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Estimating above-ground biomass

This report details three exercises undertaken to: 1) estimate aboveground biomass of individual trees using published allometric equations and a hectare expansion factor, 2) estimate combined aboveground biomass of trees at the plot level, 3) and to internally validate candidate models based on the limited data available. The current dataset was collected in Dumfries and Galloway region of southwest Scotland. A total of 167 trees were measured diameter at breast height (dbh > 1.3m), sampling populations in variable sized circular plots among four species: *Betula pendula, Betula pubescens, Sorbus aucuparia* and *Picea sitchensis.* Data analysis was conducted in R environment (v.2.1). The developed syntax is provided in the appendix.

Question 1-3; Identification of aboveground biomass equations

Biomass equations were selected based on four requirements: 1) location of study that is in closest proximity to current field site, 2) relevant species of study focus, 3) relevant use of 'dbh' as the predictor in their biomass equation, 4) and appropriate range of 'dbh' values fitted to biomass equation. Among eleven equations considered, three models were based on logarithmic transformation of the variables. The following table presents the eleven candidate equations and their summary information:

Table 1. Aboveground biomass equations by tree species. Format provided under "Equation" and a, b, D, are parameter values. Index numbers indicating original publications listed below bibliography

Species (Index#)	Range of D	Equation	α	β	Country
(M1) *Betula pendula* (32)	/	$\alpha*D^\beta$	0.2511	2.29	UK
(M2) *Betula pendula* (10)	2.9-30	$\alpha+\beta*\ln(D)$	-2.4166	2.4227	UK
(M3) *Betula pendula* (10)	2.9-26	$\alpha+\beta*\ln(D)$	-2.7584	2.6134	UK
(M4) *Betula pendula* (10)	3.3-16	$\alpha+\beta*\ln(D)$	-2.1625	2.3078	UK
(M5) *Betula pendula* (10)	3.5-23	$\alpha+\beta*\ln(D)$	-2.6423	2.4678	UK
(M6) *Betula pubescens* (35)	10-90	$\alpha*D^\beta$	-2.162	2.3078	UK
(M7) *Betula pubescens* (35)	0.8-8.5	$\alpha*D^\beta$	0.00029	2.50038	Sweden
(M8) *Picea sitchensis* (C16)	3-283	$\alpha+\beta*\ln(D)$	-3.0300	2.5567	US
(M9) *Picea sitchensis* (B04)	2-40	$\alpha*D^\beta$	0.028	2.710	Ireland
(M10) *Sorbus aucuparia* (1)	3-64	$\alpha+\beta*\ln(D)$	-2.2118	2.4133	US
(M11) *Sorbus aucuparia* (2)	3-60	$\alpha+\beta*\ln(D)$	-2.9255	2.4109	US

Table 2 Descriptive statistics for all trees measured (n=167)

Variable	Count	Mean	SD	Median	SE	Range
Mean diameter (cm)						
Betula pendula	40	23.7	23.1	13.5	3.6	76.0
Betula pubescens	20	11.1	3.9	9.5	0.9	12.0
Picea sitchensis	66	19.7	6.5	20.0	0.8	26.0
Sorbus aucuparia	1	8.0	8.0	/	≠	~~0.0~~

For silver brich, five biomass equations were available from the UK with similar range in values. To identify the best-fit equation, eleven models were fitted using response variables generated from the above equations. Descriptive analysis of these found highly dipsersed data, violation of homogeneity and non-normal distribution (Table 3). Plots were generated to examine residuals versus fitted values (Fig.1-8). Using non-linear least squared regression, models were compared by assessing the bias between predicted values and observed values. In table 4 below, the root mean square error of model residuals (RMSE) was presented in absolute terms. Models with highest RMSE values were omitted, providing final cut of eight candidate models.

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Table 3. Descriptive statistics for response variables based on 7 biomass equations. #Shaprio-Wilks's p-values reporting signficant deviation from normal distribution at 0.05, 0.01, 0.001 leve;s as *, ** and **

Variable	Mean	SD	SE	Skewness	Kurtosis	p-value[#]
M1: SBI_agb_Z05.32	872.4	1533.7	242.5	1.73	1.53	***
M2: SBI_agb_Z05.52	531.8	962.0	152.1	1.77	1.68	***
M3: SBI_agb_Z05.53	824.5	1546.3	244.5	1.82	1.90	***
M4: SBI_agb_Z05.54	429.6	758.3	119.9	1.73	1.55	***
M6: PBI_agb_B68.01	35.1	29.1	6.5	1.19	0.22	***
M7: PBI_agb_Z05.40	0.2	0.1	0.0	1.25	0.39	***
M8: SS_agb_B04.01	111.3	83.4	10.3	0.71	-0.37	***
M9: SS_agb_C14.16	118.3	85.7	10.4	0.65	-0.48	**

For silver birch, M3 model was best fit to the current dataset. Bunce, who carried out inventory survey in the nearby Meathop Wood, derived this equation (Bunce 1968). Though, the range of dbh values appears less dispersed than this current dataset. For downy birch, some confusion arose. While model diagnostics indicated M7 was best fit, descriptive results suggested this equation was heavily conservative. Therefore, final equation was chosen from M6 model, which was also considerably significant. Interestingly, M6 was also derived from the same study carried out by Bunce (ibid.). As no biomass equation was provided for Rowan in the review conducted by Zianis et al (2005), a formula was adopted from a US-based study (Chojnacky, Heath, and Jenkins 2014). In this US-base study, two equations were available for Rowan. Between these, dbh ranges were considered and the more limited scale adopted (M11, dbh=3-60, Table 1). Between two equations for Sitka spruce, the models derived from a study in Ireland, which was best fit to the data, was chosen (Black et al. 2004).

Table 4. Parameter estimates (& standard error for biomass models: NLS-NLS5. SE: standard errors. RMSE: root mean square. Signficant estimates reported at the levels of 0.05, 0.01, 0.001 as *, **, ***.

Parameter	M1 (SBI)	M2 (SBI)	M3 (SBI)	M4 (SBI)
α	56.774 (9.901)***	52.076 (9.344)***	121.037 (22.548)***	29.817 (5.220)***
β	1.027 (0.011)***	0.684 (0.010)***	1.181 (0.025)***	0.5122 (0.006)***
RMSE	28.61	27.00	2.38	15.09

Parameter	M6 (PBI)	M7 (PBI)	M8 (SS)	M9 (SS)
α	7.185 (0.346)***	0.055 (0.003)***	38.760 (1.968)***	30.372 (1.467)***
β	-2.200 (0.059)***	0.002 (0.001)***	0.526 (0.006)***	0.495 (0.004)***
RMSE	0.14	0.00	1.98	1.47

Hectare expansion factor was estimated using plot size as an attribute of the R-syntax. Using the relascope factor of 2, the radius of relascope plots was estimated using dbh, such that:

ForestInventoryRelascope_Rversion$plot_radius_m <- (35*ForestInventoryRelascope_Rversion$dbh_cm/100)
ForestInventoryRelascope_Rversion$hef <- 10000 / (pi*ForestInventoryRelascope_Rversion$plot_radius_m^2)

Using a hectare area factor, the absolute contribution of basal area ($BA\_m^2\_ha^{-1}$) and aboveground biomass ($AGB\_Mg\_ha^{-1}$) per hectare of individual trees and plots (Table 5). Having completed the exercise, it is recommended that the workflow of this analysis would benefit from beginning with hectare area factor before generating other results (see syntax in appendix)

Table 5. Total basal area and aboveground biomass of fixed size plots

Plot	BA_m2_ha	AGB_Mg_ha
1	22.4062315	86.93626169
2	33.2564659	112.5917576
3	34.13074419	260.2069904

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Figures 1-8 Scatterplot and regression lines of the relation between species dbh and the calculated aboveground biomass; Linear (red curve) vs nonlinear algorithmic regression lines (blue curve).
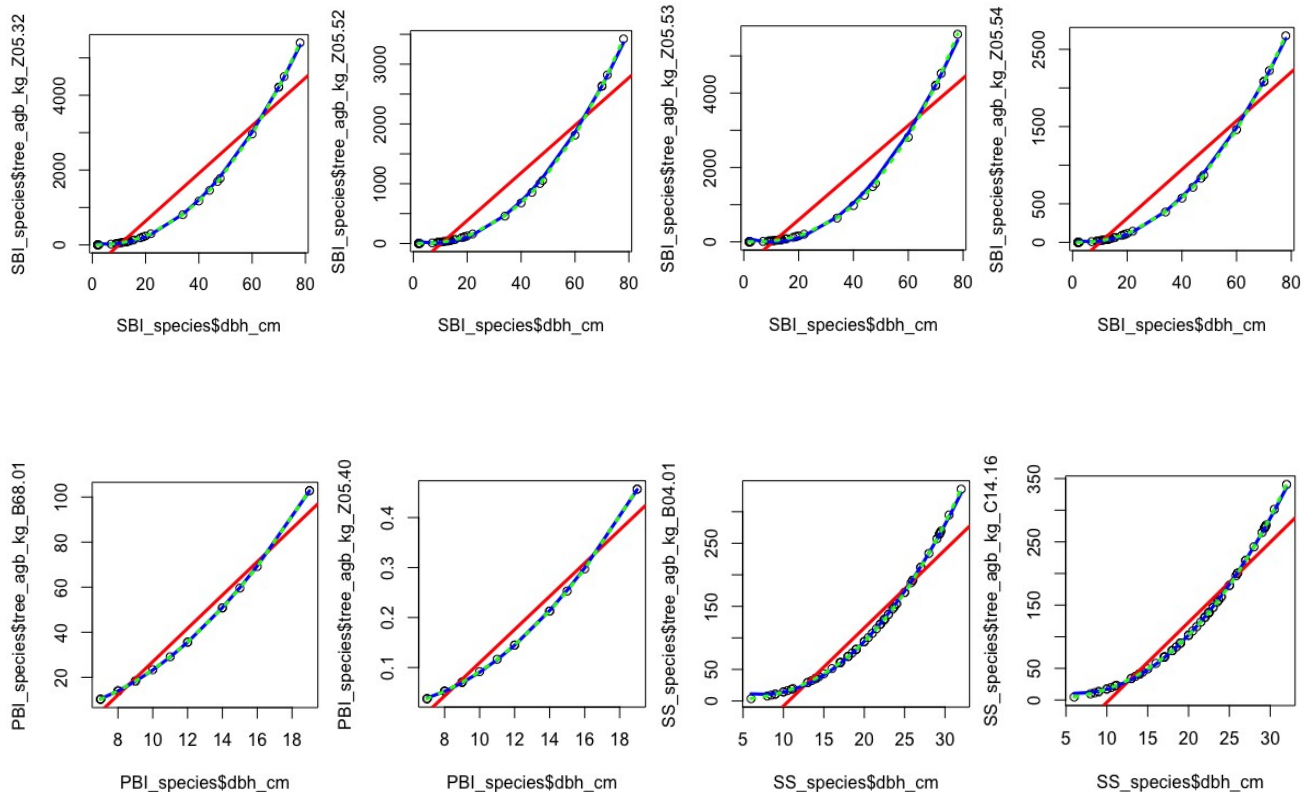
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Bunce, R G H. 1968. "Biomass and Production of Trees in a Mixed Deciduous Woodland: I. Girth and Height as Parameters for the Estimation of Tree Dry Weight." *The Journal of Ecology*: 759–75.

Chojnacky, David C, Linda S Heath, and Jennifer C Jenkins. 2014. "Updated Generalized Biomass Equations for North American Tree Species." *Forestry* 87(1): 129–51.

Zianis, Dimitris, Petteri Muukkonen, Raisa Mäkipää, and Maurizio Mencuccini. 2005. *Biomass and Stem Volume Equations for Tree Species in Europe*. FI.

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Appendix I Biomass equations

- M1 Hughes, M. K. (1971). Tree biocontent, net production and litter fall in a deciduous woodland. *Oikos*, 62-73
- M2 Bunce, R. G. H. (1968). Biomass and production of trees in a mixed deciduous woodland: I. Girth and height as parameters for the estimation of tree dry weight. *The Journal of Ecology*, 759-775.
- M3 Bunce, R. G. H. (1968). Biomass and production of trees in a mixed deciduous woodland: I. Girth and height as parameters for the estimation of tree dry weight. *The Journal of Ecology*, 759-775.
- M4 Bunce, R. G. H. (1968). Biomass and production of trees in a mixed deciduous woodland: I. Girth and height as parameters for the estimation of tree dry weight. *The Journal of Ecology*, 759-775.
- M5 Bunce, R. G. H. (1968). Biomass and production of trees in a mixed deciduous woodland: I. Girth and height as parameters for the estimation of tree dry weight. *The Journal of Ecology*, 759-775.
- M6 Johansson, T. (1999). Biomass equations for determining fractions of pendula and pubescent birches growing on abandoned farmland and some practical implications. *Biomass and bioenergy*, *16*(3), 223-238.
- M7 Johansson, T. (1999). Biomass equations for determining fractions of pendula and pubescent birches growing on abandoned farmland and some practical implications. *Biomass and bioenergy*, *16*(3), 223-238.
- M8 Chojnacky, D. C., Heath, L. S., & Jenkins, J. C. (2014). Updated generalized biomass equations for North American tree species. *Forestry*, *87*(1), 129-151.
- M9 Black, K., Tobin, B., Saiz, G., Byrne, K. A., & Osborne, B. (2004). Improved estimates of biomass expansion factors for Sitka spruce. *Irish Forestry*.
- M10 Chojnacky, D. C., Heath, L. S., & Jenkins, J. C. (2014). Updated generalized biomass equations for North American tree species. *Forestry*, *87*(1), 129-151.
- M11 Chojnacky, D. C., Heath, L. S., & Jenkins, J. C. (2014). Updated generalized biomass equations for North American tree species. *Forestry*, *87*(1), 129-151.

Appendix II – R_syntax

```
###### Inventory Monitoring and Assessment ######
######  Assignment 1 - Tree Allometry ##########
########## S.Murphy -08-03-2020 ##############

## Load data ##
## Compute HEF per plot data separately & calculate relascope plots using a:B ratio of
 1:35 ##
ForestInventoryFixedSize_Rversion$hef <- 10000 /
 (pi*ForestInventoryFixedSize_Rversion$plot_radius_m^2)
ForestInventoryConcentric_Rversion$hef <- 10000 /
 (pi*ForestInventoryConcentric_Rversion$plot_radius_m^2)
ForestInventoryKtree_Rversion$hef <- 10000 /
 (pi*ForestInventoryKtree_Rversion$plot_radius_m^2)
ForestInventoryRelascope_Rversion$plot_radius_m <-
 (35*ForestInventoryRelascope_Rversion$dbh_cm/100)
ForestInventoryRelascope_Rversion$hef <- 10000 /
 (pi*ForestInventoryRelascope_Rversion$plot_radius_m^2)

## Merge datasets ##
total_trees <- rbind(ForestInventoryFixedSize_Rversion,
 ForestInventoryConcentric_Rversion, ForestInventoryKtree_Rversion,
 ForestInventoryRelascope_Rversion)

## Generate basal area per tree using dbh ##
total_trees$tree_ba_m <- ((total_trees$dbh_cm)/200)^2*3.147
```

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```
## split data subsets ##
total_trees$species <- as.factor(total_trees$species)
total_trees$species_code <- recode(total_trees$species, 'SS'=1, 'PBI'=2, 'SBI'=3,
 'ROW'=4)
SS_species <- total_trees[ which(total_trees$species_code==1),]
PBI_species <- total_trees[ which(total_trees$species_code==2),]
SBI_species <- total_trees[ which(total_trees$species_code==3),]
ROW_species <- total_trees[ which(total_trees$species_code==4),]

## Generate "abg" response variables using selected biomass equations ##
## Equations used: zianis05.32, zianis05.52, zianis05.53, zianis05.54
## zianis05.55, zianis05.54, bunce68.01, zianis05.40, chojnacky.C14.01.172
## chojnacky.C14.02.172, black.B04.01, chojnacky.C14.16 - see bilbiography ##
SBI_species$tree_agb_kg_Z05.32 <- (((SBI_species$dbh_cm)^2.29)*0.2511)
SBI_species$tree_agb_kg_Z05.52 <- (exp(-2.4166 +2.4227*log(SBI_species$dbh_cm)))
SBI_species$tree_agb_kg_Z05.53 <- (exp(-2.7584 +2.6134*log(SBI_species$dbh_cm)))
SBI_species$tree_agb_kg_Z05.54 <- (exp(-2.1625 +2.3078*log(SBI_species$dbh_cm)))
SBI_species$tree_agb_kg_Z05.55 <- (exp(-2.6423 +2.4678*log(SBI_species$dbh_cm)))
PBI_species$tree_agb_kg_B68.01 <- (exp(-2.162 + 2.3078*log(PBI_species$dbh_cm)))
PBI_species$tree_agb_kg_Z05.40 <- (((PBI_species$dbh_cm)^2.50038)*0.00029)
ROW_species$tree_agb_kg_C14.01 <- (exp(-2.9255 + 2.4109*log(ROW_species$dbh_cm)))
ROW_species$tree_agb_kg_C14.02 <- (exp(-2.2118 + 2.4133*log(ROW_species$dbh_cm)))
SS_species$tree_agb_kg_B04.01 <- (((SS_species$dbh_cm)^2.71)*0.028)
SS_species$tree_agb_kg_C14.16 <- (exp(-3.030 + 2.5567*log(SS_species$dbh_cm)))

## Analysis; Run descriptives and check distrubtion of explanatory/response variables ##
describe(SBI_species$dbh_cm)
describe(PBI_species$dbh_cm)
describe(SS_species$dbh_cm)
describe(ROW_species$dbh_cm)

describe(SBI_species$tree_ba_m)
describe(PBI_species$tree_ba_m)
describe(SS_species$tree_ba_m)
describe(ROW_species$tree_ba_m)

describe(SBI_species$tree_agb_kg_Z05.32)
describe(SBI_species$tree_agb_kg_Z05.52)
describe(SBI_species$tree_agb_kg_Z05.53)
describe(SBI_species$tree_agb_kg_Z05.54)
describe(SBI_species$tree_agb_kg_Z05.55)
describe(PBI_species$tree_agb_kg_B68.01)
describe(PBI_species$tree_agb_kg_Z05.40)
describe(ROW_species$tree_agb_kg_C14.01)
describe(ROW_species$tree_agb_kg_C14.02)
describe(SS_species$tree_agb_kg_B04.01)
describe(SS_species$tree_agb_kg_C14.16)

plot(SBI_species$dbh_cm, SBI_species$tree_agb_kg_Z05.32)
```

```
abline(predict1.z05.32, lwd=3, col="red")
predict2.z05.32 <- lm(SBI_species$tree_agb_kg_Z05.32 ~ SBI_species$dbh_cm +
 I(SBI_species$dbh_cm^2))
lines(smooth.spline(SBI_species$dbh_cm, predict(predict2.z05.32)), lwd=3, col="blue")
predict3.z05.32 <- lm(SBI_species$tree_agb_kg_Z05.32 ~ SBI_species$dbh_cm +
 I(SBI_species$dbh_cm^2) + I(SBI_species$dbh_cm^3))
lines(smooth.spline(SBI_species$dbh_cm, predict(predict3.z05.32)), col="green", lwd=3,
 lty=3)


## Analysis; Check models for distribution, homoskedasticity##
## Compare linear/non-linear models ##
## Eq z05.32 ##

predict1.z05.32 <- lm(SBI_species$tree_agb_kg_Z05.32 ~ SBI_species$dbh_cm)
plot(SBI_species$tree_agb_kg_Z05.32, resid(predict1.z05.32))
plot(fitted(predict1.z05.32), resid(predict1.z05.32))
qqnorm(rstandard(predict1.z05.32))

plot(SBI_species$dbh_cm, SBI_species$tree_agb_kg_Z05.32)
abline(predict1.z05.32, lwd=3, col="red")
predict2.z05.32 <- lm(SBI_species$tree_agb_kg_Z05.32 ~ SBI_species$dbh_cm +
 I(SBI_species$dbh_cm^2))
lines(smooth.spline(SBI_species$dbh_cm, predict(predict2.z05.32)), lwd=3, col="blue")
predict3.z05.32 <- lm(SBI_species$tree_agb_kg_Z05.32 ~ SBI_species$dbh_cm +
 I(SBI_species$dbh_cm^2) + I(SBI_species$dbh_cm^3))
lines(smooth.spline(SBI_species$dbh_cm, predict(predict3.z05.32)), col="green", lwd=3,
 lty=3)

## Eq z05.52 ##
predict1.z05.52 <- lm(SBI_species$tree_agb_kg_Z05.52 ~ SBI_species$dbh_cm)
plot(SBI_species$tree_agb_kg_Z05.52, resid(predict1.z05.52))
plot(fitted(predict1.z05.52), resid(predict1.z05.52))
qqnorm(rstandard(predict1.z05.52))

plot(SBI_species$dbh_cm, SBI_species$tree_agb_kg_Z05.52)
abline(predict1.z05.52, lwd=3, col="red")
predict2.z05.52 <- lm(SBI_species$tree_agb_kg_Z05.52 ~ SBI_species$dbh_cm +
 I(SBI_species$dbh_cm^2))
lines(smooth.spline(SBI_species$dbh_cm, predict(predict2.z05.52)), lwd=3, col="blue")
predict3.z05.52 <- lm(SBI_species$tree_agb_kg_Z05.52 ~ SBI_species$dbh_cm +
 I(SBI_species$dbh_cm^2) + I(SBI_species$dbh_cm^3))
lines(smooth.spline(SBI_species$dbh_cm, predict(predict3.z05.52)), col="green", lwd=3,
 lty=3)

## Eq z05.53 ##
predict1.z05.53 <- lm(SBI_species$tree_agb_kg_Z05.53 ~ SBI_species$dbh_cm)
plot(SBI_species$tree_agb_kg_Z05.53, resid(predict1.z05.53))
plot(fitted(predict1.z05.53), resid(predict1.z05.53))
qqnorm(rstandard(predict1.z05.53))
```

```
plot(SBI_species$dbh_cm, SBI_species$tree_agb_kg_Z05.53)
abline(predict1.z05.53, col="red", lwd=3)
predict2.z05.53 <- lm(SBI_species$tree_agb_kg_Z05.53 ~ SBI_species$dbh_cm +
 I(SBI_species$dbh_cm^2))
lines(smooth.spline(SBI_species$dbh_cm, predict(predict2.z05.53)), lwd=3, col="blue")
predict3.z05.53 <- lm(SBI_species$tree_agb_kg_Z05.53 ~ SBI_species$dbh_cm +
 I(SBI_species$dbh_cm^2) + I(SBI_species$dbh_cm^3))
lines(smooth.spline(SBI_species$dbh_cm, predict(predict3.z05.53)), col="green", lwd=3,
 lty=3)

## Eq z05.54 ##
predict1.z05.54 <- lm(SBI_species$tree_agb_kg_Z05.54 ~ SBI_species$dbh_cm)
plot(SBI_species$tree_agb_kg_Z05.54, resid(predict1.z05.54))
plot(fitted(predict1.z05.54), resid(predict1.z05.54))
qqnorm(rstandard(predict1.z05.54))

plot(SBI_species$dbh_cm, SBI_species$tree_agb_kg_Z05.54)
abline(predict1.z05.54, col="red", lwd=3)
predict2.z05.54 <- lm(SBI_species$tree_agb_kg_Z05.54 ~ SBI_species$dbh_cm +
 I(SBI_species$dbh_cm^2))
lines(smooth.spline(SBI_species$dbh_cm, predict(predict2.z05.54)), lwd=3, col="blue")
predict3.z05.54 <- lm(SBI_species$tree_agb_kg_Z05.54 ~ SBI_species$dbh_cm +
 I(SBI_species$dbh_cm^2) + I(SBI_species$dbh_cm^3))
lines(smooth.spline(SBI_species$dbh_cm, predict(predict3.z05.54)), col="green", lwd=3,
 lty=3)

## Eq z05.55 ##
predict1.z05.55 <- lm(SBI_species$tree_agb_kg_Z05.55 ~ SBI_species$dbh_cm)
plot(SBI_species$tree_agb_kg_Z05.55, resid(predict1.z05.55))
plot(fitted(predict1.z05.55), resid(predict1.z05.55))
qqnorm(rstandard(predict1.z05.55))

plot(SBI_species$dbh_cm, SBI_species$tree_agb_kg_Z05.55)
abline(predict1.z05.55, col="red", lwd=3)
predict2.z05.55 <- lm(SBI_species$tree_agb_kg_Z05.55 ~ SBI_species$dbh_cm +
 I(SBI_species$dbh_cm^2))
lines(smooth.spline(SBI_species$dbh_cm, predict(predict2.z05.55)), lwd=3, col="blue")
predict3.z05.55 <- lm(SBI_species$tree_agb_kg_Z05.55 ~ SBI_species$dbh_cm +
 I(SBI_species$dbh_cm^2) + I(SBI_species$dbh_cm^3))
lines(smooth.spline(SBI_species$dbh_cm, predict(predict3.z05.55)), col="green", lwd=3,
 lty=3)

## Eq B68.01 ##
predict1.B68.01 <- lm(PBI_species$tree_agb_kg_B68.01 ~ PBI_species$dbh_cm)
plot(PBI_species$tree_agb_kg_B68.01, resid(predict1.B68.01))
plot(fitted(predict1.B68.01), resid(predict1.B68.01))
qqnorm(rstandard(predict.B68.01))

plot(PBI_species$dbh_cm, PBI_species$tree_agb_kg_B68.01)
```

```
abline(predict1.B68.01, col="red", lwd=3)
predict2.B68.01 <- lm(PBI_species$tree_agb_kg_B68.01 ~ PBI_species$dbh_cm +
 I(PBI_species$dbh_cm^2))
lines(smooth.spline(PBI_species$dbh_cm, predict(predict2.B68.01)), lwd=3, col="blue")
predict3.B68.01 <- lm(PBI_species$tree_agb_kg_B68.01 ~ PBI_species$dbh_cm +
 I(PBI_species$dbh_cm^2) + I(PBI_species$dbh_cm^3))
lines(smooth.spline(PBI_species$dbh_cm, predict(predict3.B68.01)), col="green", lwd=3,
 lty=3)

## Eq Z05.40 ##
predict1.z05.40 <- lm(PBI_species$tree_agb_kg_Z05.40 ~ PBI_species$dbh_cm)
plot(PBI_species$tree_agb_kg_Z05.40, resid(predict1.z05.40))
plot(fitted(predict1.z05.40), resid(predict1.z05.40))
qqnorm(rstandard(predict1.z05.40))

plot(PBI_species$dbh_cm, PBI_species$tree_agb_kg_Z05.40)
abline(predict1.z05.40, col="red", lwd=3)
predict2.z05.40 <- lm(PBI_species$tree_agb_kg_Z05.40 ~ PBI_species$dbh_cm +
 I(PBI_species$dbh_cm^2))
lines(smooth.spline(PBI_species$dbh_cm, predict(predict2.z05.40)), lwd=3, col="blue")
predict3.z05.40 <- lm(PBI_species$tree_agb_kg_Z05.40 ~ PBI_species$dbh_cm +
 I(PBI_species$dbh_cm^2) + I(PBI_species$dbh_cm^3))
lines(smooth.spline(PBI_species$dbh_cm, predict(predict3.z05.40)), col="green", lwd=3,
 lty=3)

## Eq B04.01 ##
predict1.B04.01 <- lm(SS_species$tree_agb_kg_B04.01 ~ SS_species$dbh_cm)
plot(SS_species$tree_agb_kg_B04.01, resid(predict1.B04.01))
plot(fitted(predict1.B04.01), resid(predict1.B04.01))
qqnorm(rstandard(predict1.B04.01))

plot(SS_species$dbh_cm, SS_species$tree_agb_kg_B04.01)
abline(predict1.B04.01, col="red", lwd=3)
predict2.B04.01 <- lm(SS_species$tree_agb_kg_B04.01 ~ SS_species$dbh_cm +
 I(SS_species$dbh_cm^2))
lines(smooth.spline(SS_species$dbh_cm, predict(predict2.B04.01)), lwd=3, col="blue")
predict3.B04.01 <- lm(SS_species$tree_agb_kg_B04.01 ~ SS_species$dbh_cm +
 I(SS_species$dbh_cm^2) + I(SS_species$dbh_cm^3))
lines(smooth.spline(SS_species$dbh_cm, predict(predict3.B04.01)), col="green", lwd=3,
 lty=3)

## Eq C14.16 ##
predict1_C14.16 <- lm(SS_species$tree_agb_kg_C14.16 ~ SS_species$dbh_cm)
plot(SS_species$tree_agb_kg_C14.16, resid(predict1_C14.16))
plot(fitted(predict1_C14.16), resid(predict1_C14.16))
qqnorm(rstandard(predict1_C14.16))

plot(SS_species$dbh_cm, SS_species$tree_agb_kg_C14.16)
abline(predict1_C14.16, col="red", lwd=3)
predict2_C14.16 <- lm(SS_species$tree_agb_kg_C14.16 ~ SS_species$dbh_cm +
```

```
 I(SS_species$dbh_cm^2))
lines(smooth.spline(SS_species$dbh_cm, predict(predict2_C14.16)), lwd=3, col="blue")
predict3_C14.16 <- lm(SS_species$tree_agb_kg_C14.16 ~ SS_species$dbh_cm +
 I(SS_species$dbh_cm^2) + I(SS_species$dbh_cm^3))
lines(smooth.spline(SS_species$dbh_cm, predict(predict3_C14.16)), col="green", lwd=3,
 lty=3)

## Compare model resuls ##
summary(predict2.z05.32)
summary(predict2.z05.52)
summary(predict2.z05.53)
summary(predict2.z05.54)
summary(predict2.z05.55)
summary(predict2.B68.01)
summary(predict2.z05.40)
summary(predict2.B04.01)
summary(predict2_C14.16)

## split fixed_size_data to estiamte plot level BA & AGB##
sapply(ForestInventoryFixedSize_Rversion, class)
ForestInventoryFixedSize_Rversion$species <-
 as.factor(ForestInventoryFixedSize_Rversion$species)
ForestInventoryFixedSize_Rversion$species_code <-
 recode(ForestInventoryFixedSize_Rversion$species, 'SS'=1, 'PBI'=2, 'SBI'=3, 'ROW'=4)
SS_species <-
 ForestInventoryFixedSize_Rversion[ which(ForestInventoryFixedSize_Rversion$species_co
 de==1),]
PBI_species <-
 ForestInventoryFixedSize_Rversion[ which(ForestInventoryFixedSize_Rversion$species_co
 de==2),]
SBI_species <-
 ForestInventoryFixedSize_Rversion[ which(ForestInventoryFixedSize_Rversion$species_co
 de==3),]
ROW_species <-
 ForestInventoryFixedSize_Rversion[ which(ForestInventoryFixedSize_Rversion$species_co
 de==4),]

## generate tree_agb_kg using selected biomass equations ##
SBI_species$tree_agb_kg <- (exp(-2.7584 +2.6134*log(SBI_species$dbh_cm)))
PBI_species$tree_agb_kg <- (((PBI_species$dbh_cm)^2.50038)*0.00029)
ROW_species$tree_agb_kg <- (exp(-2.9255 + 2.4109*log(ROW_species$dbh_cm)))
SS_species$tree_agb_kg <- (exp(-3.030 + 2.5567*log(SS_species$dbh_cm)))

# merge fixed_size_datasets
fixedplot_merged <- rbind(PBI_species, SBI_species, ROW_species, SS_species)

fixedplot_merged$tree_ba_m <- ((fixedplot_merged$dbh_cm)/200)^2*3.147
fixedplot_merged$BA_m <- (fixedplot_merged$tree_ba_m*fixedplot_merged$hef)
fixedplot_merged$AGB_Mg_ha <- (fixedplot_merged$tree_agb_kg*fixedplot_merged$hef)
```

Inventory, Assessment and Monitoring;

```
fixedplot_merged %>%
  group_by(plot) %>%
  summarise(sumplot_AGB = sum(fixedplot_merged$BA_m, na.rm = TRUE))
```