Plot-based aboveground biomass estimates - TropiSAR sites

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NB. All aboveground biomass (AGB) estimates are in Mg ha⁻¹. Calibration points with Area_code names including ‘h’, ‘q’ and ‘c’ represent 1ha, 0.25ha and 0.16ha, respectively.

Loading packages and datasets

```r
# PARACOU: 15 plots 6.25ha (PAR01-15) + 1 plot 25ha (PAR16); ARB = PAR17 (6.25ha) NB. all plots surveyed in 2009 except PAR16 surveyed in 2010
## NB. "Each 9 ha plot contains a buffer zone 25 m wide. Trees are monitored inside the core zone, i.e. in an area of 6.25 ha, while silvicultural treatments were applied to the whole plot."
# NOURAGUES: NOU01 (Balenfois 2ha; 100x200m), NOU02 (Grand Plateau 10ha; 100x1000m), NOU03 (Parare 6ha; 200x300m), NOU04 (Petit Plateau 12ha; 300x400m), NOU05 (Bas_Pond_1; 50x50m), NOU06 (Bas_Pond_2; 50x50m), NOU07 (Lek; 50x50m), NOU08 (Lhor; 100x100m), NOU09 (Parare_Ridge; 100x100m), NOU10 (Ringier; 100x100m), NOU11 (Wemomax; 50x50m)

# Packages
library(BIOMASS)
library(knitr)
library(kableExtra)
library(oce)  # to compute Earth magnetic declination
library(lubridate)  # convert ymd dates to decimal year
library(sp)

# Tree-level and botanical datasets
load("TropiSARstem.rdata")
load("TropiSARbota.rdata")
```

Getting wood density (WD) using names

```r
TropiSARstem$Genus <- dfbota$genusCorr[match(TropiSARstem$Name, dfbota$ID)]
TropiSARstem$Species <- dfbota$speciesCorr[match(TropiSARstem$Name, dfbota$ID)]
TropiSARstem$FamilyAPG <- dfbota$familyAPG[match(TropiSARstem$Name, dfbota$ID)]
TropiSARstem$NameCorr <- paste(TropiSARstem$Genus, TropiSARstem$Species)

# Some trees (n=48) were identified at family level in the field; we fill the family column
TropiSARstem$FamilyAPG[which(is.na(TropiSARstem$FamilyAPG) & !(is.na(TropiSARstem$Info_fam)))] <- TropiSARstem$FamilyAPG[which(is.na(TropiSARstem$FamilyAPG) & !(is.na(TropiSARstem$Info_fam)))]

dataWD <- getWoodDensity(genus=TropiSARstem$Genus, species=TropiSARstem$Species, family=TropiSARstem$FamilyAPG, stand=TropiSARstem$Plot_code)
```
## The reference dataset contains 16467 wood density values

## Your taxonomic table contains 1125 taxa

```r
TropiSARstem$WD <- dataWD$meanWD
TropiSARstem$sdWD <- dataWD$sdWD
TropiSARstem$levelWD <- dataWD$levelWD
```

### Refining permanent plot georeferencing

#### # Preliminary work in order to georeference the data

```r
load("TropiSARplotcoord.rdata")
```

```r
coordplot.nousp <- read.csv("PlotCoordNouSP.csv", sep=";", stringsAsFactors=T)
nousp.utm <- SpatialPoints(cbind(coordplot.nousp$X_utm, coordplot.nousp$Y_utm), proj4string=CRS("+proj=utm +zone=22 +north +datum=WGS84 +units=m +no_defs +ellps=WGS84 +towgs84=0,0,0"))
nousp.geo <- spTransform(nousp.utm, CRS("+proj=longlat +datum=WGS84"))
```

```r
coordplot.nousp$Longitude <- nousp.geo@coords[,1]
coordplot.nousp$Latitude <- nousp.geo@coords[,2]
```

```r
coordplot.trop$Longitude[which(is.na(coordplot.trop$Longitude))] <- coordplot.nousp$Longitude
coordplot.trop$Latitude[which(is.na(coordplot.trop$Latitude))] <- coordplot.nousp$Latitude
```

```r
spgeo <- SpatialPoints(cbind(coordplot.trop$Longitude,coordplot.trop$Latitude), proj4string=CRS("+proj=longlat +datum=WGS84"))
sputm <- spTransform(spgeo, CRS("+proj=utm +zone=22 +north +datum=WGS84 +units=m +no_defs +ellps=WGS84 +towgs84=0,0,0"))
```

```r
coordplot.trop$X_utm <- sputm@coords[,1]
coordplot.trop$Y_utm <- sputm@coords[,2]
```

```
# Get "true" bearing
tropiplot <- as.character(unique(coordplot.trop$Plot_code))
coordplot.trop$Loc <- substring(coordplot.trop$Point, 6)
coordplot.trop$True_bearing <- NA
```

```r
for (i in 1:length(tropiplot)) {
  swe.trop <- (atan2(coordplot.trop$X_utm[which(coordplot.trop$Plot_code == tropiplot[i] & coordplot.trop$Loc == "b")]-coordplot.trop$X_utm[which(coordplot.trop$Plot_code == tropiplot[i] & coordplot.trop$Loc == "a")],
                   coordplot.trop$Y_utm[which(coordplot.trop$Plot_code == tropiplot[i] & coordplot.trop$Loc == "b")]-coordplot.trop$Y_utm[which(coordplot.trop$Plot_code == tropiplot[i] & coordplot.trop$Loc == "a")]))*180/pi
  nwe.trop <- (atan2(coordplot.trop$X_utm[which(coordplot.trop$Plot_code == tropiplot[i] & coordplot.trop$Loc == "c")]-coordplot.trop$X_utm[which(coordplot.trop$Plot_code == tropiplot[i] & coordplot.trop$Loc == "d")],
                   coordplot.trop$Y_utm[which(coordplot.trop$Plot_code == tropiplot[i] & coordplot.trop$Loc == "d")]-coordplot.trop$Y_utm[which(coordplot.trop$Plot_code == tropiplot[i] & coordplot.trop$Loc == "c")]))*180/pi
  coordplot.trop$True_bearing[which(coordplot.trop$Plot_code == tropiplot[i] & coordplot.trop$Loc == "a"),] <- 90 - swe.trop
  coordplot.trop$True_bearing[which(coordplot.trop$Plot_code == tropiplot[i] & coordplot.trop$Loc == "d"),] <- 90 - swe.trop
  coordplot.trop$True_bearing[which(coordplot.trop$Plot_code == tropiplot[i] & coordplot.trop$Loc == "c"),] <- 90 - nwe.trop
  coordplot.trop$True_bearing[which(coordplot.trop$Plot_code == tropiplot[i] & coordplot.trop$Loc == "b"),] <- 90 - nwe.trop
}
```
rdplot.trop$Loc == "c")} - coordplot.trop$Y_utm[which(coordplot.trop$Plot_code == tropiplot[i] & coordplot.trop$Loc == "d")]*180/pi)

coordplot.trop$True_bearing[which(coordplot.trop$Plot_code == tropiplot[i])] <- round(mean(c(swe.trop, nwe.trop)),1) + 270
coordplot.trop$True_bearing <- round((coordplot.trop$True_bearing) %% 360,1) # modulus operator 

# Converting "true" bearing in (1) radians, and then in (2) plot rotation
coordplot.trop$TB_rad <- (pi/2 - (coordplot.trop$True_bearing*pi/180)) %% pi # TB stands for true bearing
coordplot.trop$RotAng_rad <- (coordplot.trop$TB_rad - pi/2)

TropiSARstem$TreeRad <- sqrt(TropiSARstem$X_rel^2 + TropiSARstem$Y_rel^2)
TropiSARstem$TreeAng_rel <- atan2(TropiSARstem$X_rel, TropiSARstem$Y_rel); range(TropiSARstem$TreeAng_rel, na.rm=T) # seems OK; max TreeAng is pi/2 ie tree on the Y line

## [1] 0.000000 1.570796

# Assigning plot rotation to each stem
TropiSARstem$PlotAng <- coordplot.trop$RotAng_rad[match(TropiSARstem$Plot_code, coordplot.trop$Plot_code)]

# Computing new stem coordinates after plot rotation
TropiSARstem$Xrot_rel <- TropiSARstem$X_rel * cos(TropiSARstem$PlotAng) - TropiSARstem$Y_rel * sin(TropiSARstem$PlotAng) # x' = x * cos(theta) - y * sin(theta)
TropiSARstem$Yrot_rel <- TropiSARstem$X_rel * sin(TropiSARstem$PlotAng) + TropiSARstem$Y_rel * cos(TropiSARstem$PlotAng) # y' = x * sin(theta) + y * cos(theta)

## Works because it selects the first value in the data.frame and that value is the one we need (x=0; y=0)
TropiSARstem$X_abs <- coordplot.trop$X_utm[match(TropiSARstem$Plot_code, coordplot.trop$Plot_code)] + TropiSARstem$Xrot_rel
TropiSARstem$Y_abs <- coordplot.trop$Y_utm[match(TropiSARstem$Plot_code, coordplot.trop$Plot_code)] + TropiSARstem$Yrot_rel

# CHANGING COORDINATES AFTER VISUAL INSPECTION OF BIG TREES LOCATION AND LIDAR-DERIVED CHM
df.changcoord <- data.frame(plot = tropiplot, 
modx = c(-5,-5,3,-2,0,0,0,0,0,0,0,2,2,-1,-2,0,-3,0,3,-2,-1,3,4,0, 
-1,-1,2,0),
mody = c(2,-3,3,-6,0,0,0,0,0,0,0,5,-3,-4,-2,0,-3,-3,1,-2,1,0,0,0 
,-2,-1,-2,0),
stringsAsFactors=F)
TropiSARstem$X_absCORR <- TropiSARstem$X_abs + df.changcoord$modx[match(TropiSARstem$Plot_code, df.changcoord$plot)]
TropiSARstem$Y_absCORR <- TropiSARstem$Y_abs + df.changcoord$mody[match(TropiSARstem$Plot_code, df.changcoord$plot)]

coordplot.trop$X_utmCORR <- coordplot.trop$X_utm + df.changcoord$modx[match(coordplot.trop$Plot_code, df.changcoord$plot)]
coordplot.trop$Y_utmCORR <- coordplot.trop$Y_utm + df.changcoord$mody[match(coordplot.trop$Plot_code, df.changcoord$plot)]
Creating georeferenced sets of calibration points (at 1ha and 0.25ha)

```r
site = c("NOURAGUES", "PARACOU")
scale = c(100, 50)
suffixe = c("h", "q")
partplot = c("PAR01", "PAR02", "PAR03", "PAR04", "PAR05", "PAR06", "PAR07", "PAR08", "PAR09", "PAR10", "PAR11", "PAR12", "PAR13", "PAR14", "PAR15", "PAR17")

# Creating dataframe to georeference quarter hectare features
coord_orig_q <- coordplot.trop[which(coordplot.trop$X_rel == 0 & coordplot.trop$Y_rel == 0),]
coord_orig_q$full_lengthX <- coordplot.trop$X_rel[which(coordplot.trop$Loc == "b")]
coord_orig_q$full_lengthY <- coordplot.trop$Y_rel[which(coordplot.trop$Loc == "d")]
coord_orig_temp <- coord_orig_q
coord_orig_q <- coord_orig_q[-which(coord_orig_q$Plot_code == "NOU08"),]
# Removing NOU08, a 100x100m plot without XY (so won't be able to dispatch trees in quarters)

# Creating dataframe to georeference hectare features (n=119)
coord_orig_h <- coord_orig_temp
coord_orig_h$X_rel[which(coord_orig_h$Plot_code %in% partplot)] <- 25
coord_orig_h$Y_rel[which(coord_orig_h$Plot_code %in% partplot)] <- 25
coord_orig_h$full_lengthX[which(coord_orig_h$Plot_code %in% partplot)] <- 200
coord_orig_h$full_lengthY[which(coord_orig_h$Plot_code %in% partplot)] <- 200

coord_orig_h$X_utmCORR[which(coord_orig_h$Plot_code %in% partplot)] <- coord_orig_h$X_utmCORR[which(coord_orig_h$Plot_code %in% partplot)] + cos(coord_orig_h$RotAng_rad[which(coord_orig_h$Plot_code %in% partplot)]) * pi/4) * sqrt(25^2 + 25^2) # XX <-
coord_orig_h$Y_utmCORR[which(coord_orig_h$Plot_code %in% partplot)] <- coord_orig_h$Y_utmCORR[which(coord_orig_h$Plot_code %in% partplot)] + sin(coord_orig_h$RotAng_rad[which(coord_orig_h$Plot_code %in% partplot)]) * pi/4) * sqrt(25^2 + 25^2) # YY <-
coord_orig_h <- coord_orig_h[-which(coord_orig_h$full_lengthX < 100),] # Removing 50x50m plots

scale.list <- list()
for (j in 1:length(scale)) {
  if (j == 1) coord_orig = coord_orig_h else coord_orig = coord_orig_q
  plot.df <- data.frame()
tempoplot <- as.character(coord_orig$Plot_code)

  for (k in 1:length(tempoplot)) {
    lengthX <- coord_orig$full_lengthX[which(coord_orig$Plot_code == tempoplot[k])]; lengthY
    incrX_h <- cos(coord_orig$RotAng_rad[which(coord_orig$Plot_code == tempoplot[k])]) * scale[j] # increment for X coordinates horizontally
    incrY_h <- sin(coord_orig$RotAng_rad[which(coord_orig$Plot_code == tempoplot[k])]) * scale[j] # increment for Y coordinates horizontally
  }
}
```
incrX_v <- cos(coord_orig$RotAng_rad[which(coord_orig$Plot_code == tempoplot[k])] + pi/2) * scale[j]  # increment for X coordinates vertically; also equals (-incrY_h)
incrY_v <- sin(coord_orig$RotAng_rad[which(coord_orig$Plot_code == tempoplot[k])] + pi/2) * scale[j]  # increment for Y coordinates vertically; also equals incrX_h

nbptX <- length(seq(0, lengthX, scale[j]))
nbptY <- length(seq(0, lengthY, scale[j]))
incrX.mat <- matrix(rep(0:(nbptX-1),nbptY), nrow=nbptY, ncol=nbptX, byrow = T); incrX.mat
incrY.mat <- matrix(rep(rev(0:(nbptY-1)),nbptX), nrow=nbptY, ncol=nbptX); incrY.mat

XX <- coord_orig$X_utmCORR[which(coord_orig$Plot_code == tempoplot[k])] + incrX_h * incrX.mat + incrX_v * incrY.mat
YY <- coord_orig$Y_utmCORR[which(coord_orig$Plot_code == tempoplot[k])] + incrY_h * incrX.mat + incrY_v * incrY.mat

#plot(as.vector(YY) ~ as.vector(XX))

XX_SW.mat <- XX[2:nbptY, 1:(nbptX-1)]; YY_SW.mat <- YY[2:nbptY, 1:(nbptX-1)]
XX_NW.mat <- XX[1:nbptY-1, 1:(nbptX-1)]; YY_NW.mat <- YY[1:(nbptY-1), 1:(nbptX-1)]
XX_SE.mat <- XX[2:nbptY, nbptX]; YY_SE.mat <- YY[2:nbptY, nbptX]
XX_NE.mat <- XX[1:(nbptY-1), nbptX]; YY_NE.mat <- YY[1:(nbptY-1), nbptX]

XX_SW.vect <- as.vector(XX_SW.mat); YY_SW.vect <- as.vector(YY_SW.mat)
XX_NW.vect <- as.vector(XX_NW.mat); YY_NW.vect <- as.vector(YY_NW.mat)
XX_SE.vect <- as.vector(XX_SE.mat); YY_SE.vect <- as.vector(YY_SE.mat)
XX_NE.vect <- as.vector(XX_NE.mat); YY_NE.vect <- as.vector(YY_NE.mat)

for (l in 1:(nbptX-1)) {
    XX_SW.vect[(((l-1)*(nbptY-1)+1):(l*(nbptY-1)))] <- rev(XX_SW.vect[(((l-1)*(nbptY-1)+1):(l*(nbptY-1))])
    XX_NW.vect[(((l-1)*(nbptY-1)+1):(l*(nbptY-1)))] <- rev(XX_NW.vect[(((l-1)*(nbptY-1)+1):(l*(nbptY-1))])
    XX_SE.vect[(((l-1)*(nbptY-1)+1):(l*(nbptY-1)))] <- rev(XX_SE.vect[(((l-1)*(nbptY-1)+1):(l*(nbptY-1))])
    XX_NE.vect[(((l-1)*(nbptY-1)+1):(l*(nbptY-1)))] <- rev(XX_NE.vect[(((l-1)*(nbptY-1)+1):(l*(nbptY-1))])
}

for (l in 1:(nbptX-1)) {
    YY_SW.vect[(((l-1)*(nbptY-1)+1):(l*(nbptY-1)))] <- rev(YY_SW.vect[(((l-1)*(nbptY-1)+1):(l*(nbptY-1))])
    YY_NW.vect[(((l-1)*(nbptY-1)+1):(l*(nbptY-1)))] <- rev(YY_NW.vect[(((l-1)*(nbptY-1)+1):(l*(nbptY-1))])
    YY_SE.vect[(((l-1)*(nbptY-1)+1):(l*(nbptY-1)))] <- rev(YY_SE.vect[(((l-1)*(nbptY-1)+1):(l*(nbptY-1))])
    YY_NE.vect[(((l-1)*(nbptY-1)+1):(l*(nbptY-1)))] <- rev(YY_NE.vect[(((l-1)*(nbptY-1)+1):(l*(nbptY-1))])
}

temploplot.df <- data.frame(Site = as.character(rep(coord_orig$Site[which(coord_orig$Plot_code == tempoplot[k])], (nbptX-1) * (nbptY-1))), Area_code = paste(temploplot[k], suffixe[j], c(1:((nbptX-1)*(nbptY-1))), sep=""), Plot_code = rep(temploplot[k], (nbptX-1) * (nbptY-1)), Scale = rep(paste(scale[j]^2/10^4,"ha", sep=""), (nbptX-1) * (nbptY-1)), sep=""),

RepFOS_15Feb19_TropiSAR.html[13.03.19 11:35:46]
plot.df <- rbind(plot.df, templot.df)
}
scale.list[[j]] <- plot.df
}
#scale.list

# Convert list of georef hectares/quarters into a single data.frame
df1ha <- as.data.frame(scale.list[[1]])
df0.25ha <- as.data.frame(scale.list[[2]])

georefeatures.df <- rbind(df1ha, df0.25ha)

nousp_sw.utm <- SpatialPoints(cbind(georefeatures.df$sw_x, georefeatures.df$sw_y), proj4string=CRS("+proj=utm +zone=22 +north +datum=WGS84 +units=m +no_defs +ellps=WGS84 +towgs84=0,0,0"))
nousp_sw.geo <- spTransform(nousp_sw.utm, CRS("+proj=longlat +datum=WGS84"))

georefeatures.df$Lon_sw <- nousp_sw.geo@coords[,1]; georefeatures.df$Lat_sw <- nousp_sw.geo@coords[,2]

nousp_nw.utm <- SpatialPoints(cbind(georefeatures.df$nw_x, georefeatures.df$nw_y), proj4string=CRS("+proj=utm +zone=22 +north +datum=WGS84 +units=m +no_defs +ellps=WGS84 +towgs84=0,0,0"))
nousp_nw.geo <- spTransform(nousp_nw.utm, CRS("+proj=longlat +datum=WGS84"))

georefeatures.df$Lon_nw <- nousp_nw.geo@coords[,1]; georefeatures.df$Lat_nw <- nousp_nw.geo@coords[,2]

nousp_se.utm <- SpatialPoints(cbind(georefeatures.df$se_x, georefeatures.df$se_y), proj4string=CRS("+proj=utm +zone=22 +north +datum=WGS84 +units=m +no_defs +ellps=WGS84 +towgs84=0,0,0"))
nousp_se.geo <- spTransform(nousp_se.utm, CRS("+proj=longlat +datum=WGS84"))

georefeatures.df$Lon_se <- nousp_se.geo@coords[,1]; georefeatures.df$Lat_se <- nousp_se.geo@coords[,2]

nousp_ne.utm <- SpatialPoints(cbind(georefeatures.df$ne_x, georefeatures.df$ne_y), proj4string=CRS("+proj=utm +zone=22 +north +datum=WGS84 +units=m +no_defs +ellps=WGS84 +towgs84=0,0,0"))
nousp_ne.geo <- spTransform(nousp_ne.utm, CRS("+proj=longlat +datum=WGS84"))

georefeatures.df$Lon_ne <- nousp_ne.geo@coords[,1]; georefeatures.df$Lat_ne <- nousp_ne.geo@coords[,2]

georefeatures.df <- georefeatures.df[, -c(5:12)]
georefeatures.df$Lon_cnt <- rowMeans(georefeatures.df[, c(5,7,9,11)])
georefeatures.df$Lat_cnt <- rowMeans(georefeatures.df[, c(6,8,10,12)])

## ATTRIBUTING TREES TO ONE HECTARE AREAS

partplot = c("PAR01", "PAR02", "PAR03", "PAR04", "PAR05", "PAR06", "PAR07", "PAR08", "PAR09", "PAR10", "PAR11", "PAR12", "PAR13", "PAR14", "PAR15", "PAR17")

Assigning trees to hectares (1ha) and quarters (0.25ha) based on Plot_code and relative XY
Estimating H from Feldpausch H:D relationship
Developing local H:D relationships (3 in total: 1 per site for trees + 1 for palms)

```r
# Load H:D dataset
load("TropiSARforHD.rdata")
TropiSARforHD <- TropiSARforHD[which(TropiSARforHD$Family == "Areaceae"),]

# Compute site-specific H:D models
HDmodelPerSite <- by(TropiSARforHD, TropiSARforHD$Site,
    function(x) modelHD(D=x$Diameter, H=x$Height, method="michaelis", useWeight =T),
    simplify=FALSE)
RSEmodels <- sapply(HDmodelPerSite, function(x) x$RSE)
Coeffmodels <- lapply(HDmodelPerSite, function(x) x$coefficients)
ResHD <- data.frame(Site=names(unlist(RSEmodels)),
a=round(unlist(sapply(Coeffmodels,"[",1)),3),
b=round(unlist(sapply(Coeffmodels,"[",2)),3),
RSE=round(unlist(RSEmodels),3))
kable(ResHD, row.names = F)
```

# Retrieve predicted height values in the database
# NB. HEIGHT VALUES SOMETIMES FROM SURVEYS OTHER THAN THOSE WHEN DBH WAS MEASURED... BUT THIS HAPPENS FOR RABI AS WELL
TropiSARstem$Hloc <- TropiSARstem$Height # keeping directly measured trees
TropiSARstem$HlocRSE <- 1 # to be refined?! Assume a 1-m error on directly measured trees
TropiSARstem$levelHloc <- "FIELD"

```r
Site=as.character(ResHD$Site)
for(i in 1:length(ResHD$Site)){
    filt<-TropiSARstem$Site==Site[i] & is.na(TropiSARstem$Hloc)
    TropiSARstem$Hlocal[filt]<-retrieveH(D=TropiSARstem$Diameter[filt],model=HDmodelPerSite[[Site[i]]])$H
    TropiSARstem$HlocRSE[filt]<-HDmodelPerSite[[Site[i]]]$RSE
    TropiSARstem$levelHloc[filt]<-Site[i]
}
```
Assigning mean plot coordinates to trees to get environmental factor E

```r
longitude <- tapply(coordplot.trop$Longitude, coordplot.trop$Plot_code, mean)
latitude <- tapply(coordplot.trop$Latitude, coordplot.trop$Plot_code, mean)
meancoord <- data.frame(Plot_code=names(longitude), long=as.numeric(longitude), lat=as.numeric(latitude))
TropiSARstem$long <- meancoord[match(TropiSARstem$Plot_code, meancoord$Plot_code),"long"]
TropiSARstem$lat <- meancoord[match(TropiSARstem$Plot_code, meancoord$Plot_code),"lat"]
```

Compute AGB at hectare/quarter/corner level using 3 different models

```r
TropiSARstemTREE <- TropiSARstem[-which(TropiSARstem$FamilyAPG == "Arecaceae"),]
TropiSARstemTREE <- TropiSARstemTREE[with(TropiSARstemTREE, order(Site, decreasing = c(F), method = "radix")),]
resolAGB <- c("Hect_code", "Quart_code")
coefmult <- c(1,4)
ordarea <- list(df1ha$Area_code, df0.25ha$Area_code)
```

AGB PALM

```r
sort(table(TropiSARstem$Hect_code[which(TropiSARstem$FamilyAPG == "Arecaceae")]))
sort(table(TropiSARstem$Quart_code[which(TropiSARstem$FamilyAPG == "Arecaceae")]))

source("computeAGBpalm.R")
getWoodDensity("Oenocarpus", "bataua")
computeAGB(D=25.0, WD=0.6815, H=27.0)
computeAGBpalm(D=25.0)
TropiSARstemPALM <- TropiSARstem[which(TropiSARstem$FamilyAPG == "Arecaceae"),]
AGBpalmval <- computeAGBpalm(TropiSARstemPALM$Diameter)
tempPALM <- as.data.frame(matrix(rep(AGBpalmval, 1000), length(AGBpalmval), 1000))
Tropiprop_PALM <- cbind(TropiSARstemPALM, tempPALM)
```

AGB FELDPAUSCH (agb_fph)

```r
AGB_fph.list <- list()
rm(resultMC_FeldFG); gc()
resultMC_FeldFG <- by(TropiSARstemTREE, TropiSARstemTREE[,"Site"],
  function(x) AGBmonteCarlo(D=x$Diameter, WD=x$WD, errWD=x$sdWD, H=x$Hfeld
```
tempNOU <- as.data.frame(resultMC_FeldFG$NOURAGUES$AGB_simu)
tempPAR <- as.data.frame(resultMC_FeldFG$PARACOU$AGB_simu)
tempTROP <- rbind(tempNOU, tempPAR)
Tropiprop_FELD <- cbind(TropiSARstemTREE, tempTROP)
Tropiprop_FELD <- rbind(Tropiprop_FELD, Tropiprop_PALM)

for (i in 1:length(resolAGB)) {
tempocalc <- by(Tropiprop_FELD[, resolAGB[i]],
  function(x) list(meanAGB = mean(apply(x[,46:1045], 2, sum, na.rm = T)),
  #medAGB = median(apply(x[,46:1045], 2, sum, na.rm = T)),
  #sdAGB = sd(apply(x[,46:1045], 2, sum, na.rm = T)),
  credibilityAGB = quantile(apply(x[,46:1045], 2, sum, na.rm = T), probs = c(0.025, 0.975))))

  AGB_fph.list[[i]] <- data.frame(Area_code = names(tempocalc),
  agb_fph = round(as.numeric(sapply(tempocalc, "[", 1))*coefmult[i], 1),
  cred_fph_2.5 = round(as.numeric(lapply(sapply(tempocalc, "[", 1)),
    function(x) x[1]) * coefmult[i], 1),
  cred_fph_97.5 = round(as.numeric(lapply(sapply(tempocalc, "[", 2)),
    function(x) x[2]) * coefmult[i], 1),
  stringsAsFactors = F)

  AGB_fph.list[[i]] <- AGB_fph.list[[i]][match(ordarea[[i]], AGB_fph.list[[i]]$Area_code),]
  rownames(AGB_fph.list[[i]]) <- NULL
}
#AGB_fph.list

AGB_fph.df <- Reduce(rbind, AGB_fph.list)

AGB_fph.df

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## AGB USING ENVIRONMENTAL FACTOR E (agb_chv)

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AGB_chv.list <- list()

rm(resultMC_ChavFG); gc()
resultMC_ChaveFG <- by(TropiSARstemTREE, TropiSARstemTREE[, "Site"],
  function(x) AGBmonteCarlo(D=x$Diameter, WD=x$WD, errWD=x$sdWD, coord=cb
  ind(x$long, x$lat),
           Dpropag="chave2004"), simplify=F)
tempNOU <- as.data.frame(resultMC_ChaveFG$NOURAGUES$AGB_simu)
```

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```r
tempPAR <- as.data.frame(resultMC_ChaveFG$PARACOU$AGB_simu)
tempTROP <- rbind(tempNOU,tempPAR)
Tropiprop_CHAV <- cbind(TropiSARstemTREE, tempTROP)
Tropiprop_CHAV <- rbind(Tropiprop_CHAV, Tropiprop_PALM)

for (i in 1:length(resolAGB)) {
  tempocalc <- by(Tropiprop_CHAV, Tropiprop_CHAV[,resolAGB[i]],
  function(x) list(meanAGB = mean(apply(x[,46:1045], 2, sum, na.rm = T)),
  credibilityAGB = quantile(apply(x[,46:1045], 2, sum, na.rm = T), probs = c(0.025,0.975))))

  AGB_chv.list[[i]] <- data.frame(Area_code = names(tempocalc),
  agb_chv = round(as.numeric(sapply(tempocalc,"[",1))*coefmult[i,1]),
  cred_chv_2.5 = round(as.numeric(lapply(sapply(tempocalc,"[",2),
       function(x) x[1]))*coefmult[i,1]),
  cred_chv_97.5 = round(as.numeric(lapply(sapply(tempocalc,"[",2),
        function(x) x[2]))*coefmult[i,1]), stringsAsFactors = F)

  AGB_chv.list[[i]] <- AGB_chv.list[[i]][match(ordarea[[i]], AGB_chv.list[[i]]$Area_code),]
  rownames(AGB_chv.list[[i]]) <- NULL
}

AGB_chv.list
AGB_chv.df <- Reduce(rbind, AGB_chv.list)
AGB_chv.df
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## AGB USING LOCAL H:D RELATIONSHIP (agb_loc)

```
AGB_loc.list <- list()

rm(resultMC_LocalFG); gc()
resultMC_LocalFG <- by(TropiSARstemTREE, TropiSARstemTREE[,"Site"],
function(x) AGBmonteCarlo(D=x$Diameter, WD=x$WD, H=x$Hlocal, errWD=x$sd
WD,
errH=x$HlocRSE, Dpropag ="chave2004"), simplify=F)

tempNOU <- as.data.frame(resultMC_LocalFG$NOURAGUES$AGB_simu)
tempPAR <- as.data.frame(resultMC_LocalFG$PARACOU$AGB_simu)
tempTROP <- rbind(tempNOU, tempPAR)
Tropiprop_LOCAL <- cbind(TropiSARstemTREE, tempTROP)
Tropiprop_LOCAL <- rbind(Tropiprop_LOCAL, Tropiprop_PALM)
```

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tempocalc <- by(Tropiprop_LOCAL[, resolAGB[i]],
function(x) list(meanAGB = mean(apply(x[, 46:1045], 2, sum, na.rm = T)),
               credibilityAGB = quantile(apply(x[, 46:1045], 2, sum, na.rm = T), probs = c(0.025, 0.975))))

AGB_loc.list[[i]] <- data.frame(Area_code = names(tempocalc),
                                agb_loc = round(as.numeric(sapply(tempocalc, "[", 1))*coefmult[i, 1]),
                                cred_loc_2.5 = round(as.numeric(lapply(sapply(tempocalc, "[", 2),
                                                   function(x) x[1])*coefmult[i, 1]),
                                cred_loc_97.5 = round(as.numeric(lapply(sapply(tempocalc, "[", 2),
                                                   function(x) x[2])*coefmult[i, 1]),
stringsAsFactors = F)

AGB_loc.list[[i]] <- AGB_loc.list[[i]][match(ordarea[[i]], AGB_loc.list[[i]]$Area_code),]
rownames(AGB_loc.list[[i]]) <- NULL
}
AGB_loc.list
AGB_loc.df <- Reduce(rbind, AGB_loc.list)
AGB_loc.df

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Calculating the maximum height and the Lorey’s height per (sub)plot

```
TropiSARstemTREE$Hchave <- retrieveH(D=TropiSARstemTREE$Diameter, coord=cbind(TropiSARstemTREE$long,TropiSARstemTREE$lat))$H

# Max height
maxHlocal <- tapply(TropiSARstemTREE$Hlocal, TropiSARstemTREE$Quart_code, max)
maxHchave <- tapply(TropiSARstemTREE$Hchave, TropiSARstemTREE$Quart_code, max)
maxHfeld <- tapply(TropiSARstemTREE$Hfeld, TropiSARstemTREE$Quart_code, max)

# Lorey height
TropiSARstemTREE$BAm <- (pi*(TropiSARstemTREE$Diameter/2)^2)/10000
TropiSARstemTREE$HBAm <- TropiSARstemTREE$BAm
TropiSARstemTREE$HBAlocal <- TropiSARstemTREE$Hlocal * TropiSARstemTREE$HBAm
TropiSARstemTREE$HBAchave <- TropiSARstemTREE$Hchave * TropiSARstemTREE$HBAm
TropiSARstemTREE$HBAfeld <- TropiSARstemTREE$Hfeld * TropiSARstemTREE$HBAm
LoreyLocal <- tapply(TropiSARstemTREE$HBAlocal,TropiSARstemTREE$Quart_code,sum) / tapply(TropiSARstemTREE$BAm,TropiSARstemTREE$Quart_code,sum)
LoreyChave <- tapply(TropiSARstemTREE$HBAchave,TropiSARstemTREE$Quart_code,sum) / tapply(TropiSARstemTREE$BAm,TropiSARstemTREE$Quart_code,sum)
LoreyFeld <- tapply(TropiSARstemTREE$HBAfeld,TropiSARstemTREE$Quart_code,sum) / tapply(TropiSARstemTREE$BAm,TropiSARstemTREE$Quart_code,sum)

hdf <- data.frame(Area_code = names(maxHlocal), LoreyLocal=LoreyLocal, LoreyChave=LoreyChave,LoreyFeld=LoreyFeld, maxHlocal=maxHlocal, maxHchave=maxHchave, maxHfeld=maxHfeld)
```
Reshaping the different information (estimates, coordinates) in a single object

```r
# Merge dataframes
AGB_FIN1 <- merge(georefeatures.df, AGB_fph.df, by="Area_code", sort = F, all=T)
AGB_FIN2 <- merge(AGB_FIN1, AGB_chv.df, by="Area_code", sort = F, all=T)
AGB_TropiSAR <- merge(AGB_FIN2, AGB_loc.df, by="Area_code", sort = F, all=T)
# AGB_TropiSAR[,c(14:15,17:18,20:21)] <- round(AGB_TropiSAR[,c(14:15,17:18,20:21)],1)

# Reorder columns
AGB_TropiSAR <- AGB_TropiSAR[c("Site","Area_code","Plot_code","Scale",
                           "Lon_sw","Lat_sw","Lon_nw","Lat_nw","Lon_se","Lat_se","Lon_ne",
                           "Lat_ne","Lon_cnt","Lat_cnt",
                           "LoreyLocal","LoreyChave","LoreyFeld","maxHlocal","maxHchave","maxHfeld",
                           "agb_fph","cred_fph_2.5","cred_fph_97.5","agb_chv","cred_chv_2.5",
                           "cred_chv_97.5","agb_loc","cred_loc_2.5","cred_loc_97.5")]
# AGB_TropiSAR
```