2. Introduction section charts

Sagar Shah, Rethink Priorities

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Clear memory and load files

```
rm(list=ls())
library(readxl)
library(tidyverse)
```

```
-- Attaching core tidyverse packages ------------------------ tidyverse 2.0.0 --
v dplyr     1.1.2     v readr     2.1.4
v forcats   1.0.0     v stringr   1.5.0
v ggplot2   3.4.2     v tibble    3.2.1
v lubridate 1.9.2     v tidyr     1.3.0
v purrr     1.0.1
-- Conflicts ------------------------------------------ tidyverse_conflicts() --
x dplyr::filter() masks stats::filter()
x dplyr::lag()    masks stats::lag()
i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to becom
```

```
library(magrittr)
```

```
Attaching package: 'magrittr'

The following object is masked from 'package:purrr':

    set_names

The following object is masked from 'package:tidyr':

    extract
```

```r
library(RColorBrewer)
library(scales)
```

```
Attaching package: 'scales'

The following object is masked from 'package:purrr':

    discard

The following object is masked from 'package:readr':

    col_factor
```

I first input a spreadsheet from fishcount.org, providing estimates of the mean slaughter weight and mean lifespan of the 24 most commonly farmed finfish species.

```r
lifeexp <-
  # Read file
  read_excel(
             "../1_input_data/fishcount_living.xlsx",
             range = "A9:V33") |>
  # Select collumns needed
         select(1,9:10,13:14) %>%
  # Convert collumn names to lower case
         mutate(across(1,str_to_lower))

# Rename collumns
names(lifeexp) <- c("species","weight_lower","weight_upper","lifespan_lower","lifespan_upp

lifeexp
```

```
# A tibble: 24 x 5
   species                weight_lower weight_upper lifespan_lower lifespan_upper
   <chr>                         <dbl>        <dbl>          <dbl>          <dbl>
 1 grass carp(=white am~           500         2500             12             24
 2 silver carp                     300         1500             24             24
 3 common carp                     500         2500             10             48
 4 nile tilapia                    250          800              6              7
 5 bighead carp                    500         1500             14             28
```

```
 6 carassius spp                150        400            12              19
 7 catla                        300       2000            14              21
 8 atlantic salmon             3614       8434            22              27
 9 roho labeo                   300       1500            14              21
10 pangas catfishes nei         500       1500            10              14
# i 14 more rows
```

I then select the species I'm interested in (based on consumption in the EU).

```
#Define search terms to filter collumns
species_list <- c("common carp","pangas","north african","trout",
                  "seabream","seabass","salmon","tilapia","striped") %>%
                  paste(collapse="|")

# Filter collumns based on search terms
lifeexp %<>% filter(str_detect(species,species_list))

# Assign each species line to a species group
species_data<- lifeexp %>%
mutate(
  species_group=case_when(
    str_detect(species,"carp") ~ "Common Carp",
    str_detect(species,"salmon") ~ "Salmon",
    str_detect(species,"catfish") ~ "Freshwater Catfish",
    str_detect(species,"trout") ~ "Rainbow Trout",
    str_detect(species,"seabream") ~ "Gilthead Seabream",
    str_detect(species,"seabass") ~ "European Seabass",
    str_detect(species,"tilapia") ~ "Tilapia",
    TRUE ~ "ERROR"
  )
) %>%

# Order rows by species group
  relocate(species_group) %>%
  arrange(species_group)

# Calculate upper/lower/average weights and lifespans across all species within a species
species_data  %<>%
  group_by(species_group) %>%
  summarise(
    weight_lower=min(weight_lower),
    weight_upper=max(weight_upper),
```

```
    weight_av=(min(weight_lower)+max(weight_upper))/2,
    lifespan_lower=min(lifespan_lower),
    lifespan_upper=max(lifespan_upper),
    lifespan_av=(min(lifespan_lower)+max(lifespan_upper))/2
  )

species_data
```

```
# A tibble: 7 x 7
  species_group      weight_lower weight_upper weight_av lifespan_lower
  <chr>                     <dbl>        <dbl>     <dbl>          <dbl>
1 Common Carp                 500         2500      1500             10
2 European Seabass            400          500       450             14
3 Freshwater Catfish          500         1500      1000             10
4 Gilthead Seabream           300          400       350             12
5 Rainbow Trout               210         5000      2605              9
6 Salmon                     3614         8434      6024             22
7 Tilapia                     250          800       525              6
# i 2 more variables: lifespan_upper <dbl>, lifespan_av <dbl>
```

I then supplement the fishcount data with my own figures where I think I have better numbers in the EU context than those provided by fishcount.

- (Small) Rainbow trout - Add in a median expected weight of 500g rather than the mid-point, given number of lives is likely to skew more heavily towards smaller weights given consumption is dominated by weight in countries consuming smaller trout. Used longer life expectancy based on Jokumsen & Svendsen (2010), Animal Ask Denmark report, and EUMOFA case study.
- (Large) Rainbow Trout - Used longer life expectancy based on Animal Ask Denmark report and EUMOFA case study, and various websites suggesting around 1.5 years during on-growing phase to achieve harvest weight.
- Atlantic Salmon - Used mean weight from Norwegian Fish Health report average slaughter weight and number of smolts put out to sea. Used life expectancy based on Mowi Industry report.
- Carp - Used data from EUMOFA report suggesting typical weights for consumption is 1.5 to 2kg, and typically 3 year production cycle. Small carp seem less commonly consumed in EU.

```
species_data %<>%
  rbind(
```

```r
    c("Rainbow Trout (small)",210,1200,500,12,15,13.5),
   c("Rainbow Trout (large)",1200,5000,3100,21,26,23.5),
   c("Atlantic Salmon",3614,8434,5663,22,40,31),
   c("Carp",1250,2250,1750,30,42,36)
   ) %>%
     mutate(across(2:7,as.double))

species_data
```

```
# A tibble: 11 x 7
   species_group         weight_lower weight_upper weight_av lifespan_lower
   <chr>                        <dbl>        <dbl>     <dbl>          <dbl>
 1 Common Carp                    500         2500      1500             10
 2 European Seabass               400          500       450             14
 3 Freshwater Catfish             500         1500      1000             10
 4 Gilthead Seabream              300          400       350             12
 5 Rainbow Trout                  210         5000      2605              9
 6 Salmon                        3614         8434      6024             22
 7 Tilapia                        250          800       525              6
 8 Rainbow Trout (small)          210         1200       500             12
 9 Rainbow Trout (large)         1200         5000      3100             21
10 Atlantic Salmon               3614         8434      5663             22
11 Carp                          1250         2250      1750             30
# i 2 more variables: lifespan_upper <dbl>, lifespan_av <dbl>
```

I now input data on apparent consumption of the most consumed farmed finfish species in the EU27 in 2021, taken from supply balance sheet data from EUMOFA.

Splits between large and small rainbow trout are based on the EUMOFA large trout case study.

```r
eu_consumption_2021 <- tibble(
# Define species names
  species_group=c('Atlantic Salmon',"Rainbow Trout",'Rainbow Trout (large)',"Rainbow Trout
# Add consupmtion in metric tonnes
  consumption=c(1097029,216425,94033,122392,136724,106776,102039,79726,39833)) %>%
# Convert to grammes (as fish weight reported in grammes)
  mutate(consumption=consumption*1E6)

eu_consumption_2021
```

```
# A tibble: 9 x 2
  species_group           consumption
  <chr>                         <dbl>
1 Atlantic Salmon       1097029000000
2 Rainbow Trout          216425000000
3 Rainbow Trout (large)   94033000000
4 Rainbow Trout (small)  122392000000
5 Gilthead Seabream      136724000000
6 European Seabass       106776000000
7 Freshwater Catfish     102039000000
8 Carp                    79726000000
9 Tilapia                 39833000000
```

I then add in the data with species specific data and work out number of animals slaughtered and age.

Note that my uncertainty ranges for lifespan will probably be too narrow, as I've assumed perfect correlation between slaughter weight and lifespan ranges (i.e. heaviest fish have longest lifespan, while lightest fish will have longest lifespan). Had I allowed for the opposite (lightest fish to be associated with longest lifespan), the ranges would have probably have been too wide.

```
eu_consumption_2021 %<>%
# Add fish weight and lifespan data
  left_join(species_data,by="species_group") %>%
  rowwise() %>%
  mutate(
# Number of fish slaughtered figures
    slaughter_upper=consumption/weight_lower,
    slaughter_lower=consumption/weight_upper,
    slaughter_midweight=consumption/weight_av,
# Lifespan ranges, assuming perfect correlation between weight and lifespan ranges
    lifeyears_1=consumption/weight_lower*lifespan_lower/12,
    lifeyears_2=consumption/weight_upper*lifespan_upper/12,
# Min and max lifespan
    lifeyears_lower=min(lifeyears_1,lifeyears_2),
    lifeyears_upper=max(lifeyears_1,lifeyears_2),
# Best guess of average lifespan
    lifeyears_midwl=slaughter_midweight*lifespan_av/12
  )
```

Chart1: Number of fish slaughtered for EU consumption

```r
fig1 <-   eu_consumption_2021 %>%
  filter(species_group!="Rainbow Trout") %>%
  ggplot(
    aes(
      x=reorder(str_to_title(species_group),slaughter_midweight),
      y=slaughter_midweight,
      ymin=slaughter_lower,
      ymax=slaughter_upper
    )
  ) +
  geom_col(fill="#1B9E77")+
  geom_errorbar(width=0.2,size=0.3)+
    scale_y_continuous(labels = scales::label_number_si()) +
  theme_light() +
  coord_flip() +
    labs(
    title="Number of fish slaughtered",
    subtitle="Farmed finfish to support EU27 consumption in 2021",
    y="Number slaughtered",
    x="")
```

```
Warning: Using `size` aesthetic for lines was deprecated in ggplot2 3.4.0.
i Please use `linewidth` instead.
```

```
Warning: `label_number_si()` was deprecated in scales 1.2.0.
i Please use the `scale_cut` argument of `label_number()` instead.
```

```r
fig1
```

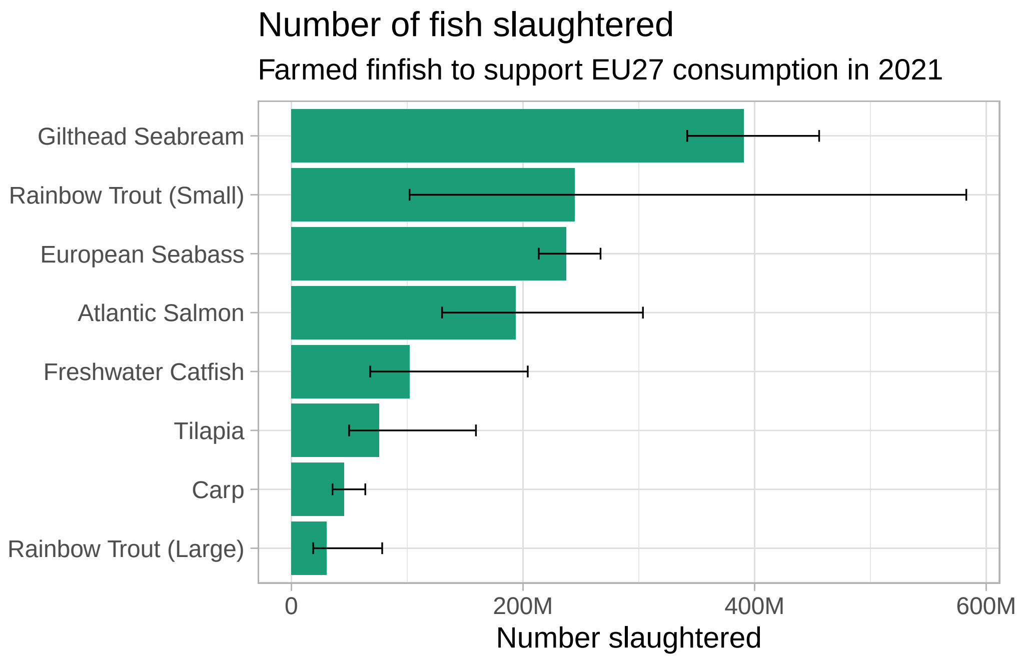


Fig 2: Share of EU farms where fish are stunned before slaughter

Source: Leaked EU impact assessment document

```
share_stunned <- tibble(
  species=c("Atlantic Salmon","Rainbow Trout","Carp","Seabream & Seabass"),
  upper=c(1,0.5,0.1,0.05),
  lower=c(0.9,0.2,0,0),
  label=c("> 90%","20% to 50%","< 10%","< 5%")) %>%
  mutate(label_pos=0.5*(upper+lower))



fig2 <- share_stunned %>%
  ggplot(
    aes(
      x=reorder(species,upper),
      ymin=lower,
      y=label_pos,
      ymax=upper
    )
  ) +
  geom_errorbar(width=0.5,size=1)+
```

```
  geom_linerange(size=8,color="#1B9E77") +
  geom_text(aes(label=label),nudge_x=0.38) +
  scale_y_continuous(labels = scales::percent) +
  theme_light() +
  coord_flip() +
    labs(
    title="Share of EU farms where fish are stunned",
    x="",
    y="")


fig2
```

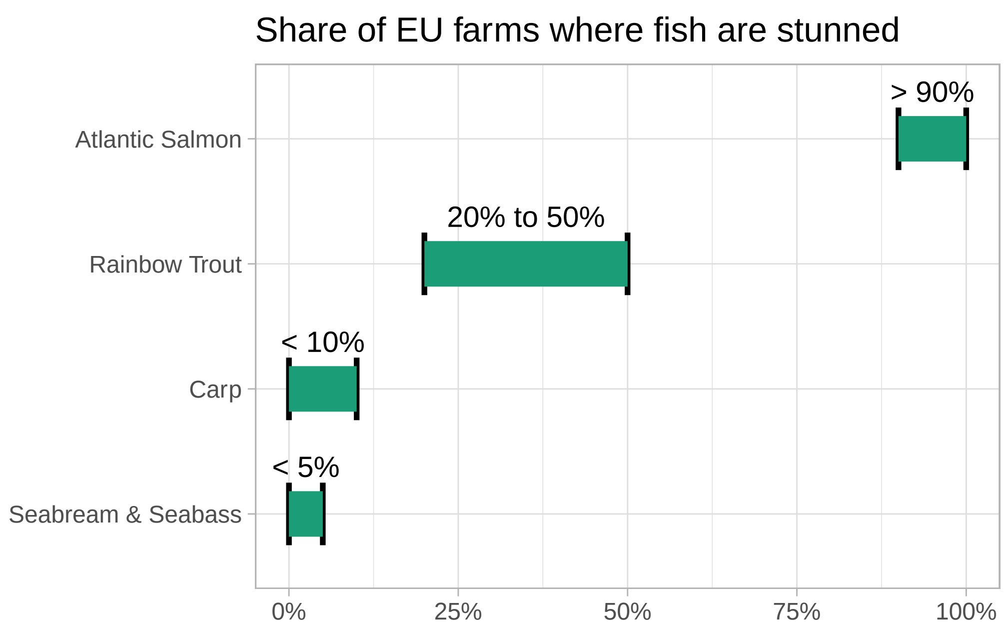


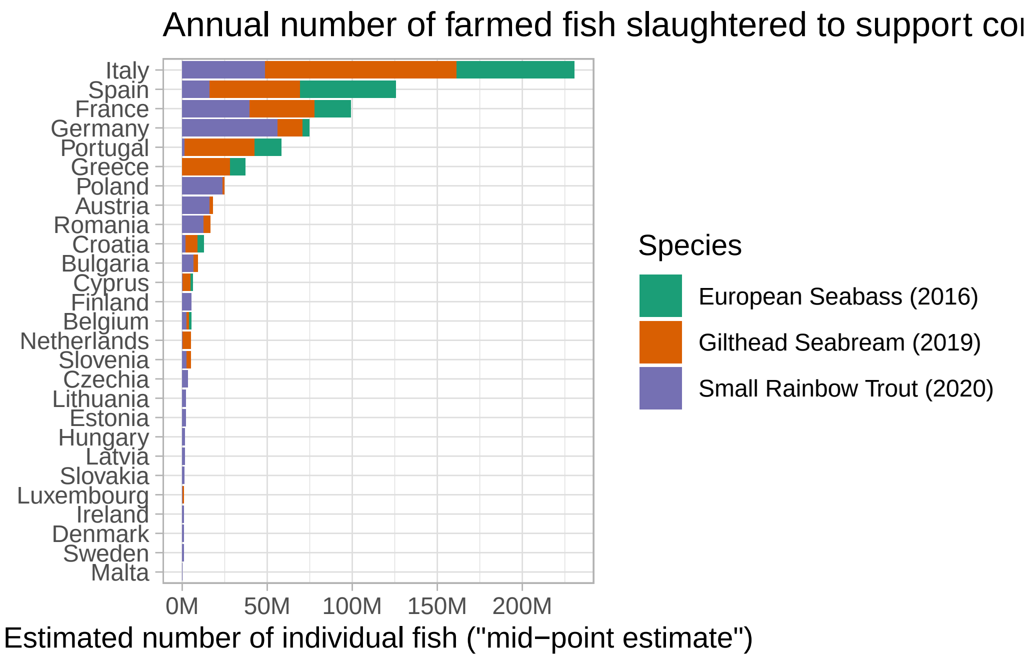
Fig 3 - Consumption by country

```
fig_3_data <-
readRDS("../3_intermediate_data/cons_data.rds") %>%
  filter(country!="United Kingdom") %>%
  mutate(species_group=case_when(
    str_detect(species,"Sea Bream") ~ "Gilthead Seabream",
    str_detect(species,"Sea Bass") ~ "European Seabass",
    str_detect(species,"Salmon") ~ "Atlantic Salmon",
    str_detect(species,"Small") ~ "Rainbow Trout (small)",
```

```
    str_detect(species,"Large") ~ "Rainbow Trout (large)",
    str_detect(species,"Carp") ~ "Carp",
    TRUE~"Error")) %>%
  left_join(species_data,by="species_group") %>%
  mutate(
    slaughter_midweight=tons*1E6/weight_av) %>%
  select(species_group,country,slaughter_midweight) %>%
  group_by(country) %>%
  mutate(
    total_cons=sum(slaughter_midweight)
  ) %>%
  ungroup()
```

```
fig3 <- fig_3_data %>%
  filter(!species_group %in% c("Atlantic Salmon","Carp","Rainbow Trout (large)")) %>%
  group_by(country) %>%
  mutate(
    total_cons=sum(slaughter_midweight)
  ) %>%
  ungroup() %>%
ggplot(aes(
      y=reorder(country,total_cons),
      x=slaughter_midweight,
      fill=species_group))+
    geom_col()+
    labs(
    title = "Annual number of farmed fish slaughtered to support consumption in EU27",
    x = "Estimated number of individual fish (\"mid-point estimate\")",
    y = "",
    fill = "Species"
  ) +
  scale_x_continuous(labels = label_number(suffix = "M", scale = 1e-6)) +
  scale_fill_brewer(palette = "Dark2",
                    labels = c("European Seabass (2016)", "Gilthead Seabream (2019)", "Sma
  theme_light() +
  theme(legend.position = "right")

fig3
```



Export charts in order used in the report

```
#Define chart export characteristics
save_chart <- function(name,plot_name) {
  plot_no_title <- plot_name+ labs(title=NULL,subtitle=NULL)
  ggsave(name,plot = plot_no_title,path ="../4_charts/", width = 6.7, height = 3.8,units =
}

#Export charts to file
save_chart("fig1_eu_slaughter_numbers.png",fig1)
save_chart("fig2_stun_shares.png",fig2)
save_chart("fig3_slaughter_by_country_consumption.png",fig3)
```