

Global Carbon Estimates

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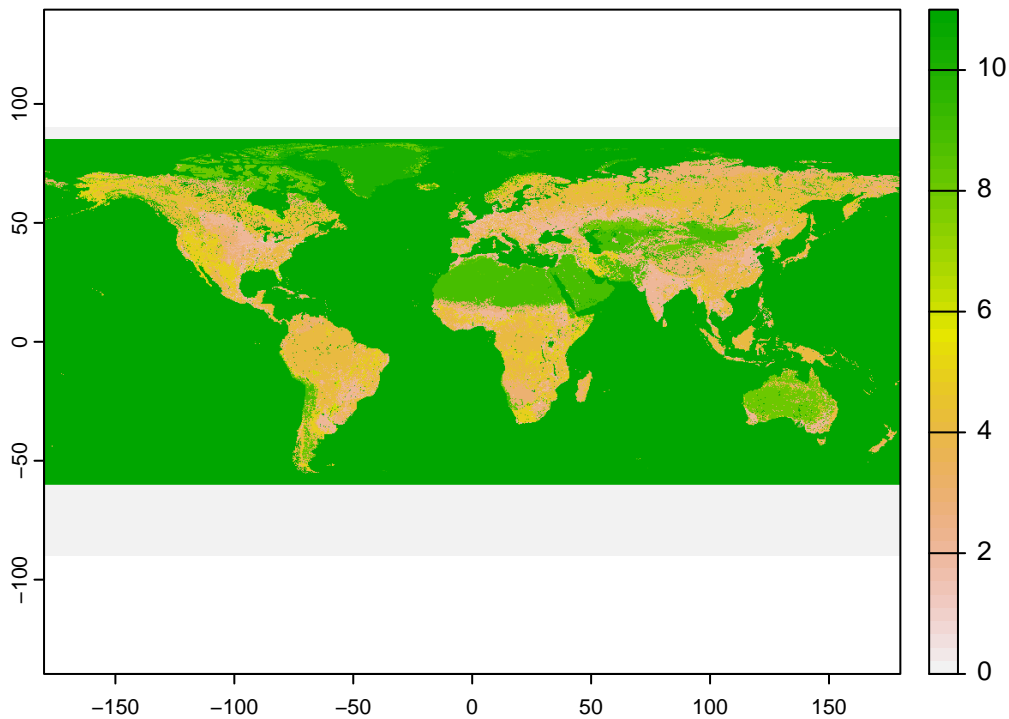
Ecosystem Cover Data

```
# Download total land cover map from FAO
#download.file("https://storage.googleapis.com/fao-maps-catalog-data/uuid/ba4526fd-cdbf-4028-a1bd-5a559
#unzip("FAO_covermap.zip", exdir = ".")
#file.remove("FAO_covermap.zip")

biomes <- rast("glc_shv10_DOM.Tif")

## Warning: [rast] can't get proj4 from srs

plot(biomes) #look at map
```



```

#make df of frequency of each value in raster
landcover <- as.data.frame(freq(biomes)) %>%
  rename("Area" = "count")

landcover$Ecosystem <- c("Null", "Artificial", "Cropland", "Grassland", "Tree Covered", "Shrubland", "H

#Split out and add ecosystems based on proportion

#Tropical forests - based on FAO 2020
tropfor <- data.frame(1,12,71015243*0.45, "Tropical Forest")
names(tropfor) <- c("layer","value","Area","Ecosystem")
landcover <- rbind(landcover, tropfor)

#Temperate forests - based on FAO 2020
tempfor <- data.frame(1,12,71015243*0.16, "Temperate Forest")
names(tempfor) <- c("layer","value","Area","Ecosystem")
landcover <- rbind(landcover, tempfor)

#Temperate grasslands - based on Dinerstein et al. 2017
tempgr <- data.frame(1,12,33129685*0.33, "Temperate Grassland")
names(tempgr) <- c("layer","value","Area","Ecosystem")
landcover <- rbind(landcover, tempgr)

#Savannas - based on Dinerstein et al. 2017, plus shrub
savshrub <- data.frame(1,12,(33129685*0.67)+18337497, "Savanna & Shrubland")
names(savshrub) <- c("layer","value","Area","Ecosystem")

```

```
landcover <- rbind(landcover, savshrub)

AMcover <- landcover[,c(3,4)] %>%
  filter(Ecosystem != "Null") %>% # filters out
  filter(Ecosystem != "Artificial") %>%
  filter(Ecosystem != "Grasslands") %>%
  filter(Ecosystem != "Tree Covered") %>%
  filter(Ecosystem != "Shrublands") %>%
  filter(Ecosystem != "Herbaceous Wetlands") %>%
  filter(Ecosystem != "Mangroves") %>%
  filter(Ecosystem != "Sparse Veg") %>%
  filter(Ecosystem != "Bare Soil") %>%
  filter(Ecosystem != "Snow & Glaciers") %>%
  filter(Ecosystem != "Water")
```

Carbon Data

```
#aboveground and root C data from Robinson 2007, Liu et al. 2015
#used proportion of root:shoot from Robinson 2007 to fill in Liu et al. 2015 root C estimates - in Pg C
plantC <- read_csv("plantC.csv")
```

```
## Rows: 21 Columns: 3
## -- Column specification -----
## Delimiter: ","
## chr (1): Ecosystem
## dbl (2): AGB_C, RootBio_C
##
## i Use 'spec()' to retrieve the full column specification for this data.
## i Specify the column types or set 'show_col_types = FALSE' to quiet this message.
```

```
#merge with cover, add ERH C based on Soudzilovskaia et al. 2015 - g/m-2 estimates. Different than C fl
coverC <- merge(AMcover, plantC,
  by="Ecosystem", all.x = T) %>% #merge
  mutate(AMbio_C = (Area*1000000)*0.0000000000000475) #add ERH
```

```
#C flux per veg type via Hawkins et al. 2023
```

```
#Croplands
```

```
cropAM <- coverC %>%
  filter(Ecosystem == "Cropland") %>%
  mutate(Allo_C = AGB_C * 0.033)
coverC2 <- merge(coverC, cropAM)
```

```
#Savannas & shrublands
```

```
ssAM <- coverC %>%
  filter(Ecosystem == "Savanna & Shrubland") %>%
  mutate(Allo_C = (AGB_C/2 * 0.065) + (AGB_C/2 * 0.023))
coverC2 <- rbind(coverC2, ssAM)
```

```
#Temperate grasslands
```

```
tgAM <- coverC %>%
```

```

    filter(Ecosystem == "Temperate Grassland") %>%
    mutate(Allo_C = AGB_C * 0.065)
coverC2 <- rbind(coverC2, tgAM)

#Temperate forests
tfAM <- coverC %>%
    filter(Ecosystem == "Temperate Forest") %>%
    mutate(Allo_C = AGB_C * 0.023)
coverC2 <- rbind(coverC2, tfAM)

#Tropical forests
trfAM <- coverC %>%
    filter(Ecosystem == "Tropical Forest") %>%
    mutate(Allo_C = AGB_C * 0.023)
coverC2 <- rbind(coverC2, trfAM)

#MAOM and POM C data from Georgiou et al. 2022
SOMC <- read_csv("MOC_synthesis.csv") %>%
    filter(Top.depth == 0) %>%
    rename("Ecosystem" = "Vegetation") %>%
    rename("MAOM_C" = "SiltClayC") %>%
    select(Ecosystem, Top.depth, Bottom.depth, Bulk.C, MAOM_C, POM_C)

## Rows: 1457 Columns: 20
## -- Column specification -----
## Delimiter: ","
## chr (6): Author, Soil.order, MineralType, Vegetation, frc_method, source
## dbl (14): Year, Lat, Lon, MAT, MAP, Top.depth, Bottom.depth, Clay, Silt, San...
##
## i Use 'spec()' to retrieve the full column specification for this data.
## i Specify the column types or set 'show_col_types = FALSE' to quiet this message.

SOMC[SOMC == 0] <- NA #replace zeros with NA
SOMC[SOMC == "Grassland"] <- "Temperate Grassland"
SOMC[SOMC == "Savanna"] <- "Savanna & Shrubland"
SOMC[SOMC == "Shrubland"] <- "Savanna & Shrubland"

SOMCmeans <- SOMC %>%
    group_by(Ecosystem) %>%
    summarise_if(is.numeric, mean, na.rm = TRUE)

#Scale to area of biome, using average bulk density & sampling depth
coverC3 <- merge(coverC2, SOMC) %>%
    select(-Top.depth) %>%
    mutate(PgC = (1.33*Bottom.depth*10000000000)*
        (Bulk.C/10000000000000000000)*Area) %>%
    mutate(MAOM_PgC = (1.33*Bottom.depth*10000000000)*
        (MAOM_C/10000000000000000000)*Area) %>%
    mutate(POM_PgC = (1.33*Bottom.depth*10000000000)*
        (POM_C/10000000000000000000)*Area)

Cpoolmeans <- coverC3 %>%
    group_by(Ecosystem) %>%

```

```

summarise_if(is.numeric, mean, na.rm = TRUE)

#Scale to area of biome, using average bulk density & sampling depth
coverC4 <- merge(coverC2, SOMCmeans) %>%
  select(-Top.depth) %>%
  mutate(PgC = (1.33*Bottom.depth*10000000000)*
    (Bulk.C/1000000000000000000)*Area) %>%
  mutate(MAOM_PgC = (1.33*Bottom.depth*10000000000)*
    (MAOM_C/1000000000000000000)*Area) %>%
  mutate(POM_PgC = (1.33*Bottom.depth*10000000000)*
    (POM_C/1000000000000000000)*Area)

#write_csv(coverC3, "Cpools.csv")
#write_csv(Cpoolmeans, "Cpoolmeans.csv")

```