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# Forest Biomass in Bangladesh: An historical review of forest inventories to assist national estimat
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# Calculating Biomass
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# Effacer memoire
rm(list=ls())
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# Verification du working directory
getwd()
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# remove graphs
dev.off()
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# run library
#install.packages("")
library(tidyverse)
library(ggthemes)
library(grid)
library(gridExtra)
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# Setting working directory
setwd("/media/gs/OSDisk/Users/solag/Documents/Work/Bangladesh article harmo/Analysis/data")
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# Set the plot theme
source("R-corrections/theme_gs_print.R")
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#-----#
#                               Load data and h-d model
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# Read the table table_all
tree <- read.csv("results/table_all_01b_treesandplots_sup10.csv", header=T, stringsAsFactors = FALSE)
dim(tree)
length(unique(tree$id))
# Create new id
tree$main_tree_id <- paste(tree$entity_ab, tree$id_tree, sep="_")
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# Remove non vegetated trees
tree <- tree[-which(tree$lccs1 == "A"),]
length(unique(tree$id))
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# load the h-d model results
load("H-D_Model/model_params.Rdata")
param_lccs3 <- model_params$param_lccs3
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#-----#
#   Estimates h of all trees based on best model (lccs3)
#-----#
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# Calculating h estimated by Weibull lccs3
tree$h_est_lccs3 <- NA
lccs3_class <- sort(unique(tree$lccs3))
for(i in 1:length(lccs3_class)){
  a <- param_lccs3[i,1]
  b <- param_lccs3[i,2]
  c <- param_lccs3[i,3]
  lc <- lccs3_class[i]
  tree[tree$lccs3 == lc, "h_est_lccs3"] <-
    1.3 + a*(1 - exp(-b*tree[which(tree$lccs3 == lc), "dbh_cm"]^c))
}
summary(tree$h_est_lccs3)
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# Create h_all
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tree$h_all <- ifelse(is.na(tree$h_m),
                    tree$h_est_lccs3,
                    tree$h_m)

# Check
tree$lccs3_modif <- factor(tree$lccs3)
levels(tree$lccs3_modif) <- c("Cultivated vegetation",
                             "Cultivated vegetation (partially) flooded",
                             "Natural vegetation",
                             "Natural vegetation (partially) flooded",
                             "Rural settlements")

ggplot() +
  geom_point(data = tree[!is.na(tree$h_m),], aes(x=dbh_cm, y=h_all), col = 'grey50', cex=0.5) +
  geom_line(data = tree[is.na(tree$h_m),], aes(x=dbh_cm, y=h_all)) +
  facet_wrap(~lccs3_modif) +
  labs(x = "Diameter at breast height (cm)", y = "Tree total height (m)")

# save plot
ggsave("results/gr_measured and estimated tree height_sup10.png", width = 15, height = 12, units = "cm")

tree_save <- tree
tree <- tree_save

#-----#
#           Calculate aboveground biomass tree and plots
#-----#

# Tree agb
tree$agb_kg <- 0.0673*(tree$wd*(tree$dbh_cm)^2*tree$h_all)^0.976
summary(tree$agb_kg)

# calculate agb weight of each tree_sub per ha
tree$agb_t_ha <- tree$agb_kg * tree$scale_factor /1000

# create a plot level table
plot_data <- Reduce(function(...)merge(..., by = "id"),
                    list(
                      a = unique(tree[,c("id","entity_ab", "fao_biome", "bfi_zone",
                                           "lccs1", "lccs2", "lccs3", "lccs4", "lccs5", "lccs6")]),
                      b = aggregate(agb_t_ha~id, data=tree, FUN=sum),
                      c = aggregate(ba_ha~id, data=tree, FUN=sum),
                      d = aggregate(plot_size_ha~id, data=tree, FUN=max),
                      e = aggregate(scale_factor~id, data=tree, FUN=sum)
                    )
)

names(plot_data)[14] <- "nstem_ha"

length(unique(tree$id))

# Check
ggplot(plot_data) +
  geom_boxplot(aes(x=entity_ab, y=agb_t_ha)) +
  facet_wrap(~bfi_zone) +
  coord_flip()

# Control: average AGB classes per lccs6 and entity_ab
agb_avg <- aggregate(agb_t_ha~entity_ab+lccs6, data = plot_data, FUN = mean)
agb_avg

#-----#
#           write the tables
#-----#
write.csv(tree, file= "results/tree_final_sup10.csv", row.names=FALSE)
write.csv(plot_data, file= "results/plot_agb_sup10.csv", row.names=FALSE)

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