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# Forest Biomass in Bangladesh: An historical review of forest inventories to assist national estimat
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# Gael Sola, FAO, gael.sola@fao.org,
# Liam Costello, liam.costello@fao.org
# 04/2016
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# Develloping HxD models
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#####
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```
# Erase Memory
rm(list=ls())
```

```
# remove graphs
dev.off()
```

```
# Load / install packages
library(tidyverse)
library(grid)
library(gridExtra)
library(nlme)
library(lmfor)
# install.packages('tidyverse', dependencies=TRUE, type="source")
```

```
# Setting working directory
setwd("/media/gs/OSDisk/Users/solag/Documents/Work/Bangladesh article harmo/Analysis/data")
```

```
# Set graph style
source("R-corrections/theme_gs_print.R")
```

```
# Load a function for modeling and compa h-D relationship models
source("H-D_Model/hd_compa_10nov.R")
```

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```
# Read the table
tree <- read.csv("results/t_hd_alltrees.csv", stringsAsFactors = FALSE)
```

```
summary(tree$dbh_cm)
summary(tree$h_m)
```

```
# Plot h-d with FRMP displayed in the back
mytable <- tree
mytable %>%
  arrange(desc(entity_ab)) %>%
  ggplot(aes(x=dbh_cm,y=h_m)) +
  geom_point(aes(colour = entity_ab, shape = entity_ab), cex=0.8) +
# geom_text(aes(label = id_tree_2), cex=3) +
  facet_wrap(~bfi_zone) +
  theme(legend.position = c(0.8,0.2))
```

```
# mytable %>%
#   arrange(desc(entity_ab)) %>%
#   ggplot(aes(x=dbh_cm,y=h_m)) +
#   geom_point(aes(colour = entity_ab, shape = entity_ab), cex=0.8) +
#   facet_wrap(~lccs2) +
#   theme(legend.position = c(0.8,0.2))
```

```
# Check low height big dbh trees in village zone
tree[tree$bfi_zone == "Villages" & tree$dbh_cm > 100,]
```

```
# Remove trees from non vegetation lccs
tree_save <- tree
tree <- tree_save
```

```
tree <- tree[-which(tree$lccs1 == "A"),]
```

```
# Remove trees bigger than 150 cm to avoid bias of data towards small height in village
tree <- tree[-which(tree$bfi_zone == "Villages" & tree$dbh_cm > 100),]
```

```

# Remove outliers for Coastal
tree <- tree[-which(tree$id_tree_2 == "292678"),]
tree <- tree[-which(tree$id_tree_2 == "297374"),]

# Check number of tree per bfi zone and lccs
summary(factor(tree$bfi_zone))
summary(factor(tree$lccs1))
summary(factor(tree$lccs2))
summary(factor(tree$lccs3))

# Create a table with plot id and forest type
t_plot <- tree[,c("id","bfi_zone")]
t_plot <- unique(t_plot)

# create a vector with forest type names
t_bfi <- unique(tree$bfi_zone)
t_bfi[1]

# RUN JUST ONCE: Create a table vec containing 20 % of the plots for validation
# vec <- NA
# for(i in 1:length(t_bfi)){
#   v_sample <- t_plot[which(t_plot$bfi_zone == t_bfi[i]),]$id
#   vec <- c(vec, sample(v_sample, round(length(v_sample)*0.3)))
# }
# vec <- vec[!is.na(vec)]
# save(vec, file="H-D_Model/plot code for validation_10nov.Rdata")

# Load the plot id of the random selection
load("H-D_Model/plot code for validation_10nov.Rdata")

# Create the table tree_valid and tree_model
tree$attrib <- ifelse(tree$id %in% vec, "valid", "model")
table(tree$attrib)

tree_valid <- tree[tree$attrib == "valid",]
tree_model <- tree[tree$attrib == "model",]

# verif
dim(tree_valid)[1] + dim(tree_model)[1]
dim(tree)[1]

# plot
ggplot(tree) +
  geom_point(aes(x=dbh_cm, y=h_m, color=attrib, shape=attrib)) +
  facet_wrap(~bfi_zone) +
  theme(legend.position = c(0.8,0.2))

# ggplot(tree)+
#   geom_point(aes(x=dbh_cm, y=h_m, colour=attrib, pch=attrib)) +
#   facet_wrap(~lccs2)

# Select the relevant columns
tree2 <- tree_model[,c("id_tree_2","dbh_cm","h_m","id","entity_ab","bfi_zone","fao_biome", "lccs1",

#-----#
#           Develop and compare random effects
#-----#

### No random effect
# gomp
m_gomp <- hd_mod(model_form = "gomp",
                 mystart     = startHDgomperz(d = tree2$dbh_cm, h = tree2$h_m),
                 nb_iter    = 50)

# rat
m_rat <- hd_mod(model_form = "rat",

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        mystart      = startHDratkowsky(d = tree2$dbh_cm, h = tree2$h_m),
        nb_iter      = 50)
# weib
m_weib <- hd_mod(model_form = "weib",
                 mystart      = c(23.4, 0.05, 0.9),
                 nb_iter      = 50)

test2 <- fixef(m_weib)
# pow
#mystart <- coef(lm(log(tree2$h_m)~log(tree2$dbh_cm)))
#mystart[1] <- exp(mystart[1])
m_pow <- hd_mod(model_form = "pow",
                 mystart      = startHDPower(d = tree2$dbh_cm, h = tree2$h_m), #mystart,
                 nb_iter      = 50)

# compa no ranef
no_ranef <- compa_hd()
no_ranef$res_AIC
names(no_ranef$res_AIC)[2] <- "AIC_noraneef"
no_ranef$res_p_value
no_ranef$plot_models

grid.arrange(no_ranef$plot_res)

#-----#

### FAO zone effect
# gomp
m_gomp <- hd_mod(model_form = "gomp",
                 mystart      = c(20, 2, 0.1),
                 nb_iter      = 50,
                 myeffect     = "fao_biome")

# rat
m_rat <- hd_mod(model_form = "rat",
                 mystart      = startHDratkowsky(d = tree2$dbh_cm, h = tree2$h_m),
                 nb_iter      = 100,
                 myeffect     = "fao_biome")

# weib
m_weib <- hd_mod(model_form = "weib",
                 mystart      = c(23.4, 0.05, 0.9),
                 nb_iter      = 50,
                 myeffect     = "fao_biome")

# pow
#mystart <- coef(lm(log(tree2$h_m)~log(tree2$dbh_cm)))
#mystart[1] <- exp(mystart[1])
m_pow <- hd_mod(model_form = "pow",
                 mystart      = startHDPower(d = tree2$dbh_cm, h = tree2$h_m), #mystart,
                 nb_iter      = 50,
                 myeffect     = "fao_biome")

# compa fao
fao <- compa_hd(myeffect = "fao_biome")
fao$res_AIC
names(fao$res_AIC)[2] <- "AIC_fao"
fao$res_p_value
fao$plot_models

grid.arrange(fao$plot_res)

#-----#

### BFI zone effect
# gomp
m_gomp <- hd_mod(model_form = "gomp",
                 mystart      = c(20, 2, 0.1), #startHDPower(d = tree2$dbh_cm, h = tree2$h_m),#c(17
                 nb_iter      = 1000,
                 myeffect     = "bfi_zone")

```

```

# rat
m_rat <- hd_mod(model_form = "rat",
               mystart     = startHDRatkowsky(d = tree2$dbh_cm, h = tree2$h_m),
               nb_iter     = 100,
               myeffect    = "bfi_zone")

# weib
m_weib <- hd_mod(model_form = "weib",
                 mystart     = c(23.4, 0.05, 0.9),
                 nb_iter     = 100,
                 myeffect    = "bfi_zone")

# pow
mystart <- coef(lm(log(tree2$h_m)~log(tree2$dbh_cm)))
mystart[1] <- exp(mystart[1])
m_pow <- hd_mod(model_form = "pow",
                mystart     = startHDPower(d = tree2$dbh_cm, h = tree2$h_m), #mystart,
                nb_iter     = 50,
                myeffect    = "bfi_zone")

# compa bfi
bfi <- compa_hd(myeffect = "bfi_zone")
bfi$res_AIC
names(bfi$res_AIC)[2] <- "AIC_bfi"
bfi$res_p_value
bfi$plot_models

grid.arrange(bfi$plot_res)

#-----#

### LCCS1
# gomp
m_gomp <- hd_mod(model_form = "gomp",
                 mystart     = c(20, 2, 0.1), #startHDPomperz(d = tree2$dbh_cm, h = tree2$h_m),#c(17
                 nb_iter     = 1000,
                 myeffect    = "lccs1")

# rat
m_rat <- hd_mod(model_form = "rat",
               mystart     = startHDRatkowsky(d = tree2$dbh_cm, h = tree2$h_m),
               nb_iter     = 100,
               myeffect    = "lccs1")

# weib
m_weib <- hd_mod(model_form = "weib",
                 mystart     = c(23.4, 0.05, 0.9),
                 nb_iter     = 100,
                 myeffect    = "lccs1")
test <- fixef(m_weib)

# pow
m_pow <- hd_mod(model_form = "pow",
                mystart     = startHDPower(d = tree2$dbh_cm, h = tree2$h_m), #mystart,
                nb_iter     = 50,
                myeffect    = "lccs1")

# compa lccs1
lccs1 <- compa_hd(myeffect = "lccs1")
lccs1$res_AIC
names(lccs1$res_AIC)[2] <- "AIC_lccs1"
lccs1$res_p_value
lccs1$plot_models

grid.arrange(lccs1$plot_res)

```

#-----#

LCCS2

gomp

```
m_gomp <- hd_mod(model_form = "gomp",
  mystart      = c(20, 2, 0.1), #startHDgomperz(d = tree2$dbh_cm, h = tree2$h_m),#c(17
  nb_iter      = 1000,
  myeffect     = "lccs2")
```

rat

```
m_rat <- hd_mod(model_form = "rat",
  mystart      = c(19.7, 21.1, 13.7), #startHDratkowsky(d = tree2$dbh_cm, h = tree2$h_m
  nb_iter      = 1000,
  myeffect     = "lccs2")
```

weib

```
m_weib <- hd_mod(model_form = "weib",
  mystart      = startHDweibull(d = tree2$dbh_cm, h = tree2$h_m),
  nb_iter      = 100,
  myeffect     = "lccs2")
```

haha <- fixef(m_weib)

pow

```
m_pow <- hd_mod(model_form = "pow",
  mystart      = startHDPower(d = tree2$dbh_cm, h = tree2$h_m), #mystart,
  nb_iter      = 50,
  myeffect     = "lccs2")
```

compa lccs2

```
lccs2 <- compa_hd(myeffect = "lccs2")
lccs2$res_AIC
names(lccs2$res_AIC)[2] <- "AIC_lccs2"
lccs2$res_p_value
lccs2$plot_models
```

grid.arrange(lccs2\$plot_res)

#-----#

LCCS3

summary(as.factor(tree2\$lccs3))

gomp

```
m_gomp <- hd_mod(model_form = "gomp",
  mystart      = c(20, 2, 0.1), #startHDgomperz(d = tree2$dbh_cm, h = tree2$h_m),#c(17
  nb_iter      = 1000,
  myeffect     = "lccs3")
```

rat

```
m_rat <- hd_mod(model_form = "rat",
  mystart      = c(19.7, 21.1, 13.7), #startHDratkowsky(d = tree2$dbh_cm, h = tree2$h_m
  nb_iter      = 1000,
  myeffect     = "lccs3")
```

weib

```
m_weib <- hd_mod(model_form = "weib",
  mystart      = startHDweibull(d = tree2$dbh_cm, h = tree2$h_m),
  nb_iter      = 100,
  myeffect     = "lccs3")
```

pow

```
m_pow <- hd_mod(model_form = "pow",
  mystart      = startHDPower(d = tree2$dbh_cm, h = tree2$h_m), #mystart,
  nb_iter      = 50,
  myeffect     = "lccs3")
```

compa lccs3

```

lccs3 <- compa_hd(myeffect = "lccs3")
lccs3$res_AIC
names(lccs3$res_AIC)[2] <- "AIC_lccs3"
lccs3$res_p_value
lccs3$plot_models

grid.arrange(lccs3$plot_res)

#-----#
#                               Model selection
#-----#

# Compa effects AIC
AIC_all <- Reduce(function(...)merge(..., by = "model"),
                  list(no_ranef$res_AIC, fao$res_AIC, bfi$res_AIC,
                       lccs1$res_AIC, lccs2$res_AIC, lccs3$res_AIC
                    )
                )
AIC_all[,2:5] <- round(AIC_all[,2:5], 0)
AIC_all

write.csv(AIC_all, file="H-D_Model/compa_AIC.csv", row.names=FALSE)

# ==>>> Best models selected:
#   - Weibull LCCS3 (best effect)
#   - Weibull BFI (runner-up effect weibul good compromise residual behavior/AIC)
#   - Weibull no effect
no_ranef$plot_models
ggsave("H-D_Model/gr_models and data_noranef.png", width = 15, height = 12, units = "cm", dpi = 300)

bfi$plot_models
ggsave("H-D_Model/gr_models and data_bfi.png", width = 15, height = 12, units = "cm", dpi = 300)

lccs3$plot_models
ggsave("H-D_Model/gr_models and data_lccs3.png", width = 15, height = 12, units = "cm", dpi = 300)

# Re-run models
m_weib_noef <- hd_mod(model_form = "weib",
                     mystart   = c(23.4, 0.05, 0.9),
                     nb_iter   = 100)

m_weib_bfi <- hd_mod(model_form = "weib",
                     mystart   = startHDweibull(d = tree2$dbh_cm, h = tree2$h_m),
                     nb_iter   = 100,
                     myeffect  = "bfi_zone")

m_weib_lcc <- hd_mod(model_form = "weib",
                     mystart   = startHDweibull(d = tree2$dbh_cm, h = tree2$h_m),
                     nb_iter   = 100,
                     myeffect  = "lccs3")

AIC(m_weib_noef)
fixef(m_weib_noef)
ranef(m_weib_noef)

AIC(m_weib_bfi)
fixef(m_weib_bfi)
ranef(m_weib_bfi)

AIC(m_weib_lcc)
fixef(m_weib_lcc)
ranef(m_weib_lcc)

#-----#
#                               Bias calculation
#-----#

# Create a table with all the parameters

```

```

# BFI Weibull
param_bfi <- ranef(m_weib_bfi)
for (i in 1:length(fixef(m_weib_bfi))){
  param_bfi[,i] <- param_bfi[,i] + fixef(m_weib_bfi)[i]
}

# LCCS3 Weibull
param_lcc <- ranef(m_weib_lcc)
for (i in 1:length(fixef(m_weib_lcc))){
  param_lcc[,i] <- param_lcc[,i] + fixef(m_weib_lcc)[i]
}
param_lcc

# Calculating h estimated by Weibull BFI
tree_valid$h_est_bfi <- NA
bfi_zones <- sort(unique(tree_valid$bfi_zone))
for(i in 1:length(bfi_zones)){
  a <- param_bfi[i,1]
  b <- param_bfi[i,2]
  c <- param_bfi[i,3]
  bz <- bfi_zones[i]
  tree_valid[tree_valid$bfi_zone == bz,"h_est_bfi"] <-
    1.3 + a*(1 - exp(-b*tree_valid[which(tree_valid$bfi_zone == bz),"dbh_cm"]^c))
}

summary(tree_valid$h_est_bfi)

# Calculating h estimated by Weibull lccs3
tree_valid$h_est_lcc <- NA
lccs3_class <- sort(unique(tree_valid$lccs3))
for(i in 1:length(lccs3_class)){
  a <- param_lcc[i,1]
  b <- param_lcc[i,2]
  c <- param_lcc[i,3]
  lc <- lccs3_class[i]
  tree_valid[tree_valid$lccs3 == lc,"h_est_lcc"] <-
    1.3 + a*(1 - exp(-b*tree_valid[which(tree_valid$lccs3 == lc),"dbh_cm"]^c))
}
summary(tree_valid$h_est_lcc)

# Calculate the h_est by weibull no ranef
a <- fixef(m_weib_noef)[1]
b <- fixef(m_weib_noef)[2]
c <- fixef(m_weib_noef)[3]
tree_valid$h_est_noef <- 1.3 + a*(1 - exp(-b*tree_valid$dbh_cm^c))

# Calculate h_est by feldpausch article
# (2012 - Integrating height into global forest biomass estimates, table 3)
tree_valid$h_est_F12 <- 57.122*(1-exp(-0.0332*tree_valid$dbh_cm^0.8468))

# (2011 - Height-diameter allometry of tropical forest trees)
tree_valid$h_est_F11 <- exp(1.2194)*tree_valid$dbh_cm^0.5767

ggplot(tree_valid) +
  geom_point(aes(x=dbh_cm, y=h_m), col='grey', alpha = 0.6) +
  geom_line(aes(x=dbh_cm, y=h_est_bfi)) +
  geom_line(aes(x=dbh_cm, y=h_est_noef), linetype = "longdash") +
  geom_line(aes(x=dbh_cm, y=h_est_F11), linetype = "dashed") +
  geom_line(aes(x=dbh_cm, y=h_est_F12), linetype = "dotted") +
  facet_wrap(~bfi_zone) +
  labs(caption = "line: Weibull BFI; long dash line: Weibull no random effect; dashed line: Feldpausch",
       x = "Diameter at breast height (cm)",
       y = "Tree total height (m)")

ggsave("H-D_Model/gr_model_validation_bfi.png", width = 15, height = 12, units = "cm", dpi = 300)

ggplot(tree_valid) +
  geom_point(aes(x=dbh_cm, y=h_m), col='grey', alpha = 0.6) +
  geom_line(aes(x=dbh_cm, y=h_est_lcc)) +

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geom_line(aes(x=dbh_cm, y=h_est_noef), linetype = "longdash") +
geom_line(aes(x=dbh_cm, y=h_est_F11), linetype = "dashed") +
geom_line(aes(x=dbh_cm, y=h_est_F12), linetype = "dotted") +
facet_wrap(~lccs3) +
labs(caption = "line: Weibull lccs3; long dash line: Weibull no random effect; dashed line: Feldpausch et al. 2011; dotted line: Feldpausch et al. 2011",
      x       = "Diameter at breast height (cm)",
      y       = "Tree total height (m)")

ggsave("H-D_Model/gr_model_validation_lcc.png", width = 15, height = 12, units = "cm", dpi = 300)

# Calculate bias
bias_noraneef <- sum((tree_valid$h_m - tree_valid$h_est_noef))/sum(tree_valid$h_m)*100
bias_noraneef

bias_bfi <- sum((tree_valid$h_m - tree_valid$h_est_bfi))/sum(tree_valid$h_m)*100
bias_bfi

bias_lccs3 <- sum((tree_valid$h_m - tree_valid$h_est_lcc))/sum(tree_valid$h_m)*100
bias_lccs3

bias_F11 <- sum((tree_valid$h_m - tree_valid$h_est_F11))/sum(tree_valid$h_m)*100
bias_F11

bias_F12 <- sum((tree_valid$h_m - tree_valid$h_est_F12))/sum(tree_valid$h_m)*100
bias_F12

# Save the bias as a table
bias_all <- data.frame(Model = c("No random effect", "BFI", "LCCS3", "Feldpausch et al. 2011", "Feldpausch et al. 2011"),
                      Bias = c(bias_noraneef,bias_bfi, bias_lccs3, bias_F11, bias_F12)
                      )

bias_all

write.csv(bias_all, file="H-D_Model/bias_models.csv", row.names=FALSE)

# Save the params as R file
model_params <- list(param_noraneef = fixef(m_weib),
                    param_bfi = param_bfi,
                    param_lccs3 = param_lcc
                    )

save(model_params, file="H-D_Model/model_params.Rdata")
#####
#####
#####

```