Title: Mapping the soil carbon stocks of Bangladesh

Year: 2016

Author: Poultouchidou, A., Chowdhury, S., Hoque, S., Nazmul Hasan, Md., Henry, M., Akther, M., Costello, L., Rahman, L., Bernoux, M.

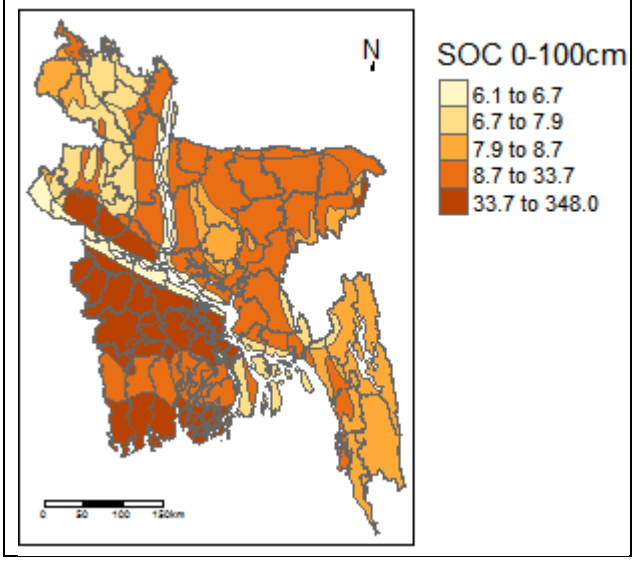
Reference: Poultouchidou, A., Chowdhury, S., Hoque, S., Nazmul Hasan, Md., Henry, M., Akther, M., Costello, L., Rahman, L., Bernoux, M. (2016), Mapping the soil carbon stocks of Bangladesh, Bangladesh Forest Department and Food and Agriculture Organization of the United Nations. Dhaka, Bangladesh.

Methodology: Data from the Harmonized World Soil Database (HWSD) used to develop the map of SOC stocks for Bangladesh. The variables of HWSD database considered were: MU_GLOBAL (a code that links the GIS layer to the attribute database), SHARE (the share % of the soil unit within the mapping unit), soil organic carbon (% weight), gravel content (% vol), sand fraction (%wt), clay fraction (%wt), reference bulk density (kg/dm^3). An intersection shape file was created between the HWSD shapefile and the district boundaries.

The soil properties were extracted from the global HWSD database and allocated to the intersected maps. In total, 27 soil mapping units relevant for Bangladesh have been extracted from the global HWSD database. The FAO-UNESCO 1974 legend was used to link the soil mapping units with the interpretation of each of soil properties on the map. The area was estimated based on the Bangladesh Transverse Mercator (BTM) projection system.

Results:

Image



Data:

The map is available at the FAO team, Forest Department in Dhaka, Bangladesh.

Contact FAO:

matieu.henry@fao.org

R Script:

```
# Import the data

HWSD <- read.csv("HWSD_DATA.csv")
GLO <- read.csv("GLO.csv")
BD <- readOGR(dsn = "G:/SOC/SRDI_HWSD", layer = "HWSD_Bgd_District")

# Extract from the global database HWSD the relevant data for Bangladesh

SBD <- HWSD[HWSD$MU_GLOBAL %in% unique(BD$MU_GLOBAL) , ]

# Sinusoidal projection

proj_BTM<- "+proj=tmerc +lon_0=90e +x_0=500000 +y_0=-2000000 +ellps=evrst30"
BD_BTM <-spTransform(BD, CRS=proj_BTM)

# Calculate the soil organic carbon stocks per major soil type

SBD_74 <- data.frame(T_SOC= SBD$T_SOC, Major_74= SBD$Major_74)
mean_T_SOC_M <- tapply(SBD_74$T_SOC, SBD_74$Major_74, mean)
sd_T_SOC_M<- tapply(SBD_74$T_SOC, SBD_74$Major_74, sd)
n_T_SOC_M<- tapply(SBD_74$T_SOC, SBD_74$Major_74, length)
min_T_SOC_M<- tapply(SBD_74$T_SOC, SBD_74$Major_74, min)
max_T_SOC_M<- tapply(SBD_74$T_SOC, SBD_74$Major_74, max)
table_T_SOC_M<- data.frame(mean=mean_T_SOC_M, sd=sd_T_SOC_M, n=n_T_SOC_M,
min=min_T_SOC_M, max=max_T_SOC_M)

SBD_74 <- data.frame(S_SOC= SBD$S_SOC, Major_74= SBD$Major_74)
mean_S_SOC_M <- tapply(SBD_74$S_SOC, SBD_74$Major_74, mean)
sd_S_SOC_M<- tapply(SBD_74$S_SOC, SBD_74$Major_74, sd)
n_S_SOC_M<- tapply(SBD_74$S_SOC, SBD_74$Major_74, length)
min_S_SOC_M<- tapply(SBD_74$S_SOC, SBD_74$Major_74, min)
max_S_SOC_M<- tapply(SBD_74$S_SOC, SBD_74$Major_74, max)
```

```
table_S_SOC_M<- data.frame(mean=mean_S_SOC_M, sd=sd_S_SOC_M, n=n_S_SOC_M,
min=min_S_SOC_M, max=max_S_SOC_M)

SBD_74 <- data.frame(Tot_SOC= SBD$T_SOC+SBD$S_SOC, Major_74= SBD$Major_74)
mean_Tot_SOC_M <- tapply(SBD_74$Tot_SOC, SBD_74$Major_74, mean)
sd_Tot_SOC_M <- tapply(SBD_74$Tot_SOC, SBD_74$Major_74, sd)
n_Tot_SOC_M <- tapply(SBD_74$Tot_SOC, SBD_74$Major_74, length)
min_Tot_SOC_M <- tapply(SBD_74$Tot_SOC, SBD_74$Major_74, min)
max_Tot_SOC_M <- tapply(SBD_74$Tot_SOC, SBD_74$Major_74, max)
table_Tot_SOC_M <- data.frame(mean=mean_Tot_SOC_M, sd=sd_Tot_SOC_M,
n=n_Tot_SOC_M, min=min_Tot_SOC_M, max=max_Tot_SOC_M)

# Calculate the SOC stocks per MU

SBD$T_SOC2 <- SBD$T_SOC*SBD$SHARE/100
SBD$S_SOC2 <- SBD$S_SOC*SBD$SHARE/100

T_SOC <- tapply(SBD$T_SOC2, SBD$MU_GLOBAL, sum)
T_SOC2 <- data.frame(MU_GLOBAL=names(T_SOC), T_SOC=T_SOC)
S_SOC <- tapply(SBD$S_SOC2, SBD$MU_GLOBAL, sum)
S_SOC2 <- data.frame(MU_GLOBAL=names(S_SOC), S_SOC=S_SOC)

SBD$S_SOC2[is.na(SBD$S_SOC2)]<-0
SBD$T_SOC2[is.na(SBD$T_SOC2)]<-0
SBD$Tot_SOC2<- SBD$T_SOC2 + SBD$S_SOC2
Tot_SOC <- tapply(SBD$Tot_SOC2, SBD$MU_GLOBAL, sum)
Tot_SOC2 <- data.frame(MU_GLOBAL=names(Tot_SOC), Tot_SOC=Tot_SOC)
dim(Tot_SOC2$Tot_SOC)
MU <- data.frame(MU_GLOBAL=names(Tot_SOC), T_SOC=T_SOC, S_SOC=S_SOC,
Tot_SOC=Tot_SOC)

# Allocate to the spatial dataframe the SOC values and soil names

BD_BTM$T_SOC <- T_SOC2$T_SOC[
  match(BD_BTM$MU_GLOBAL, T_SOC2$MU_GLOBAL)]

BD_BTM$S_SOC <- S_SOC2$S_SOC[
  match(BD_BTM$MU_GLOBAL, S_SOC2$MU_GLOBAL)]

BD_BTM$Tot_SOC <- Tot_SOC2$Tot_SOC[
  match(BD_BTM$MU_GLOBAL, Tot_SOC2$MU_GLOBAL)]
```

```
BD_BTM$FAO_74_Name <- SBD$FAO_74_Name[
  match(BD_BTM$MU_GLOBAL, SBD$MU_GLOBAL)]

BD_BTM$Major_74 <- SBD$Major_74[
  match(BD_BTM$MU_GLOBAL, SBD$MU_GLOBAL)]

# Clean BD_BTM database from the water bodies

BD_BM <- subset(BD_BTM, BD_BTM$T_SOC>0)

# Map representing the SOC for the 0-100 cm soil layer
tm_shape(BD_BM) +
  tm_fill("Tot_SOC", style="kmeans",
          labels=levels(BD_BM$Tot_SOC),
          title="SOC 0-100cm")+
  tm_borders()+
  tm_layout(legend.outside = TRUE)+
  tm_scale_bar(size = 0.3, position = c("left", "bottom"))+
  tm_compass(size= 0.3, position = c("right", "top"))
```