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Comparison of uncertainty in per unit area estimates of aboveground biomass for two selected model sets

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ABSTRACT

Uncertainty in above ground forest biomass (AGB) estimates at broad-scale depends primarily on three sources of error that interact and propagate: measurement error, model error, and sampling error. Using Monte Carlo simulations, we compare the total propagated error for two sets of regional-level component equations for lodgepole pine AGB, and for two sets of high-precision instruments by accounting for all three of these sources of error. The two sets of models compared included a set of newly-developed component ratio method (CRM) equations, and a set of component AGB equations currently used by the Forest Inventory and Analysis (FIA) unit of the United States Department of Agriculture (USDA) Forest Service.

Relative contributions for measurement, model, and sampling error using the current regional equations were 5%, 2% and 93%, respectively, and 13%, 55% and 32%, respectively using the CRM equations. Relative standard error (RSE) values for the current regional and CRM equations with all three error types accounted for were 20.7% and 36.8%, respectively. Results for the model comparisons indicate that per acre estimates of AGB using the CRM equations are far less precise than those produced with the current set of regional equations. Results for the instrument comparisons indicate the terrestrial lidar scanning reduce uncertainty in broad-scale estimates of AGB attributed to measurement error.

1. Introduction

Increasingly central to the planning and monitoring-related goals of disciplines such as forestry and ecology, the production of defensibly precise broad-scale estimates of above ground biomass (AGB) but requires a thorough recognition of their primary associated sources of variability (Temesgen et al., 2007). The widespread sample-based approach of acquiring these AGB estimates for forested areas typically involves applying individual-tree regression equations to trees selected within randomly selected sample plots to obtain tree-level estimates of AGB. All individual-tree estimates are then summed to obtain plot-level estimates, with all plot values subsequently expanded up to per unit area levels of ABG. The reported precision of these per unit area estimates using this approach commonly reflect only the sampling error; the variability resulting from among-plot differences in plot-level values of ABG. In addition to sampling error, two other primary sources of error have been shown to interact and propagate during the process of scaling individual-tree estimates of AGB up to per unit area levels; namely measurement error and model error (Cunia, 1965). Measurement error is defined as the difference between a defined "true" value and the measured value of a given attribute. Model errors are sourced mainly from the residual variability around the model predictions and uncertainty in the parameter estimates. Because only sampling error is accounted for, uncertainty estimates for AGB are often an underestimation of the actual uncertainty. If uncertainty estimates for AGB are to be statistically credible, all three of these error types must be accounted for.

Measurement error is a source of uncertainty that has received broad attention in the forestry literature. A number of authors have

Abbreviations: AGB, aboveground biomass; CRM, component ratio method; CRM-FIA, component ratio method used by FIA; CV, coefficient of variation; DBH, diameter at breast height; DNF, Deschutes National Forest; DOB, diameter outside bark; FIA, Forest Inventory and Analysis; HT, total tree height; HTCB, height to the base of live crown; NFI, National Forest Inventory; RMSE, root mean square error; RRMSE, relative root mean square error; RSE, relative standard error; SE, standard error; STM, standing tree measurements; SUR, seemingly unrelated regression; TTWOF, total tree aboveground biomass without foliage; WNF, Willamette National Forest.

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investigated the measurement error of particular instruments used in forestry applications (Behre, 1926; Bell and Gourley, 1980; McRoberts et al., 1994; Williams et al., 1994; Skovsgaard et al., 1998; Plamondon, 1999; Kalliovirta et al., 2004), while others have characterized the distributions of measurement errors for measured tree variables (McRoberts et al., 1994; Canavan and Hann, 2004). Work has also been done to investigate the effects of measurement error on the uncertainty of forest model predictions (Westfall and Patterson, 2007; Suty et al., 2013; Berger et al., 2014). Westfall and Patterson (2007) used the two stage error distribution method, also described by Canavan and Hann (2004), to model measurement variation distributions. Using quality assurance data from 682 inventory plots implemented by the Forest Inventory and Analysis (FIA) unit of the United States Department of Agriculture (USDA) Forest Service, they were able to assess the effects of measurement variability on several volume change estimates, including ingrowth, accretion, removals and mortality. Error due to measurement variability was minimal compared to the sampling variability, with accretion being the most sensitive to systematic measurement errors. Suty et al. (2013) used Taylor series expansion and empirical comparisons between two volume growth prediction methods to illustrate the effect of introduced bias from random measurement errors to inputs for non-linear volume growth models used in the Swedish National Forest Inventory (NFI). Similarly, Berger et al. (2014) used Taylor series expansion and Monte Carlo simulations to approximate the effects of measurement errors in four independent variables on the relative error of stem volume equations currently used in the Austrian NFI. None of these studies, however, investigated how measurement error affected broad-scale AGB estimates.

The effects of model errors on the variability of broad-scale forest inventory estimates are well described. Breidenbach et al. (2014) assessed how variability in models used by the Norwegian NFI affects biomass stock and change estimates for Norway spruce. A parametric bootstrap approach was employed to quantify the contributions of parameter estimate uncertainty, inflated model residual variance and within-plot correlation to the total uncertainty of biomass stock and change in Norway. McRoberts and Westfall (2014) used Monte Carlo simulations to examine how volume model-related variability influences broad-area estimates generated from 2178 FIA plots across a study area in northeastern Minnesota, USA. A comparison was made of the gains using species-specific models versus coniferous/deciduous nonspecific models, calibrated from a species-specific dataset collected from 2102 trees across 24 states of the northern and northeastern Unites States. Both of these authors found the model errors to be minimal contributors to the total uncertainty. However, neither studies investigated the effects of measurement error as well.

Unfortunately, very few studies have addressed the effects of all primary sources of error on broad-scale forestry inventory estimates (Temesgen et al., 2015). Mowrer and Frayer (1986) addressed the effects of measurement error, model error and sampling error by measuring the cumulative variance of five 10-year projections from a growth and yield model for pure even-aged clonal quaking aspen using both Taylor series expansion and Monte Carlo simulations. Gertner (1990) approximated the effect of all three sources for non-linear individual-tree volume functions used to estimate stand-level volume per acre. Chave et al. (2004) examined the effects of these different sources of error using permanent plot data from the moist forests of the canal region of Panama. In addition to the three aforementioned error sources, the magnitude of uncertainty from the specific model form chosen was assessed. This study is similar in that all three forms of error were empirically compared for two different sets of component models developed for lodgepole pine (*Pinus contorta*) for use in the Pacific Northwest region. In doing so, we were able to produce credible depictions of uncertainties useful for determining which model is the most reliable for future use.

1.1. Component ratio method

The FIA is charged with the task of providing stock and change estimates for a large number of national-scale forest-related variables, with their estimates of AGB being drawn upon and used for a wide range of applications. Regional-level equations for small to mid-level estimation in specific regions are publicly available and used by many individuals seeking species-specific localized component estimates of AGB. However, these suites of equations often source from an array of different studies, inconsistent methodologically and in sample size, often yielding AGB estimates that differ across regions for trees of identical size and species. To address consistency issues in estimation across regions, the national-level Jenkins equations were developed and used by FIA for national-scale estimation (Jenkins et al., 2003). Stemming from extensive meta-analysis of 2640 published equations for component and total-tree biomass, the resultant Jenkins equations are a group of 10 generalized component and total tree biomass equations with diameter at breast height (DBH) as the only independent variable.

Reservations about the low-level of species specificity of these generalized models arose when large variations of AGB estimates were observed when applied to smaller-scale operations. This was illustrated by Zhou and Hemstrom (2009) who observed Jenkins estimates of total AGB of softwoods in the state of Oregon to be 17% greater compared to regional species-specific equations. Hence, in 2009 a new component ratio method (CRM) was proposed as the standard for nationwide AGB reporting. This method uses a combination of the component ratios from the Jenkins equations, regional bole volume equations and percent bark estimates, so as to ensure consistency with regional tree-level volume estimates (Heath et al., 2008; Woodall et al., 2011). However, despite the conformance with regional-based estimates of bole volume, the reliance on the national-scale generalized Jenkins component ratios yields the same non-specificity for regional and finer-scale applications.

A new set of species-specific CRM component equations for lodgepole pine (*P. contorta*) are presented here for comparing total uncertainties with those produced from the current regional equations. These new CRM equations are heretofore referred to as the CRM equations; the hybrid CRM method described in the previous paragraph will be referred to as CRM-FIA. These new CRM equations originate from a pilot research study aimed at developing new regional-level models for AGB consistent across regions. Rather than rely on the component ratios from the Jenkins models and the current regional volume models, these equations directly predict the proportion of tree-level AGB for bole wood, bark, branch wood and foliage. With these new CRM equations for component AGB stemming from one study, rather than a host of different studies as with the current regional equations, and with the specificity for use in smaller, more localized operations, the prior stated issues with consistency, specificity and congruence are addressed. The three independent variables for these new models are DBH, total height (HT) and height to crown base (HTCB).

To evaluate the performance of these new equations relative to the current regional approach for estimating tree-level AGB for lodgepole pine, comparisons of the magnitude of the cumulative propagated error will be made between the two sets of equations. Using Monte Carlo simulations, and applying both sets of equations to cluster sample plot data associated with destructively sampled trees used for development of the new CRM models, we were able to quantify the effects of measurement and model error

on the precision of per unit area estimates of AGB for both approaches.

2. Methods

2.1. Study locations

In order to capture regional differences in tree form, the data for this study were collected from both the Willamette National Forest (WNF) and the Deschutes National Forest (DNF) in western and central Oregon, respectively, All locations were within a mid-elevation band, with the WNF locations spanning from 1160 to 1340 m in elevation and the DNF locations from 1280 to 1340 m in elevation. The WNF locations encompassed two forest types: (1) a diverse mixed-species coniferous forest, with observed species being Douglas-fir (*Pseudotsuga menziesii*), western hemlock (*Tsuga heterophylla*), lodgepole pine, mountain hemlock (*Tsuga mertensiana*), noble fir (*Abies procera*), Engelmann spruce (*Picea engelmanii*), and western white pine (*Pinus monticola*); and (2) a homogenous coniferous forest composed of primarily lodgepole pine and with a small element of grand fir (*Abies grandis*). The DNF locations encompassed one forest type of homogenous coniferous species composition, with observed species being lodgepole pine and ponderosa pine (*Pinus ponderosa*).

2.2. Field data

For all locations, accessible sample trees were subjectively selected based upon morphological characteristics that included DBH, HT, and crown ratio (CR), as well as absence of defect or abnormalities. Efforts were taken to select sample trees either located in different forest stands types, or sufficiently distanced apart so as to avoid issues with spatial autocorrelation. A total of 32 trees were measured over a four week period during July and August 2013. DBH, HT and CR ranged from 13.5 to 42.9 cm, 9.2 to 31.9 m and 0.30 to 0.948, respectively.

Standing-tree measurements were conducted prior to felling, with DBH being measured to nearest 0.254 cm using a Spencer combination tape and with both HT and height to crown base (HTCB) being measured to the nearest 0.03 m using a Trupulse Laser Rangefinder 360R. For this study, HTCB was defined as the bole height of the first live limb. Downed-tree measurements of HT and HTCB were measured with a 30.48 m open reel fiberglass tape. Due to the need for determining the point on the bole where 1.3 m. above the uphill side of the tree was located prior to felling, and because DBH was measured with strict attention to detail while the sample trees still stood, standing-tree measurements of DBH were considered to be the "true" values and were not subsequently re-measured. It should also be noted that a large number of additional measurements that were not independent variables into the models were taken on the felled trees for the creation of the new CRM equations.

For estimation of component biomass per unit area, ground plot data was collected from the forest stands from which the 32 sample trees were sourced. All trees (>10 cm diameter) within a cluster plot comprised of four circular fixed area subplots arranged around each sample tree were measured for attributes such as species, DBH, HT and HTCB, among others. A 0.017 hectare plot was the primary subplot (radius 7.32 m) with the pith of the sample tree as the center. The centers of the other three circular subplots were located 36.58 m at azimuths of 120°, 240° and 360° from the pith of the sample tree. The secondary subplots were 0.008 hectares in area (radius 5.18 m), this reduction in plot size being a reflection of the relative importance of these plots to the central goal of maximizing the number of trees sampled.

2.3. Models compared

The Pacific Northwest unit of the FIA currently uses three different equations for bole, bark and branch AGB, and a published wood specific gravity value (USDA Forest Products Laboratory, 2010) to estimate lodgepole pine component AGB for region-specific applications (Zhou and Hemstrom, 2010). The summation of all three component estimates of AGB is the total tree estimate of AGB, without foliage. Bole AGB for lodgepole pine is estimated by first predicting total bole wood volume using the following equation published by Brackett (1977):

$$\mathrm{CVTS}_i = 10^{-2.615591+1.847504\times\log(\mathrm{DBH}_i)+1.085772\times\log(\mathrm{HT}_i)} \quad (1)$$

where CVTS_i is the predicted total main bole wood volume including top and stump (ft^3), DBH is in inches, height is in feet, and $\log(\cdot)$ is the logarithm function (base 10). This prediction is then multiplied by the following species-specific average wood density value to obtain bole AGB:

$$\text{Bole AGB}_i = (\mathrm{CVTS}_i \times \mathrm{WD})^{*}0.45359 \quad (2)$$

with

$$\mathrm{WD} = \mathrm{SG} \times W \quad (3)$$

where Bole AGB_i is the predicted oven-dry bole biomass (kg) for the ith tree, WD is the calculated wood density value (lbs/ft^3), 0.45359 is factor converting pounds to kilograms, SG is the published wood specific gravity value for lodgepole pine (0.38) and W is the density of water (62.4 lbs/ft^3).

Bark and branch AGB for lodgepole pine are estimated by using the following equations published by Standish et al. (1985):

$$\text{Bark AGB}_i = 3.2 + 9.1 \times \left(\frac{\mathrm{DBH}_{\mathrm{cm},i}}{100}\right)^2 \times \mathrm{HT}_{m,i} \quad (4)$$

$$\text{Branch AGB}_i = 7.8 + 12.3 \times \left(\frac{\mathrm{DBH}_{\mathrm{cm},i}}{100}\right)^2 \times \mathrm{HT}_{m,i} \quad (5)$$

where Bark AGB_i is the predicted oven-dry bark biomass for the standing tree bole up to a 2.5 cm bole diameter (kg) for the ith tree, Branch AGB_i is the predicted oven-dry branch biomass of wood and bark of live limbs attached to the main bole (kg) for the ith tree, $\mathrm{DBH}_{\mathrm{cm},i}$ is diameter at breast height (cm) and $\mathrm{HT}_{\mathrm{m},i}$ is total tree height (m).

The new CRM equations under comparison here directly predict the proportion of AGB for the bole, bark, branch and foliage components. These proportions can then be multiplied by an estimate for total tree AGB of the user's choice. In this study, the total tree biomass equation used was produced using the same data used to create the CRM equations for lodgepole pine. Both the CRM equations and the total tree biomass equation were fit in separate systems of equations using the seemingly unrelated regression method (SUR) in SAS statistical software (SAS Institute Inc., v9.4). The four CRM component equations and the total tree equation by Poudel (2014) are of the form:

$$\mathrm{pBole}_i = \exp\left[\beta_0 + \beta_1 \times \ln(\mathrm{DBH}_i) + \beta_2 \times \ln(\mathrm{HT}_I) + \frac{\sigma^2}{2}\right] \quad (6)$$

$$\mathrm{pBark}_i = \exp\left[\beta_3 + \beta_4 \times \ln(\mathrm{DBH}_i) + \frac{\beta_5}{\ln(\mathrm{HTCB}_i)} + \frac{\sigma^2}{2}\right] \quad (7)$$

$$\mathrm{pBranch}_i = \exp\left[\beta_6 + \beta_7 \times \ln(\mathrm{DBH}_i) + \beta_8 \times \ln(\mathrm{HTCB}_i) + \frac{\sigma^2}{2}\right] \quad (8)$$

$$\mathrm{pFoliage}_i = \exp\left[\beta_9 + \beta_{10} \times \ln(\mathrm{DBH}_i) + \beta_{11} \times \ln(\mathrm{HTCB}_i) + \frac{\sigma^2}{2}\right] \quad (9)$$

$$\text{Total Tree}_i = \exp\left[\beta_{12} + \frac{\beta_{13}}{\text{DBH}_i} + \frac{\sigma^2}{2}\right] \quad (10)$$

where pBole_i, pBark_i, pBranch_i and pFoliage_i are the estimated proportions of component AGB for bole wood, bark, branches and foliage, respectively, $\exp(\cdot)$ is the exponential function, $\ln(\cdot)$ is the natural logarithm function and the βss are the estimated parameters from the SUR procedure. The $\frac{\sigma^2}{2}$ is the correction factor, as described by Baskerville (1972) and McRoberts and Westfall (2014), for the resulting bias when back-transforming model predictions from the logarithmic to the initial scale of interest, where $\hat{\sigma}^2$ is the estimated mean squared error, or residual variance. In the above equations, the values of the $\hat{\beta}$s and $\hat{\sigma}^2$ are expressed on the logarithmic scale. For ease of future readability, all models, whether CRM, total tree or current regional models will be generally referred to as component models, unless where the mentioning of a specific model is deemed necessary.

2.4. Measurement error variability

For HT and HTCB, the differences between the standing-tree measurements and the downed-tree measurements were calculated for all 32 trees. In this study, the downed-tree measurements are considered to be the known "true" values due to the ease with which measurements could be taken as accurately as possible. The summary data for these differences were subsequently calculated for each input variable for the models (Table 1).

Using a grouping method detailed by Hosmer and Lemeshow (1989), and implemented by Berger et al. (2014), a simple linear regression model through the origin was constructed to predict the standard deviation of the measurement errors. In order to conduct regressions of standard deviation of measurement errors on input variables, the data required grouping. Using the notation and general methodology of Berger et al. (2014) for the example of HT: (1) the data were sorted in ascending order with respect to downed-tree measurement HT values; (2) with the minimum 10 groups, as recommended by Hosmer and Lemeshow (1989), the sorted HT values were grouped into groups of size 3, with the last group including the remainder of the HT values; (3) for every gth group, the means of the HT measurements from step 1 and $\text{SD}_{\text{ME},g}$ were estimated, where $\text{SD}_{\text{ME},g} = \frac{1}{n-1}\sqrt{\sum_{g=1}^{n}(\text{ME}_{\text{HT},g} - \overline{\text{ME}_{\text{HT},g}})^2}$ is the standard deviation of the measurement errors for HT and $\text{ME}_{\text{HT},g} = \text{HT}_D - \text{HT}_S$ are the HT measurement errors, where HT_D is the downed-tree height measurement and HT_S is the standing-tree height measurement; (4) the following model form was fit to the grouped data for HT using the method of ordinary least squares:

$$\widehat{\text{SD}}_{ME,HT} = \hat{\beta}_1 \times \text{HT} \quad (11)$$

where $\widehat{\text{SD}}_{\text{ME,HT}}$ is the estimated standard deviation of the measurement errors for HT and $\hat{\beta}_1$ is the model parameter estimate.

2.5. Integrating simulated measurement errors into model uncertainty

We based our methods of integrating the measurement error into the model uncertainty on those described by Berger et al. (2014). Using the standard deviations from Table 1 and Eq. (11), Monte Carlo simulations, conducted using R software (R Core Team, 2012), were used to approximate model uncertainties reflective of the additional uncertainty due to measurement error. Within each simulation, we were able to produce measurement errors that were then applied to "true" input values from the downed-tree measurements to produce "contaminated" input values for the equations. Input variable contamination was a two part process. For consistency, we will stay with the example of HT. First, for the kth component model, a multiplicative factor $\sim N(1, \text{SD}_{\text{HT}}^2)$ was randomly generated and multiplied together with the input variables, where SD_{HT} is the standard deviation of the height measurement errors in Table 1; and (2) an additive factor $\sim N(0, \widehat{\text{SD}}_{\text{ME,HT}}^2)$ was randomly generated and added to the input variables, where $\widehat{\text{SD}}_{\text{ME,HT}}$ is the predicted standard deviation from Eq. (11) (Berger et al., 2014).

The resultant contaminated model predictions were recorded over 5000 iterations, for all component models. The impact of the additional uncertainty was assessed by calculating the mean prediction and root mean square error (RMSE) and the relative RMSE (RRMSE) over all iterations using the dataset of 32 trees with the following formulas:

$$\text{mean} = \frac{1}{n}\sum_{i=1}^{n}\widehat{Y}_i \quad (12)$$

$$\text{RMSE} = \sqrt{\frac{1}{n}\sum_{i=1}^{n}(Y_i - \widehat{Y}_i)^2} \quad (13)$$

where Y_i is the observed value and $\widehat{Y}_i$ is the prediction for the ith tree. RRMSE is calculated by simply dividing RMSE by the mean.

To convert the CRM predicted ratios and RMSEs to tree-level units (oven-dry kg) as displayed in Table 2, two steps were taken; (1) the CRM ratios were multiplied by the prediction for total tree biomass produced by Eq. (10) to obtain tree-level predictions of component AGB; (2) to produce absolute RMSEs for this product, the square root of the sum of the squared relative RMSEs was multiplied by the predictions in step 1. The following formula for the combined RMSEs is

$$\delta\text{AGB}_{\text{Comp}} = \widehat{\text{AGB}}_{\text{Comp}} \times \sqrt{\left(\frac{\delta\text{AGB}_{\text{Ratio}}}{\widehat{\text{AGB}}_{\text{Ratio}}}\right)^2 + \left(\frac{\delta\text{AGB}_{\text{TT}}}{\widehat{\text{AGB}}_{\text{TT}}}\right)^2} \quad (14)$$

where $\delta\text{AGB}_{\text{Comp}}$ is the combined RMSE in tree-level units, $\delta\text{AGB}_{\text{Ratio}}$ is the RMSE for the CRM component ratios and $\delta\text{AGB}_{\text{TT}}$ is the RMSE for total tree AGB (Eq. (10)).

2.6. Integrating models errors into sampling uncertainty

In order to integrate the model errors, contaminated or not, into the sampling uncertainty, the magnitude of the model errors integrated needed to be contingent upon the magnitude of the model predictions. Using the previously described grouping approach with respect to the model errors, a simple linear regression model through the origin was constructed to predict the magnitude of the model errors. Following the notation and general methodology of McRoberts and Westfall (2014): (1) for the kth component model, a joined list of ε_i, Y_i and $\widehat{Y}_i$ was created and sorted in ascending order with respect to, $\widehat{Y}_i$ where $\varepsilon_i = \widehat{Y}_i - Y_i$; (2) with the minimum 10 groups, as recommended by Hosmer and Lemeshow (1989), the sorted triads of observations were grouped into groups of size 3, with the last group including the remainder of the means; (3) for every gth group, the mean observation $\overline{Y}_g = \frac{1}{n_g}\sum_{g=1}^{n_g} Y_g$, the mean prediction $\overline{\widehat{Y}_g} = \frac{1}{n_g}\sum_{g=1}^{n_g}\widehat{Y}_g$ and the mean square error

Table 1
Summary statistics of the measurements errors for HT and HTCB.

	n	Min.	Mean	Max.	SD
HT (m)	32	−2.56	−0.82	2.26	0.83
HTCB (m)	32	−1.04	−0.07	1.37	0.49

Table 2
Model predictions and RMSE values for CRM ratios, CRM tree-level estimates and tree-level estimates for the regional equations, without measurement error. Total minus foliage, the sum of the tree-level component estimates, is used as another means for comparison between the models. Tree-levels units are in kilograms of dry biomass.

Model means-without measurement error				Model RMSEs-without measurement error			
Total tree (SUR)	284.83			Total tree (SUR)	73.78		
Component	CRM ratios	CRM tree-level	Regional tree-level	Component	CRM ratios	CRM tree-level	Regional tree-level
Bole	0.677	192.83	182.44	Bole	0.081	55.04	79.56
Bark	0.054	15.42	14.21	Bark	0.031	9.76	10.59
Branch	0.192	54.79	20.78	Branch	0.061	22.34	30.74
Foliage	0.080	22.69	NA	Foliage	0.023	8.81	NA
Total minus foliage		263.04	217.43	Total minus foliage		87.14	120.89

$\sigma_g^2 = \frac{1}{n_g - 1}\sum_{g=1}^{n} e_g^2$ were calculated, where n_g is the number of trees in the gth group; (4) the following model form was fit to the grouped data for each component model using the method of ordinary least squares

$$\hat{\sigma}_i = \hat{\beta}_1 * \widehat{Y}_i \tag{15}$$

where $\hat{\sigma}_i$ is the predicted model error for the ith tree, $\hat{\beta}_1$ is the model parameter estimate and $\widehat{Y}_i$ is the model prediction for the ith tree. It should be noted that with measurement error integrated into the model errors, the value of $\hat{\beta}_1$ is expected to increase, reflecting this additionally accounted for source of uncertainty.

A bootstrapping technique, in conjunction with Eq. (15), was used to simulate the effects of model errors on the uncertainty of per unit area estimates of component AGB for all models. A similar Monte Carlo simulation sequence and notation described by McRoberts and Westfall (2014) was used for each component model.

First, the data set containing the "true" values of the 32 sample trees was randomly sampled with replacement to produce a bootstrapped-sample of size 32. Similar to the previously described method of simulating measurement errors, contaminated model predictions for all 32 pseudo-sampled trees were produced by adding a randomly generated residual, $\varepsilon_i \sim N(0, \hat{\sigma}_i^2)$, to the prediction for the ith pseudo-sampled tree produced using the kth component model, where $\hat{\sigma}_i$ is estimated using Eq. (15). Using the contaminated predictions and the pseudo sample data, a new model, of the same form as the kth component model, was refit. For Eqs. (1), (6)–(9) and (10), due to their original model form, the contaminated predictions and the pseudo sample data required transformation to the $\log_{10}$–$\log_{10}$ and ln–ln scale, respectively, prior to refitting.

Second, the refit equations were applied to the ground plot data set. For the ith tree in the jth plot, predictions of tree-level component AGB were produced by adding the model predictions to a randomly generated constrained residual, $\lambda\varepsilon_i$ where ε_i is the randomly generated residual $\sim N(0, \hat{\sigma}_i^2)$, and λ is a multiplicative constraining factor that yields model efficiency values of 0.95. Model efficiency, calculated as

$$Q^2 = 1 - \left(\frac{\sum_{i=1}^{n_{pl}} e_i^2}{\sum_{i=1}^{n_{pl}} (Y_i - \overline{Y})^2}\right) \tag{16}$$

where n_{pl} is the number of trees in the ground plot data set, and Q^2 is a goodness-of-fit statistic similar to the more familiar r^2 from the ordinary least squares procedure, where the higher the value the better the fit of the model to a given data set (Vanclay and Skovsgaard, 1997; McRoberts and Westfall, 2014). This multiplicative factor constraint was implemented in order to have a standardized quality of fit of the model to the ground plot data for purposes of comparing the standard errors of the mean for all component models. Due to recent published findings illustrating the minimal effect correlation among trees within plots has on the standard error of the estimates, correlation among residuals was not integrated into the analysis of this study (Berger et al., 2014; Breidenbach et al., 2014; McRoberts and Westfall, 2014).

Third, to obtain the estimated per hectare values of component AGB on the jth cluster plot, the summation of all subplot-level per unit area component AGB predictions on the lth subplot were calculated as

$$Y_j = \sum_{l=1}^{4} Y_l \tag{17}$$

with

$$Y_l = \frac{\sum_{i=1}^{n_l} Y_{i,l}}{\text{Subplot Area}_{\text{hectares}}} \tag{18}$$

where n_l is the number of trees observed in the lth subplot and $Y_{i,l}$ is the ith tree on the lth subplot.

Fourth, for each simulation cycle the mean and variance of the mean across all cluster plots were calculated as

$$\overline{Y} = \frac{1}{n_{cl}}\sum_{j=1}^{n_{cl}} Y_j \tag{19}$$

$$\widehat{\text{Var}}(\overline{Y}) = \frac{1}{n_{cl}(n_{cl}-1)}\sum_{j=1}^{n_{cl}} (Y_j - \overline{Y})^2 \tag{20}$$

where n_{cl} is the number of cluster plots (32 in this study).

Finally, the mean prediction and mean within-simulation variance over 5000 simulation cycles were calculated as

$$\hat{\mu}_{\text{sim}} = \frac{1}{5000}\sum_{1}^{5000} \overline{Y} \tag{21}$$

$$\widehat{\text{Var}}_{\text{sim}} = \frac{1}{5000}\sum_{1}^{5000} \widehat{\text{Var}}(\overline{Y}) \tag{22}$$

The mean predictions as well as final propagated error were compared for all component models for both approaches. Metrics used for comparison include RMSE, RRMSE, standard error of the mean (SE) from Eq. (20) and relative SE (RSE).

3. Results and discussion

3.1. Model predictions and uncertainty

Once the predicted CRM component ratios were produced, they were multiplied by the predicted total tree biomass obtained using the SUR equation. When measurement error is not integrated into the model errors, the CRM predicts comparable amounts of tree-level AGB for each component, except for branches where the CRM predicts over 2.5 times that of the currently used

Table 3
Model predictions and RMSE values for CRM ratios, CRM tree-level estimates and tree-level estimates for the regional equations, with measurement error. Total minus foliage, the sum of the tree-level component estimates, is used as another means for comparison between the models. Tree-levels units are in kilograms of dry biomass.

Model means-with measurement error				Model RMSEs-with measurement error			
Total tree (SUR)	284.83			Total tree (SUR)	73.78		
Component	CRM ratios	CRM tree-level	Regional tree-level	Component	CRM ratios	CRM tree-level	Regional tree-level
Bole	0.607	172.92	338.50	Bole	0.324	157.07	573.95
Bark	0.044	12.40	14.13	Bark	0.057	16.62	49.99
Branch	0.207	58.93	20.67	Branch	0.079	27.22	72.87
Foliage	0.090	25.52	NA	Foliage	0.040	13.07	NA
Total minus foliage		244.24	373.29	Total minus foliage		200.91	696.80

Table 4
Model RRMSE values for CRM ratios, CRM tree-level estimates and tree-level estimates for the regional equations, with and without measurement error. Total minus foliage, the sum of the tree-level component estimates, is used as another means for comparison between the models.

Model RRMSEs-without measurement error				Model RRMSEs-with measurement error			
Total tree (SUR)	24.1%						
Component	CRM ratios (%)	CRM tree-level (%)	Regional tree-level (%)	Component	CRM ratios (%)	CRM tree-level (%)	Regional tree-level (%)
Bole	12.0	28.5	43.6	Bole	53.4	77.5	169.6
Bark	57.7	63.3	74.5	Bark	131.6	155.7	353.9
Branch	31.5	40.8	147.9	Branch	38.2	62.4	352.6
Foliage	28.9	38.8	NA	Foliage	44.2	68.3	NA
Total minus foliage		42.9	55.6	Total minus foliage		77.8	186.7

Standish et al. (1985) equations (Table 2). This difference could likely be explained by differences between the geographic location of the two study locations, as well as differences in the field protocol for sub-sampling branches. The Standish et al. (1985) equations were fit from a dataset stemming from throughout the province of British Columbia, Canada where a difference in growing season duration and conditions may result in less branch AGB than in the mid latitudes of lodgepole pines range, where the data in this study are sourced. The sub-sampled branches selected in the Standish et al. (1985) study were randomly selected from three diameter classes, two from each class, whereas in this study branches were randomly selected, independent of size, from three different live crown height strata, with four from the bottom, three from the middle and two from the top stratum, giving greater weight to the portion of the crown where larger branches typically occur. As a result of this difference in predicted branch AGB, the predicted total tree AGB without foliage (TTWOF) when measurement error is not accounted for is greater than that of the regional equations. This result contrasts to the results found by Chojnacky (2012) who found the aforementioned hybrid CRM approach to yield predictions that were less than those from the current regional suite of equations for all but two genera. RMSE values for tree-level component and TTWOF estimates were generally larger for the regional models, with the RMSE for the regional bole and branch component models being 53% and 41% higher, respectively, than the CRM component model RMSEs. The TTWOF RMSE for the regional estimate was also 45% higher than the CRM estimate.

With the integration of measurement error into the model errors, this difference between TTWOF RMSE values was substantially larger (Table 3). As expected, all RMSE values increased for all tree-level component and TTWOF RMSE values, but the 621% increase from 79.56 kg without measurement error to 573.95 kg with measurement error for the regional bole component model RMSE was dramatic. RRMSE values for all regional models showed substantial increase as well (Table 4). This substantial imprecision is most likely due to extrapolation, which occurred through the random simulation of measurement errors. The measurement error simulation procedure produced intermittently extreme values of DBH and HT for inputs into the equation. Hence, this dramatic increase illustrates the model not being suitable for extrapolation outside the range of DBH and HT for which it was intended. With the TTWOF RMSE value for the regional equations being almost five times that of the CRM TTWOF RMSE value, the CRM was the more precise approach for tree level estimation of AGB. The model prediction for the regional bole component model also increased a substantial 86% with simulated measurement error integrated, resulting in a 72% increase for TTWOF. The CRM model predictions for branch and foliage AGB increased slightly, while the predictions for bole and bark AGB decreased with simulated measurement error, resulting in a 7% decrease for TTWOF for the CRM prediction.

3.2. Per unit area estimates and uncertainty

When only sampling error is considered for per unit area estimation, the standard error of the means for the CRM were greater in magnitude than those produced using the current regional equations (Table 5), showing a reversal in the trend observed with the model RMSEs. As was the case with the tree-level predictions, the bole and branch component models comprise the two greatest portions of the TTWOF variability, with the CRM branch model precision being substantially less than the regional branch model. This relatively large TTWOF RSE value can likely be attributed to two reasons relating to the ground plot data. First, the ground plot data were combined from different forest locations, with different species compositions, stand densities and structure. Thus, the variability between the 32 cluster plots was expectedly large. Second, the small sample size of only 32 cluster plots could be contributing to these large RSE values as well. Similar to the tree-level predictions when measurement error was integrated, the CRM predictions for all components and TTWOF were larger than those produced by the regional equations.

When the model error was integrated into the simulations for per unit area estimation, the precision of the current regional equation predictions was relatively unchanged; showing less than a 2% increase in the SE for TTWOF, suggesting the model error of the

Table 5
Per hectare estimates and SE values for CRM and regional equations, without accounting for measurement or model error. Total minus foliage, the sum of the per hectare component estimates, is used as another means for comparison between the models. Tree-levels units are in kilograms of dry biomass per hectare.

Sampling error only					
Mean			SE		
Component	CRM plot-level	Regional plot-level	Component	CRM plot-level	Regional plot-level
Bole	24690.09	17875.77	Bole	4373.71	3383.30
Bark	1862.87	1578.96	Bark	330.47	284.07
Branch	6489.43	2497.86	Branch	1130.67	436.49
Foliage	2603.83	NA	Foliage	438.48	NA
Total minus foliage	33042.39	21952.59	Total minus foliage	5834.85	4103.86

Table 6
Per hectare estimates and SE values for CRM and regional equations, accounting only for model error and for both measurement and model error. Total minus foliage, the sum of the per hectare component estimates, is used as another means for comparison between the models. Tree-levels units are in kilograms of dry biomass per hectare.

Mean			SE		
Component	CRM plot-level	Regional plot-level	Component	CRM plot-level	Regional plot-level
Sampling error (with model error)					
Bole	32768.33	16940.20	Bole	11649.73	3341.45
Bark	3253.51	1602.48	Bark	1253.84	295.64
Branch	9896.37	2971.86	Branch	3130.85	548.02
Foliage	3109.95	NA	Foliage	742.51	NA
Total minus foliage	45918.20	21514.55	Total minus foliage	16034.43	4185.12
Sampling error (with model and measurement error)					
Bole	33287.96	16701.94	Bole	12245.38	3566.87
Bark	6673.57	1600.91	Bark	2893.22	296.29
Branch	10227.99	2968.04	Branch	3335.24	547.98
Foliage	3272.53	NA	Foliage	803.54	NA
Total minus foliage	50189.53	21270.89	Total minus foliage	18473.84	4411.13

Table 7
RSE values for CRM and regional equations, for all three scenarios depicted in the previous three tables. Total minus foliage, the sum of the per hectare component estimates, is used as another means for comparison between the models.

Component	Sampling error (RSEs)					
	Sampling only		Model errors		Measurement and model errors	
	CRM plot-level (%)	Regional plot-level (%)	CRM plot-level (%)	Regional plot-level (%)	CRM plot-level (%)	Regional plot-level (%)
Bole	17.7	18.9	35.6	19.7	36.8	21.4
Bark	17.7	18.0	38.5	18.4	43.4	18.5
Branch	17.4	17.5	31.6	18.4	32.6	18.5
Foliage	16.8	NA	23.9	NA	24.6	NA
Total minus foliage	18.5	18.7	34.9	19.5	36.8	20.7

regional models are trivial contributors to the total uncertainty (Table 6). This is in line with the results of several authors who have looked at the effects of model uncertainty on per unit area estimates of forestry parameters (Berger et al., 2014; Breidenbach et al., 2014; McRoberts and Westfall, 2014; Ståhl et al., 2014). With the relatively small sample size of only 32 trees, this small increase in uncertainty could partially be attributed to the $Q^2 = 0.95$ constraint for establishing a baseline of comparison between the two sets of equations. However, we anticipate the SE values would only marginally increase without this constraint, as shown by McRoberts and Westfall (2014).

The precision of the CRM predictions, however, showed a substantial change with integration of model errors, with the SE for TTWOF increasing nearly threefold. With the CRM approach, where two estimates with their own amounts of uncertainty are multiplied together, the resulting estimate of total component AGB is hierarchical in nature; with the residuals of the total tree and component ratio equations being serially correlated. When this degree of serial correlation is present between the residuals of two hierarchical responses, predictions themselves will be unbiased and consistent, but will also be highly inefficient with the uncertainty estimates being enlarged (Kutner et al., 2004, p.481). Thus, as suggested by the results of the simulations in this study, the effect of applying both CRM estimates to plot data and multiplying the resultant estimates together, without accounting for the correlation structure between these two models, can produce per unit area estimates with a low degree of reliability. Future inventory-based efforts will be able to incorporate field-based measurements from FIA plots of errors in measurement of tree and other attributes (Pollard et al., 2006).

The effect of accounting for measurement error in addition to model and sampling error was seen in an increase in the SE and RSE values for both sets of equations (Tables 6 and 7). The TTWOF SE for the CRM and regional equations increased by 15% and 5%, respectively. The relative proportions of SE due to measurement, model and sampling error for the regional equations were 5%, 2% and 93%, respectively. Gertner (1990) found similar results for proportion of total variance while looking at the effect of all three sources of error while estimating stand-level volume per acre. The same relative proportions of SE for the CRM equations

were 13%, 55% and 32%, for measurement, model and sampling error, respectively. The relative proportion of the SE due to measurement error being as large as it is (13%) indicates the measurement error also contributed fairly heavily to the total per unit area uncertainty for the CRM estimates.

With a relatively small dataset of only 32 lodgepole pine trees that were subjectively selected, rather than probabilistically, from a fairly limited portion of the species' range, the predictions and their respective uncertainties reported in this study likely have some amount of bias. However, despite these admitted inferential limits, a clear depiction of the general contributions of measurement, model and sampling error to the total propagated error was given for both models.

4. Conclusion

As defensibly precise estimates of AGB across a range of scales are increasingly sought after by FIA and others users of individual-tree biomass equations, the need to produce reliable depictions of their associated uncertainty will continue to develop. This study has confirmed that not accounting for both measurement and model error does in fact result in an underestimation of per unit area uncertainty of AGB. Due to the substantial contribution of the models errors with the CRM equations, the per unit area estimates produced with those equations were much less precise than the current regional equations. With an increased sample size, issues with precision may be mitigated. However, these issues likely stem predominantly from the equation forms selected; specifically the new CRM approach described here.

Ultimately, if FIA were to implement the usage of these CRM equations for lodgepole pine in the Pacific Northwest region, accounting for the uncertainty of the combined equations should accompany this implementation. This would result in reliability statements with increased credibility. While the predicted means from the CRM equations could theoretically yield more accurate estimates when applied to different stands of lodgepole pine, the results of this study suggest those estimates would be less precise than those that would be produced by the current regional equations. The results of this study also provide an impetus for future research to depict the anticipated reduction in uncertainty associated with accounting for the aforementioned correlation structure. Further, given these results it is reasonable to assume the precision of the estimates produced by the CRM-FIA approach are substantially underestimated. While the issue of consistency with the current regional models is still prevalent, the comparatively greater reliability of their estimates of AGB on a per unit area basis, using the trees in this study, dissuades their replacement for small to midscale usage by the CRM equations evaluated here.

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