

# Above Ground Biomass and Carbon Sequestration PT SMM

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### 1. Load packages

```
library(dplyr)
library(BIOMASS)
library(knitr)
```

### 2. Reading and preparing data

```
primer <- read.csv("./primer_tree_measurement.csv")
sekunder <- read.csv("./secunder_tree_measurement.csv")
```

### 3. Retrieve wood density

```
##Check and retrieve taxonomy First, check for any typo in the taxonomy
Taxo <- correctTaxo(genus = primer$genus, species = primer$species, useCache = T, verbose = F)
primer$genusCorr <- Taxo$genusCorrected
primer$speciesCorr <- Taxo$speciesCorrected
#If needed, retrieve APG III families and orders from genus names
APG <- getTaxonomy(primer$genusCorr, findOrder = T)
primer$familyAPG <- APG$family
primer$orderAPG <- APG$order
#Retrieve wood density using the plot level average if no genus level information is available
dataWD <- getWoodDensity(
  genus = primer$genusCorr,
  species = primer$speciesCorr,
```

```
stand = primer$plotId
)

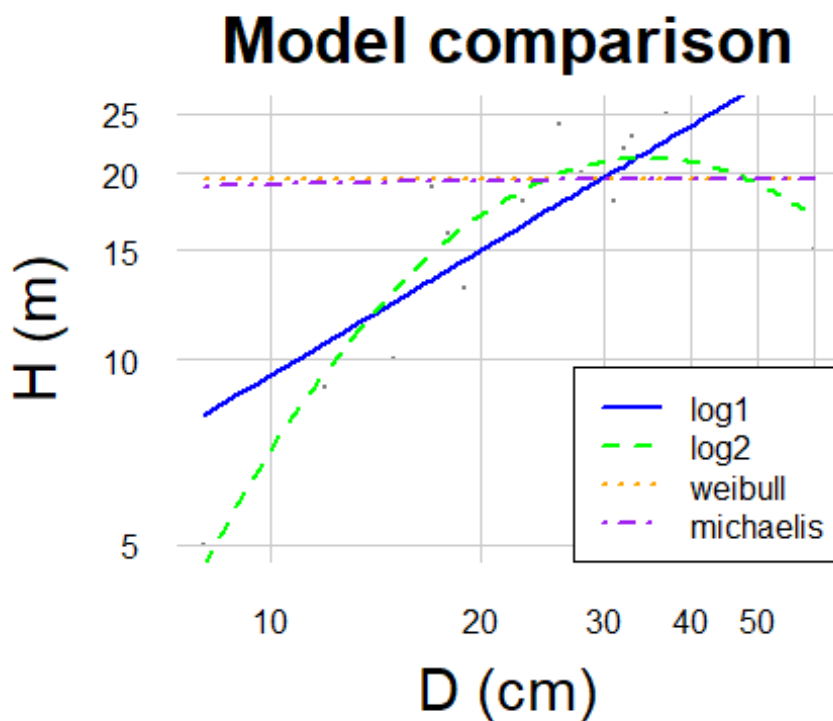
## The reference dataset contains 16467 wood density values
## Your taxonomic table contains 11 taxa
```

#### 4. Build Height-Diameter Models

*##compare different models at once*

```
result <- modelHD(
  D = sekunder$D,
  H = sekunder$H,
  useWeight = TRUE
)

## To build a HD model you must use the parameter 'method' in this function
```



```
kable(result)
```

method	color	RSE	RSElog	Average_bias
log1	blue	5.405612	0.2917245	0.0192297
log2	green	2.786206	0.1630367	-0.0002287
weibull	orange	6.886383	NA	0.1550681
michaelis	purple	6.465894	NA	0.1493854

```
##Compute the Local H-D model with the Lowest RSE
HDmodel <- modelHD(
```

```

D = sekunder$D,
H = sekunder$H,
method = "log2",
useWeight = TRUE
)

```

## 5. Retrieve Height Data

```

##Retrieve height data from a Local Height-diameter model
dataHlocal <- retrieveH(
  D = primer$D,
  model = HDmodel)
##Retrieve height data from a Feldpaush et al. (2012) averaged model
dataHfeld <- retrieveH(
  D = primer$D,
  region = "SEAsia")
##Retrieve height data from Chave et al. (2012) equation 6
dataHchave <- retrieveH(
  D = primer$D,
  coord = primer[, c("long", "lat")])

```

## 6. Estimate AGB (Above Ground Biomass) and Carbon Sequestration

```

##organize data
primer$WD <- dataWD$meanWD
primer$H <- dataHlocal$H
primer$Hfeld <- dataHfeld$H
##Compute AGB(Mg) per tree
AGBtree <- computeAGB(
  D = primer$D,
  WD = primer$WD,
  H = primer$H)
##Compute AGB(Mg) per plot (need to be divided by plot area to get Mg/ha)
AGBplot <- summaryByPlot(AGBtree, primer$plotId)
AGBplot$TonHa <- AGBplot$AGB*100
kable(AGBplot)

```

plot	AGB	TonHa
Blok10	2.6108412	261.08412
Blok2	1.8073477	180.73477
Blok6	1.5666391	156.66391
Blok9	2.2431566	224.31566
Blok7	2.5231818	252.31818
Blok1	2.0278802	202.78802
Blok5	1.4554484	145.54484
Blok8	0.3687516	36.87516
Blok4	0.2982196	29.82196
Blok3	1.6727782	167.27782

```

##Compute AGB(Mg) per tree without height information (Eq. 7 from Chave et al. (2014))
AGBplotChave <- summaryByPlot(
  computeAGB(
    D = primer$D, WD = primer$WD,
    coord = primer[, c("long", "lat")]),
  primer$plotId)
##Compute AGB(Mg) per tree with Feldpausch et al. (2012) regional H-D model
AGBplotFeld <- summaryByPlot(
  computeAGB(
    D = primer$D, WD = primer$WD,
    H = primer$Hfeld
  ),
  plot = primer$plotId)
##Mean AGB
mean(AGBplot$TonHa)

## [1] 165.7424 Ton/Ha (Above Ground Biomass)

##Carbon sequestration
mean(AGBplot$TonHa)/2

## [1] 82.87122 Ton C/Ha

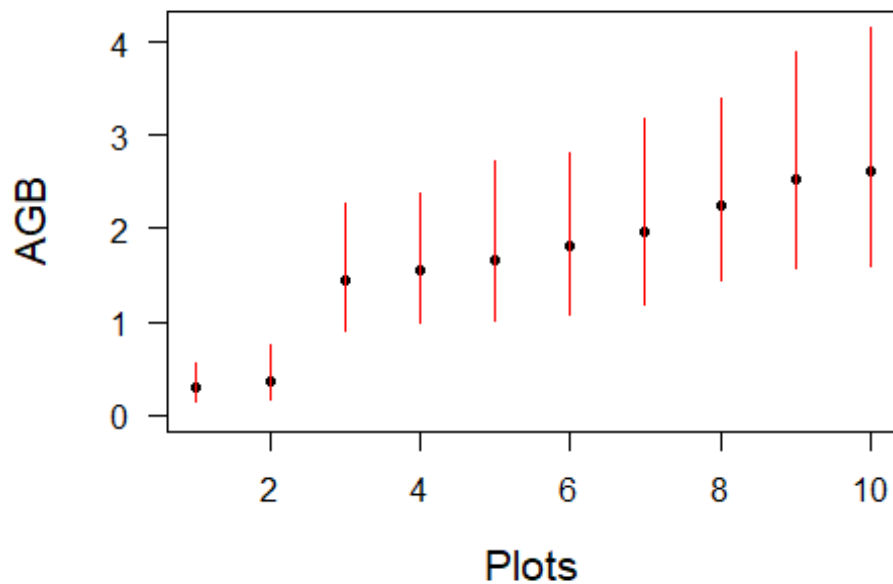
```

## 7. Propagate AGB Errors

```

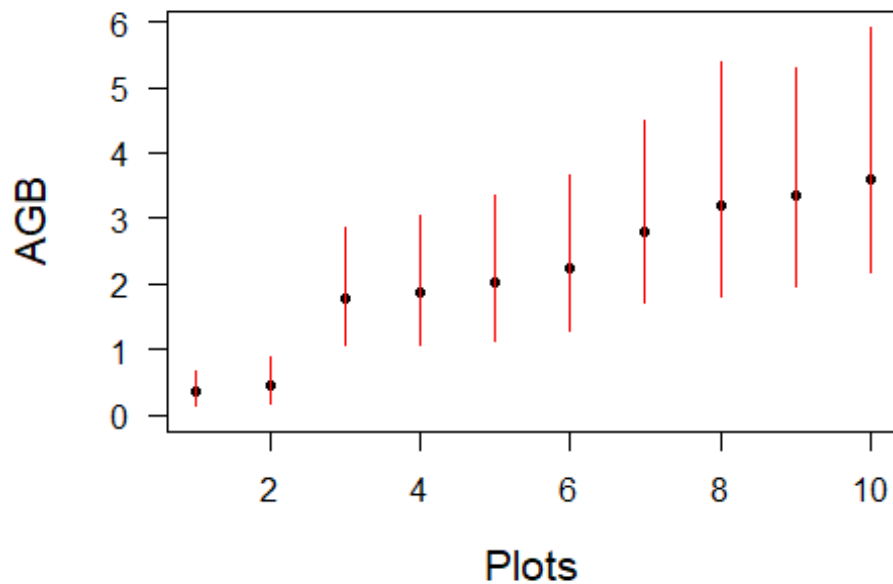
##Organize data
primer$sdWD <- dataWD$sdWD
primer$HfeldRSE <- dataHfeld$RSE
##Propagate error for all tree at once using the local HD model constructed above (modelHD),
##i.e. non-independent allometric errors will be assigned to all trees at each iteration, independently of plots.
resultMC <- AGBmonteCarlo(D = primer$D, WD = primer$WD, errWD = primer$sdWD, HDmodel = HDmodel, Dpropag = "chave2004")
Res <- summaryByPlot(resultMC$AGB_simu, primer$plotId)
Res <- Res[order(Res$AGB), ]
plot(Res$AGB, pch = 20, xlab = "Plots", ylab = "AGB", ylim = c(0, max(Res$Cred_97.5)), las = 1, cex.lab = 1.3)
segments(seq(nrow(Res)), Res$Cred_2.5, seq(nrow(Res)), Res$Cred_97.5, col = "red")

```

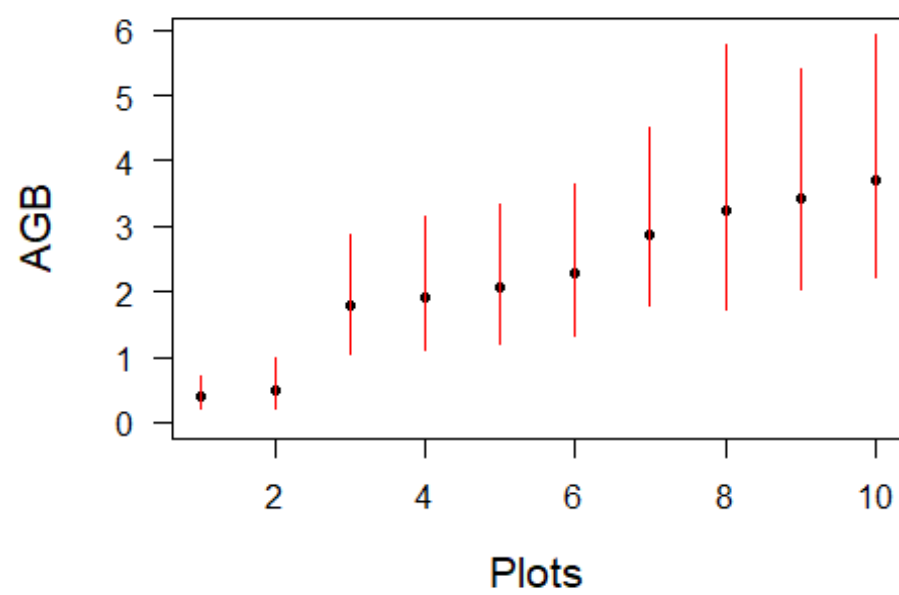


```
##Using the Feldpaush regional HD averaged model (code only given)
resultMC <- AGBmonteCarlo(
  D = primer$D,
  WD = primer$WD,
  errWD = primer$sdWD,
  H = primer$Hfeld,
  errH = primer$HfeldRSE,
  Dpropag = "chave2004"
)

Res <- summaryByPlot(resultMC$AGB_simu, primer$plotId)
Res <- Res[order(Res$AGB), ]
plot(Res$AGB, pch = 20, xlab = "Plots", ylab = "AGB", ylim = c(0, max(Res$Cred_97.5)), las = 1, cex.lab = 1.3)
segments(seq(nrow(Res)), Res$Cred_2.5, seq(nrow(Res)), Res$Cred_97.5, col = "red")
```



```
##Per plot using the Chave et al. (2014) Equation 7 (code only given)
resultMC <- AGBmonteCarlo(
  D = primer$D,
  WD = primer$WD,
  errWD = primer$sdWD,
  coord = primer[, c("long", "lat")],
  Dpropag = "chave2004"
)
Res <- summaryByPlot(resultMC$AGB_simu, primer$plotId)
Res <- Res[order(Res$AGB), ]
plot(Res$AGB, pch = 20, xlab = "Plots", ylab = "AGB", ylim = c(0, max(Res$C
red_97.5)), las = 1, cex.lab = 1.3)
segments(seq(nrow(Res)), Res$Cred_2.5, seq(nrow(Res)), Res$Cred_97.5, col =
"red")
```



## LAMPIRAN

Tabel 1. Data Primer Tree Sampling Hutan Sekunder Bentang Alam Makam Balok

plotId	treeld	family	genus	species	D	lat	long
Blok10	8	Euphorbiaceae	Triadica	cochinchinensis	19	-3.04188	107.8921
Blok2	13	Euphorbiaceae	Triadica	cochinchinensis	20	-3.04417	107.8928
Blok6	34	Euphorbiaceae	Triadica	cochinchinensis	17	-3.04347	107.8904
Blok9	47	Euphorbiaceae	Triadica	cochinchinensis	16	-3.04281	107.8929
Blok2	14	Meliaceae	Aglaia	elliptica	15	-3.04417	107.8928
Blok6	35	Meliaceae	Aglaia	elliptica	15	-3.04347	107.8904
Blok9	48	Meliaceae	Aglaia	elliptica	15	-3.04281	107.8929
Blok10	9	Meliaceae	Aglaia	forbesii	37	-3.04188	107.8921
Blok2	15	Meliaceae	Aglaia	forbesii	33	-3.04417	107.8928
Blok9	49	Meliaceae	Aglaia	forbesii	35	-3.04281	107.8929
Blok6	33	Meliaceae	Aglaia	hiernii	17	-3.04347	107.8904
Blok7	38	Meliaceae	Aglaia	hiernii	12	-3.04353	107.8949
Blok1	1	Leguminosae	Archidendron	jiringa	55	-3.04472	107.8959
Blok7	39	Leguminosae	Archidendron	jiringa	53	-3.04353	107.8949
Blok1	2	Rutaceae	Murraya	koenigii	8	-3.04472	107.8959
Blok1	3	Rutaceae	Murraya	koenigii	9	-3.04472	107.8959
Blok2	16	Rutaceae	Murraya	koenigii	10	-3.04417	107.8928
Blok2	17	Rutaceae	Murraya	koenigii	9	-3.04417	107.8928
Blok5	27	Rutaceae	Murraya	koenigii	9	-3.04271	107.8939
Blok8	44	Rutaceae	Murraya	koenigii	9	-3.04413	107.8901
Blok8	45	Rutaceae	Murraya	koenigii	9	-3.04413	107.8901
Blok9	50	Rutaceae	Murraya	koenigii	9	-3.04281	107.8929
Blok4	24	Calophyllaceae	Calophyllum	nodosum	20	-3.04277	107.8904
Blok8	46	Calophyllaceae	Calophyllum	nodosum	24	-3.04413	107.8901
Blok1	4	Burseraceae	Dacryodes	rostrata	24	-3.04472	107.8959
Blok5	28	Burseraceae	Dacryodes	rostrata	22	-3.04271	107.8939
Blok1	5	Leguminosae	Albizia	saponaria	13	-3.04472	107.8959
Blok1	6	Leguminosae	Albizia	saponaria	11	-3.04472	107.8959
Blok10	10	Leguminosae	Albizia	saponaria	9	-3.04188	107.8921
Blok3	19	Leguminosae	Albizia	saponaria	12	-3.04212	107.8928
Blok3	20	Leguminosae	Albizia	saponaria	12	-3.04212	107.8928
Blok4	25	Leguminosae	Albizia	saponaria	12	-3.04277	107.8904
Blok4	26	Leguminosae	Albizia	saponaria	12	-3.04277	107.8904
Blok5	29	Leguminosae	Albizia	saponaria	12	-3.04271	107.8939
Blok5	30	Leguminosae	Albizia	saponaria	12	-3.04271	107.8939
Blok7	40	Leguminosae	Albizia	saponaria	12	-3.04353	107.8949
Blok9	51	Leguminosae	Albizia	saponaria	12	-3.04281	107.8929



Blok1	7	Meliaceae	Dysoxylum	sp	31	-3.04472	107.8959
Blok10	11	Meliaceae	Dysoxylum	sp	33	-3.04188	107.8921
Blok10	12	Meliaceae	Dysoxylum	sp	31	-3.04188	107.8921
Blok2	18	Meliaceae	Dysoxylum	sp	30	-3.04417	107.8928
Blok3	21	Meliaceae	Dysoxylum	sp	28	-3.04212	107.8928
Blok3	22	Meliaceae	Dysoxylum	sp	22	-3.04212	107.8928
Blok5	31	Meliaceae	Dysoxylum	sp	29	-3.04271	107.8939
Blok5	32	Meliaceae	Dysoxylum	sp	28	-3.04271	107.8939
Blok6	36	Meliaceae	Dysoxylum	sp	28	-3.04347	107.8904
Blok7	41	Meliaceae	Dysoxylum	sp	28	-3.04353	107.8949
Blok7	42	Meliaceae	Dysoxylum	sp	28	-3.04353	107.8949
Blok7	43	Meliaceae	Dysoxylum	sp	28	-3.04353	107.8949
Blok9	52	Meliaceae	Dysoxylum	sp	28	-3.04281	107.8929
Blok9	53	Meliaceae	Dysoxylum	sp	28	-3.04281	107.8929
Blok3	23	Meliaceae	Aglaia	sp1	32	-3.04212	107.8928
Blok6	37	Meliaceae	Aglaia	sp1	30	-3.04347	107.8904

Tabel 2. Data Sampling Sekunder Height-Diameter Model Hutan Sekunder Makam Balok

plotId	genus	species	D	H	lat	long
Blok1	Dacryodes	rostrata	24	17	-3.04472	107.8959
Blok2	Dillenia	excelsa	26	24	-3.04417	107.8928
Blok3	Cryptocarya	sp	18	16	-3.04212	107.8928
Blok4	Archidendron	jiringa	60	15	-3.04277	107.8904
Blok5	Aglaia	hiernii	17	19	-3.04271	107.8939
Blok6	Aglaia	elliptica	15	10	-3.04347	107.8904
Blok7	Aglaia	forbesii	37	25	-3.04353	107.8949
Blok8	Aglaia	macrocarpa	33	23	-3.04413	107.8901
Blok9	Aglaia	sp1	32	22	-3.04281	107.8929
Blok10	Aglaia	sp2	28	20	-3.04188	107.8921
Blok6	Dysoxylum	sp	31	18	-3.04347	107.8904
Blok4	Triadica	cochinchinensis	19	13	-3.04277	107.8904
Blok1	Albizia	saponaria	12	9	-3.04472	107.8959
Blok9	Murraya	koenigii	8	5	-3.04281	107.8929
Blok5	Calophyllum	nodosum	23	18	-3.04271	107.8939