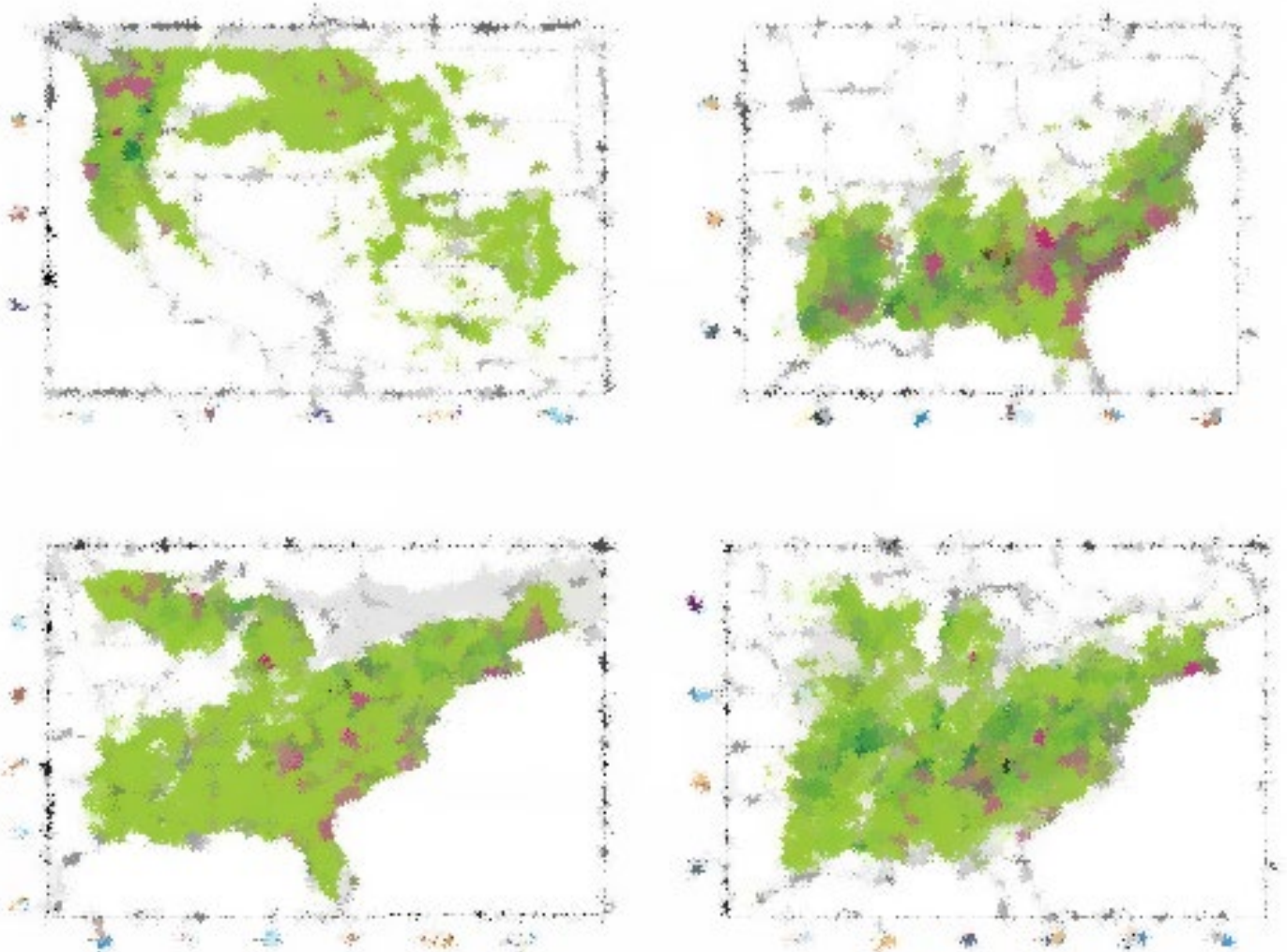




Gaps in Available Data for Modeling Tree Biomass in the United States

Jereme Frank, Aaron Weiskittel, David Walker,
James A. Westfall, Philip J. Radtke, David L.R. Affleck,
John Coulston, David W. MacFarlane



Abstract

When estimating tree-level biomass and carbon, it is common practice to develop generalized models across numerous species and large spatial extents. However, sampling efforts are generally incomplete and trees are not randomly selected. In this analysis, of the more than 1,000 biomass-related articles that were reviewed, trees were destructively sampled in over 300 studies to estimate biomass in the United States. Studies were summarized and past sampling efforts were explored to illuminate where the largest data gaps occurred in terms of tree components sampled, tree size, tree form, tree species, and location. The most prominent gaps were in large trees, particularly in Douglas-fir trees in the Pacific Northwest. In addition, tree roots were notably undersampled. Lastly, trees of poor or unusual form and low vigor were often not sampled, and this may introduce a systematic bias if not dealt with appropriately. More than 200 species did not have a biomass model or a single data point. The gaps presented here can be viewed as suggestions for future destructive sampling efforts, but the magnitude of a gap for a given model will ultimately depend on the selected modeling framework and the user's objectives.

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INTRODUCTION

Rationale

Given increasing interest in accounting for forest biomass and carbon stocks (Aalde et al. 2006, Pan et al. 2011) across the world, and specifically in the United States, there is a need to more closely examine limitations to current tree biomass estimation methods. At a broad level, biomass estimation methods are often categorized as (1) regional biomass conversion/expansion factors (e.g., Fang and Wang 2001), (2) stand-level biomass models, or (3) tree-level biomass models (Temesgen et al. 2015). In particular, there are two primary factors that influence biomass estimation accuracy: limitations to modeling techniques, and sampling gaps that limit available data and the geographic extent of model applicability. This review explores gaps in previous sampling efforts that limit the available data required to develop tree-level biomass models across the United States. Other important limitations of biomass estimation methods (including modeling techniques) are discussed in Weiskittel et al. (2015).

Generalized Allometric Models

Tree-level biomass models are generally derived by destructively sampling a subset of live trees, drying and weighing the separate tree components (e.g., stems, branches, foliage), and using allometry to relate some easily measured metric (e.g., diameter and sometimes height) to the dry weight of the entire tree or some portion or component of the tree. Destructive sampling is extremely costly and time intensive; thus, most biomass studies sample a relatively small number of trees over a generally small area. In addition, sampling units are difficult to select objectively or at random due to operating restrictions and landowner limitations. Consequently, sampling efforts are often coordinated with ongoing management objectives or otherwise constrained to areas where destructive sampling is feasible. As such, it is difficult to be entirely representative in both site and tree selection.

Variations in wood and bark properties, crown architecture, and stem form can result from different climatic, soil, or management factors (Larson 1963), making it challenging to extrapolate biomass to a different location or larger area. Those seeking to derive stand- and landscape-level biomass and carbon estimates often turn to geographically generalized tree-level allometric models, which use data from multiple studies and locations to refit models to a larger area (e.g., Schmitt and Grigal 1981).

In addition to considering how sites are selected, it is important to consider how individual trees are selected. Standards for sampling trees for volume and yield tables (e.g., Behre et al. 1926), and by extension biomass models, generally exclude trees with abnormalities and defects from model fitting because they detract from a study's ability to identify allometric relationships. This selection effect can result in a significant amount of systematic bias, leading to overestimates, particularly in hardwood biomass (e.g., MacFarlane and Weiskittel 2016).

Previous Tree Biomass Allometric Model Compilations

The plethora of published allometric models and their frequent use in estimating biomass and carbon across various scales has necessitated literature syntheses to understand limitations in both the models and the data used to build them. In Europe, Zianis et al. (2005) summarized the number of biomass models in terms of species by tree component and country. Similar syntheses have summarized models in Australia (Keith et al. 2000), sub-Saharan Africa (Henry et al. 2011), southeast Asia (Yuen et al. 2016), South America (Cifuentes-Jara et al. 2013), and North America (Ter-Mikaelian and Korzukhin 1997). Jenkins et al. (2004)

summarized biomass models from 177 biomass studies for tree species commonly found in the United States. More recently, Chojnacky et al. (2014) updated these models. While most of these compilations focus on developing or comparing models, recent work in the United States has led to a compilation of actual tree-level volume, biomass, and component biomass data (Radtke et al. 2015).

Current Biomass Estimation Approaches for the U.S. Forest Inventory

Perhaps the most widely used standing tree inventory available in the United States is the USDA Forest Service, Forest Inventory and Analysis Database (FIADB) (O'Connell et al. 2016). This database is also considered the best source for estimating biomass and carbon at the landscape level in the United States. For example, the Forest Inventory and Analysis (FIA) program reports its carbon estimates to the United Nations Framework Convention on Climate Change (UNFCCC) (USEPA 2017), and the Department of Energy relies on FIA's estimates of biomass (Aalde et al. 2006). Furthermore, biomass is the basic unit of productivity used in numerous ecological studies (e.g., Clark et al. 2001, Parker and Schneider 1975, Whittaker et al. 1974), and it is clearly important that mean biomass predictions and characterizations of uncertainty are accurate.

To estimate tree-level biomass, FIA uses the Component Ratio Method (CRM) (Woodall et al. 2011b), having switched in 2008 from previously using regionally-specific biomass models (e.g., Wharton and Griffith 1993). CRM uses species-specific regional volume models, deducts cull to estimate sound cubic-foot wood volume, and uses biomass conversion and expansion factors (BCEFs) to estimate total aboveground biomass without foliage. These BCEFs include wood and bark density values (as presented in Miles and Smith 2009) as well as nationally and taxonomically generalized CRM models (as presented in Jenkins et al. 2003). These models are then applied to the tree list in the FIADB to estimate state, regional, and national biomass. Despite this recent switch to the CRM, assessment of the new approach has been minimal (e.g., Domke et al. 2012). A recent analysis using observed tree-level biomass data from the eastern states suggests that the CRM method underestimates biomass by 6-15 percent across the eastern United States (Radtke et al. 2017). Because a fully comprehensive destructive sampling effort to obtain tree biomass data across the United States has not been conducted, it is also important to understand how sampling gaps may influence past and future assessments.

An important underlying assumption of this work is that tree biomass can vary between species, diameter at breast height (d.b.h.) or d.b.h./height, and region even when other factors are held constant. Basic allometry suggests that for a given species within a region, biomass will increase as d.b.h. increases (Jenkins et al. 2003). In addition, for a given tree size, biomass will vary between species within a region due to differences in wood density (Miles and Smith 2009) and tree architecture. Regional differences, however, are more difficult to detect. For instance, Jenkins et al. (2003) found that biomass regressions of the same species varied considerably, but no regional patterns were apparent. This brings up the question as to whether apparent biomass differences should be attributed to regional variation, noise in biomass measurements, or high site-to-site variability.

Objectives and Expectations

The primary objectives for this study were threefold:

1. Report on the number of studies that have been conducted and the number of trees sampled by core component groups to estimate biomass in the United States.
2. Assess the sample sizes and diameter ranges for key species evaluated in previous studies.
3. Characterize the sampling locations of certain species and compare that to the geographic range of the species.

Data collected across these studies will ultimately be used to test the assumptions mentioned in the previous section. Thus, data gaps were considered in terms of (1) how they may affect generalized models and CRM estimators used to assess biomass at various scales across the United States; (2) how the data can serve to validate current models; and (3) how they might restrict future model applicability when using actual data. Ideally, from a validation perspective, the relative representation of data from destructively sampled trees would match the standing tree inventory. However, from a modeling perspective, ensuring sampling across the range of attributes may be preferred (i.e., ensuring some samples of large trees at the tail of size distribution rather than a high number of trees at the peak). To illustrate, the publicly available FIADB was used to compare and formally assess gaps in terms of tree size classes, species, and location.

METHODS

Recording Information for the Gap Analysis

Literature Review

To complete this analysis, an exhaustive search of the literature on tree biomass studies in the United States was conducted. First, previous tree biomass model syntheses and databases (Chojnacky et al. 2014, Jenkins et al. 2004, Ter-Mikaelian and Korzukhin 1997) were examined, and the literature describing the studies cited in these articles were used as a source for additional resources. The literature review leveraged these past works by providing additional details on each study, synthesizing the additional information, and incorporating newer datasets. In addition, this review encompassed a recent (and ongoing) compilation of biomass data from destructively sampled trees (Radtke et al. 2015), hereafter referred to as the “legacy tree database.” The data search for the legacy tree database extended beyond the peer-reviewed literature and incorporated a number of unpublished studies. As a matter of accounting and considering the widespread use of the models developed by Jenkins et al. (2004) and Chojnacky et al. (2014) in the United States, it was noted if the reviewed studies appeared in these works. It was also recorded if actual biomass data or only a model could be obtained from each study. For studies that had a model, it was noted if the model contained height as a predictor and if the author reported standard error. The objective was to quantify the number of trees greater than 1 inch d.b.h. within the United States for which at least one tree component was destructively sampled for dry weight. Studies were not included in the analysis if they were located outside of the United States, were compilations, were more theoretical or statistical in nature, measured only external characteristics (without any destructive sampling) on standing trees, sampled only seedlings (i.e., trees less than 1 inch d.b.h.) or shrubs, measured only green weight or volume, or focused on biomass estimates at the stand or regional level rather than the tree level. Exceptions to these rules included studies where both seedlings and larger trees were sampled and the number of each could not be determined. In these cases, the total number of sampled trees included seedlings.

Tree Components

The primary interest of this study was in estimating aboveground biomass (AGB). However, given that other researchers may be interested in the mass of individual tree components, all components sampled were reported. For instance, the CRM and biomass expansion factors (BEFs) in general rely on the relationship between a component (particularly bole biomass) and AGB (without foliage). In addition, recent studies suggest that variations in whole-tree mass are related to differences in the way mass is allocated to tree components (e.g., the crown) (Goodman et al. 2014), and that bole volume is strongly affected by the allocation of wood to branches (MacFarlane and Weiskittel 2016). Filling gaps in tree component data is also important because tree utilization is best understood when the tree is modeled as the sum of its interrelated parts (MacFarlane 2015). Finally, branch and bark models might provide preliminary estimates for bioenergy harvests (Conner and Johnson 2011, USDOE 2011), while foliage estimates are integral for ecosystem process modeling (e.g., Chapin et al. 2002).

The USDA Forest Service National Biomass Estimation Library (Wang 2014), an extension of the Jenkins et al. (2004) database, identified 47 different tree component classes, many of which can be seen as subclasses of other components. For this analysis, gaps in available data were assessed for nine tree component groups: (1) total stem (wood and bark) biomass; (2) branch wood and bark biomass; (3) total above-stump biomass (including foliage); (4) root biomass; (5) stem wood biomass; (6) stem bark biomass; (7) total above-stump wood and bark biomass (excluding foliage); (8) crown (foliage and branch) biomass; and (9) foliage biomass. Studies vary considerably in how they differentiate between size classes of roots or branches, and often models calculate the biomass of the entire component and do not separate by size. In this analysis, a study was considered to have examined root biomass if any portion of the root biomass was measured. For branches (wood and bark), the study had to include at least the live branch component, although for most studies, the branch component included both live and dead branches. There were also differences in how components were separated. For example, in most cases the foliage component was separated from the twig; however, in some cases, foliage was defined as leaf and twig (e.g., Lambert et al. 2005, Whittaker et al. 1974). Finally, studies varied in how they defined the stem, specifically whether it constituted the entire stem or merchantable stem, and how the merchantable stem was delimited (i.e., “topped”). For this analysis, the stem was considered to be sampled if the entire merchantable stem was sampled regardless of where it was delimited.

Tree and Site Selection Criteria

For each reviewed study, the author, year, species, and location were recorded. In addition, for each location by species combination, the sample size; average, minimum, and maximum tree diameter; and tree components sampled were recorded. Each study was then examined to determine if tree-sampling restrictions were imposed as evidenced by avoiding trees of poor form (e.g., low forks, excessive branching, or broken tops) or poor health (e.g., showing signs of low vigor, damage, or disease, and at high risk of mortality). The best available information for site locations was used to estimate latitude and longitude for each study. Frequently, coordinates could be estimated to within 0.05°, although accuracy was much lower for studies that had a location description that was either too general or the extent of the area sampled was too large and little site-specific information was provided. Based on the location data, trees were assigned to one of four FIA regional units: Northern, which was split into Northeast (NE) and North Central (NC); Southeastern (SE); Intermountain West (IMW); and Pacific Northwest (PNW).

The lack of uniformity in recording site characteristics across studies makes it difficult to utilize site factors in the modeling framework. Authors of many articles do not adequately explain how sites are selected and do not describe physiography, landscape, or stand attributes. Some studies utilize classification systems, but groupings often differ across studies or use qualitative descriptors such as poor and good, which makes intra-study comparisons difficult. Site index can be used to classify studies, but in a previous review, site index was recorded in fewer than 10 studies (Ter-Mikaelian and Korzukhin 1997). Instead, in this analysis, data gaps were assessed by location and region, two factors that can be viewed as proxies for variations in climatic conditions, edaphic characteristics (such as soil type or depth), and treatment.

Assessment and Quantification of Data Gaps by Location, Species, and Diameter

This analysis examined available models and actual data (i.e., data available in the legacy tree database) and includes summaries of (1) the total number of trees sampled across all studies; (2) the total number of studies conducted; and (3) the number of trees available in the legacy tree database across all species by components and region. The summaries can be seen as a first assessment of gaps in available data.

As a means to assess gaps in data by tree diameter, diameter distributions for a given species were compared between the FIADB and the legacy tree database. Boxplots showing the maximum, minimum, median, and 25th and 95th quantiles were used to show discrepancies between the distributions of the two datasets and to highlight the limitations in the range of trees sampled in the legacy tree database. Distributions of the data were further examined for species groups and species by proportion of trees and proportion of biomass.

To visualize and assess spatial gaps in data (i.e., do the number of trees sampled represent the biomass across a species' range), maps showing the FIADB-estimated biomass per acre for the 30 species with the most biomass across the continental United States were overlaid with the locations of past biomass studies. Latitudinal and longitudinal biases were depicted by calculating and plotting spherical centroids weighted by FIA plot biomass data and sample size in the legacy tree database. The FIA estimate for total tree biomass was calculated as oven-dry biomass in the merchantable bole + dry biomass of tops and limbs of timber species (DRYBIO_BOLE + DRYBIO_TOP in O'Connell et al. 2016). Percent error was calculated by taking the ratio of the distance between the centroids and the diagonal distance between the minimum and maximum coordinates and then converting this to a percentage.

A goal of this study was to quantify whether past sampling efforts undersampled trees of different sizes and species relative to the amount of biomass reported for trees of the specified sizes and species represented in the U.S. forest carbon inventory. The number of trees for a given species, diameter size class (d.b.h. <5 inches = 1; 5 to <15 inches = 10, 15 to <25 inches = 20, etc.), and FIA region in the legacy tree database and the percentage of the biomass present for the same groups in the FIADB were calculated. Potential gaps were described for illustrative purposes by using a baseline tree sampling objective equal to the FIADB biomass percentage x 10. As a measure of sampling effectiveness, the sampling completeness value (SCV) was calculated as the product of the number of trees in the legacy tree database and the sampling objective. In addition, representation for a biomass pool was calculated as the difference between the percentage of the number of trees in the legacy tree database and the percentage of biomass in the FIADB.

RESULTS

Over 1,060 studies were identified that were potentially related to tree-level biomass estimation. After eliminating studies determined not to contain data relevant to this analysis, 844 studies were further examined. A preliminary review of these 844 studies determined that 351 had actual tree-level aboveground or component biomass (e.g., stem, foliage, roots, or branches) measurements assessed in the United States. Trees were destructively sampled in most of the studies, but in some cases trees were cored and climbed with limited branch sampling (e.g., Sillett et al. 2015). Of the biomass studies that used destructive sampling, 25 were duplicates and were removed, leaving 326 unique studies with a combined total of 47,684 trees in the analysis (see Appendix 1 for a list of all studies). A total of 240 of these studies (74 percent) were not included in Jenkins et al. (2003), which developed generalized models using numerous finer-scale models to generate pseudodata.

Tree and Component Mass

A total of 24,791 trees (52 percent of the 47,684 trees sampled) were identified from 199 studies that employed destructive sampling for above-stump biomass across the United States ([Table 1](#); tables begin on p. 17). Stem biomass was measured for 27,080 trees (57 percent); stem wood biomass estimates were available for 25,618 trees (54 percent); and wood biomass estimates were provided for 20,283 trees (43 percent). Stem measurements generally were taken from a variable stump (generally ≤ 1 foot) to a variable top, which was almost always reported as a value < 4 inches diameter outside bark. Branch, crown, and foliage biomass was estimated for 22,197 (47 percent); 19,154 (40 percent); and 21,262 (45 percent) trees, respectively. Estimates for the stump and root portions of the tree were less common, with root biomass measurements identified for only 2,840 (6 percent) trees.

When considering legacy tree data only, the percentage of known trees measured ranged from 72 percent (14,548 out of 20,283 trees) for stem bark biomass to 13 percent for root biomass (363 out of 2,840 trees). Trees that had both stem and above-stump biomass measured included 11,402 trees from the legacy tree database and 17,251 trees across all studies. In the legacy tree database, above-stump biomass (with or without foliage) was measured for 14,073 trees. This number is slightly higher than the number of trees with above-stump biomass and the number of trees with total wood biomass ([Table 1](#)) because it included trees both with and without foliage. For the 30 species with the greatest biomass in the FIADB, subalpine fir¹, Sitka spruce, white fir, and grand fir were lacking in total aboveground estimates. Mountain hemlock and pignut hickory were undersampled for all components and have no known destructively sampled trees. Data for all 148 species that had at least one tree sampled can be found in Table S1 (supplemental files for tables S1-S8 and Appendix S2 are available at <https://doi.org/10.2737/NRS-GTR-184.s2>).

Tree Selection

Species

Gaps in species data were depicted by tree component ([Table 1](#)), study type ([Table 2](#)), and region ([Table 3](#)). Excluding more general taxonomic groupings and species in the Caribbean and Pacific, 354 unique tree species were identified in the FIADB. Models or legacy tree data were available for 148 of these species (see Appendix S2 in supplemental tables file for list), leaving 206 species for which a published biomass model could not be located. These 206 species, however, accounted for less than 10 percent of the total biomass in the FIADB. The

¹Scientific names for all tree species are listed in Appendix 2.

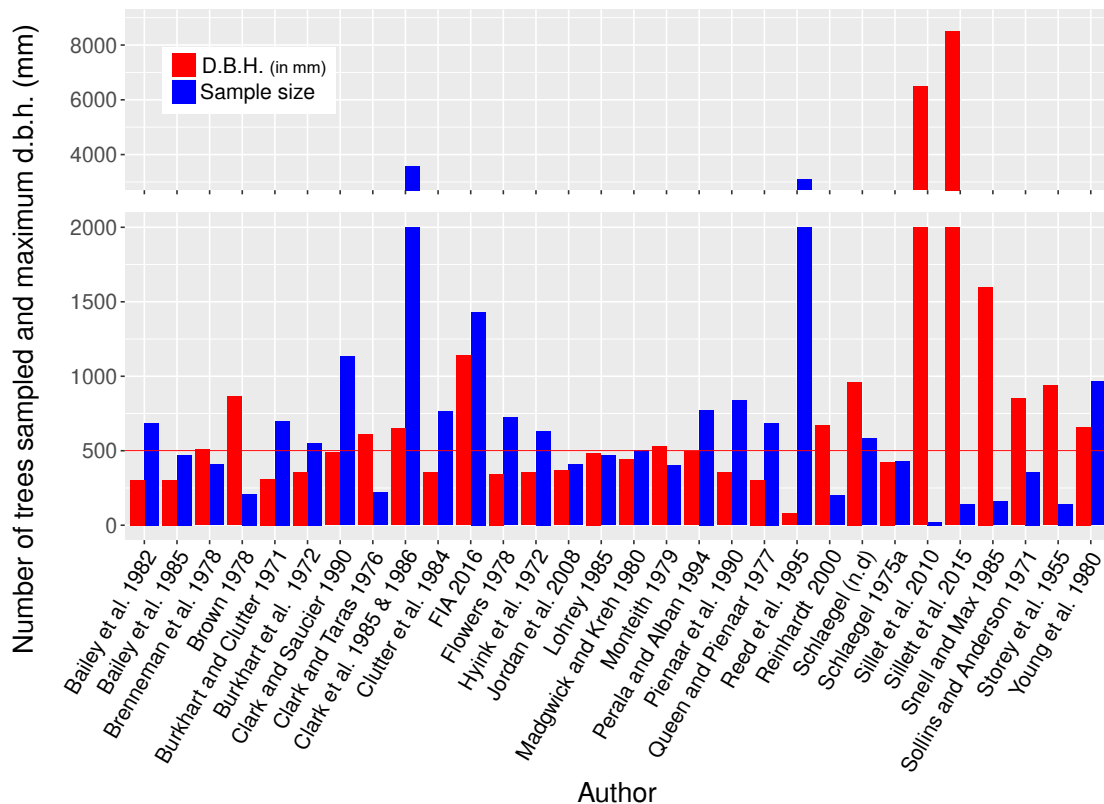


Figure 1.—Sample size and maximum d.b.h. (in mm = inches * 25.4) sampled for the 30 studies with the greatest importance index (simply sample size * maximum d.b.h. (mm) sampled). A threshold of 500 (red line) highlights the studies that sampled a maximum diameter tree greater than 19.7 inches (500 mm) or sampled more than 500 trees. Please note the discontinued scale. (See Appendix 1 for study citations.)

10, 20, and 30 species with the greatest amount of biomass in the FIADB made up 42 percent, 57 percent, and 67 percent, respectively, of the total biomass in the FIADB and 33 percent, 42 percent, and 61 percent, respectively, of the destructively sampled trees in the literature. The species with the greatest number of trees was loblolly pine, with 9,967 trees sampled (Table 2). By comparison, only 1,177 Douglas-fir trees have been sampled for at least one component of tree biomass. Of the 30 species with the greatest amount of biomass in the FIADB, pignut hickory and mountain hemlock had no samples in the legacy tree database (Table 2). Additional species with no samples included Pacific silver fir, shagbark hickory, and common pinyon (Table S2). It is worth noting that although more hickory trees were sampled, they were rarely identified to species (e.g., Clark et al. 1986, Wiart 1977). Additional ash, poplar, elm, birch, hackberry, and oak species were also sampled, but were not identified to species (see Appendix 2 in this document and Appendix S2 in supplemental tables file for the complete list of species and genera in this study).

Sample Size, Size Classes, and Diameter Distributions

Relatively few studies sample trees over 20 inches (500 mm) in d.b.h. and sample more than 500 trees. Given this finding, studies that sampled a high number of trees, including large trees, were noted as higher in importance. An importance index (sample size * maximum d.b.h. in inches/100) was calculated for each study, and the studies with the 30 highest importance indexes (Table 4, Fig. 1) contained 21,659 of the 47,684 trees evaluated for this analysis. These included the work of Alexander Clark (Clark and Saucier 1990; Clark and Schroeder 1986; Clark et al. 1985, 1986), which contributed 4,712 trees in a rather comprehensive sampling of the southeast region; Young et al. (1980), who sampled an estimated 965 trees in Maine; and

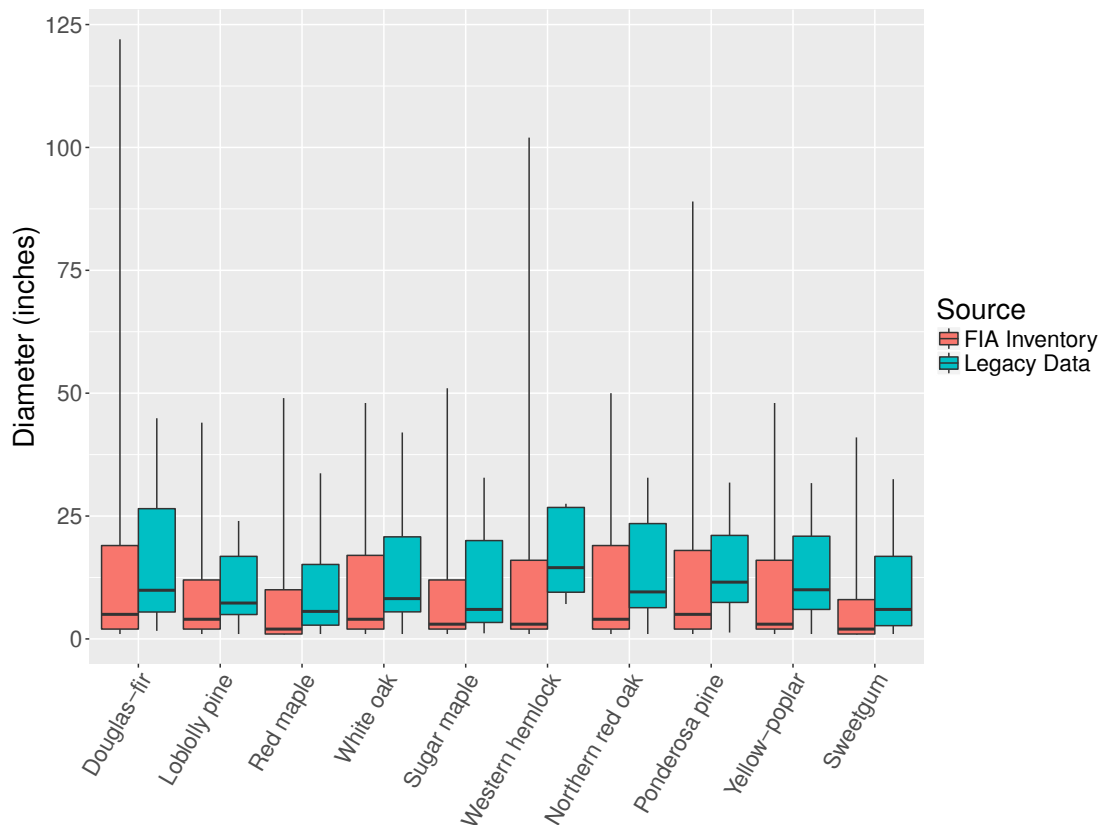


Figure 2.—The boxplot shows the diameter distributions of forest land trees in the FIA database compared to trees in the legacy tree database for the 10 species with the most biomass. The 25th and 95th quantiles are represented by the bottom and top of the box, respectively, and maximum and minimum values are represented by the top and bottom of the lines, respectively. The line that dissects the box marks the median value. Additional figures for the remaining 30 species with the most biomass in the FIADB are available as supplemental materials ([Figs. S2.2 and S2.3](#)).

Perala and Alban (1994), who sampled extensively across the Great Lakes region (NC region). The works of Sillett et al. (2010, 2015) are highly influential, being the only U.S. studies to measure above-stump biomass for trees over 50 inches in d.b.h. The redwoods sampled in California are by far the largest trees sampled across North America. Otherwise, the majority of the 30 studies with the highest importance index occurred in the eastern United States, with more than half from the southeast ([Table 4](#)).

For most species, the largest trees were generally undersampled (Fig. 2). Across the United States, the largest tree sampled for biomass was generally greater than 95 percent of the trees in the FIADB; however, for a given species, the largest destructively sampled tree was often less than half the size of the largest tree in the FIADB (Fig. 2). By count, hardwood trees with a d.b.h. from 1 to 19 inches and conifers with a d.b.h. from 1 to 23 inches represented 99 percent of trees across the landscape. While the vast majority of trees were in the smaller diameter classes, the greatest proportion of biomass was in the mid-range diameter classes (Fig. 3). By individual species, distribution peaks consistently shifted from saplings (1 to <5 inches d.b.h.) when examining the proportion of trees by count to small trees (5 to <15 inches d.b.h.) when examining the proportion of biomass by size class (Figs. S3.1 to S3.30). A shift in the peaks of the distribution from small diameter classes in the FIADB to larger diameter classes in the legacy tree database was also generally observed, suggesting that trees were destructively sampled to cover a selected range of diameters rather than being sampled strictly according to the distribution. However, these trends likely vary by state based on current composition and past management.

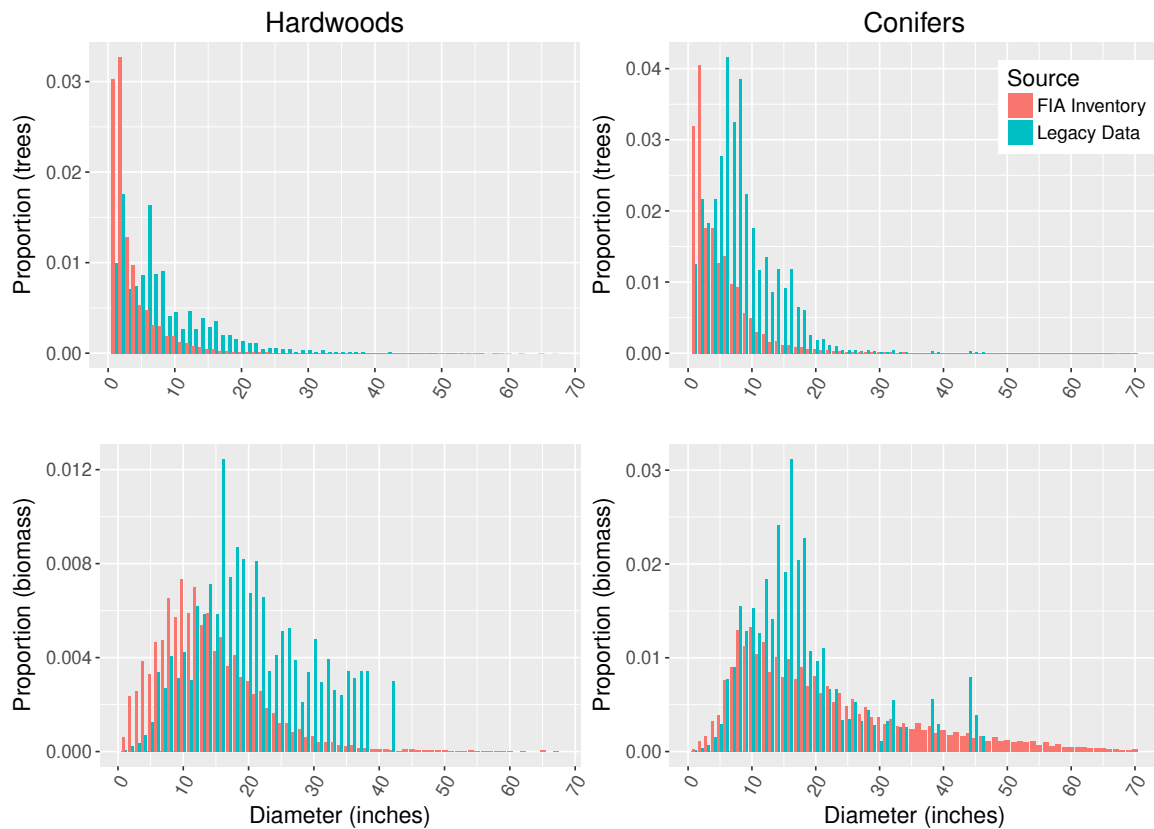


Figure 3.—Tree frequency by diameter class in the FIA and legacy tree databases for hardwoods and conifers (top panels) and the proportion of biomass by diameter in the FIA and legacy tree databases (bottom panels). Given the overwhelming proportion of biomass in redwood trees in the legacy tree database, they were excluded from this figure. Individual species figures for the 30 species with the most biomass in the FIADB are available as supplemental materials ([Fig. S3](#)).

Tree Sampling Restrictions Based on Form, Risk of Mortality, or Vigor

For many studies, it was difficult to determine whether sampling restrictions were imposed. Of the 326 studies (47,684 trees) examined, it was determined that 67 studies (10,080 trees) imposed sampling restrictions, while 46 studies (10,903 trees) described their sampling design as random and did not indicate any sampling restrictions. For the remaining 211 studies, tree selection methods were unclear. Clark et al. (1985, 1986) classified trees as growing stock, rough, and rotten/cull, and we assumed that there were no sampling restrictions; Perala and Alban (1994) randomly selected trees and recorded rot and stain, while Schlaegel (1975) took diligent note of external defect and measured rot and stain. Generally, sampling restrictions were evidenced in methodologies that avoided trees that were open grown, heavily defoliated, broken at the top, low-forked, diseased, or otherwise distorted (Brown 1978). In other cases, only good to average form or “healthy” trees were selected (Hocker and Earley 1983, Levia 2008). In one case, if trees were over 12 inches d.b.h., only poor form or less vigorous trees were selected (Bridge 1979). In other cases, the sample may have been biased toward a particular class of trees according to the objectives of a thinning study (Goldsmith and Hocker 1978).

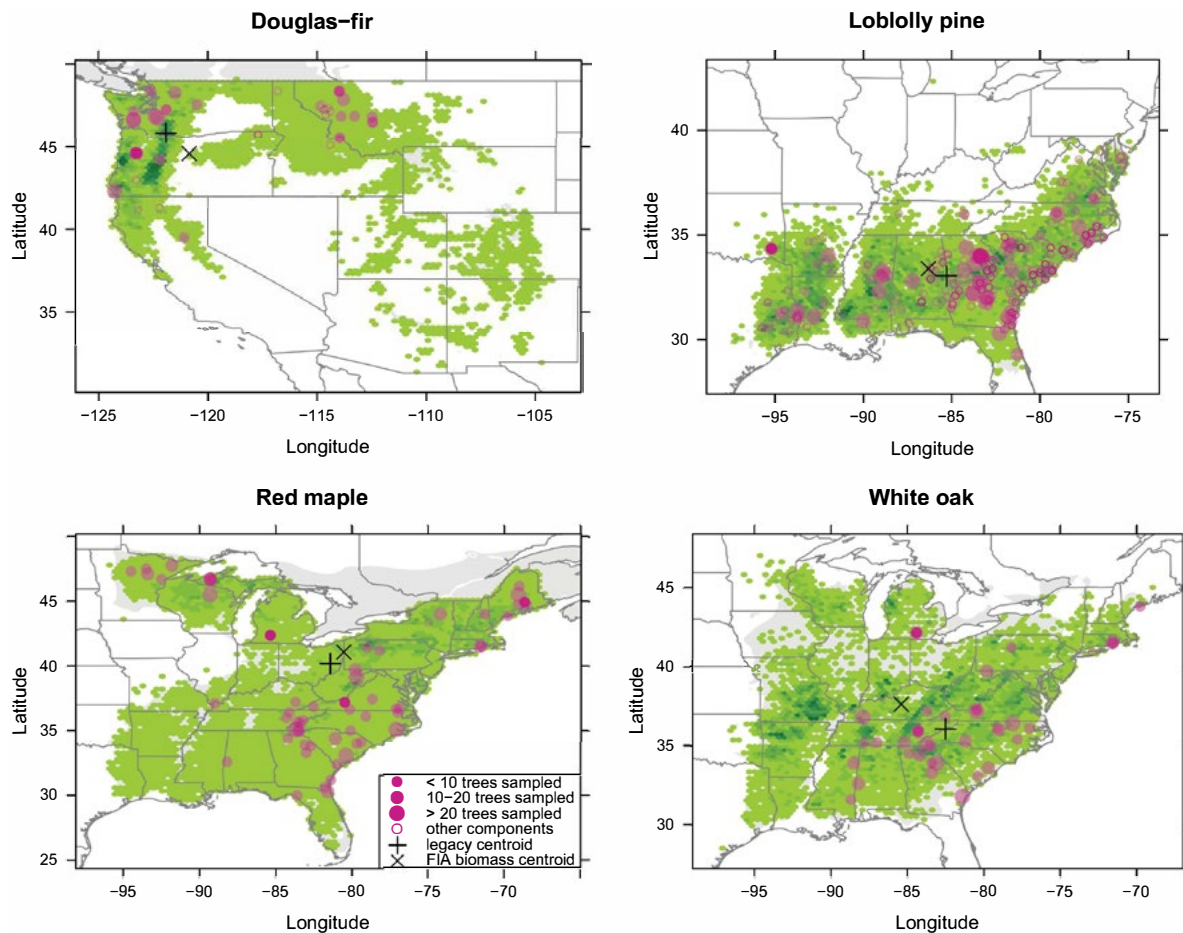


Figure 4.—Known biomass study locations and maximum sample size sampled for the four most prevalent species by biomass across the United States plotted over biomass per acre as estimated from the FIA database. Low biomass sites appear in lighter shades of yellow and green and high biomass sites appear in shades of dark green and blue. Species level maps for the 30 species with the most biomass in the FIADB are available as supplemental materials (Fig. S4).

Geography, Site Selection, and Location

A comparison of FIADB-estimated biomass per acre across the species range and known biomass study locations showed some variation for the four species with the most biomass (Fig. 4). For red maple, over 95 percent of reported biomass was in only 22 of the 31 states where this species occurs. In particular, the Allegheny Plateau in northwestern Pennsylvania and southwestern New York represented areas of high red maple biomass. However, prior to FIA sampling in 2014, no more than eight red maple trees had been sampled in these areas (Wood 1971), and none of these trees had a d.b.h. greater than 11.8 inches. In contrast, sampling for loblolly pine appeared to be relatively complete across its range, while Douglas-fir could be further studied in the southeast portion of its range, and white oak could be further studied in eastern Missouri. Comparisons between the legacy and FIA biomass centroids for Douglas-fir, loblolly pine, and red maple showed relatively good agreement, with differences of 6.4, 4.0, and 3.5 percent, respectively (Table 5). By comparison, white oak showed a southeasterly sampling bias of approximately 9.7 percent (311 miles), which would be alleviated by sampling towards the western edge of its range. Individual maps comparing the FIADB-estimated biomass per acre across the species range and known biomass study locations are available for the 30 species with the greatest biomass (Fig. S4.1-S4.30).

Over half of the trees sampled in the United States came from the southeastern region ([Table 3](#)), which included states as far west as Texas. While 42,962 trees were sampled in the eastern states (NE, NC, SE), only 4,722 trees (9.9 percent) were sampled in the western states (PNW and IMW).

Data Gaps by Region, Tree Species, and Diameter Class

The percentage of total biomass and the number of legacy trees sampled for aboveground wood and bark biomass (with or without foliage) were calculated for species by region by diameter class combinations. The 30 combinations with the greatest amount of biomass accounted for approximately a third of the cumulative biomass in the FIADB, and tentative sampling objectives were met for most of these groupings ([Table 6](#)). The sampling objective was not met in all cases, however, and the 30 species with the most biomass where the sampling objective was not met (i.e., $SCV < 1$) are highlighted in [Table 7](#). In the SE, species including loblolly pine, yellow-poplar, and white oak were adequately sampled in both the 10 and 20 inch diameter classes, as were slash pine, red maple, and water oak in the 10 inch diameter class. However, when examining all groupings, species such as pignut hickory and sugar maple in the 10 inch diameter class and loblolly pine in the 30 inch diameter class were undersampled (see [Table S7](#) for all tree groupings). In the PNW, large Douglas-fir (40 to 50 inch diameter classes) and western hemlock (10 to 30 inch diameter classes) were noticeably undersampled, along with 20 to 30 inch Douglas-fir and grand fir in the IMW. In the north-central region, no 20 inch black oak, 10 inch green ash, or 10 inch black ash trees were sampled. In the northeast region, species such as red maple and northern red oak (*Quercus rubra* L.) in the 20 inch diameter class were notably undersampled. Large Douglas-fir was also underrepresented, while loblolly pine was perhaps overrepresented with more than 1,400 trees sampled in the 10 inch diameter class (i.e., 10 inch loblolly pine make up 4.6 percent of the biomass in the FIADB and 10.1 percent of the trees in the legacy tree database). In addition to 20-40 inch Douglas-fir, the most underrepresented trees included 10 inch red maple, 20 inch western hemlock, 10 inch lodgepole pine, and 10 inch sugar maple ([Table 8](#)).

DISCUSSION

Alternatives for Further Sampling

The main objective of this research was to identify current gaps in tree biomass data so that future studies might optimize sampling, and thereby reduce uncertainty in predictive biomass models. This work highlighted some of the gaps that exist in currently available data by tree components ([Table 1](#)), species ([Table 2](#)), and regions ([Table 3](#)). In addition, the maps (Figs. 4 and 4S) can be used to assess where spatial gaps exist for a given species. For example, a total of 219 Douglas-fir; 2,168 loblolly pine; 445 red maple; and 360 white oak legacy trees were destructively sampled for above stump biomass (above stump legacy trees in [Table 1](#)). This might provide an adequate sample for predicting aboveground biomass for these species if the trees were spatially well-distributed. However, because they are not (see Fig. 4), additional sampling may be necessary to fill gaps across the species ranges where key landscapes and habitats are not represented, thereby minimizing the potential influence of spatially distinct patterns. Lastly, the results illustrate the lack of a representative sample in terms of diameter distributions, which are shifted towards larger trees but rarely contain the largest trees. (Figs. 2 and 3).

Overall, the most robust assessment of gaps seems to come from comparing biomass pool proportions in the FIADB to sample sizes in the legacy tree database. To match the effective population, the largest gaps for a given biomass pool are defined as having a low number of trees and a high amount of biomass in the FIADB. Regionally, the most prominent data gaps were in the PNW and IMW regions and tended to align with tree size rather than species. Despite being well represented in the FIADB, groupings in the 20- to 50-inch diameter classes appeared to be the most undersampled. For future sampling efforts, one approach might be to set a tentative sampling completeness value (SCV) goal of one and sample from each group until this goal is met. In particular, this approach would suggest sampling large Douglas-fir trees in the PNW region as well as northern red oak and red maple in the NE region ([Table 7](#)). The sampling objectives presented in Tables 6 and 7 could be increased based on user's objectives and available resources. Representation (i.e., the proportion of trees in the legacy tree database compared to the proportion of biomass for a given biomass pool) is important to consider because an unrepresentative database would result in erroneous projections of model error if not dealt with appropriately.

Although these are imperfect assessments, they serve as reasonable prioritizations of current needs (i.e., by species, diameter class, and region) until a more robust assessment of uncertainty and required sample size is undertaken within a specific modeling framework. For instance, recent work by Clough et al. (2016) suggests that the greatest relative uncertainties in AGB are in the southern portions of the IMW (where woodland species dominate) and eastern portions of the PNW. Ultimately, continued sampling for a given biomass pool would be determined by the number of trees sampled and model uncertainty after accounting for diameter and height.

Sampling to mirror the effective population is practical for many applications. From a modeling perspective, however, it may be useful to sample across the range of attributes in the population. Using this approach, the legacy tree database and literature may have oversampled small trees, undersampled large trees, and failed to sample species up to the edge of their range, and thus, the current literature and available data may not adequately capture the full range of attributes or variability in the population. In contrast to sampling to match the effective population, an alternative approach would be to sample at the “fringe” to best understand the broad range of variability for a population. This would include sampling less prevalent species, sampling at the edge of a species' range, and sampling the largest trees. For instance, large trees are presently a relatively small part of the landscape, but shifts in management practices may create the potential to greatly increase carbon stores (Stephenson et al. 2014).

Model-based Approaches to Fill Data Gaps

The cost of extensive sampling may make it prohibitive to adequately represent species and size classes across the entire United States. As such, in this section modeling techniques are considered, including (1) validating and developing species-group models; (2) using spatially explicit models; and (3) using pseudodata to fill gaps where the greatest paucity of data exists. These approaches may offer solutions for modeling gaps in available data, but species-group and spatial models may support a rationale to sample across the widest range of possible attributes rather than sampling to match the effective population. Errors associated with each approach are largely unquantified so these approaches will need testing, and continued sampling is recommended to update and validate a selected modeling approach.

Nonspecific Models and Species-group Models

When few data points are available for a given species, a species-group approach (i.e., predicting biomass for a single species using species that share similar traits or phylogeny) may be useful. However, a model fit to genus-level data then applied to individual species may incur bias, and this bias has largely been unquantified (Weiskittel et al. 2015). The literature review revealed that only a few studies have grouped species. When employed, the grouping was mainly based on apical dominance (e.g., Brenneman et al. 1978). Hence, the relative advantages and disadvantages of grouping species remain largely unexplored. The species groups presented in Jenkins et al. (2003) were based primarily on phylogenetic similarities, while Chojnacky et al. (2013) incorporated species' specific gravity. A nonspecific modeling approach was supported when quantifying volume across a large area since estimates and uncertainties using nonspecific models did not substantially deviate from specific models (i.e., models developed for each species). Mean volume estimates were within 3 percent, and standard errors improved with the nonspecific models for both coniferous and deciduous species (McRoberts and Westfall 2014).

A species-group approach may further support sampling a broad spectrum of species, including the 200+ species that currently do not have a model or data point. This approach also suggests sampling less common species with no observations to validate species-group models since there is a theoretical threshold at which the sampling of the most common species ceases to improve predictions of biomass and uncertainty. In addition, considering that species distributions and abundance are ever-changing in the face of climate change (Iverson and Prasad 1998), disease and pest outbreaks (e.g., eastern hemlock and white ash), and human disturbance (e.g., red maple [Abrams 1998]), models that are sensitive to these factors should be sought. These prospects may warrant model exploration that extends beyond taxonomy to include physiologically meaningful categories such as species tolerances (e.g., Niinemets and Valladares 2006), or not grouping at all and predicting with wood properties such as wood density. For instance, modeling approaches that incorporate wood density across many species have been shown to work well in the tropics (e.g., Chave et al. 2014) and in the northern United States (MacFarlane 2015).

Spatial Considerations and Spatially Explicit Models

Since site selection is generally opportunistic, bias may occur; thus users will need to consider whether a model is suitable for a given application. Ideally, site-related factors would be included in models, but as noted earlier, problems arise because there is little consistency in how sites and treatments are described, and different authors use various classification systems for soils and geographic factors. Incorporating tree height may help to account for these potential site differences, but only 44 percent of the studies with models incorporated height as a predictor variable (Table 4). It is interesting that height is not incorporated into biomass models more frequently. This may, in part, be due to the study scope. For example, studies that collect data only across homogeneous growing conditions probably warrant a diameter-only regression model. In contrast, studies that sample across a wide range of sites require height in their models (e.g., Clark et al. 1985, 1986) or height and site for some species (e.g., Perala and Alban 1994). Incorporating height (which is generally available in the legacy tree database) into models will likely help to explain site and stand characteristics that cannot be explained in diameter-only models. Additional variation may be explained by age and soil, but this information is not always easily measured in an inventory.

The general lack of a representative sample across the entire United States may require that users employ more sophisticated modeling techniques to improve parameter and error estimates that result from spatial dependence and clustering for some species. Work in

the northeastern United States suggests spatial variability in height-diameter relationships between sites, but no systematic relationship to latitude and longitude were found (Westfall 2015). Mixed-effects modeling may offer a solution considering that the fixed-effects structure predicts across the entire dataset, while the inclusion of random effects parameters may improve local predictions (De-Miguel et al. 2014, Westfall 2016). By assessing differences in a fixed-only versus mixed-modeling approach, one may determine whether variation between ecoregions (e.g., Bailey 1995) or states exists and to what extent the variation exists, but sample size may be a limiting factor. Models that include explicit spatial modifiers on parameters and parameter standard error estimates might be most appropriate (e.g., Babcock et al. 2013). The effect of this would likely be expressed as greater uncertainty as predictions are made beyond the general availability of existing data.

Pseudodata Vs. Actual Data

The number of destructively sampled trees in terms of the whole body of “literature” (i.e., all studies with and without models) and the number of trees in the legacy tree database were quantified. Over half of the trees (25,187) that were identified as having been destructively sampled are not currently available in the legacy tree database, but the majority of these trees (24,388) had associated models. The trees in the legacy tree database can be viewed as actual data, and while using actual data is preferred, a model could be used to predict pseudodata where large spatial, species, or size gaps exist.

The generalized models presented in Jenkins et al. (2003) were fit after generating pseudodata from regression models reported in the literature (Pastor et al. 1984). Models developed from pseudodata, however, have some important limitations (see Lambert et al. 2005) and may introduce error when back-predicting from the original regression model (Baskerville 1972, Snowdon 1991). Additionally, the models have only a tenuous link to empirical data, and the error estimates are propagated using pseudo-ranges (see Jenkins et al. 2004). As such, while the approach may lead to reasonable mean estimates across multiple studies and large regions, it does not provide realistic error estimates, particularly within a site or study.

Generating more realistic measures of uncertainty is integral to providing more realistic simulated data. This requires measures of uncertainty, such as the standard error, that accompany models used to generate pseudodata. Of the 326 studies that were reviewed, 252 studies presented models to predict biomass of at least one tree component. Across all studies, standard error (generally on the mean rather than the parameters) was reported for 55 percent of the models. R^2 values were reported more frequently, and recent work shows that using R^2 values may provide improved pseudodata estimates (Wayson et al. 2015). Bayesian approaches to simulating data are also proposed in Henry et al. (2015). However, questions remain about the suitability of pseudodata, and standard errors on the parameter estimates tend to be underestimated (Magnussen and Negrete 2015). The legacy tree database could be a valuable tool for testing methodologies for generating pseudodata. However, when available, we advocate using actual data in all model development.

Sampling for Trees of Varying Form, Risk, and Vigor, and Improving Estimates of Component Allometry

Of the 113 studies for which tree selection methods were determined, more than half of the studies imposed sampling restrictions by selecting trees of average and better vigor and by avoiding forked (as noted by MacFarlane and Weiskittel 2016) and otherwise deformed trees. Using models that avoid trees that are poorly formed (e.g., low forking or with a broken top) or at a high risk of mortality (i.e., of low vigor), as evidenced by broken branches, severe

mechanical damage, and fungal pathogens (Pelletier et al. 2013), may overestimate the biomass of low vigor/high risk trees, leading to overestimates at larger strata.

The height to the tree's lowest branch and the size of the largest branch may help explain the proportion of bole-to-branch biomass (MacFarlane 2011) and bole-to-AGB. Height to the lowest branch was almost never included as a predictor, and only a few biomass studies assessed the influence of form or health on biomass estimates (e.g., Bickelhaupt 1979). In addition, classifying trees in terms of form and risk (Pelletier et al. 2013) may improve estimates of tree merchantable volume (Castle et al. 2017) and decay (Frank et al. 2018), which in turn affects volume and biomass estimates when discounted from gross volume. It is recommended that future studies examine how variation in tree form and health may influence biomass estimates by sampling diseased and deformed trees. Further, a clear and broadly applicable classification or measurement protocol is necessary for assessing standing tree form and risk to mortality.

Although root biomass can constitute approximately 30 percent of the total tree biomass (aboveground + belowground) (Grier and Milne 1981, Young et al. 1980), roots were the most undersampled component. Of the studies observed, only 4 sampled root biomass for Douglas-fir and only 13 sampled root biomass for loblolly pine, while only a single study examined red maple root mass, and no studies included belowground biomass for western hemlock. Hence, it is important to investigate root biomass in western hemlock and red maple. In addition, although above-stump biomass (including foliage) is available in over 12,000 trees in the legacy tree database, only 9,383 of the trees were sampled for all major components (i.e., stem wood, stem bark, branch, and foliage). We recommend weighing all major aboveground components separately for any destructive sampling endeavor.

SUMMARY, LIMITATIONS, AND RECOMMENDATIONS FOR FUTURE RESEARCH

Summary

This review included 326 studies with 47,684 trees that were destructively sampled for at least one tree component. This is a conservative estimate of the data available because not all existing biomass studies were located and reviewed, and more trees have been sampled since these numbers were tabulated. For example, the following articles are known to contain relevant root biomass data in the United States, but were located after this analysis was completed: Samuelson et al. 2014 (36 longleaf pine trees); Litton et al. 2003 (45 lodgepole pine trees); Omdal et al. 2001 (80 lodgepole pine trees); Pearson et al. 1984 (89 ponderosa pine trees); Foster (1985 (9 balsam fir trees). Additional studies and root biomass data are also presented in Cairns et al. (1997).

As of March 2016, the actual data from 159 studies have been located, accounting for 22,497 trees in the continental United States (including Alaska), including 9,383 trees that have data for each major component (i.e., stem wood, stem bark, branch, and foliage). Presently, these data are available in a permanent online repository available at legacytreedata.org (Radtke et al. 2015) where researchers can share data and analyses to improve biomass and carbon estimation at various scales.

Based on this comprehensive assessment of existing literature, the most notable gaps in tree biomass data included (1) very large trees (>40 inches d.b.h.), particularly large conifers in the PNW region; (2) root and stump biomass from most species; and (3) trees that diverge

from an idealized form for timber production or that have low vigor. In addition, although the literature was not formally explored for these factors, very few studies included open-grown trees, trees in urban landscapes, and dead and dying standing trees. The lack of studies of the latter supports recommendations that additional research is required to quantify this carbon pool and meet UNFCCC reporting requirements (Woodall et al. 2011a).

Limitations

This gap assessment focused on how existing data and past studies are limited in terms of the species, tree components, and size classes of trees sampled, but there are some limitations to this approach. The most obvious data gaps were defined and compared to the effective tree population, which was estimated using the FIA database. However, exactly matching the effective population ultimately may not be necessary because the variation in a biomass pool determines whether there are enough trees sampled. In addition, depending on the adopted modeling framework (e.g., a nonspecific approach could replace a specific approach), sampling a wider range of less common species may be warranted rather than sampling a higher number of common species.

In addition to limitations in this gap assessment approach, how these data were collected must also be considered. First, since the data were often collected opportunistically and do not reflect a representative sample, more sophisticated modeling techniques may be necessary, and careful consideration should be given to the appropriateness of a model for a given biomass pool. Second, within-tree variation is often not accounted for and protocols can vary widely between studies, leading to random sources of variation.

Recommendations for Continued Research

The data that are preserved in the legacy tree database provide a valuable resource for addressing questions pertaining to biomass and carbon estimation at multiple scales (ranging from within-tree to national). A substantial number of biomass prediction studies hailing from the past 60 years have been preserved; however, data are missing from nearly half of the trees sampled. This result highlights the value of archiving all data because models and data generated from these efforts can be useful for large-scale modeling efforts. The FIA program continues to collaborate with university and industry partners to archive and digitize past datasets and to target trees for destructive sampling from those species and size classes needed to fill in data gaps. Additional collaboration is sought where feasible, and future destructive sampling efforts should consider adopting existing protocols (available at legacytreedata.org) to improve data compatibility across studies.

Studies that examine within-tree variation and compare different methodologies are needed and may shift prioritizations of future sampling requirements. In addition, optimal sample sizes will need to be considered as a function of uncertainty for a given biomass pool, as these will offer more appropriate objectives for future sampling.

Table 1.—Summary of number of trees and studies sampled for component biomass for the 30 species with the greatest biomass in the FIADB. For each tree component, estimates are given for (1) the total numbers sampled in the literature (including trees in the legacy tree database); (2) the number of studies in the literature (including trees in the legacy tree database; in brackets); and (3) the number of trees available in the legacy tree database. Zero indicates that there are no known destructively sampled trees or studies. Data for all 148 species sampled are available in Table S1.

Common name	Stem			Branch			Above stump			Stem and above stump			Roots		
	Total # of trees	# of studies	# trees in DB	Total # of trees	# of studies	# trees in DB	Total # of trees	# of studies	# trees in DB	Total # of trees	# of studies	# trees in DB	Total # of trees	# of studies	# trees in DB
Douglas-fir	761	[16]	332	829	[21]	431	598	[16]	219	585	[14]	211	134	[4]	9
Loblolly pine	5307	[46]	4203	2962	[44]	1810	2743	[41]	2168	2265	[29]	2078	515	[13]	156
Red maple	921	[22]	544	783	[17]	488	825	[21]	445	700	[15]	412	70	[1]	0
White oak	528	[13]	444	451	[10]	431	428	[11]	360	359	[8]	348	18	[2]	4
Sugar maple	427	[17]	273	326	[14]	196	421	[16]	238	377	[15]	238	56	[2]	14
Western hemlock	79	[4]	60	90	[5]	71	37	[3]	18	30	[2]	11	0	[0]	0
Northern red oak	257	[11]	204	313	[12]	171	137	[9]	82	102	[7]	78	14	[1]	0
Ponderosa pine	366	[11]	246	459	[15]	394	232	[10]	161	226	[9]	161	0	[1]	0
Yellow-poplar	411	[13]	335	377	[11]	331	291	[11]	210	224	[9]	208	0	[1]	0
Sweetgum	1040	[10]	806	1188	[10]	793	879	[8]	734	868	[7]	723	59	[3]	0
Lodgepole pine	205	[8]	135	202	[10]	202	95	[7]	76	91	[6]	76	0	[1]	0
Chestnut oak	193	[8]	140	209	[9]	140	159	[6]	87	127	[5]	87	0	[0]	0
Black oak	90	[5]	64	90	[5]	64	89	[5]	55	43	[2]	43	0	[0]	0
Engelmann spruce	113	[4]	84	121	[6]	92	51	[3]	19	48	[2]	19	0	[0]	0
Quaking aspen	717	[13]	672	438	[15]	393	389	[13]	240	249	[10]	214	46	[3]	8
American beech	196	[10]	134	146	[8]	84	150	[11]	86	134	[9]	72	58	[2]	15
Black cherry	113	[8]	82	102	[7]	82	130	[9]	61	91	[6]	60	0	[0]	0
White ash	90	[5]	72	58	[4]	40	65	[4]	7	25	[3]	7	0	[0]	0
Eastern white pine	299	[9]	221	263	[8]	190	189	[7]	136	155	[6]	102	43	[1]	0
Water oak	206	[2]	206	396	[3]	206	215	[3]	215	206	[2]	206	0	[0]	0
Slash pine	2582	[21]	1281	1318	[18]	784	1308	[17]	988	1176	[13]	988	94	[5]	58
White fir	22	[2]	10	34	[3]	22	12	[1]	0	12	[1]	0	0	[0]	0
Post oak	30	[3]	30	30	[3]	30	63	[3]	30	28	[1]	28	0	[0]	0
Mountain hemlock	6	[1]	0	6	[1]	0	6	[1]	0	6	[1]	0	0	[0]	0
Subalpine fir	72	[4]	63	68	[4]	59	9	[1]	0	9	[1]	0	0	[0]	0
Sitka spruce	40	[2]	23	24	[2]	6	17	[1]	0	17	[1]	0	0	[0]	0
Grand fir	27	[1]	27	69	[3]	69	0	[0]	0	0	[0]	0	0	[0]	0
Pignut hickory	0	[0]	0	0	[0]	0	0	[0]	0	0	[0]	0	0	[0]	0
Eastern hemlock	167	[7]	120	136	[6]	89	83	[5]	36	83	[5]	36	47	[1]	0
Scarlet oak	141	[5]	141	127	[4]	127	80	[3]	80	78	[2]	78	0	[0]	0
All 148 species	27080	[221]	17301	22197	[197]	12783	24791	[199]	12177	17251	[160]	11402	2840	[38]	363

Table 1.—continued

Common name	Stem wood			Stem bark			Total wood			Crown			Foliage		
	Total # of trees	# of studies	# trees in DB	Total # of trees	# of studies	# trees in DB	Total # of trees	# of studies	# trees in DB	Total # of trees	# of studies	# trees in DB	Total # of trees	# of studies	# trees in DB
Douglas-fir	503	[10]	147	503	[10]	147	694	[16]	315	906	[21]	434	926	[25]	489
Loblolly pine	7280	[41]	5418	4003	[34]	3583	2057	[26]	1695	2726	[29]	2280	2897	[45]	2015
Red maple	595	[11]	418	591	[10]	418	930	[23]	537	682	[14]	414	680	[16]	415
White oak	397	[8]	379	393	[7]	379	605	[15]	468	375	[9]	364	363	[8]	363
Sugar maple	265	[11]	231	265	[11]	231	444	[14]	196	377	[15]	238	349	[13]	195
Western hemlock	40	[3]	21	40	[3]	21	65	[4]	46	164	[6]	66	97	[5]	78
Northern red oak	170	[5]	170	170	[5]	170	302	[14]	185	158	[8]	78	162	[9]	82
Ponderosa pine	77	[6]	50	77	[6]	50	255	[11]	184	444	[14]	397	529	[18]	424
Yellow-poplar	327	[8]	283	327	[8]	283	468	[14]	377	224	[9]	208	225	[8]	210
Sweetgum	1146	[7]	802	1146	[7]	802	1195	[11]	795	783	[5]	723	1085	[8]	725
Lodgepole pine	63	[4]	48	63	[4]	48	139	[7]	120	239	[11]	224	206	[11]	202
Chestnut oak	130	[4]	130	130	[4]	130	270	[11]	143	129	[5]	90	129	[5]	90
Black oak	87	[4]	61	87	[4]	61	173	[8]	107	69	[3]	43	55	[4]	55
Engelmann spruce	79	[3]	50	79	[3]	50	108	[5]	76	98	[5]	69	99	[6]	67
Quaking aspen	690	[11]	671	664	[10]	645	415	[14]	363	279	[12]	244	292	[13]	250
American beech	65	[6]	65	65	[6]	65	216	[10]	98	135	[9]	73	131	[9]	69
Black cherry	58	[4]	58	58	[4]	58	132	[8]	86	91	[6]	60	81	[6]	61
White ash	39	[3]	39	39	[3]	39	113	[6]	80	26	[3]	8	26	[3]	8
Eastern white pine	121	[4]	121	121	[4]	121	206	[6]	153	207	[6]	154	273	[9]	200
Water oak	396	[3]	206	396	[3]	206	396	[3]	206	206	[2]	206	396	[3]	206
Slash pine	3423	[23]	2137	1526	[19]	1255	844	[11]	784	1048	[12]	988	1327	[18]	784
White fir	12	[1]	0	12	[1]	0	22	[2]	10	34	[3]	22	34	[3]	22
Post oak	29	[2]	29	29	[2]	29	32	[3]	32	28	[1]	28	63	[3]	30
Mountain hemlock	6	[1]	0	6	[1]	0	6	[1]	0	6	[1]	0	6	[1]	0
Subalpine fir	43	[3]	34	46	[3]	37	50	[3]	41	69	[4]	60	51	[3]	42
Sitka spruce	0	[0]	0	0	[0]	0	23	[2]	6	24	[2]	6	24	[2]	6
Grand fir	0	[0]	0	0	[0]	0	15	[1]	15	72	[4]	72	73	[3]	73
Pignut hickory	0	[0]	0	0	[0]	0	0	[0]	0	0	[0]	0	0	[0]	0
Eastern hemlock	64	[4]	64	64	[4]	64	126	[6]	58	104	[5]	57	138	[7]	91
Scarlet oak	138	[5]	138	138	[5]	138	147	[6]	147	92	[3]	92	80	[3]	80
All 148 species	25618	[164]	17328	20283	[150]	14548	22560	[178]	12308	19154	[166]	13057	21262	[206]	12511

Table 2.—Tree sample sizes and number of studies [shown in brackets] for the 30 tree species with the greatest biomass in the FIADB (for at least one tree component) and the minimum (min.) and maximum (max.) diameters for trees previously summarized in Jenkins et al. (2003) compared to legacy tree data presently accumulated. Totals also include legacy tree data from previously summarized articles (Both) and from articles that were not previously summarized and that have no legacy tree data (Additional literature). Additional literature was further separated into studies with models and studies without models. Total n = 47,684 trees for all species. Data for all 148 species sampled are available in Table S2.

Common name	Tree sample size [number of studies] by study type						D.B.H. range (inches)			
	Legacy tree database	Jenkins database	Both	Additional literature with models	Additional literature without models	Total	Jenkins min.	Jenkins max.	Legacy min.	Legacy max.
Douglas-fir	458 [15]	555 [7]	54 [3]	61 [2]	49 [3]	1177 [30]	0.3	63.0	1.0	44.9
Loblolly pine	6318 [37]	200 [5]	86 [4]	3347 [26]	16 [1]	9967 [73]	1.3	22.1	1.0	24.0
Red maple	202 [7]	479 [9]	400 [10]	65 [4]	23 [1]	1169 [31]	0.1	26.0	1.0	33.7
White oak	98 [5]	182 [6]	383 [6]	82 [4]	6 [1]	751 [22]	0.1	25.2	1.0	42.0
Sugar maple	136 [5]	247 [6]	137 [6]	85 [2]	26 [2]	631 [21]	0.1	27.4	1.1	32.8
Western hemlock	65 [3]	98 [2]	38 [2]	0 [0]	0 [0]	201 [7]	1.1	43.3	1.1	30.6
Northern red oak	36 [2]	96 [5]	182 [7]	108 [3]	33 [1]	455 [18]	0.1	28.7	1.0	32.8
Ponderosa pine	445 [11]	47 [2]	42 [1]	107 [3]	6 [1]	647 [18]	1.0	34.0	1.0	41.3
Yellow-poplar	90 [5]	102 [5]	291 [4]	55 [3]	59 [2]	597 [19]	0.2	25.6	1.0	31.7
Sweetgum	79 [3]	0 [0]	738 [2]	485 [9]	0 [0]	1302 [14]	1.0	20.7	1.0	32.5
Lodgepole pine	189 [7]	0 [0]	35 [3]	55 [2]	4 [1]	283 [13]	1.1	11.3	1.0	23.6
Chestnut oak	7 [1]	110 [4]	136 [4]	49 [3]	16 [1]	318 [13]	1.1	22.6	1.2	26.5
Black oak	7 [2]	60 [2]	100 [4]	40 [1]	0 [0]	207 [9]	0.2	34.8	1.1	24.0
Engelmann spruce	98 [4]	29 [1]	9 [1]	0 [0]	3 [1]	139 [7]	1.1	30.0	1.1	33.3
Quaking aspen	549 [9]	47 [2]	185 [3]	143 [3]	7 [1]	931 [18]	1.1	19.5	1.0	23.8
American beech	42 [4]	101 [3]	106 [5]	19 [1]	0 [0]	268 [13]	0.1	26.0	1.1	31.4
Black cherry	32 [3]	75 [4]	54 [3]	20 [1]	0 [0]	181 [11]	0.1	20.0	1.0	28.0
White ash	49 [3]	55 [2]	63 [2]	18 [1]	0 [0]	185 [8]	0.2	20.0	1.3	32.2
Eastern white pine	172 [4]	78 [3]	93 [4]	0 [0]	0 [0]	343 [11]	0.1	26.0	1.0	32.0
Water oak	13 [2]	0 [0]	202 [1]	190 [1]	0 [0]	405 [4]	1.0	20.0	1.0	20.0
Slash pine	2163 [16]	100 [1]	0 [0]	2508 [14]	0 [0]	4771 [31]	-	-	1.0	21.0
White fir	22 [2]	12 [1]	0 [0]	0 [0]	0 [0]	34 [3]	2.8	38.6	7.5	26.2
Post oak	1 [1]	0 [0]	31 [2]	33 [1]	0 [0]	65 [4]	3.0	20.9	3.0	20.9
Mountain hemlock	0 [0]	6 [1]	0 [0]	0 [0]	0 [0]	6 [1]	6.7	21.5	-	-
Subalpine fir	66 [3]	0 [0]	16 [1]	9 [1]	0 [0]	91 [5]	1.0	12.7	1.0	24.6
Sitka spruce	23 [1]	18 [1]	0 [0]	0 [0]	0 [0]	41 [2]	1.2	30.6	7.8	23.1
Grand fir	52 [3]	0 [0]	32 [1]	0 [0]	0 [0]	84 [4]	1.0	15.6	1.0	33.2
Pignut hickory	0 [0]	0 [0]	0 [0]	0 [0]	0 [0]	0 [0]	-	-	-	-
Eastern hemlock	89 [5]	68 [2]	34 [2]	0 [0]	0 [0]	191 [9]	0.1	33.5	1.0	33.5
Scarlet oak	4 [1]	0 [0]	157 [6]	0 [0]	0 [0]	161 [7]	1.1	22.2	1.1	27.8
All 148 species	16013 [133]	5704 [60]	6484 [26]	18684 [94]	799 [13]	47684 [326]	0.1	63.0	1.0	334.9

Table 3.—Estimates of the number of trees sampled by species and region for the 30 tree species with the greatest biomass in the FIADB. For each region estimates are given for (1) the total numbers sampled in the literature (including trees in the legacy tree database); (2) the number of studies in the literature (including trees in the legacy tree database; in brackets); and (3) the number of trees available in the legacy tree database. A dash indicates the species is not present in a given region in the FIA database, and zero indicates that there are no known destructively sampled trees or studies. Studies may bridge more than one region, leading to discrepancies between the apparent number of studies listed here and the totals listed in Table 2. Data for all 148 species sampled are available in Table S3.

Common name	Intermountain West (IMW)			Pacific Northwest (PNW)			Northeast (NE)			Southeast (SE)			North Central (NC)		
	Total # of trees	# of studies	# trees in DB	Total # of trees	# of studies	# trees in DB	Total # of trees	# of studies	# trees in DB	Total # of trees	# of studies	# trees in DB	Total # of trees	# of studies	# trees in DB
Douglas-fir	203	[8]	130	974	[24]	382	0	[0]	0	0	[0]	0	0	[0]	0
Loblolly pine	-	-	-	-	-	-	0	[0]	0	9967	[72]	6404	0	[0]	0
Red maple	-	-	-	-	-	-	495	[18]	188	346	[9]	259	328	[6]	155
White oak	-	-	-	-	-	-	217	[10]	65	478	[12]	400	56	[2]	16
Sugar maple	-	-	-	-	-	-	380	[12]	115	11	[3]	10	240	[8]	148
Western hemlock	12	[1]	12	189	[6]	91	-	-	-	-	-	-	-	-	-
Northern red oak	-	-	-	-	-	-	203	[11]	78	142	[6]	108	110	[5]	32
Ponderosa pine	383	[13]	316	264	[7]	171	-	-	-	0	[0]	0	0	[0]	0
Yellow-poplar	-	-	-	-	-	-	189	[9]	43	352	[10]	282	56	[2]	56
Sweetgum	-	-	-	0	[0]	0	0	[0]	0	1302	[14]	817	0	[0]	0
Lodgepole pine	138	[8]	134	145	[7]	90	-	-	-	-	-	-	0	[0]	0
Chestnut oak	-	-	-	-	-	-	95	[5]	21	207	[8]	122	16	[1]	0
Black oak	-	-	-	-	-	-	89	[4]	55	78	[4]	52	40	[1]	0
Engelmann spruce	125	[6]	93	14	[1]	14	-	-	-	0	[0]	0	0	[0]	0
Quaking aspen	48	[3]	41	160	[3]	27	30	[3]	30	0	[0]	0	693	[10]	636
American beech	-	-	-	-	-	-	200	[10]	80	52	[4]	52	16	[1]	16
Black cherry	-	-	-	-	-	-	141	[8]	46	34	[3]	34	6	[1]	6
White ash	-	-	-	-	-	-	114	[6]	41	31	[1]	31	40	[1]	40
Eastern white pine	-	-	-	-	-	-	115	[4]	72	183	[6]	163	45	[4]	30
Water oak	-	-	-	-	-	-	0	[0]	0	405	[4]	215	0	[0]	0
Slash pine	-	-	-	-	-	-	-	-	-	4771	[31]	2163	-	-	-
White fir	12	[1]	12	22	[2]	10	-	-	-	0	[0]	0	0	[0]	0
Post oak	-	-	-	-	-	-	0	[0]	0	65	[4]	32	0	[0]	0
Mountain hemlock	0	[0]	0	6	[1]	0	-	-	-	-	-	-	-	-	-
Subalpine fir	91	[5]	82	0	[0]	0	-	-	-	0	[0]	0	-	-	-
Sitka spruce	-	-	-	41	[2]	23	-	-	-	-	-	-	-	-	-
Grand fir	50	[2]	50	34	[3]	34	-	-	-	-	-	-	-	-	-
Pignut hickory	-	-	-	-	-	-	0	[0]	0	0	[0]	0	0	[0]	0
Eastern hemlock	-	-	-	-	-	-	104	[5]	36	71	[5]	71	16	[1]	16
Scarlet oak	-	-	-	-	-	-	49	[3]	49	112	[4]	112	0	[0]	0
All species	1555	[28]	1173	3167	[52]	1526	6121	[50]	1774	29901	[167]	16094	6940	[0]	1930

Table 4.—The 30 studies with the highest importance (import.) index (=sample size * maximum d.b.h.[in inches]/100) ranked from highest to lowest. Indicator (ind.) values of 1 = yes and 0 = no identify if a biomass model (Eq.) was presented, height (Ht.) was included, standard (Std.) error given, or sampling restrictions (Samp. rest.) imposed based on form/risk/vigor class. It is also noted if the article was present in the legacy tree database (Leg. tree), Jenkins et al. (2004), or Chojnacky et.al (2014). A proportion between 0 and 1 indicates that only a portion of the data has the given attribute. Data for all studies are available in Table S4.

Author	Region	Import. index	Sample size (no.)	Min. d.b.h. (inches)	Max. d.b.h. (inches)	Eq. ind.	Ht. ind.	Std. error ind.	Samp. rest. ind.	Leg. tree ind.	Chojnacky et al. 2014	Jenkins et al. 2004
Clark et al. 1985, 1986	SE	916	3580 ^a	1	25.6	1	1	1	0	1	1	1
FIA 2016	All	642	1430	1	44.9	0	-	-	1	1	0	0
Sillett et al. 2015	PNW	466	139	1.6	334.9	1	0	1	0	1	0	0
Young et al. 1980	NE	251	965	0.1	26	1	0	0	-	0	1	1
Schlaegel (n.d.) ^b	SE	221	582	1	37.9	-	-	-	-	1	0	0
Clark and Saucier 1990	SE	217	1132	5	19.2	0	-	-	-	1	0	0
Perala and Alban 1994	NC	151	774	1.1	19.5	1	1	0	1	1	1	1
Sollins and Anderson 1971	SE	120	357	1.1	33.5	1	1	0	-	1	1	1
Pienaar et al. 1990	SE	117	838	3	14	1	1	0	-	0	0	0
Clutter et al. 1984	SE	107	762	2	14	1	1	0	-	0	0	0
Snell and Max 1985	PNW	101	160	3.9	63	1	0	0	1	0	1	1
Flowers 1978	SE	98	724	2.2	13.6	1	1	0	1	1	0	0
Reed et al. 1995	NC	96	3083	0.1	3.1	1	1	0	0	0	0	0
Lohrey 1985	SE	89	467	1.3	19.1	1	1	1	-	1	0	0
Hyink et al. 1972	SE	88	632	5	14	1	1	0	0	0	0	0
Madgwick and Kreh 1980	SE	87	501	0.6	17.4	1	1	1	-	0	0	0
Burkhart and Clutter 1971	SE	86	701	3.1	12.2	1	1	0	-	1	0	0
Monteith 1979	NE	84	402	1	20.8	1	1	-	1	0.8	1	1
Bailey et al. 1982	SE	82	686	3	12	1	1	0	-	0	0	0
Queen and Pienaar 1977	SE	82	685	2.6	12	1	1	0	1	1	0	0
Brenneman et al. 1978	NE	81	407	2	20	1	0	0	0	0	1	1
Burkhart et al. 1972	SE	78	551	2.5	14.1	0	-	-	1	1	0	0
Brown 1978	IMW	71	210	1	34	1	1	1	1	1	1	1
Schlaegel 1975a	NC	71	426	1.1	16.7	1	1	1	0	1	0	0
Jordan et al. 2008	SE	59	407	5.5	14.4	-	-	-	-	1	0	0
Bailey et al. 1985	SE	57	472	1	12	1	1	0	-	0	0	0
Sillet et al. 2010	PNW	54	21	22.8	255.1	0	-	-	-	1	0	0
Clark and Taras 1976	SE	53	221	5.6	24	0	-	-	-	1	0	0
Reinhardt 2000	IMW	53	201	1	26.4	0	0	0	1	1	0	0
Storey et al. 1955	IMW+ PNW	53	143	1.5	37	1	1	1	1	1	1	0

^aThe figure of 3,580 trees sampled by Alexander Clark likely includes trees sampled from Clark et al. (1985), Clark et al. (1986), and Clark and Schroeder (1986). These studies along with Clark and Saucier (1990) reused data from four previous species-specific studies that he did on yellow-poplar, southern red oak, northern red oak, and scarlet oak. These four studies were not cited in this analysis.

^bSchlaegel (n.d.) includes multiple bottomland hardwood reports from the early to mid-1980s.

Table 5.—Centroid coordinates for the legacy and FIA databases for the 30 species with the greatest estimated biomass across the United States. Distances between the centroids and the diagonal distance across the range of the species' are given in miles (mi). Error (%) is calculated using the centroid error and the diagonal distance error. A dash indicates that there was insufficient data to determine the legacy centroids.

FIA species code	Legacy centroid longitude	Legacy centroid latitude	FIA centroid longitude	FIA centroid latitude	Distance between centroids (mi)	Longitudinal difference (mi)	Latitudinal difference (mi)	FIA diagonal distance (mi)	Error (%)
Douglas-fir	-121.9	45.9	-120.8	44.6	167.4	-83.7	145.0	2613.0	6.4
Loblolly pine	-85.3	33.0	-86.3	33.4	102.8	95.3	-38.5	2555.0	4.0
Red maple	-81.4	40.2	-80.5	41.1	124.6	-74.6	-99.8	3566.9	3.5
White oak	-82.5	36.1	-85.4	37.6	310.9	257.9	-173.7	3193.1	9.7
Sugar maple	-83.7	45.0	-81.8	43.2	254.5	-158.0	199.5	3229.9	7.9
Western hemlock	-124.3	46.4	-124.9	49.3	320.9	41.5	-318.2	3427.4	9.4
Northern red oak	-82.0	38.6	-82.4	41.2	297.7	34.7	-295.7	3300.0	9.0
Ponderosa pine	-115.1	39.1	-116.3	42.2	358.0	102.0	-343.2	3221.1	11.1
Yellow-poplar	-83.0	36.1	-82.3	36.8	99.1	-65.2	-74.6	2510.4	3.9
Sweetgum	-83.5	33.7	-85.9	34.0	221.9	219.9	-29.9	4511.9	4.9
Lodgepole pine	-114.6	43.2	-115.2	44.3	133.8	45.8	-125.7	3644.8	3.7
Chestnut oak	-82.6	36.5	-81.5	37.6	157.9	-97.7	-124.0	2090.1	7.6
Black oak	-79.5	38.3	-85.4	38.9	518.4	514.1	-67.3	3107.4	16.7
Engelmann spruce	-111.2	43.7	-111.3	42.9	91.7	6.9	91.4	2403.6	3.8
Quaking aspen	-93.2	48.3	-96.5	44.6	480.6	250.8	410.1	6592.9	7.3
American beech	-79.3	40.5	-78.8	40.9	56.9	-34.8	-45.0	3127.7	1.8
Black cherry	-80.5	38.3	-81.4	40.5	258.5	84.6	-244.2	3771.2	6.9
White ash	-84.9	37.4	-80.6	41.1	555.3	-371.9	-412.5	3429.6	16.2
Eastern white pine	-81.6	38.5	-79.0	42.9	530.2	-217.7	-483.5	2924.0	18.1
Water oak	-82.5	32.5	-87.6	32.5	479.3	479.3	3.4	2456.8	19.5
Slash pine	-88.0	31.3	-84.5	30.7	339.0	-331.5	70.8	2228.8	15.2
White fir	-123.0	44.1	-119.8	40.4	488.1	-266.9	408.8	2288.0	21.3
Post oak	-86.8	36.4	-92.0	35.0	495.4	470.4	155.7	3148.8	15.7
Mountain hemlock	-	-	-125.4	49.7	-	-	-	3755.0	-
Subalpine fir	-113.3	45.2	-113.7	44.9	37.4	26.2	26.7	3639.6	1.0
Sitka spruce	-133.2	55.9	-135.2	55.7	126.6	125.3	18.3	3336.1	3.8
Grand fir	-121.1	45.7	-118.1	46.0	234.1	-232.8	-24.8	1434.0	16.3
Pignut hickory	-	-	-83.9	36.9	-	-	-	3124.1	-
Eastern hemlock	-82.3	38.8	-77.1	43.1	648.4	-441.2	-475.4	2535.8	25.6
Scarlet oak	-82.1	36.8	-82.2	37.4	62.2	9.1	-61.5	2426.9	2.6

Table 6.—Percentage of biomass (% bio) and cumulative biomass percentage estimated by using the FIADB, number of trees in the legacy tree database (nleg) with above-stump woody biomass (with or without foliage), and diameter at breast height or diameter at ground line for the 30 region/species/d.b.h. class combinations with the greatest biomass in the FIADB. Diameter classes are grouped by saplings (1 to <5 inches) then by 10 inch increments (d.b.h. class 10 = 5 to <15 inch trees, etc.) The sampling completeness value (SCV) = $nleg/\%bio * 10$ and indicates how well sampled a group is. Representation (Rep.) is the difference between the percentage that the group comprises out of the entire legacy tree database by number and the percentage of biomass that the group comprises in the FIA database. In total 14,073^a trees with aboveground biomass (with and without foliage) were used here. Data for all region/species/d.b.h. class combinations are available in Table S6.

Region	Common name	D.b.h. class	% of biomass (%)	Cumulative biomass (%)	Number of trees in legacy tree database	Sampling Objective	SCV	Rep.
SE	Loblolly pine	10	4.6	4.6	1431	46	30.9	5.5
PNW	Douglas-fir	20	2.4	7.0	83	24	3.4	-1.8
PNW	Douglas-fir	10	1.9	8.9	116	19	6.2	-1.0
NE	Red maple	10	1.7	10.6	80	17	4.7	-1.1
SE	Loblolly pine	20	1.6	12.2	240	16	14.7	0.3
PNW	Douglas-fir	30	1.5	13.7	16	15	1.1	-1.4
SE	White oak	10	1.2	14.9	237	12	20.6	0.8
IMW	Lodgepole pine	10	1.1	16.0	38	11	3.3	-0.8
NE	Sugar maple	10	1.1	17.1	38	11	3.4	-0.8
SE	Sweetgum	10	1.1	18.2	444	11	40.8	2.7
PNW	Western hemlock	20	1.1	19.3	14	11	1.3	-1.0
IMW	Douglas-fir	10	1.1	20.4	30	11	2.8	-0.8
SE	White oak	20	1.0	21.4	86	10	8.4	-0.3
IMW	Douglas-fir	20	1.0	22.4	1	10	0.1	-1.0
PNW	Douglas-fir	40	1.0	23.4	6	10	0.6	-0.9
PNW	Western hemlock	10	0.9	24.3	21	9	2.2	-0.7
SE	Slash pine	10	0.9	25.2	599	9	67.0	4.5
NE	Northern red oak	20	0.8	26.0	7	8	0.9	-0.7
SE	Red maple	10	0.8	26.8	134	8	17.7	0.5
SE	Yellow-poplar	20	0.7	27.5	65	7	8.9	-0.1
SE	Post oak	10	0.7	28.2	26	7	3.6	-0.5
NE	Red maple	20	0.7	28.9	5	7	0.7	-0.7
NC	Sugar maple	10	0.7	29.6	66	7	9.9	0.0
SE	Yellow-poplar	10	0.7	30.3	159	7	23.8	0.9
NE	Sugar maple	20	0.6	30.9	15	6	2.3	-0.5
PNW	Western hemlock	30	0.6	31.5	4	6	0.6	-0.6
IMW	Engelmann spruce	20	0.6	32.1	10	6	1.7	-0.5
IMW	Engelmann spruce	10	0.6	32.7	36	6	6.2	-0.2
SE	Water oak	10	0.6	33.3	98	6	17.3	0.4
PNW	Douglas-fir	50	0.6	33.8	0	6	0.0	-0.6

Table 7.—The 30 groups that were most undersampled by region/species/d.b.h. class group where SCV was less than one. All groupings are ranked according to the percentage of biomass in the FIA database. Data for all region/species/d.b.h. class combinations are available in Table S7.

Region	Common name	D.B.H. class	% of biomass	FIADB Rank	Number of trees in legacy tree database	Sampling Objective	SCV
IMW	Douglas-fir	20	1.0	14	1	10	0.1
PNW	Douglas-fir	40	1.0	15	6	10	0.6
NE	Northern red oak	20	0.8	18	7	8	0.9
NE	Red maple	20	0.7	22	5	7	0.7
PNW	Western hemlock	30	0.6	26	4	6	0.6
PNW	Douglas-fir	50	0.6	30	0	6	0.0
NE	White ash	10	0.5	43	3	5	0.7
NE	Eastern hemlock	10	0.4	45	1	4	0.3
IMW	Utah juniper	20	0.4	49	3	4	0.8
PNW	Mountain hemlock	20	0.4	50	0	4	0.0
NE	Yellow-poplar	20	0.4	53	2	4	0.5
SE	Pignut hickory	10	0.3	58	0	3	0.0
SE	Mockernut hickory	10	0.3	59	0	3	0.0
NE	White oak	20	0.3	62	2	3	0.6
PNW	Ponderosa pine	30	0.3	63	0	3	0.0
NE	Black cherry	20	0.3	64	1	3	0.3
NE	Chestnut oak	20	0.3	67	2	3	0.6
PNW	Mountain hemlock	10	0.3	69	0	3	0.0
NE	White ash	20	0.3	70	2	3	0.7
IMW	Common or two-needle pinyon	10	0.3	77	0	3	0.0
NE	Eastern hemlock	20	0.3	85	0	3	0.0
PNW	Douglas-fir	60	0.3	87	0	3	0.0
PNW	Sitka spruce	20	0.3	89	2	3	0.8
PNW	Western hemlock	40	0.3	91	0	3	0.0
IMW	Douglas-fir	30	0.3	92	0	3	0.0
PNW	Sitka spruce	30	0.3	96	0	3	0.0
PNW	Pacific silver fir	20	0.3	98	0	3	0.0
PNW	White fir	30	0.2	100	1	2	0.4
NE	Black oak	20	0.2	101	1	2	0.4
PNW	Canyon live oak	10	0.2	104	0	2	0.0

Table 8.—The 30 most underrepresented region/species/d.b.h class combinations. Representation was calculated as the percentage of trees in legacy tree database – percentage of biomass in the FIADB. Data for all region/species/d.b.h. class combinations are available in Table S8.

Region	Common name	D.B.H class	% of biomass	FIADB Rank	Number of trees in legacy tree database	Representation
PNW	Douglas-fir	20	2.4	2	83	-1.8
PNW	Douglas-fir	30	1.5	6	16	-1.4
NE	Red maple	10	1.7	4	80	-1.1
IMW	Douglas-fir	20	1.0	14	1	-1.0
PNW	Western hemlock	20	1.1	11	14	-1.0
PNW	Douglas-fir	10	1.9	3	116	-1.0
PNW	Douglas-fir	40	1.0	15	6	-0.9
IMW	Lodgepole pine	10	1.1	8	38	-0.8
NE	Sugar maple	10	1.1	9	38	-0.8
IMW	Douglas-fir	10	1.1	12	30	-0.8
PNW	Western hemlock	10	0.9	16	21	-0.7
NE	Northern red oak	20	0.8	18	7	-0.7
NE	Red maple	20	0.7	22	5	-0.7
PNW	Western hemlock	30	0.6	26	4	-0.6
PNW	Douglas-fir	50	0.6	30	0	-0.6
NE	Sugar maple	20	0.6	25	15	-0.5
IMW	Engelmann spruce	20	0.6	27	10	-0.5
SE	Post oak	10	0.7	21	26	-0.5
IMW	Ponderosa pine	20	0.5	33	9	-0.4
NE	White ash	10	0.5	43	3	-0.4
NE	Eastern hemlock	10	0.4	45	1	-0.4
PNW	Mountain hemlock	20	0.4	50	0	-0.4
SE	Pignut hickory	10	0.3	58	0	-0.3
SE	Mockernut hickory	10	0.3	59	0	-0.3
NE	Eastern white pine	20	0.4	46	4	-0.3
IMW	Utah juniper	20	0.4	49	3	-0.3
NE	Yellow-poplar	20	0.4	53	2	-0.3
PNW	Ponderosa pine	30	0.3	63	0	-0.3
IMW	Quaking aspen	10	0.5	42	12	-0.3
NE	Black cherry	20	0.3	64	1	-0.3

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Appendix 2: Common and scientific names for species mentioned in the text and the 30 tree species with the most biomass in the FIADB

Common name ^a	Genus	Species	Full scientific name with authority ^b	FIA Species code ^c
Pacific silver fir	<i>Abies</i>	<i>amabilis</i>	<i>Abies Amabilis</i> Dougl. ex Forbes	11
White fir	<i>Abies</i>	<i>concolor</i>	<i>Abies concolor</i> (Gord. & Glend.) Lindl. Ex Hildebr.	15
Grand fir	<i>Abies</i>	<i>grandis</i>	<i>Abies grandis</i> (Dougl. ex D. Don) Lindl.	17
Subalpine fir	<i>Abies</i>	<i>lasiocarpa</i>	<i>Abies lasiocarpa</i> (Hook.) Nutt.	19
Engelmann spruce	<i>Picea</i>	<i>engelmannii</i>	<i>Picea engelmannii</i> Parry ex Engelm.	93
Sitka spruce	<i>Picea</i>	<i>sitchensis</i>	<i>Picea sitchensis</i> (Bong.) Carr.	98
Common or two-needle pinyon	<i>Pinus</i>	<i>edulis</i>	<i>Pinus edulis</i> Engelm.	106
Lodgepole pine	<i>Pinus</i>	<i>contorta</i>	<i>Pinus contorta</i> Dougl. ex. Loud.	108
Slash pine	<i>Pinus</i>	<i>elliottii</i>	<i>Pinus elliottii</i> Engelm.	111
Ponderosa pine	<i>Pinus</i>	<i>ponderosa</i>	<i>Pinus ponderosa</i> Dougl. ex Laws.	122
Eastern white pine	<i>Pinus</i>	<i>strobus</i>	<i>Pinus strobus</i> L.	129
Loblolly pine	<i>Pinus</i>	<i>taeda</i>	<i>Pinus taeda</i> L.	131
Douglas-fir	<i>Pseudotsuga</i>	<i>menziesii</i>	<i>Pseudotsuga menziesii</i> (Mirb.) Franco	202
Redwood	<i>Sequoia</i>	<i>sempervirens</i>	<i>Sequoia sempervirens</i> (D. Don) Endl.	211
Eastern hemlock	<i>Tsuga</i>	<i>canadensis</i>	<i>Tsuga canadensis</i> (L.) Carr.	261
Western hemlock	<i>Tsuga</i>	<i>heterophylla</i>	<i>Tsuga heterophylla</i> (Raf.) Sarg.	263
Mountain hemlock	<i>Tsuga</i>	<i>mertensiana</i>	<i>Tsuga mertensia</i> (Bong.) Carr.	264
Red maple	<i>Acer</i>	<i>rubrum</i>	<i>Acer rubrum</i> L.	316
Sugar maple	<i>Acer</i>	<i>saccharum</i>	<i>Acer saccharum</i> Marsh.	318
Birch spp.	<i>Betula</i>	spp.	<i>Betula</i> L.	370
Pignut hickory	<i>Carya</i>	<i>glabra</i>	<i>Carya glabra</i> (Mill.) Sweet	403
Shagbark hickory	<i>Carya</i>	<i>ovata</i>	<i>Carya ovata</i> (Mill.) K. Koch	407
Hackberry spp.	<i>Celtis</i>	spp.	<i>Celtis</i> L.	460
American beech	<i>Fagus</i>	<i>grandifolia</i>	<i>Fagus grandifolia</i> Ehrh.	531
Ash spp.	<i>Fraxinus</i>	spp.	<i>Fraxinus</i> L.	540
White ash	<i>Fraxinus</i>	<i>americana</i>	<i>Fraxinus americana</i> L.	541
Black ash	<i>Fraxinus</i>	<i>nigra</i>	<i>Fraxinus nigra</i> Marsh.	543
Green ash	<i>Fraxinus</i>	<i>pennsylvanica</i>	<i>Fraxinus pennsylvanica</i> Marsh.	544
Sweetgum	<i>Liquidambar</i>	<i>styraciflua</i>	<i>Liquidambar styraciflua</i> L.	611
Yellow-poplar	<i>Liriodendron</i>	<i>tulipifera</i>	<i>Liriodendron tulipifera</i> L.	621
Cottonwood and poplar spp.	<i>Populus</i>	spp.	<i>Populus</i> L.	740
Quaking aspen	<i>Populus</i>	<i>tremuloides</i>	<i>Populus tremuloides</i> Michx.	746
Black cherry	<i>Prunus</i>	<i>serotina</i>	<i>Prunus serotina</i> Ehrh.	762
Oak spp.	<i>Quercus</i>	spp.	<i>Quercus</i> L.	800
White oak	<i>Quercus</i>	<i>alba</i>	<i>Quercus alba</i> L.	802
Scarlet oak	<i>Quercus</i>	<i>coccinea</i>	<i>Quercus coccinea</i> Muenchh.	806
Water oak	<i>Quercus</i>	<i>nigra</i>	<i>Quercus nigra</i> L.	827
Chestnut oak	<i>Quercus</i>	<i>prinus</i>	<i>Quercus prinus</i> L.	832
Northern red oak	<i>Quercus</i>	<i>rubra</i>	<i>Quercus rubra</i> L.	833
Post oak	<i>Quercus</i>	<i>stellata</i>	<i>Quercus stellata</i> Wangenh.	835
Black oak	<i>Quercus</i>	<i>velutina</i>	<i>Quercus velutina</i> Lam.	837
Elm spp.	<i>Ulmus</i>	spp.	<i>Ulmus</i> L.	970

^a A list of all species examined in this analysis is available in Appendix S2 located in [supplemental tables file](#).

^b Scientific names from Burns and Honkala 1990a and 1990b.

^c Forest Inventory and Analysis species codes (O'Connell et al. 2016).

Frank, Jereme; Weiskittel, Aaron; Walker, David; Westfall, James A.; Radtke, Philip J.; Affleck, David L.R.; Coulston, John; MacFarlane, David W. 2019. **Gaps in available data for modeling tree biomass in the United States**. Gen. Tech. Rep. NRS-184. Newtown Square, PA: U.S. Department of Agriculture, Forest Service, Northern Research Station. 57 p. <https://doi.org/10.2737/NRS-GTR-184>.

When estimating tree-level biomass and carbon, it is common practice to develop generalized models across numerous species and large spatial extents. However, sampling efforts are generally incomplete and trees are not randomly selected. In this analysis, of the more than 1,000 biomass-related articles that were reviewed, trees were destructively sampled in over 300 studies to estimate biomass in the United States. Studies were summarized and past sampling efforts were explored to illuminate where the largest data gaps occurred in terms of tree components sampled, tree size, tree form, tree species, and location. The most prominent gaps were in large trees, particularly in Douglas-fir trees in the Pacific Northwest. In addition, tree roots were notably undersampled. Lastly, trees of poor or unusual form and low vigor were often not sampled, and this may introduce a systematic bias if not dealt with appropriately. More than 200 species did not have a biomass model or a single data point. The gaps presented here can be viewed as suggestions for future destructive sampling efforts, but the magnitude of a gap for a given model will ultimately depend on the selected modeling framework and the user's objectives.

KEY WORDS: U.S. Forest Carbon Inventory, allometric modeling, tree component biomass, gaps, tree form and vigor

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