Biomass Distribution 1961-2018

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INTRODUCTION

This project helps in properly visualising as well as understanding the rapid change in biomass distribution in the last ~60 years. Bar-On, Phillips, and Milo (2018) It is a way to fact check all the different headlines that have been going around recently like how humans contribution to the present state of the planet has been more than 83% but by themselves they only make up 0.01% of the life present on earth. "Humans Just 0.01" (2018)

How the population sizes of mammals, fish, birds, reptiles, and amphibians have declined an average of 68% between 1970 and 2016, according to World Wildlife Fund's (WWF) Living Planet Report 2020. Populations in Latin America and the Caribbean have fared worst, with an average decline of 94%. Global freshwater species have also been disproportionately impacted, declining 84% on average. As an important indicator of planetary health, these drastic species population trends signal a fundamentally broken relationship between humans and the natural world, the consequences of which—as demonstrated by the ongoing COVID-19 pandemic—can be catastrophic. `@wwf_2020`

In order better understand the actual meaning behind these numbers, biomass distribution has been used which can be used to depict the size of a species with respect to all the lifeforms.

DATA

This project consists of data pulled from 2006 IPCC Guidelines for National Greenhouse Gas Inventories ("2006 IPCC Guidelines for NATIONAL Greenhouse Gas Inventories" (n.d.)) and Food and Agriculture Organization of the United Nations ("FAO Global Statistical Yearbook, FAO Regional Statistical Yearbooks" (n.d.)) for data regarding the mass index and distribution of poultry and livestock in different regions of the world (North and Latin America, Asia, Indian Subcontinent, Oceania and Africa). The aim of this project was to map out the change in the biomass distribution and analyze how human activities have affected the environment in the past 60 years. The main focus will be on terrestrial lifeforms (animals) and humans.

The project can be broken down into two sections: Wrangling and Visualization. As I will be referring to various data sets in this project, cleaning and structuring is a big part of it.

WRANGLING

70% humany body is water => 30% carbon x 50% carbon out of the dry weight. Also the average of the human body is being assumed at 50 kgs. Also, 1kg is equal to 0.15 C which is stored in the variable `to_carbon` *Hern (1999).* `bird_bm` *and* `mammal_bm` *store the total biomass of the birds and mammals on earth and* `wild_animal_biomass` *stores the total biomass of the wild animals on earth. These values have been used as constants in this notebook for easy conversion. For this project, the total biomass on earth has been assumed to be ~550 Gt C, being such a large number any change in it is bound to be insignificant concerning only a span of 60 years.*

```
regions <- sort(c("Africa", "Latin America", "Asia", "Eastern Europe", "Northern America", "Oceania", "
converter = 1000*0.15/1e15 #kg to Gt
wild_animal_biomass = 550 * 3 * 1e-6
birds_bm = 0.007 #Gt C
mammmal_bm = 550 * 3 * 1e-4
```

```r
to_carbon = 0.15
human_carbon_mass = 5e4 * to_carbon
```

Loading the data on human population over the years and converting it into Gt C and calculating the changing biomass and %age biomass over the years

```r
human_pop <- readxl::read_excel("../../_data/Data_Extract_From_World_Development_Indicators.xlsx") %>% s
    select(! contains("Series") & ! contains("Country")) %>%
    pivot_longer(cols = names(.),names_to = "Year", values_to = "Population") %>%
    mutate(Year = as.numeric(str_extract(Year, '[^\\s]+'))) %>%
    mutate(`Total Biomass (Gt C)` = as.double(`Population`) * human_carbon_mass * 1e-15) %>%
    mutate(`% Mammal Biomass (Gt C)` = `Total Biomass (Gt C)` / (mammmal_bm * 1e-2))


tail(human_pop)
```

```
## # A tibble: 6 x 4
##    Year Population `Total Biomass (Gt C)` `% Mammal Biomass (Gt C)`
##   <dbl>      <dbl>                  <dbl>                     <dbl>
## 1  2013 7169675197                 0.0538                      32.6
## 2  2014 7254292848                 0.0544                      33.0
## 3  2015 7339076654                 0.0550                      33.4
## 4  2016 7424484741                 0.0557                      33.7
## 5  2017 7509410228                 0.0563                      34.1
## 6  2018 7592475615                 0.0569                      34.5
```

Loading the mass Index for poultry and modifying the Area name and Region as per the requirement, the areas under focus have been listed down below

```r
birds_index <- read.csv('../../_data/birds.csv') %>%
  mutate(Area = case_when(
    Area == "Southern Asia" ~ "Indian Subcontinent",
    Area == "Americas" ~ "Latin America",
    TRUE ~ Area
  )) %>%
  filter(Area %in% regions) %>%
  arrange(Area, Item)
head(birds_index)
```

```
##   Domain.Code       Domain Area.Code   Area Element.Code Element Item.Code
## 1          QA Live Animals      5100 Africa         5112  Stocks      1057
## 2          QA Live Animals      5100 Africa         5112  Stocks      1057
## 3          QA Live Animals      5100 Africa         5112  Stocks      1057
## 4          QA Live Animals      5100 Africa         5112  Stocks      1057
## 5          QA Live Animals      5100 Africa         5112  Stocks      1057
## 6          QA Live Animals      5100 Africa         5112  Stocks      1057
##       Item Year.Code Year      Unit  Value Flag
## 1 Chickens      1961 1961 1000 Head 274201    A
## 2 Chickens      1962 1962 1000 Head 282821    A
## 3 Chickens      1963 1963 1000 Head 292008    A
## 4 Chickens      1964 1964 1000 Head 305707    A
## 5 Chickens      1965 1965 1000 Head 316576    A
## 6 Chickens      1966 1966 1000 Head 330808    A
##                                                            Flag.Description
## 1 Aggregate, may include official, semi-official, estimated or calculated data
## 2 Aggregate, may include official, semi-official, estimated or calculated data
```

```
## 3 Aggregate, may include official, semi-official, estimated or calculated data
## 4 Aggregate, may include official, semi-official, estimated or calculated data
## 5 Aggregate, may include official, semi-official, estimated or calculated data
## 6 Aggregate, may include official, semi-official, estimated or calculated data
```

```
unique(as.data.frame(birds_index[,"Area"]))
```

```
##      birds_index[, "Area"]
## 1                   Africa
## 291                   Asia
## 581         Eastern Europe
## 813    Indian Subcontinent
## 1045         Latin America
## 1277      Northern America
## 1509               Oceania
## 1741        Western Europe
```

Using bird_index the information on chicken is extracted out which only the Area, Year and Value columns are seleccted. The Values of Latin America and Asia are modified by subtracting Northern America and Indian Subcontinent respectively to avoid repitition.

```
chicken <- filter(birds_index, Item == "Chickens") %>%
  select(Area, Year, Value) %>%
  pivot_wider(names_from = Area, values_from = Value) %>%
  mutate(`Latin America` = `Latin America` - `Northern America`, Asia = Asia - `Indian Subcontinent`) %
  column_to_rownames('Year')
head(chicken)
```

```
##      Africa    Asia Eastern Europe Indian Subcontinent Latin America
## 1961 274201  918518         623953              172296        365212
## 1962 282821  962503         672343              176622        373697
## 1963 292008 1001039         689495              186306        395109
## 1964 305707 1040895         623901              193017        423850
## 1965 316576 1078200         638318              199930        428824
## 1966 330808 1108430         671476              209242        441242
##      Northern America Oceania Western Europe
## 1961           821016   26304         361024
## 1962           847087   27059         364607
## 1963           847720   27313         365832
## 1964           863594   27991         380597
## 1965           904276   28949         386324
## 1966           926914   29316         349822
```

The dataset on chickens laying eggs is loaded and stored in `chicken_layers` *and is formatted to match the table above.*

```
chicken_layers <- read.csv('../../_data/FAOSTAT_egg_chicken.csv') %>%
  mutate(Area = case_when(
    Area == "Southern Asia" ~ "Indian Subcontinent",
    Area == "Americas" ~ "Latin America",
    TRUE ~ Area
  )) %>%
  filter(Area %in% regions & Element == "Laying") %>%
  arrange(Area) %>%
  select(Area, Year, Value) %>%
  pivot_wider(names_from = Area, values_from = Value) %>%
  mutate(`Latin America` = `Latin America` - `Northern America`, Asia = Asia - `Indian Subcontinent`) %
```

```r
  column_to_rownames('Year')

head(chicken_layers)
```

```
##      Africa   Asia Eastern Europe Indian Subcontinent Latin America
## 1961 122114 546011         393793               56750        150247
## 1962 126039 575480         405868               61033        151731
## 1963 129208 568808         390208               64255        153821
## 1964 134420 593492         384892               65305        160602
## 1965 141982 614320         414677               69055        171345
## 1966 145630 628879         438041               74105        167284
##      Northern America Oceania Western Europe
## 1961           323081   18033         167066
## 1962           326236   18301         163560
## 1963           323869   17925         164074
## 1964           327459   18117         169345
## 1965           327171   19248         168955
## 1966           329247   19579         199529
```

To calculate the biomass of chicken first chicken is seperated into two categories- broilers and layers. The resulting separate dataframes are multiplied by the avg weight as per the "2006 IPCC Guidelines for NATIONAL Greenhouse Gas Inventories" (n.d.) standards i.e. 0.9 and 1.8 kgs. The output obtained is then stored together in `chicken_all` where the added weights are converted into Biomass(Gt C) then the actual %age of Total Biomass is calculated as well. The chicken_all dataframe adds both the dataframes together. The sum of all the regions are added based on the year using `rowSums()` and the %Total Birds mass is calculated using the constant birds_bm

```r
chicken_broilers <- (chicken - chicken_layers)*0.9
chicken_layers <- (chicken_layers)* 1.8

chicken_all <- (chicken_broilers + chicken_layers) %>%
  rowSums() %>%
  as.data.frame() * converter

names(chicken_all)[1] <- "Total Biomass (Gt C)"

chicken_all <- chicken_all %>%
  mutate(`% Total Birds` = (`Total Biomass (Gt C)`/birds_bm) * 1e5) %>%
  mutate(`Total Biomass (Gt C)` = `Total Biomass (Gt C)` * 1e-1)

tail(chicken_all)
```

```
##      Total Biomass (Gt C) % Total Birds
## 2013         3.656286e-07      52.23266
## 2014         3.694877e-07      52.78396
## 2015         3.786571e-07      54.09388
## 2016         3.962678e-07      56.60968
## 2017         4.023285e-07      57.47550
## 2018         4.086130e-07      58.37328
```

For ducks (and Turkey), the data is first loaded to `ducks(Turkeys)` from `bird_index` similarly as chickens before. The `ducks_all(Turkey_all)` then adds all the different regions together which is then multiplied by their avg weight (as per "2006 IPCC Guidelines for NATIONAL Greenhouse Gas Inventories" (n.d.)) of 2.7 and then converted into Gt C using `converter`.

```r
ducks <- filter(birds_index, Item == 'Ducks') %>%
  select(Area, Year, Value) %>%
  pivot_wider(names_from = Area, values_from = Value) %>%
  column_to_rownames('Year') %>%
  mutate(`Latin America` = `Latin America` - `Northern America`, Asia = Asia - `Indian Subcontinent`)

ducks_all <- ducks %>%
  rowSums() %>%
  as.data.frame() * converter * 2.7
names(ducks_all)[1] <- "Total Biomass (Gt C)"
ducks_all <- ducks_all %>%
  #mutate(`% Total Animal Biomass (Gt C)` = `Total Biomass (Gt C)`/(wild_animal_biomass)) %>%
  mutate(`% Total Birds` = `Total Biomass (Gt C)`/birds_bm) * 1e5


head(ducks_all)
```

```
##      Total Biomass (Gt C) % Total Birds
## 1961          0.007619913      1.088559
## 1962          0.007960680      1.137240
## 1963          0.008356851      1.193836
## 1964          0.008590374      1.227196
## 1965          0.008861400      1.265914
## 1966          0.009144859      1.306409
```

```r
Turkey <- filter(birds_index, Item == 'Turkeys') %>%
  select(Area, Year, Value) %>%
  pivot_wider(names_from = Area, values_from = Value) %>%
  column_to_rownames('Year') %>%
  mutate(`Latin America` = `Latin America` - `Northern America`, Asia = Asia - `Indian Subcontinent`)

Turkey_all <- Turkey %>%
  rowSums() %>%
  as.data.frame() * converter * 2.7
names(Turkey_all)[1] <- "Total Biomass (Gt C)"
Turkey_all <- Turkey_all %>%
  #mutate(`% Total Animal Biomass (Gt C)` = `Total Biomass (Gt C)`/(wild_animal_biomass)) %>%
  mutate(`% Total Birds` = `Total Biomass (Gt C)`/birds_bm) * 1e5


head(Turkey_all)
```

```
##      Total Biomass (Gt C) % Total Birds
## 1961          0.007942334     1.1346191
## 1962          0.006744587     0.9635124
## 1963          0.006216345     0.8880493
## 1964          0.005902389     0.8431984
## 1965          0.005909071     0.8441531
## 1966          0.006389240     0.9127485
```

Livestock index loads the dataset on the weight of livestocks in different regions of the world as per the "2006 IPCC Guidelines for NATIONAL Greenhouse Gas Inventories" (n.d.). The columns are renamed and rearranged as per the requirement

```r
livestock_index <- read.csv("../../_data/animal_weight.csv",
                      col.names = c('Area','Cattle_dairy', 'Cattle_non_dairy', 'Buffaloes','Swine_marke
                      ) %>%
  select(! starts_with("d")) %>%
  filter(! Area == "Middle east") %>%
  arrange(Area) %>%
  column_to_rownames('Area')
livestock_index
```

```
##                      Cattle_dairy Cattle_non_dairy Buffaloes Swine_market
## Africa                        275              173       380           28
## Asia                          350              391       380           50
## Eastern Europe                550              391       380           50
## Indian Subcontinent           275              110       295           28
## Latin America                 400              305       380           28
## Northern America              604              389       380           46
## Oceania                       500              330       380           45
## Western Europe                600              420       380           50
##                      Swine_breeding Sheep Goats Horses Asses Mules Camels
## Africa                           28  28.0  30.0    238   130   130    217
## Asia                            180  48.5  38.5    377   130   130    217
## Eastern Europe                  180  48.5  38.5    377   130   130    217
## Indian Subcontinent              28  28.0  30.0    238   130   130    217
## Latin America                    28  28.0  30.0    238   130   130    217
## Northern America                198  48.5  38.5    377   130   130    217
## Oceania                         180  48.5  38.5    377   130   130    217
## Western Europe                  198  48.5  38.5    377   130   130    217
```

As for most of the data, similar wrangling is required, `wrangling_livestock` function has been created which helps in loading the `FAOSTAT_livestock` data(in most cases) and then filtering them out based on the category.

```r
wrangling_livestock <- function (category, file_name = "FAOSTAT_livestock"){
  temp <- read.csv(sprintf('../../_data/%s.csv', file_name)) %>%
    mutate(Area = case_when(
      Area == "Southern Asia" ~ "Indian Subcontinent",
      Area == "Americas" ~ "Latin America",
      TRUE ~ as.character(Area)
    )) %>%
    filter(Area %in% regions) %>%
    arrange(Area, Item) %>%
    filter(Item == sprintf('%s', category)) %>%
    select(Area, Year, Value) %>%
    pivot_wider(names_from = Area, values_from = Value) %>%
    column_to_rownames('Year') %>%
    mutate(`Latin America` = `Latin America` - `Northern America`, Asia = Asia - `Indian Subcontinent`)

  return(temp)
}
```

Dairy and non-dairy cattles have different diets and hence different weights. So, to make the calculations more accurate the data on dairy cattles is loaded from `FAOSTAT_cattle_dairy.csv` which is then filtered to match the regions which we are focussing on. Due to different column naming `wrangling_livestock` function is skipped but is to load data on non-dairy cattles.

```r
cattle_dairy <- read.csv('../../_data/FAOSTAT_cattle_dairy.csv') %>%
    mutate(Area = case_when(
      Area == "Southern Asia" ~ "Indian Subcontinent",
      Area == "Americas" ~ "Latin America",
      TRUE ~ Area
    )) %>%
    filter(Area %in% regions) %>%
    arrange(Area, Item) %>%
    filter(Element == 'Milk Animals') %>%
    select(Area, Year, Value) %>%
    pivot_wider(names_from = Area, values_from = Value) %>%
    column_to_rownames('Year') %>%
    mutate(`Latin America` = `Latin America` - `Northern America`, Asia = Asia - `Indian Subcontinent`)
cattle <- wrangling_livestock('Cattle') - cattle_dairy


head(cattle)
```

```
##         Africa     Asia Eastern Europe Indian Subcontinent Latin America
## 1961 105529681 86089461       51332404           198560283     158687950
## 1962 107228969 83195165       56757782           200223885     162380226
## 1963 109072042 85148252       60337536           201085315     162233211
## 1964 112410585 87364184       58670982           205939424     168267429
## 1965 115554186 91991748       60065138           206173971     175688128
## 1966 115675777 92478459       66390091           201876014     181666686
##      Northern America  Oceania Western Europe
## 1961         88166740 18975600       27582914
## 1962         91504879 19729034       29253640
## 1963         96536759 20297538       29125845
## 1964        100998695 20968039       28375526
## 1965        103289512 20898726       28795538
## 1966        104017227 20502454       30221061
```

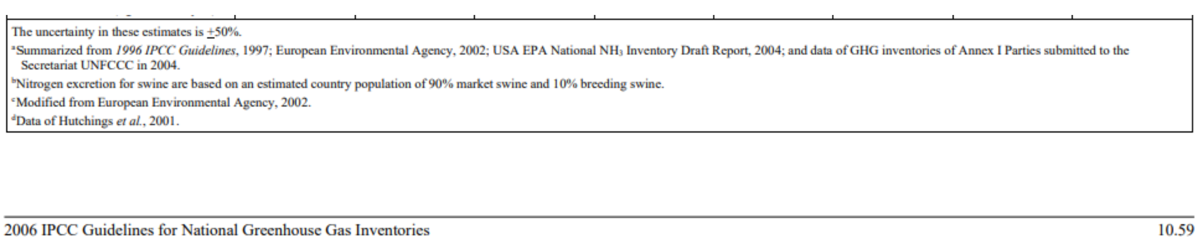
```r
head(cattle_dairy)
```

```
##        Africa    Asia Eastern Europe Indian Subcontinent Latin America
## 1961 17007415 6862907       45941801            27498908      17161126
## 1962 17237363 7316815       47520221            25057900      17531215
## 1963 17390909 7490111       48870567            24423500      18210796
## 1964 17747291 7761084       49030454            23406763      18519113
## 1965 18469973 7924174       49501925            22818605      19151689
## 1966 19118918 8270102       50004087            28560745      20170925
##      Northern America Oceania Western Europe
## 1961         20230855 5115736       19921153
## 1962         19798540 5224001       20012785
## 1963         19175636 5286648       19724129
## 1964         18584172 5125422       19515994
## 1965         17840320 5081390       19749062
## 1966         16748828 5034903       19855998
```

To calculate the mass of all the cattles they are multiplied by their respective regional masses and category(dairy/non-dairy) form the `livestock_index` dataframe, the resulting dfs are then added togehter and stored in `cattle_all` where all the different regions are summed together based on the year to get the total biomass/year as well %age total biomass/year

```
for (r in 1:length(regions)){
  cattle[regions[r]] <- as.double(livestock_index[regions[r],'Cattle_non_dairy']) * cattle[regions[r]]
  cattle_dairy[regions[r]] <- as.double(livestock_index[regions[r],'Cattle_dairy']) * cattle_dairy[regi
}
cattle_all <- (cattle + cattle_dairy) %>%
  rowSums() %>%
  as.data.frame()%>%
  `colnames<-`(c("Total Biomass (Gt C)")) %>%
  mutate(`Total Biomass (Gt C)` = `Total Biomass (Gt C)`* converter) %>%
  mutate(`% Mammal Biomass (Gt C)` = `Total Biomass (Gt C)`/(mammmal_bm*1e-2))

head(cattle_all)
```

```
##      Total Biomass (Gt C) % Mammal Biomass (Gt C)
## 1961           0.04018161                24.35249
## 1962           0.04097010                24.83036
## 1963           0.04172734                25.28930
## 1964           0.04238290                25.68660
## 1965           0.04335895                26.27815
## 1966           0.04436850                26.89000
```


The uncertainty in these estimates is ±50%.
[a]Summarized from *1996 IPCC Guidelines*, 1997; European Environmental Agency, 2002; USA EPA National NH_3 Inventory Draft Report, 2004; and data of GHG inventories of Annex I Parties submitted to the Secretariat UNFCCC in 2004.
[b]Nitrogen excretion for swine are based on an estimated country population of 90% market swine and 10% breeding swine.
[c]Modified from European Environmental Agency, 2002.
[d]Data of Hutchings *et al.*, 2001.

2006 IPCC Guidelines for National Greenhouse Gas Inventories 10.59

Figure 1: Estimated Population of Swine

For swine(pigs) the "2006 IPCC Guidelines for NATIONAL Greenhouse Gas Inventories" (n.d.) assumption is assumed here where close to 90% of them are used for breeding and only 1% are available for market. Based on this assumption ***`swine_breeding`*** *and* ***`swine_market`*** *dataframes are created using the wrangling_livestock function (loading FAOSTAT_livestock.csv) and then multiplied by their respective weights in different regions. These are then combined to form swine_all where using rowSums the data is categorized into Total Biomass/year and %age Total Mammal Biomass/year.*

```
swine_breeding <- wrangling_livestock("Pigs") * 0.9
swine_market <- swine_breeding / 9

for (r in 1:length(regions)){
   swine_breeding[regions[r]] <- as.double(livestock_index[regions[r],'Swine_breeding']) * swine_breedi
  swine_market[regions[r]] <- as.double(livestock_index[regions[r],'Swine_market']) * swine_market[regi
}

swine <- (swine_breeding + swine_market)


swine_all <- swine %>%
  rowSums() %>%
  as.data.frame() %>%
  `colnames<-`(c("Total Biomass (Gt C)")) %>%
  mutate(`Total Biomass (Gt C)` = `Total Biomass (Gt C)` * converter) %>%
```

```r
  mutate(`% Mammal Biomass (Gt C)` = `Total Biomass (Gt C)`/(mammmal_bm*1e-2))

head(swine_all)
```

```
##      Total Biomass (Gt C) % Mammal Biomass (Gt C)
## 1961          0.008243982                4.996352
## 1962          0.008659171                5.247982
## 1963          0.009241365                5.600827
## 1964          0.009410881                5.703564
## 1965          0.010282287                6.231689
## 1966          0.010649067                6.453980
```

In the case of buffaloes, most of the process is same as in cattle except the regions(buffaloes are not present in northern America and west Europe) which are modified to match rest of the tables

```r
buffaloes <- read.csv('../../_data/FAOSTAT_livestock.csv') %>%
    mutate(Area = case_when(
      Area == "Southern Asia" ~ "Indian Subcontinent",
      Area == "Americas" ~ "Latin America",
      TRUE ~ Area
    )) %>%
    filter(Area %in% regions) %>%
    arrange(Area, Item) %>%
    filter(Item == "Buffaloes") %>%
    select(Area, Year, Value) %>%
    pivot_wider(names_from = Area, values_from = Value) %>%
    column_to_rownames('Year') %>%
    mutate(Asia = Asia - `Indian Subcontinent`, `Western Europe` = 0) %>%
    cbind(`Northern America` = 0)

for (r in 1:length(regions)){
  buffaloes[regions[r]] <- (buffaloes[regions[r]] * as.double(livestock_index[r, "Buffaloes"]))
}

buffaloes_all <- buffaloes %>%
  rowSums() %>%
  as.data.frame() %>%
  `colnames<-`(c("Total Biomass (Gt C)")) %>%
  mutate(`Total Biomass (Gt C)` = `Total Biomass (Gt C)` * converter) %>%
  mutate(`% Mammal Biomass (Gt C)` = `Total Biomass (Gt C)`/(mammmal_bm*1e-2))

head(buffaloes_all)
```

```
##      Total Biomass (Gt C) % Mammal Biomass (Gt C)
## 1961          0.004257691                2.580419
## 1962          0.004305583                2.609444
## 1963          0.004329264                2.623797
## 1964          0.004517807                2.738065
## 1965          0.004568208                2.768611
## 1966          0.004810559                2.915490
```

Sheeps, Goats, Horses, asses and mules follow the same procedure as in cattle and their final values are stored sheep_all, horses_all, asses_all and mules_all respectively.

```r
sheep <- wrangling_livestock("Sheep")
```

```r
for (r in 1:length(regions)){
  sheep[regions[r]] <- (sheep[regions[r]] * as.double(livestock_index[r, "Sheep"]))
}

sheep_all <- sheep %>%
  rowSums() %>%
  as.data.frame() %>%
  `colnames<-`(c("Total Biomass (Gt C)")) %>%
  mutate(`Total Biomass (Gt C)` = `Total Biomass (Gt C)` * converter) %>%
  mutate(`% Mammal Biomass (Gt C)` = `Total Biomass (Gt C)`/(mammmal_bm*1e-2))


head(sheep_all)
```

```
##      Total Biomass (Gt C) % Mammal Biomass (Gt C)
## 1961          0.005442698                3.298605
## 1962          0.005478983                3.320596
## 1963          0.005519002                3.344850
## 1964          0.005605461                3.397249
## 1965          0.005692616                3.450070
## 1966          0.005742036                3.480022
```

```r
goat <- wrangling_livestock("Goats")

for (r in 1:length(regions)){
  goat[regions[r]] <- goat[regions[r]] * as.double(livestock_index[r, "Goats"])
}

goat_all <- goat %>%
  rowSums() %>%
  as.data.frame() %>%
  `colnames<-`(c("Total Biomass (Gt C)")) %>%
  mutate(`Total Biomass (Gt C)` = `Total Biomass (Gt C)`*converter) %>%
  mutate(`% Mammal Biomass (Gt C)` = `Total Biomass (Gt C)`/(mammmal_bm*1e-2))


head(goat_all)
```

```
##      Total Biomass (Gt C) % Mammal Biomass (Gt C)
## 1961          0.001663703                1.008305
## 1962          0.001747766                1.059252
## 1963          0.001784774                1.081682
## 1964          0.001775618                1.076132
## 1965          0.001765696                1.070119
## 1966          0.001770902                1.073274
```

```r
horses <- wrangling_livestock("Horses")

for (r in 1:length(regions)){
  horses[regions[r]] <- (horses[regions[r]] * as.double(livestock_index[r, "Goats"]))
}

horses_all <- horses %>%
  rowSums() %>%
  as.data.frame() %>%
```

```r
  `colnames<-`(c("Total Biomass (Gt C)")) %>%
  mutate(`Total Biomass (Gt C)` = `Total Biomass (Gt C)`* converter) %>%
  mutate(`% Mammal Biomass (Gt C)` = `Total Biomass (Gt C)`/(mammmal_bm*1e-2))


head(horses_all)
```

```
##      Total Biomass (Gt C) % Mammal Biomass (Gt C)
## 1961         0.0003073617               0.1862798
## 1962         0.0002959165               0.1793433
## 1963         0.0002889394               0.1751148
## 1964         0.0002845318               0.1724435
## 1965         0.0002904977               0.1760592
## 1966         0.0002938808               0.1781096
```

```r
mules <- wrangling_livestock("Mules")

mules_all <- (mules*130*converter) %>%
  rowSums() %>%
  as.data.frame() %>%
  #mutate(`% Biomass (Gt C)` = `.`/(wild_animal_biomass * 1e-2)) %>%
  mutate(`% Mammal Biomass (Gt C)` = `.`/(mammmal_bm*1e-2)) %>%
  `colnames<-`(c("Total Biomass (Gt C)", "% Mammal Biomass (Gt C)"))

head(mules_all)
```

```
##      Total Biomass (Gt C) % Mammal Biomass (Gt C)
## 1961         0.0001676369               0.1015981
## 1962         0.0001791703               0.1085880
## 1963         0.0001708586               0.1035507
## 1964         0.0001764372               0.1069317
## 1965         0.0001784144               0.1081299
## 1966         0.0001813179               0.1098896
```

```r
asses <- wrangling_livestock("Asses")

asses_all <- (asses*130*converter) %>%
  rowSums() %>%
  as.data.frame() %>%
  #mutate(`% Biomass (Gt C)` = `.`/(wild_animal_biomass * 1e-2)) %>%
  mutate(`% Mammal Biomass (Gt C)` = `.`/(mammmal_bm*1e-2)) %>%
  `colnames<-`(c("Total Biomass (Gt C)", "% Mammal Biomass (Gt C)"))

head(asses_all)
```

```
##      Total Biomass (Gt C) % Mammal Biomass (Gt C)
## 1961         0.0006781587               0.4110053
## 1962         0.0006521343               0.3952329
## 1963         0.0006479494               0.3926966
## 1964         0.0006640885               0.4024779
## 1965         0.0006817642               0.4131905
## 1966         0.0006959867               0.4218101
```

Camels are not found in Europe, Northern America, Latin America much as livestocks so they have been set to zero for the purpose of calculation. The wild camels in Australia(Oceania) will come under wild Animals (included in analysis later)

```
camels <- read.csv('../../_data/FAOSTAT_livestock.csv') %>%
    mutate(Area = case_when(
      Area == "Southern Asia" ~ "Indian Subcontinent",
      Area == "Americas" ~ "Latin America",
      TRUE ~ Area
    )) %>%
    filter(Area %in% regions) %>%
    arrange(Area, Item) %>%
    filter(Item == "Camels") %>%
    select(Area, Year, Value) %>%
    pivot_wider(names_from = Area, values_from = Value) %>%
    column_to_rownames('Year') %>%
    mutate(Asia = Asia - `Indian Subcontinent`, `Western Europe` = 0) %>%
    cbind(`Northern America` = 0, `Latin America` = 0, `Oceania` = 0)

camels_all <- (camels*217*converter) %>%
  rowSums() %>%
  as.data.frame() %>%
  #mutate(`% Biomass (Gt C)` = `.`/(wild_animal_biomass * 1e-2)) %>%
  mutate(`% Mammal Biomass (Gt C)` = `.`/(mammmal_bm*1e-2)) %>%
  `colnames<-`(c("Total Biomass (Gt C)", "% Mammal Biomass (Gt C)"))

head(camels_all)
```

```
##      Total Biomass (Gt C) % Mammal Biomass (Gt C)
## 1961         0.0004207621               0.2550073
## 1962         0.0004283833               0.2596262
## 1963         0.0004431511               0.2685764
## 1964         0.0004608473               0.2793014
## 1965         0.0004746598               0.2876726
## 1966         0.0004953378               0.3002047
```

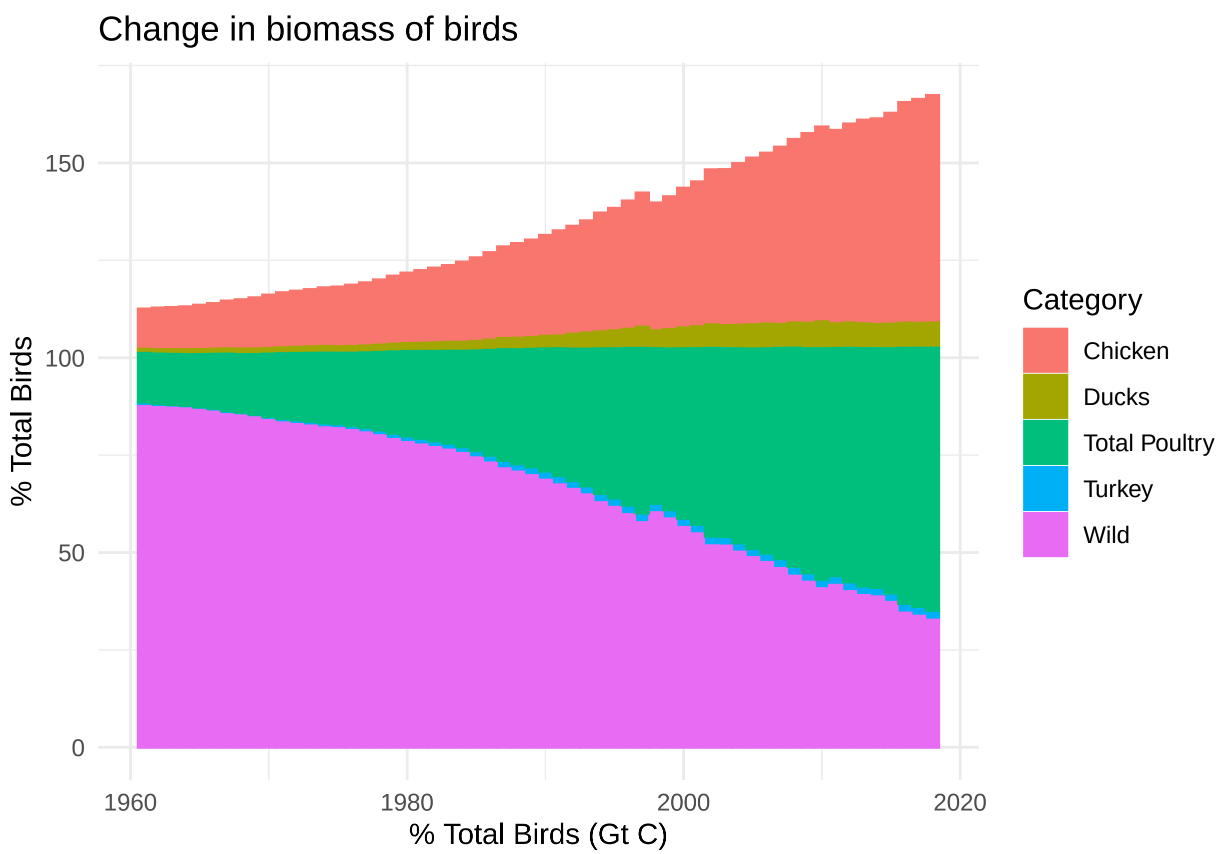
The result obtained from poultry and livestocks have been clubbed together below to get much more clearer picture of the distribution of biomass.

```
poultry <- (chicken_all + Turkey_all + ducks_all) %>%
  select(`Total Biomass (Gt C)`, `% Total Birds`)

wild_birds <- poultry %>%
  mutate(`Total Biomass (Gt C)` = (100 - `% Total Birds`) * birds_bm * 1e-2) %>%
  mutate(`% Total Birds` = (100 - `% Total Birds`))

livestocks <- (cattle_all + buffaloes_all + sheep_all + goat_all + horses_all + mules_all + asses_all +
  select(`Total Biomass (Gt C)`, `% Mammal Biomass (Gt C)`)

wild_animal_biomass <- livestocks %>%
  mutate(`Total Biomass (Gt C)` = (100 - `% Mammal Biomass (Gt C)`) * mammmal_bm*1e-2 - human_pop$`Total
  mutate(`% Mammal Biomass (Gt C)` = (100 - `% Mammal Biomass (Gt C)` - human_pop$`% Mammal Biomass (Gt
```

VISUALIZATION

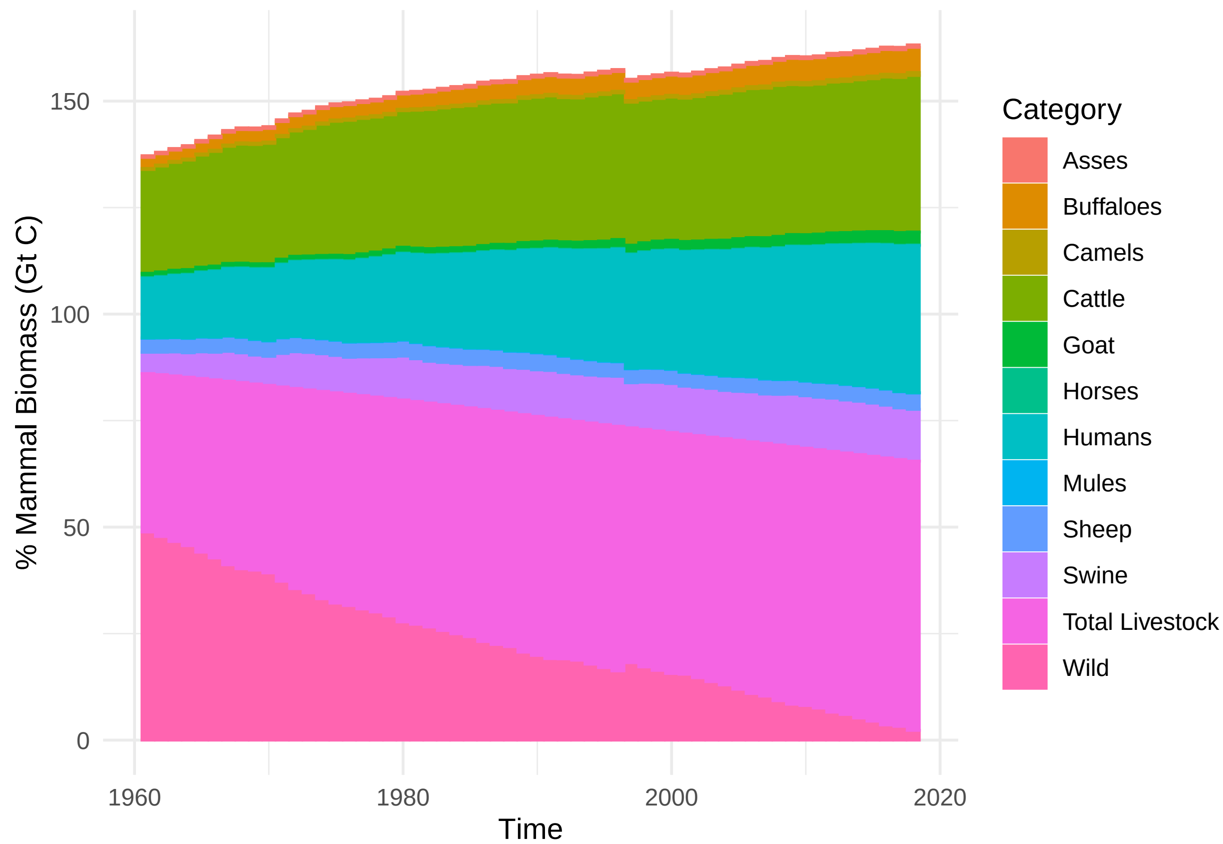
The graph below helps in the visualization of the change in biomass of the birds from 1961-2018. It is easy to observe from it that there has been a drastic drop in the wild bird population; from occupying more than 60% of the total biomass of the birds they have dropped to 30% in 2018 whereas the poultry is occupying more than 60%.

```r
rbind(cbind(chicken_all, Category = "Chicken"), cbind(Turkey_all, Category = "Turkey"), cbind(ducks_all
  mutate(Time = rep(seq.Date(as.Date('1961-01-01'), length = 58, by = "1 year"),5)) %>%
  ggplot(aes(Time, `% Total Birds`, color = Category, fill = Category)) +
  geom_bar(stat = "identity") + theme_minimal() +
  labs(title = "Change in biomass of birds", x = "% Total Birds (Gt C)")
```



Like in the case of birds, similar situation can be observed in the mammals where the drop is more significant. The wild animals have dropped from almost 50% to ~2% in less than 60 years. The humans have grown to occupy more than 35% of the total biomass in the mammals and the livestock occupy more than 60% of the total biomass.

```r
rbind(cbind(cattle_all, Category = "Cattle"), cbind(swine_all, Category = "Swine"), cbind(buffaloes_all
  mutate(Time = rep(seq.Date(as.Date('1961-01-01'), length = 58, by = "1 year"),12)) %>%
  ggplot(aes(Time, `% Mammal Biomass (Gt C)`, fill = Category, color = Category)) +
  geom_bar(stat = "identity") + theme_minimal()
```



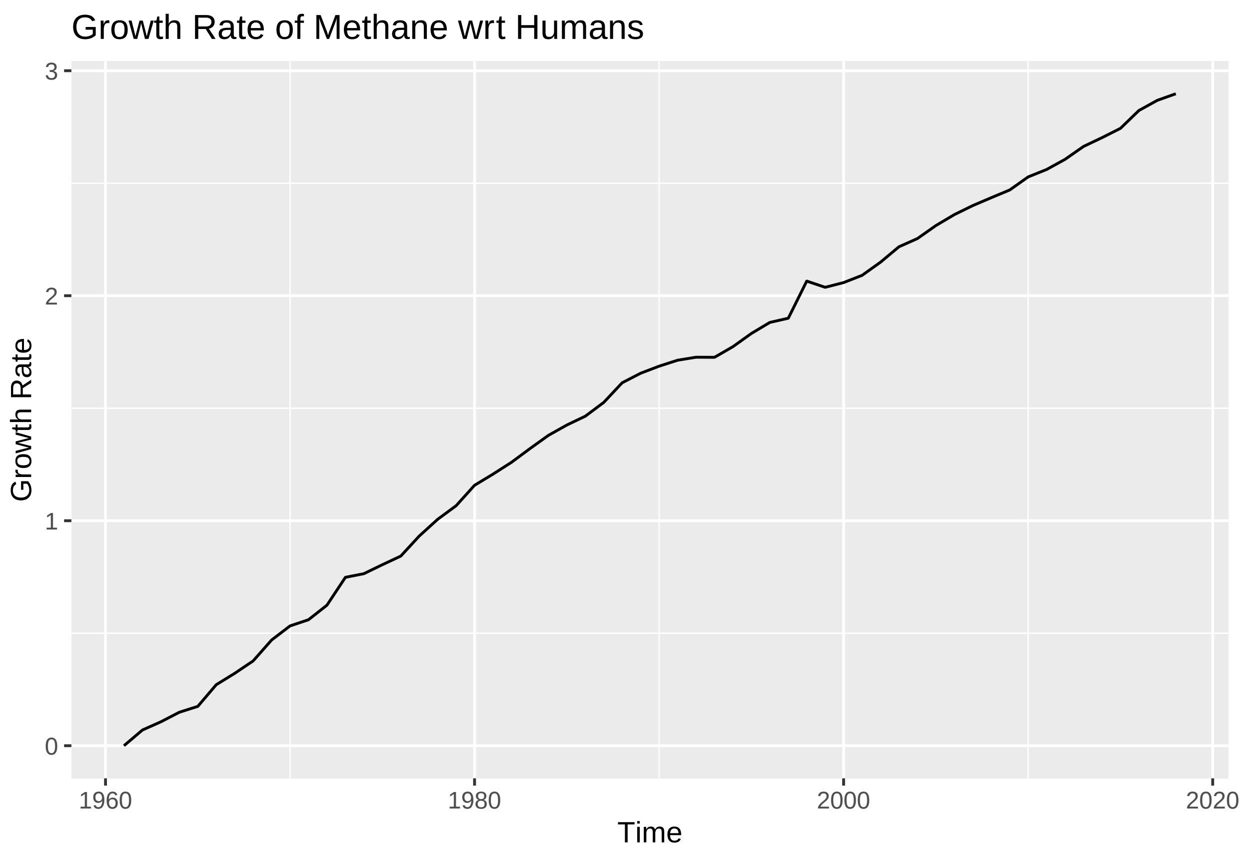
While most nations have started dealing with carbon emissions, methane(which has a shorter life cycle) is coming under greater focus each year. The largest source of anthropogenic methane emissions is agriculture, responsible for around a quarter of the total, closely followed by the energy sector, which includes emissions from coal, oil, natural gas and bio fuels. With the visualization below I try to showcase the relation between human population growth and methane emission. It is often thought that only livestock are the major contributors but from the visualization obtained it is apparent that other human activities have a significant impact on the emission.

```
methane <- read.csv("../../_data/ghg-concentrations_fig-1.csv", skip = 6) %>%
  slice(1860:1964) %>%
  `colnames<-`(c("Year", "d", "Methane (ppm of CO2)")) %>%
  select(contains("e")) %>%
  fill(`Methane (ppm of CO2)`, .direction = "updown")%>%
  filter(as.numeric(Year) %in% human_pop$Year) %>%
  slice(-c(38))
head(methane)
```

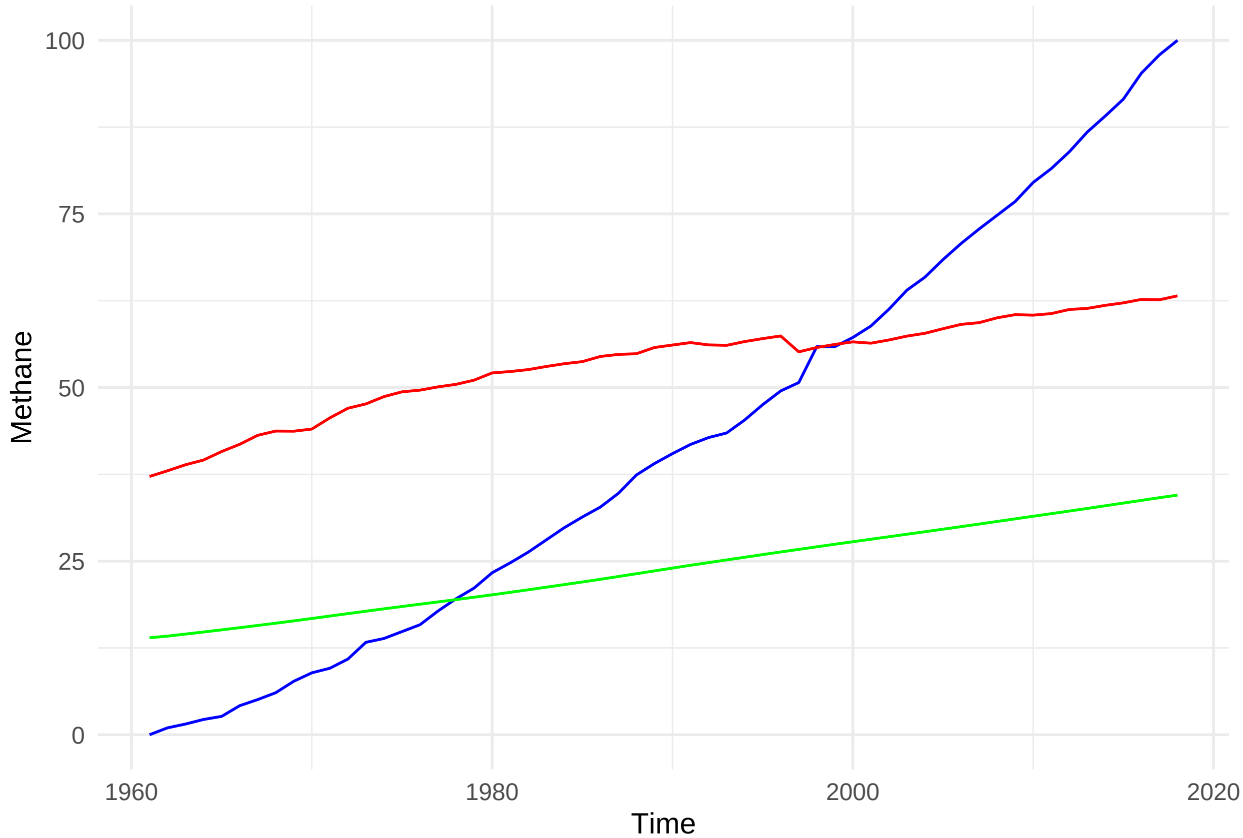
```
##   Year Methane (ppm of CO2)
## 1 1961                317.6
## 2 1962                318.5
## 3 1963                319.0
## 4 1964                319.6
## 5 1965                320.0
## 6 1966                321.4
```

```
livestocks %>%
  mutate(Methane = methane$`Methane (ppm of CO2)`, Time = seq.Date(as.Date('1961-01-01'), length = 58, 
  mutate(Methane = sapply(Methane, function(x){
```

```
    return (100*(x- min(Methane))/(max(Methane) - min(Methane)))
  }) ) %>%
  mutate(factor = Methane/Humans) %>%
  ggplot(aes(x = Time)) +
  geom_line(aes(y = factor)) +
  labs(y = "Growth Rate", title = "Growth Rate of Methane wrt Humans")
```

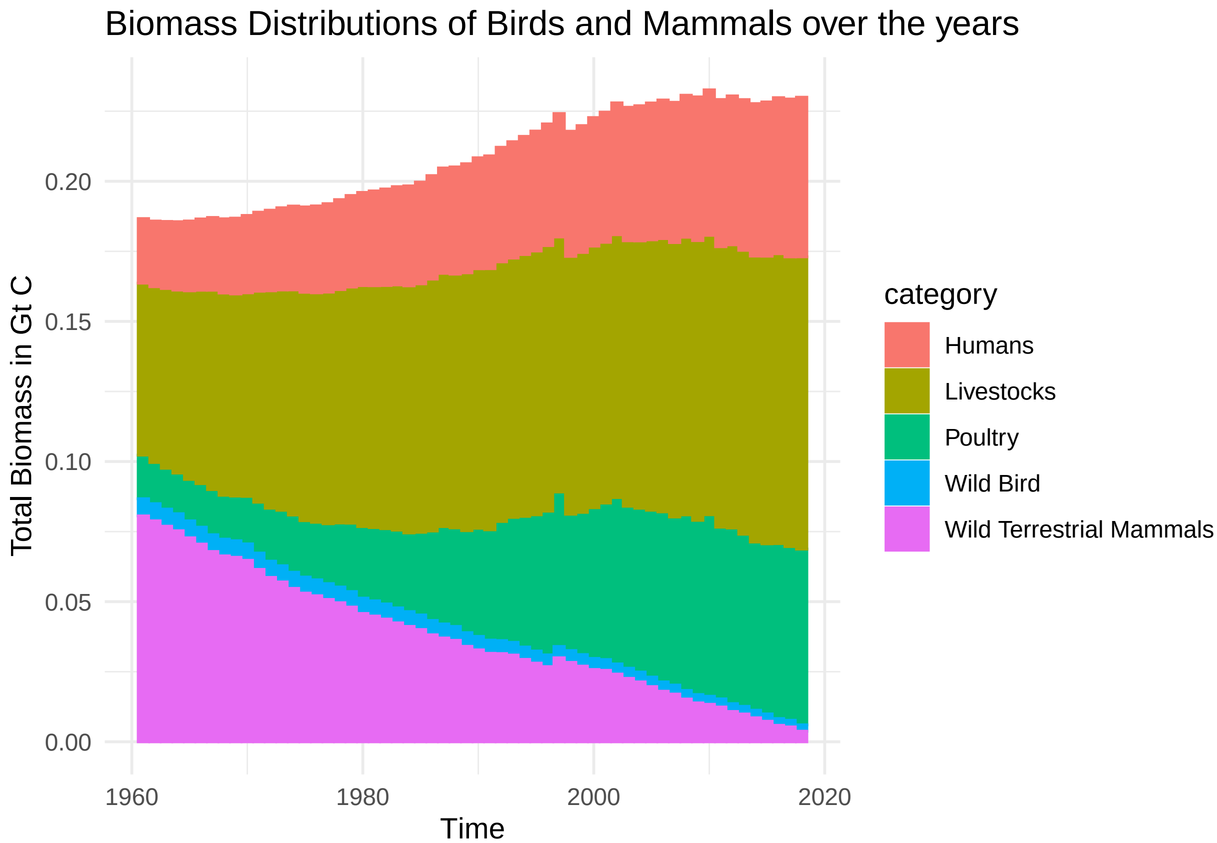



```
livestocks %>%
  mutate(Methane = methane$`Methane (ppm of CO2)`, Time = seq.Date(as.Date('1961-01-01'), length = 58, b
  mutate(Methane = sapply(Methane, function(x){
    return (100*(x- min(Methane))/(max(Methane) - min(Methane)))
  }) ) %>%
  ggplot(aes(Time)) +
  geom_line(aes(y = Methane), color = "blue", fill = "blue", stat = "identity") +
  geom_line(aes(y = `% Mammal Biomass (Gt C)`), color = "red", fill = "red", stat = "identity") +
  geom_line(aes(y = Humans), color = "green", fill = "green", stat = "identity") + theme_minimal()
```



To sum up all of my findings from this project together, the visualization below showcases the change in biomass of birds and mammals in the past ~60 years in Gt C. Although the share of birds has always been low, the drop in wild animals is very concerning.

```
as.data.frame(rbind(cbind(poultry$`Total Biomass (Gt C)`, category = "Poultry"), cbind(livestocks$`Total
  mutate(Time = rep(seq.Date(as.Date('1961-01-01'), length = 58, by = "1 year"), 5), `Total Biomass` =
  ggplot(aes(x = Time, y = `Total Biomass`, fill = category, color = category)) +
  geom_bar(stat = "identity") +
  theme_minimal() +
  labs(title = "Biomass Distributions of Birds and Mammals over the years", y = "Total Biomass in Gt C")
```



REFLECTION *Due to dealing with multiple(10) sheets in this project, I had to deal with repetitive coding as structure of each sheet was different.I have used piping extensively in this project in order to decrease the number of variables. I decided to focus on poultry, livestock and humans in this project as I wanted to showcase human impact. I dived deep and segregated the data as much as possible to get an accurate result. For the purpose of maintaining standards and to be able to compare it with actual results in the world I decided to follow IPCC and FAOSTAT for all the information regarding weight and population. As the data was classified on the basis of the regions, I chose to focus on different regions of the world based on the geography. As a result I ended up separating Asia into Asia and Indian Subcontinent and clubbing Australia and surrounding countries Oceania. Also, a major assumption made is that the total biomass on earth 550 Gt C. Although I ended up merging all of the regions together for the sake of visualization, if allowed to continue this project I would like to study all of the different regions separately as well as this might give insights on which region is experiencing most of the changes. Desertification is major problem in Africa and is surely to be major factor in the obtained results*

INFERENCE

Though we have been aware of climate change and importance of a healthy Eco-system for more than three decades, the continuing sharp decline in the wild is concerning and proves that we are much farther away from a solution than we think. Though this project focuses on biomass distribution over the years some of the information can be linked with present situations to get verify the current situations. The rapid decline in the wildlife population is also an indication to the rapid deforestation, which has been a rising problem over the years. Besides this, we can also observe how the livestock have almost doubled in population when compared to humans. Today, the global cattle population amounted to about one billion, which makes it increasingly believable than Iceland has more sheep than human (that's close to 3 sheep per person). This also,raises the topic of till what time will earth be able to sustain the growing food demands. Earth Overshoot Day is the date that marks that we have consumed all the resources that our planet is capable of generating in one year. Each year it is calculated by dividing the planet's bio capacity by humanity's ecological footprint and multiplying by 365, for the number of days in a year. In 2021, 29th July was the Earth Overshoot Day. It was first recorded *in 1970 and the overshoot day was 29 December.*

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