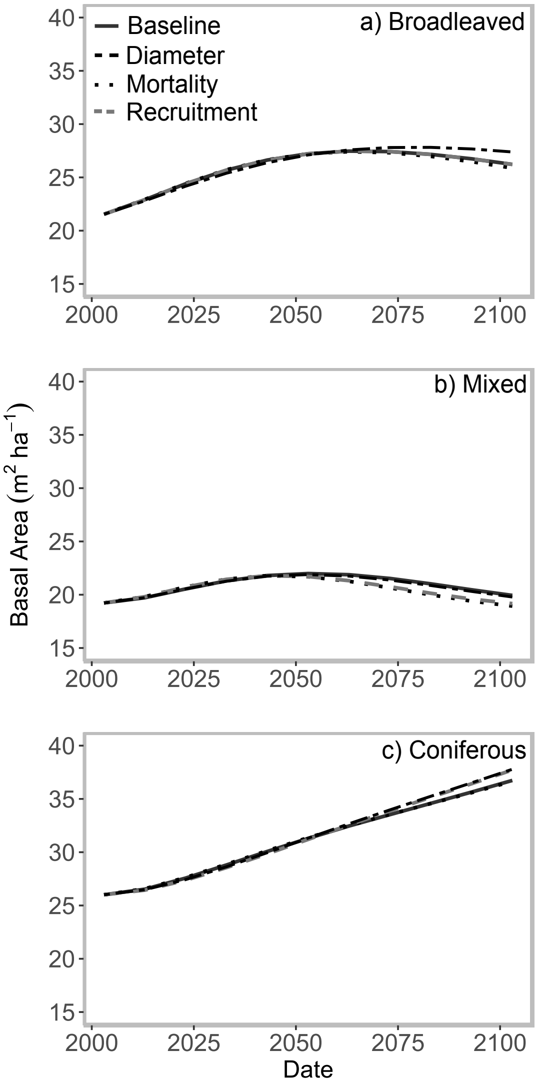

Figure 3: Mean predicted basal area (m^2ha^{-1}) illustrated for each ecotype. The growth curves are related with the full stochastic and the partial stochastic predictions (disabling diameter, mortality and recruitment sub-models).

The conifer ecotype presented the highest growth, followed by the broadleaved and the mixed ecotypes. For the broadleaved and mixed ecotypes, the predicted basal areas showed a quadratic pattern with an optimum around 2050 and 2060. While the broadleaved ecotype remained close to the optimum until 2103, the mixed ecotype slightly declined. For coniferous ecotype, a steady growth was predicted.

The contribution of the model- and sampling-related variance components in the full stochastic predictions are shown in Table 2 and Fig. 4. The results were consistent for the three ecotypes. The total variance sharply decreased during the first half of the projection and then stabilized until the end. For the broadleaved and the coniferous ecotypes, the total variance at the end of the projection was half that of the beginning. For the mixed ecotype, the variance decreased by 95% over the projection length.

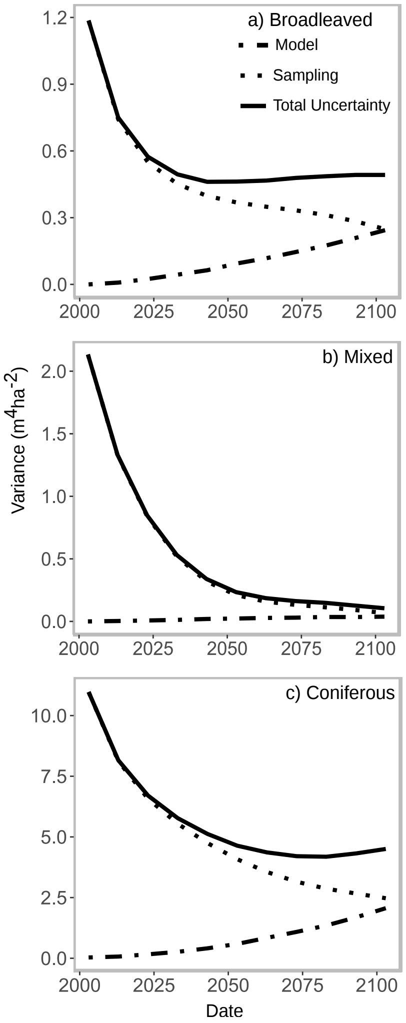

Figure 4: Contribution of the model and the sampling to the total variance of the full stochastic predictions in basal area.

Table 2: Model- and sampling-related variance contribution ($\mathrm{m}^4\mathrm{ha}^{-2}$) in the full stochastic predictions per ecotype. The relative contribution appears in parentheses.

Ecotype	Year	Model-related	Sampling-related	Total Variance
Broadleaved	2003	0.000 (0.0%)	1.186 (100.0%)	1.186
	2013	0.008 (1.1%)	0.742 (98.9%)	0.750
	2023	0.024 (4.2%)	0.550 (95.8%)	0.574
	2033	0.044 (8.9%)	0.451 (91.1%)	0.495
	2043	0.064 (13.8%)	0.398 (86.2%)	0.461
	2053	0.094 (20.4%)	0.368 (79.6%)	0.462
	2063	0.118 (25.2%)	0.349 (74.8%)	0.467
	2073	0.146 (30.5%)	0.333 (69.5%)	0.479
	2083	0.175 (35.9%)	0.312 (64.1%)	0.486
	2093	0.209 (42.4%)	0.284 (57.6%)	0.492
	2103	0.244 (49.5%)	0.248 (50.5%)	0.492
Mixed	2003	0.000 (0.0%)	2.133 (100.0%)	2.133
	2013	0.003 (0.3%)	1.327 (99.7%)	1.331
	2023	0.007 (0.9%)	0.847 (99.1%)	0.847
	2033	0.012 (2.3%)	0.531 (97.7%)	0.531
	2043	0.020 (5.8%)	0.339 (94.2%)	0.339
	2053	0.023 (9.8%)	0.234 (90.2%)	0.234
	2063	0.028 (15.0%)	0.186 (85.0%)	0.186
	2073	0.030 (18.5%)	0.132 (81.5%)	0.163
	2083	0.036 (23.9%)	0.113 (76.1%)	0.149
	2093	0.035 (27.6%)	0.092 (72.4%)	0.127
	2103	0.038 (36.2%)	0.067 (63.8%)	0.105
Coniferous	2003	0.000 (0.0%)	10.939 (100.0%)	10.939
	2013	0.037 (0.5%)	8.089 (99.5%)	8.126
	2023	0.129 (1.9%)	6.541 (98.1%)	6.670
	2033	0.232 (4.0%)	5.508 (96.0%)	5.740
	2043	0.377 (7.4%)	4.713 (92.6%)	5.090
	2053	0.557 (12.1%)	4.048 (87.9%)	4.606
	2063	0.808 (18.7%)	3.521 (81.3%)	4.329
	2073	1.053 (25.2%)	3.119 (74.8%)	4.173
	2083	1.317 (31.7%)	2.834 (68.3%)	4.151
	2093	1.654 (38.6%)	2.633 (61.4%)	4.287
	2103	2.031 (45.4%)	2.440 (54.6%)	4.471

The sampling showed the greatest contribution to the total variance. This contribution decreased all along the projection length and more sharply during the first half. It mainly explained the decrease in the total variance. The model-related variance represented a smaller proportion of the total variance, with no contribution at all at the beginning of the projection. However, this variance increased along the projection length until it represented almost half the total variance at the end of the projection. More precisely, the model-related variances represented 49.5%, 45.4% and 36.2% of the 2103 variance in the broadleaved, mixed and coniferous ecotypes, respectively.

As evoked in our first hypothesis, we expected that the model-related variance would increase over time. Considering the increasing pattern for all ecotypes, there was no evidence

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that the model-related variance would not represent the greatest share of the prediction variance if the projection length was longer than 100 years. Kangas (1998) also described an increasing model-related variance in long-term volume predictions at the stand level.

The decreasing pattern of the sampling-related variance over time was the main reason for which the total variance also decreased. This is probably due to the convergence of the feed-forward coupled model, which balances itself and reaches a steady state in long-term predictions (Vanclay, 1994, p.46), especially in the absence of disturbances. Moreover, the sampling-related variance defined in Fortin et al. (2018) is actually the designed-based variance of the estimator of the mean calculated from mean predicted basal areas and not from observed basal areas. The model convergence effect yields plot-level predicted values that are more alike over time. However, this does not mean that the forest will be more homogeneous in the future. While the variance of the predicted basal areas decreases over time, the residual error in these predictions increases and this contributes to a greater heterogeneity among the plots.

It could be argued that these trends are not related to the convergence of the model but to the region instead. In order to check this assertion, we carried out some simulations for the administrative region of Mauricie, also located in the province of Quebec. We obtained similar results indicating that the model was truly responsible for the declining sampling-related variances.

An additional insight into the context of hybrid inference is related to the sample size. As shown in Eq. 2, the greater the sample size is, the smaller the variance of the mean estimate will be. Thus, sampling variance is affected by sample size. However, Fortin et al. (2016, 2018) showed that the model-related variance is almost insensitive to sample size. This has important implications for large-area predictions. For instance, large-area predictions based on national or regional forest inventories have larger sample sizes than those of this study. As a consequence, the sampling-related variance would probably be smaller, whereas the model-related variance would remain constant. In such conditions, the model-related variance could become the main source of uncertainty, not only in a long-term prediction (i.e., 100 years), but sooner. If we double the sample size for the broadleaved ecotype, for example, as of the year 2050 when sampling-related variance really begins to decrease, model-related variance could become significant at an earlier date.

It is plausible to assume that variance behavior is dependent on the inherent variability of the ecotypes. Because mixed forests are more heterogeneous, we could expect that growth patterns would show greater variability. When comparing the sampling-related variances across the ecotypes, the sample size may hide the inherent variability. To eliminate the sample size effect, we compared the estimates of the initial population variance, i.e. that of 2003. The mixed and coniferous ecotypes were close, with population variances estimated at 200 and 240 $\mathrm{m}^4\mathrm{ha}^{-2}$, respectively. Consequently, the larger sampling variance of the coniferous ecotype (Fig. 4) was essentially due to the smaller sample size and not so much to a greater population variance. Again, it must be stressed that 2003 is the only year for which the population variance can be derived from the sampling-related variance because this latter accounts for all the variability. For all the other years, the population variance derived from the sampling-related variance represents the variance of the predicted basal areas. The residual error in the predictions must be taken into account in the estimation of the population variance. However, the current implementation of the bootstrap variance estimator in Fortin et al. (2018) does not allow for this estimation and further developments are required.

The variance estimates obtained in the partial stochastic predictions revealed that the mortality sub-model induced the greatest share of variance in basal area predictions for all ecotypes (Fig. 5 and Table 3). When the stochasticity of this sub-model was disabled, the total variance decreased by 35% to 60% at the end of the projections. Disabling the stochasticity of the diameter increment or recruitment sub-models decreased the variance by 10% to 25% in the broadleaved and coniferous ecotypes. The mixed ecotype showed a different pattern. Disabling the stochasticity of the diameter increment sub-model resulted in slightly higher variances when compared to the full stochastic predictions. More precisely, the total variance was increased by 6% in the last two decades of the projection.

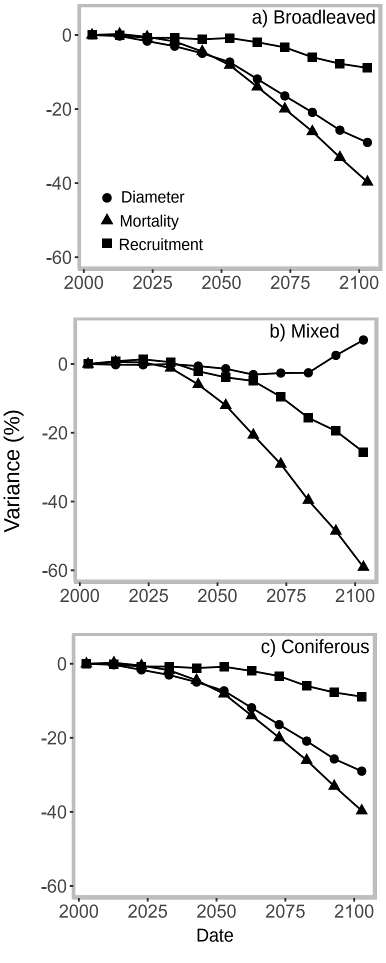

Figure 5: Variance contribution of each sub-model that compose the ARTEMIS growth model by ecotype. This contribution is calculated as the relative decrease in the total variance (%) once the stochasticity of the sub-model has been disabled.

Table 3: Variance values (m^4ha^{-2}) of the full stochastic prediction and the respective disabled growth sub-models represented per ecotype.

Ecotype	Year	Full Stochastic	Recruitment disabled	Mortality disabled	Diameter disabled
Broadleaved	2003	1.186	1.186	1.186	1.186
	2013	0.750	0.755	0.749	0.752
	2023	0.574	0.574	0.561	0.570
	2033	0.495	0.502	0.467	0.482
	2043	0.461	0.479	0.420	0.449
	2053	0.462	0.481	0.397	0.436
	2063	0.467	0.484	0.381	0.450
	2073	0.479	0.484	0.370	0.462
	2083	0.486	0.501	0.353	0.471
	2093	0.492	0.498	0.328	0.480
	2103	0.492	0.483	0.296	0.488
Mixed	2003	2.133	2.133	2.133	2.133
	2013	1.331	1.328	1.339	1.341
	2023	0.847	0.845	0.851	0.858
	2033	0.531	0.530	0.524	0.533
	2043	0.339	0.337	0.319	0.332
	2053	0.234	0.231	0.206	0.225
	2063	0.186	0.180	0.147	0.177
	2073	0.163	0.158	0.115	0.147
	2083	0.149	0.145	0.090	0.125
	2093	0.127	0.130	0.065	0.102
	2103	0.105	0.113	0.043	0.078
Coniferous	2003	10.939	10.939	10.939	10.939
	2013	8.106	8.147	8.126	8.115
	2023	6.591	6.636	6.670	6.618
	2033	5.646	5.639	5.740	5.696
	2043	5.025	4.863	5.090	5.031
	2053	4.560	4.230	4.606	4.568
	2063	4.215	3.723	4.329	4.244
	2073	4.070	3.340	4.173	4.033
	2083	4.039	3.069	4.151	3.902
	2093	4.164	2.870	4.287	3.955
	2103	4.413	2.696	4.471	4.074

In the light of these results, we could only partially validate our second hypothesis. The differences between the different growth components were relatively small for all ecotypes during the first decades, and it is only after 2050 that the departures increased (Fig. 5). On the long term, we observed that mortality accounted for the greatest share of variance. The recruitment sub-model, however, did not bring as much variance as we had expected on the long term. Tree mortality is complex and stochastic, leading to large variations over time. Indeed, it remains one of the most difficult growth components to explain (Hamilton, 1986). Kangas (1998) reported mortality as the main source of error in stand volume predictions. In our study, the contribution of mortality to prediction variance could have been emphasized by the fact that we worked with basal area. Since larger trees are more likely to die (Vanclay, 1994, p.189), they induce a greater variability in basal area predictions. If we had been working with stem density, this would not have been the case. The same rationale applies to the recruitment. Since ARTEMIS recruits small trees, the impact on basal area predictions is rather small.

In this study, we used a Monte Carlo technique. Although it is computationally intensive and time-consuming, a large-scale application of this method made it possible to propagate errors from multiple sources into ARTEMIS. The differences we observed between the predictions in fully or partially stochastic modes (Fig. 3) were also highlighted by some authors. Omitting some errors leads to different predictions (Zhou and Buongiorno, 2004; Fortin and Langevin, 2012). In addition, stochastic models turned out to be more realistic and theoretically superior than deterministic models (Fox et al., 2001).

Studies on the uncertainty assessment of large-area forest predictions exist (e.g., Kangas, 1999; Makinen et al., 2010; Yang et al., 2016; Eyvindson and Kangas, 2016). Most studies focus on either model or sampling uncertainty, but rarely on both sources. Furthermore, it seems that model uncertainty has attracted more attention than sampling uncertainty. The fact that sampling uncertainty has remained overlooked in most studies on large-area growth predictions can be related to the complex error propagation in forest growth models.

Some studies have relied on upscaling techniques based on model input aggregation to produce large-area predictions (e.g., Kangas, 1996, 1998; Fischer et al., 2014). The idea is to create an average plot for which growth is then predicted using the model (Wu et al., 2006). Although this approach has some advantages (Bugmann et al., 2000), averaging explanatory variable values over a greater scale with nonlinear models potentially leads to biases, a phenomenon that is known as Jensen's (1906) inequality and that is seldom mentioned in ecological studies (Ruel and Ayres, 1999). In our study, we managed to avoid Jensen's inequality by averaging prediction through the direct extrapolation method (Wu et al., 2006). The method consists of first running the model locally and subsequently averaging model outputs to a greater unit of area (Wu et al., 2006).

Model- and sampling-related variances in large-area estimates of biomass have been predicted using design-based variance estimators and considering the model-related variance through a first-order approximation (e.g., Stahl et al., 2014; Fu et al., 2017). However, first-order approximations imply an additional source of error and provide estimates of the statistical moments, not a distribution (Dettinger and Wilson, 1981). In the presence of a complex system such as nonlinear and time-varying errors, traditional uncertainty methods based on algebra are not adequate for the corrected estimation (Wilson and Smith, 2013). As an alternative to approximations, Breidenbach et al. (2014) and McRoberts and Westfall (2014) proposed the use of a bootstrap variance estimator. In the context of hybrid inference, this bootstrap estimator can be biased and a corrected estimator has been suggested by Fortin et al. (2018), which is the one we used in this study.

Decomposing the variance of complex models requires advanced techniques (Xu and Gertner, 2008). In this case study, we found smaller variances in the partial stochastic predictions compared with those in full stochastic mode for one sub-model, namely the diameter increment sub-model. We thought that this could be due to unstable variance estimates. We therefore increased the number of Monte Carlo realizations and tested whether the variance estimates had stabilized. After 10,000 realizations, both sampling- and model-related variance components were found to be stable. The model implementation was also checked.

From then on, we considered that these unforeseen results were reliable.

The variance decomposition approach assumes that uncertainties from the different sources are independent. Nevertheless, they may not be independent due to model complexity and highly nonlinear interactions propagated throughout the system. Such uncertainties may occur in an unpredictable manner in the future (Willems, 2012). Part of the prediction uncertainty in ARTEMIS is also a consequence of its architecture. For instance, if the order of the sub-models had been different from that shown in Fig. 1, we would be dealing with different interactions between the sub-models and different predictions of forest growth. Thus, the variance contribution could have been affected.

In a preliminary trial, we also considered the variance decomposition the other way around. We compared deterministic predictions with partial stochastic predictions, where we alternately enabled the stochasticity of one sub-model at a time. Results similar to those presented here were observed and are thus not presented.

In many studies on uncertainty in forestry, the main variable is the volume per hectare. In this study, we chose to estimate the variance in the predictions in basal area. This was motivated by the fact that we wanted to avoid additional sources of uncertainty from the static sub-models of height-diameter relationship and volume.

4 Conclusions

In this study, we managed to estimate both model- and sampling-related variance of growth predictions at a regional level. This uncertainty estimation required a bootstrap variance estimator for hybrid inference (Fortin et al., 2018) as well as a tree-level growth model that allowed for full stochastic predictions. Additionally, the variances induced by the mortality, diameter increment and recruitment sub-models were individually estimated through a variance decomposition approach. Our study provides insights into how model- and sampling-related variances change along projection length in the context of hybrid inference, as does the growth model component that contributes the most to prediction uncertainty.

The originality of our work includes the temporal perspective in the context of hybrid inference, the variance decomposition information and flexible methods, adaptable to different ecotypes and complex growth models. Sampling-related variance was reported as the most important component of large-area estimates by many authors (e.g., Stahl et al., 2014; Breidenbach et al., 2014; McRoberts and Westfall, 2014). In our study, the time scale turned out to be an original angle since it indicated that the extent of sampling- and model-related variance is a function of time. Sampling error is the most important source of variance in short-term predictions, while in long-term predictions, the model contribution is as important as that of the sampling. Consequently, efforts should focus on increasing the sampling size and developing an efficient sampling design in order to decrease the overall variance. Similar recommendations were made by McRoberts and Westfall (2014). In long-term predictions, the model should be the target of attention. By decomposing the variance, we were able to point out that the mortality sub-model should first and foremost be improved since it has a greater contribution to the prediction variance.

As a future perspective, we recognize the importance of natural or anthropogenic disturbances, which were deliberately omitted in our predictions for the sake of simplicity. Further investigations should be conducted to take these into account. Finally, since forest management planning is a long-term process, we conclude that efforts on modeling techniques should be considered in order to reduce total uncertainty in growth predictions.

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