Marine Data Science

Universität Hamburg
DER FORSCHUNG | DER LEHRE | DER BILDUNG

Data Analysis with R

10 - Handling and visualization of categorical data

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Computer Programming

Factors

Recall:

Factors are

- vectors that can contain only **predefined values**,
- used to store **categorical data**,
- built **on top of integer** vectors using two attributes:
    - the **class**, “factor”, which makes them behave differently from regular integer vectors,
    - and the **levels**, which defines the set of allowed values.

Recall:

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- used to store **categorical data**,
- built **on top of integer** vectors using two attributes:
    - the **class**, “factor”, which makes them behave differently from regular integer vectors,
    - and the **levels**, which defines the set of allowed values.
- a useful tidyverse package for factors is **forcats**

String vs. factor

Imagine that you have a vector or variable that contains months:

```r
x1 <- c("Dec", "Apr", "Jan", "Mar")
```

Using a string to record this variable has two problems:

String vs. factor

Imagine that you have a vector or variable that contains months:

```
x1 <- c("Dec", "Apr", "Jan", "Mar")
```

Using a string to record this variable has two problems:

1. It **doesn’t sort** in a useful way.
2. There are only twelve possible months, and there’s nothing saving you from **typos**.

```
sort(x1)
```

```
## [1] "Apr" "Dec" "Jan" "Mar"
```

```
x2 <- c("Dec", "Apr", "Jam", "Mar")
```

Creating factors

You can fix both of these problems with a factor. To create a factor you can convert any vector using the function `factor()`

```r
f1 <- factor(x1)
f1
```

```
## [1] Dec Apr Jan Mar
## Levels: Apr Dec Jan Mar
```

Creating factors

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```r
f1 <- factor(x1)
f1
```

```
## [1] Dec Apr Jan Mar
## Levels: Apr Dec Jan Mar
```

But this does **not yet** fix the problems...

```r
sort(f1)
```

```
## [1] Apr Dec Jan Mar
## Levels: Apr Dec Jan Mar
```

As you can see, the factor elements get sorted in the order of the levels - which is an alphabetical order.

Creating factors (cont)

Solution:

Create a vector of the valid levels and add it as `levels` argument:

```r
month_levels <- c(
  "Jan", "Feb", "Mar", "Apr", "May", "Jun",
  "Jul", "Aug", "Sep", "Oct", "Nov", "Dec"
)
f1 <- factor(x1, levels = month_levels)
f1
```

```
## [1] Dec Apr Jan Mar
## Levels: Jan Feb Mar Apr May Jun Jul Aug Sep Oct Nov Dec
```

Note:

- Whatever order you choose here will be the output order.
- You can include levels here that are not necessarily in your vector.

Creating factors (cont)

Any values not in the level vector will be silently converted to NA:

```
f2 <- factor(x2, levels = month_levels)
f2
```

```
## [1] Dec  Apr  <NA> Mar
## Levels: Jan Feb Mar Apr May Jun Jul Aug Sep Oct Nov Dec
```

To access the set of valid levels directly use `levels()`:

```
levels(f1)
```

```
##  [1] "Jan" "Feb" "Mar" "Apr" "May" "Jun" "Jul" "Aug" "Sep" "Oct" "Nov"
## [12] "Dec"
```

Factor levels

Sometimes you'd prefer that the order of the levels match the order of the first appearance in the data. You can do that when creating the factor by setting levels to `unique(x)` or after the factor conversion with `fct_inorder()` (in forcats):

```
f1 <- factor(x1, levels = unique(x1))
f1
```

```
## [1] Dec Apr Jan Mar
## Levels: Dec Apr Jan Mar
```

```
library(forcats)
f2 <- x1 %>% factor() %>% fct_inorder()
f2
```

```
## [1] Dec Apr Jan Mar
## Levels: Dec Apr Jan Mar
```

You can do many other things with a factor using the `forcats` library

- Reorder factor levels **by hand**: `fct_relevel()`
- Reorder factors levels **by first appearance or frequency**: `fct_infreq()`
- **Reverse** order of factor levels: `fct_rev()`
- Reorder factor levels **by sorting along another variable**: `fct_reorder()`
- **Collapse factor levels** into manually defined groups: `fct_collapse()`

Factor labels

You can change the way how the factor levels are **displayed**. That can be useful if you want to **reduce typing effort**:

Factor labels

You can change the way how the factor levels are **displayed**. That can be useful if you want to **reduce typing effort**:

```
x <- c(1,2,4,2,4,5,2,5,6,3,5,6,7,3,6,8,2,8)
months <- factor(x, # your vector containing the months
  levels = 1:12, # allowed values (in that order)
  labels = c("jan","feb","mar","apr","may","jun","jul","aug","sep","oct","nov","dec"))
months
```

```
##  [1] jan feb apr feb apr may feb may jun mar may jun jul mar jun aug feb
## [18] aug
## Levels: jan feb mar apr may jun jul aug sep oct nov dec
```

To compare without labels

```
factor(x, levels = 1:12)
```

```
##  [1] 1 2 4 2 4 5 2 5 6 3 5 6 7 3 6 8 2 8
## Levels: 1 2 3 4 5 6 7 8 9 10 11 12
```

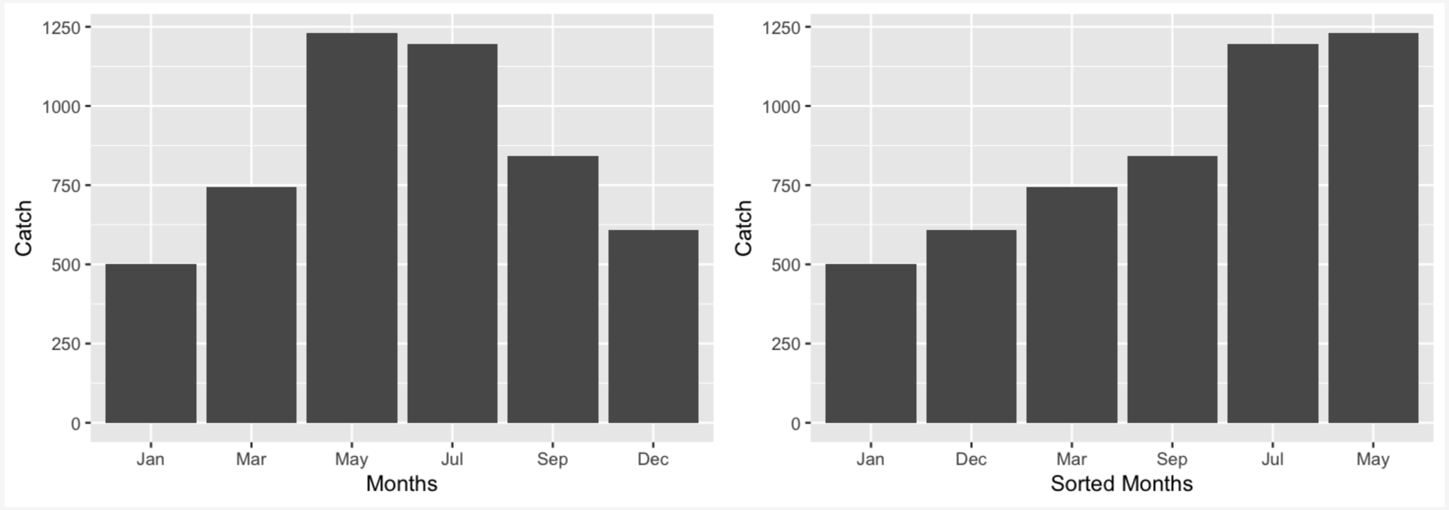
Your turn...

Exercise

Create the following dataset

```
manta_rays <- data.frame(
  month = c(9, 3, 5, 1, 7, 12),
  catch = c(843, 743, 1229, 500, 1197,607)
  )
```

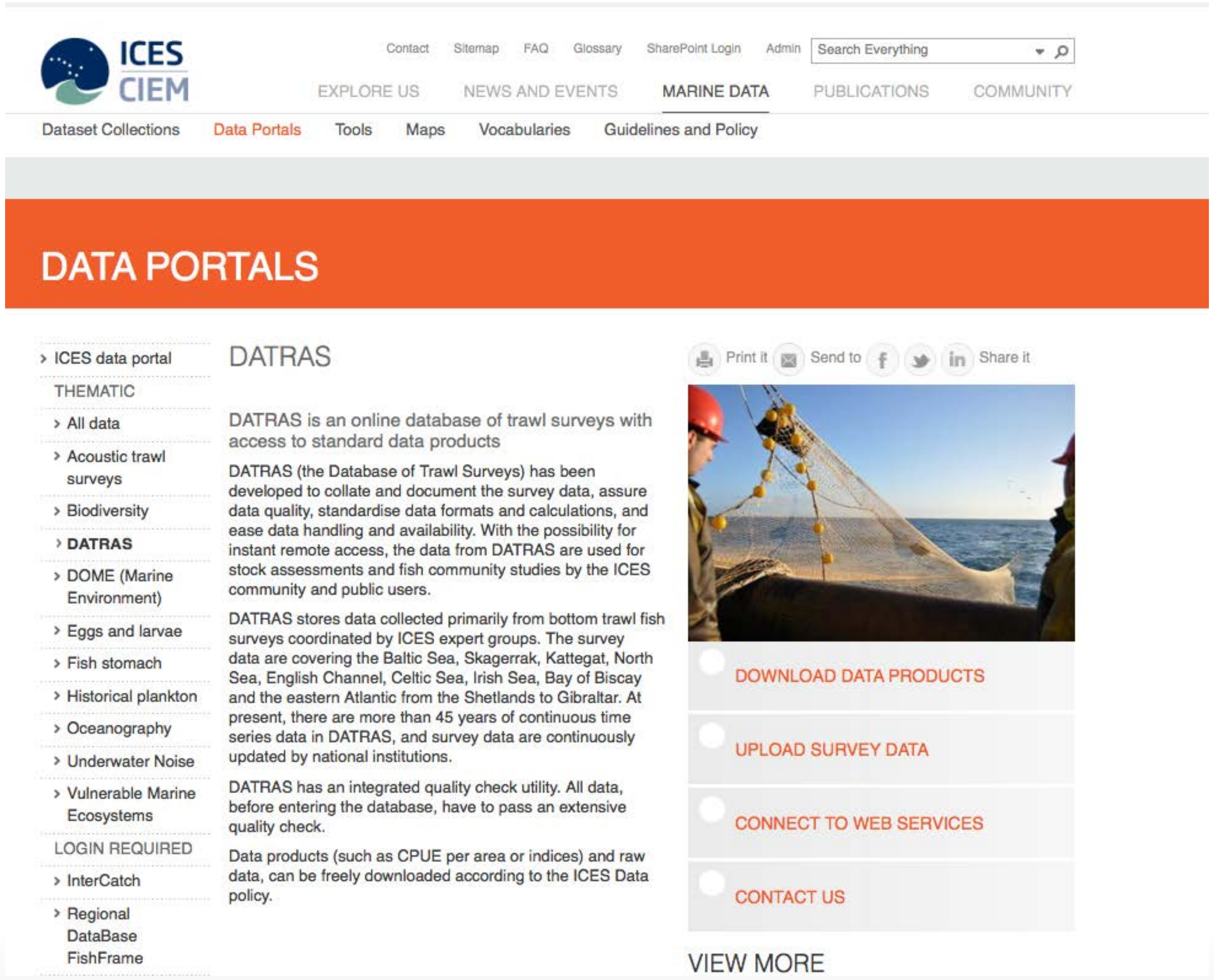
Now modify **manta_rays** to get these 2 plots:



Data Exploration
& Visualization

A real data demonstration with ICES DATRAS fish data

We will query data from the DATRAS database



DATRAS

DATRAS is an online database of trawl surveys with access to standard data products

DATRAS (the Database of Trawl Surveys) has been developed to collate and document the survey data, assure data quality, standardise data formats and calculations, and ease data handling and availability. With the possibility for instant remote access, the data from DATRAS are used for stock assessments and fish community studies by the ICES community and public users.

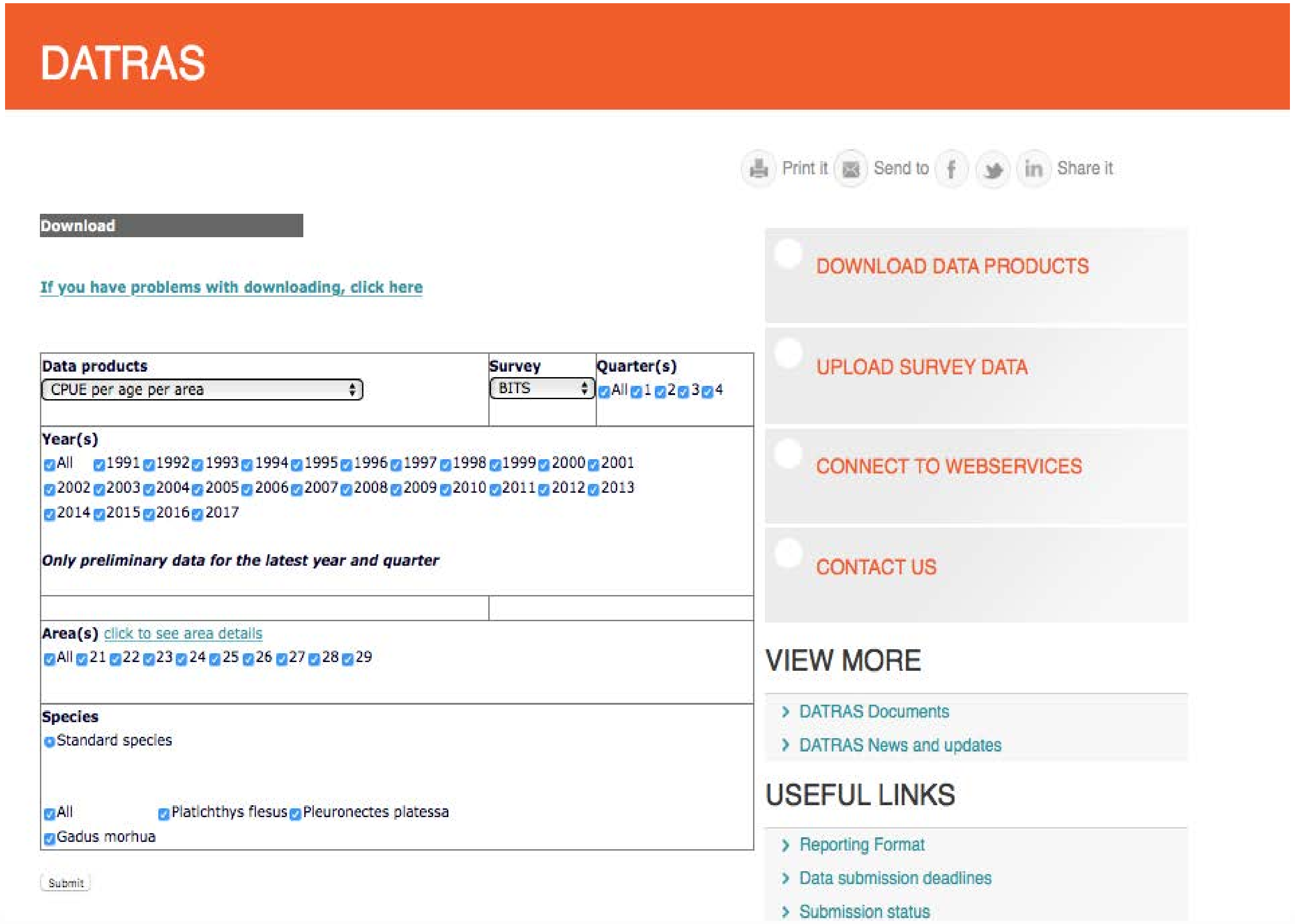
DATRAS stores data collected primarily from bottom trawl fish surveys coordinated by ICES expert groups. The survey data are covering the Baltic Sea, Skagerrak, Kattegat, North Sea, English Channel, Celtic Sea, Irish Sea, Bay of Biscay and the eastern Atlantic from the Shetlands to Gibraltar. At present, there are more than 45 years of continuous time series data in DATRAS, and survey data are continuously updated by national institutions.

DATRAS has an integrated quality check utility. All data, before entering the database, have to pass an extensive quality check.

Data products (such as CPUE per area or indices) and raw data, can be freely downloaded according to the ICES Data policy.

Screenshot from the ICES webpage: http://www.ices.dk/marine-data/data-portals/Pages/DATRAS.aspx

Query CPUE per age per area



DATRAS

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Data products CPUE per age per area

Survey BITS

Quarter(s) ☑All ☑1 ☑2 ☑3 ☑4

Year(s)
☑All ☑1991 ☑1992 ☑1993 ☑1994 ☑1995 ☑1996 ☑1997 ☑1998 ☑1999 ☑2000 ☑2001
☑2002 ☑2003 ☑2004 ☑2005 ☑2006 ☑2007 ☑2008 ☑2009 ☑2010 ☑2011 ☑2012 ☑2013
☑2014 ☑2015 ☑2016 ☑2017

Only preliminary data for the latest year and quarter

Area(s) click to see area details
☑All ☑21 ☑22 ☑23 ☑24 ☑25 ☑26 ☑27 ☑28 ☑29

Species
● Standard species

☑All ☑Platichthys flesus ☑Pleuronectes platessa
☑Gadus morhua

Submit

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- DATRAS Documents
- DATRAS News and updates

USEFUL LINKS

- Reporting Format
- Data submission deadlines
- Submission status

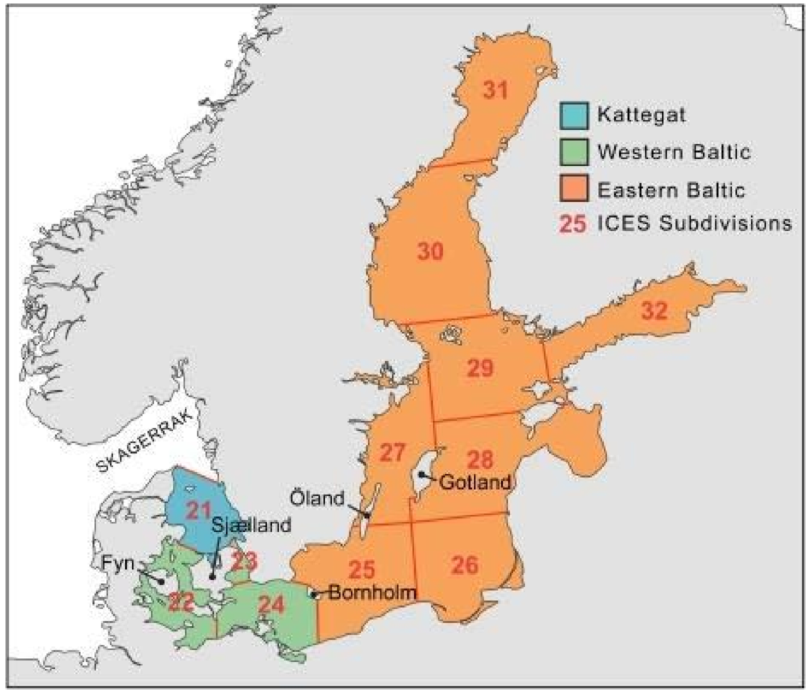
Load the data (using your file path)

```r
cpue <- read_csv("data/CPUE per age per area_2017-11-20 06_48_16.csv")
print(cpue, n = 5)
```

```
## # A tibble: 801 x 17
##   Survey  Year Quarter  Area AphiaID Species Age_0 Age_1 Age_2 Age_3 Age_4
##   <chr>  <int>   <int> <int>   <int> <chr>   <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 BITS    1991       1    24  126436 Gadus …     0 2.24   6.81  6.48  7.24
## 2 BITS    1991       1    25  126436 Gadus …     0 3.47  24.6  39.9  58.8
## 3 BITS    1991       1    26  126436 Gadus …     0 8.79   8.52 38.1  29.6
## 4 BITS    1991       1    27  126436 Gadus …     0 0      0     0     0
## 5 BITS    1991       1    28  126436 Gadus …     0 0.173 25.8  42.5  34.5
## # ... with 796 more rows, and 6 more variables: Age_5 <dbl>, Age_6 <dbl>,
## #   Age_7 <dbl>, Age_8 <dbl>, Age_9 <dbl>, Age_10 <dbl>
```

So what are the `Areas`?

ICES subdivisions (SD) in the Baltic Sea



source: EAA and EFTTA position paper, Sept 30th, 2016 (http://www.eaa-europe.org)

Now check whether the data is tidy

- Any NAs?
- Is the format long or wide? Do you want to change it?
- **Do the columns have the appropriate data type?**

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  - Are you satisfied with `Survey`, `Quarter`, `Area`, or `Species` being character or integer vectors?

Now check whether the data is tidy

- Any NAs?
- Is the format long or wide? Do you want to change it?
- **Do the columns have the appropriate data type?**
  - Are you satisfied with `Survey`, `Quarter`, `Area`, or `Species` being character or integer vectors?
  - Why not convert them into **factors** ...?

```
cpue$Quarter <- factor(cpue$Quarter)
cpue$Area <- factor(cpue$Area)
cpue$Species <- factor(cpue$Species)
```

Data transformation

Lets plot the **total CPUE** of **Atlantic cod** (*Gadus morhua*) in the **first** quarter of **2015** per area:

```
cpue_total <- cpue %>%
  filter(Species == "Gadus morhua", Year == 2015, Quarter == 1) %>%
  select(Area, contains("Age")) %>%
    mutate(total_cpue = rowSums(select(., contains("Age"))))
```

Note:

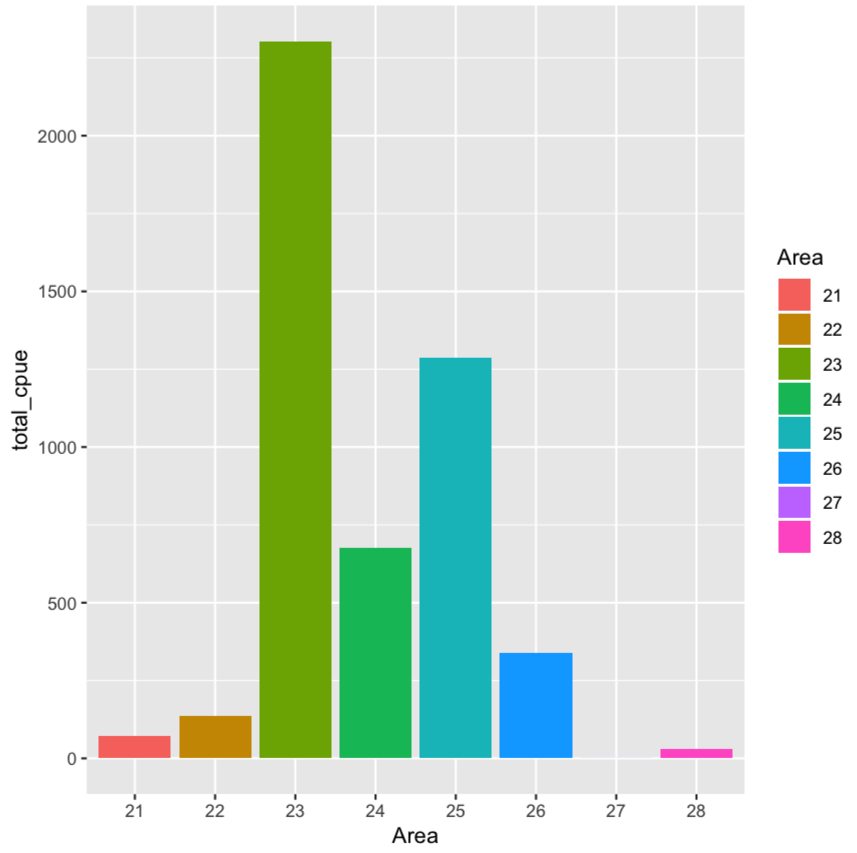
When using the pipe operator and the **select function** within another function (here `rowMeans()`) you need to use as first argument the **dot as placeholder** for the data!

Area sorted automatically

```
cpue_total %>%
  ggplot(aes(x = Area, y= total_cpue,
    fill = Area)) +
  geom_col()
```

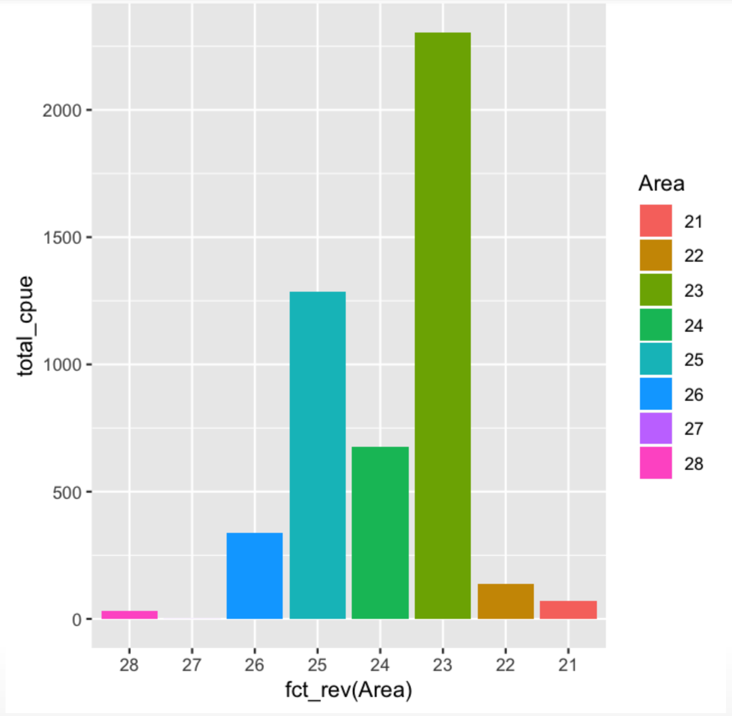
Note:

Not every plot type is suitable for categorical data, for instance a scatterplot. Instead, use **barplots**, piecharts, or boxplots. In ggplot the layer function for a barplot would be `geom_bar()` and `geom_col()`. We use the **latter** here as we already know the height of each bar and don't need it calculated from the number of cases in each group.

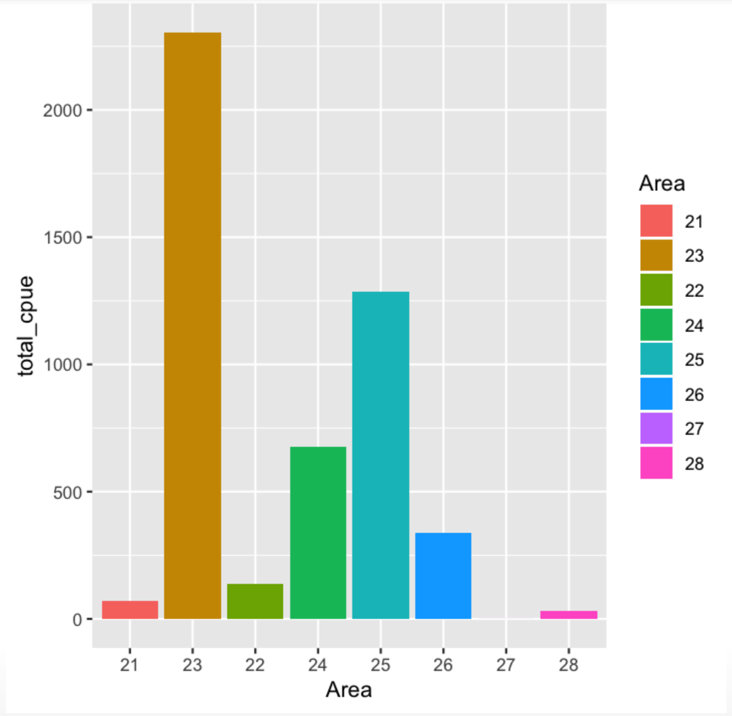


Now lets reorder the Area factor

```r
# Simply reverse order
cpue_total %>%
  ggplot(aes(x = fct_rev(Area),
    y = total_cpue, fill = Area)) +
  geom_col()
```

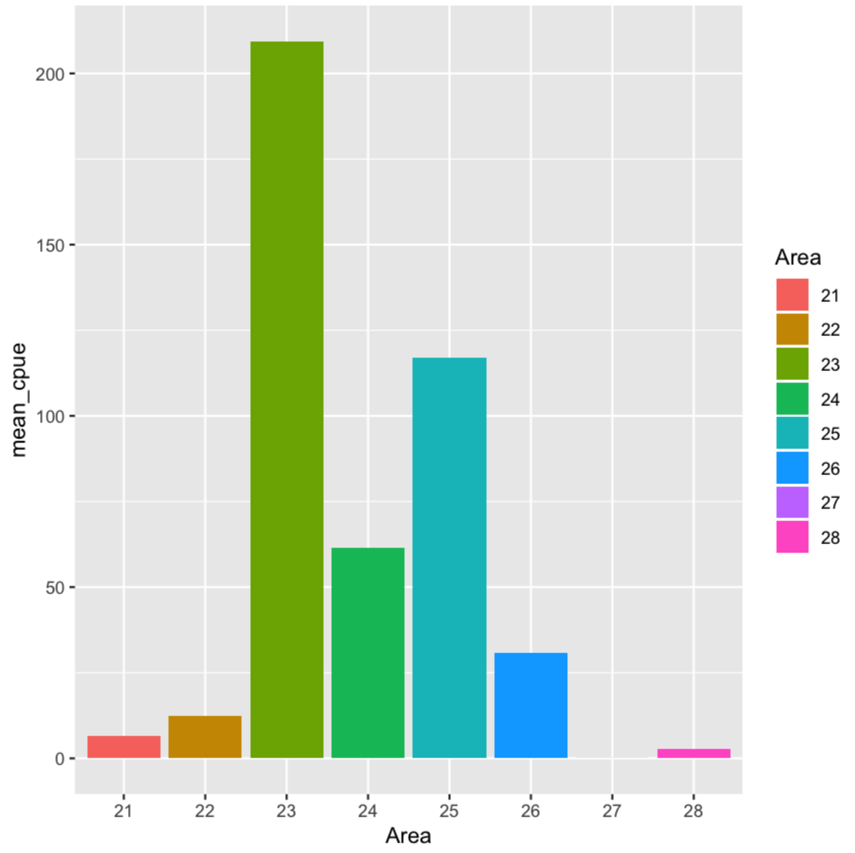


```r
# Reorder manually
cpue_total %>% mutate(Area=fct_relevel(
  Area, "22", after = 2)) %>%
  ggplot(aes(x=Area, y=total_cpue,
    fill = Area)) + geom_col()
```



What would be if we plot the mean instead of total CPUE:

```r
cpue_mean <- cpue %>%
  filter(Species == "Gadus morhua",
    Year == 2015, Quarter == 1) %>%
  select(Area, contains("Age")) %>%
  mutate(mean_cpue = rowMeans(select(.,
    contains("Age"))))
cpue_mean %>%
  ggplot(aes(x = Area, y= mean_cpue,
    fill = Area)) +
  geom_col()
```



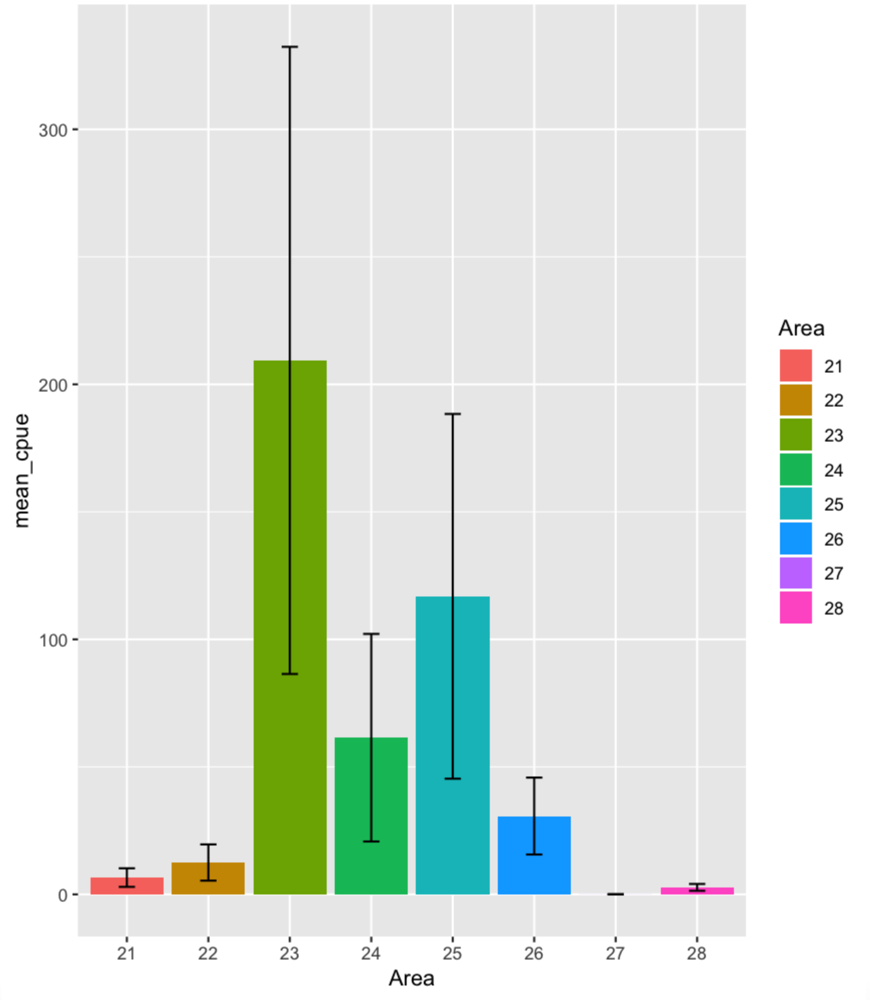
How representatives are the means?

Data Exploration & Visualization

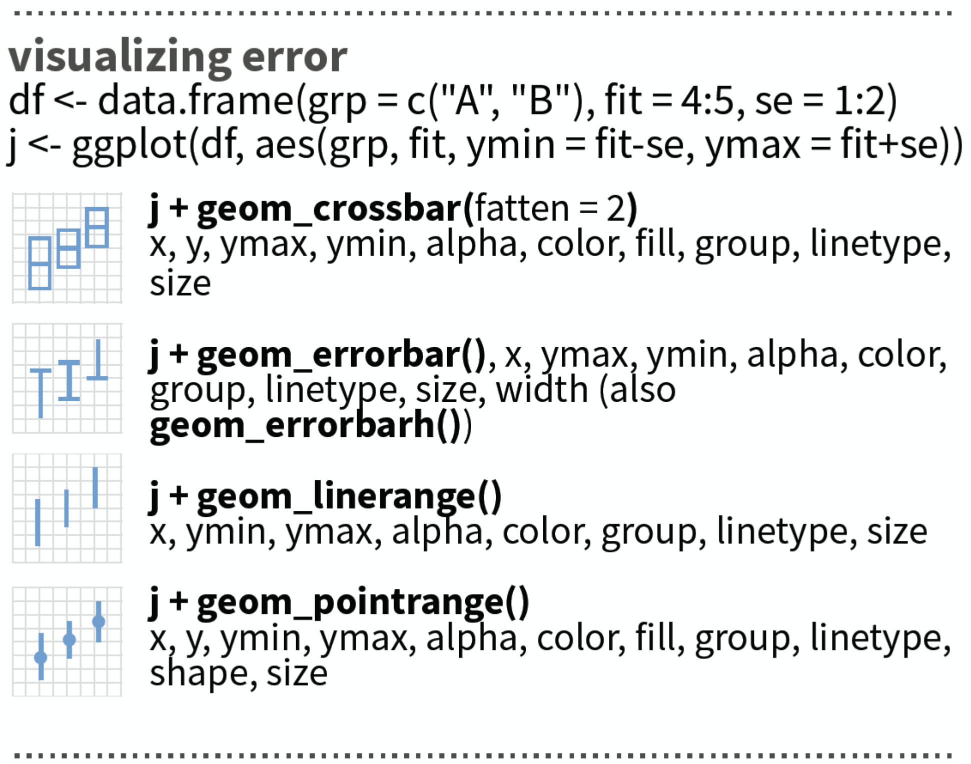
Visualizing errors

Visualizing errors using e.g. `geom_errorbar()`

```
cpue_mean %>%
  mutate(sd_cpue = apply(
    select(., contains("Age")), 1, sd),
    se_cpue = sd_cpue/ sqrt(11)
  ) %>%
  ggplot(aes(x = Area, y= mean_cpue,
    fill = Area)) +
  geom_col() +
  geom_errorbar(aes(
    ymin = mean_cpue - se_cpue,
    ymax = mean_cpue + se_cpue),
    width = .2)
    # Width of the error bars
```



Visualizing errors: other options



visualizing error

```
df <- data.frame(grp = c("A", "B"), fit = 4:5, se = 1:2)
j <- ggplot(df, aes(grp, fit, ymin = fit-se, ymax = fit+se))
```

j + geom_crossbar(fatten = 2**)**
x, y, ymax, ymin, alpha, color, fill, group, linetype, size

j + geom_errorbar(), x, ymax, ymin, alpha, color, group, linetype, size, width (also **geom_errorbarh()**)

j + geom_linerange()
x, ymin, ymax, alpha, color, group, linetype, size

j + geom_pointrange()
x, y, ymin, ymax, alpha, color, fill, group, linetype, shape, size

source: older version of Data Visualization with ggplot cheat sheet (licensed under CC-BY-SA)

Your turn...

Exercise

Pick another species and the year 2015 and find out if there are spatial differences (between areas)

1. in **total** CPUE
2. **mean** CPUE (with error bar)
3. in CPUE of **each age**

Were does the variability in the wide error bars come from?

At the end of the presentation you find a solution code!

base functions for factors: `factor(x, levels)`, `unique(x)`, `levels()`

base functions applied on margin of dataframes: `rowSums()`, `rowMeans()`, `apply(data, MARGIN, FUN)`

dplyr package: select helper function `contains()`

ggplot2 package: `geom_col()`, `geom_errorbar()`

forcats package: `fct_inorder()`, `fct_relevel()`, `fct_infreq()`, `fct_rev()`, `fct_reorder()`, `fct_collapse()`

Overview of functions you learned today

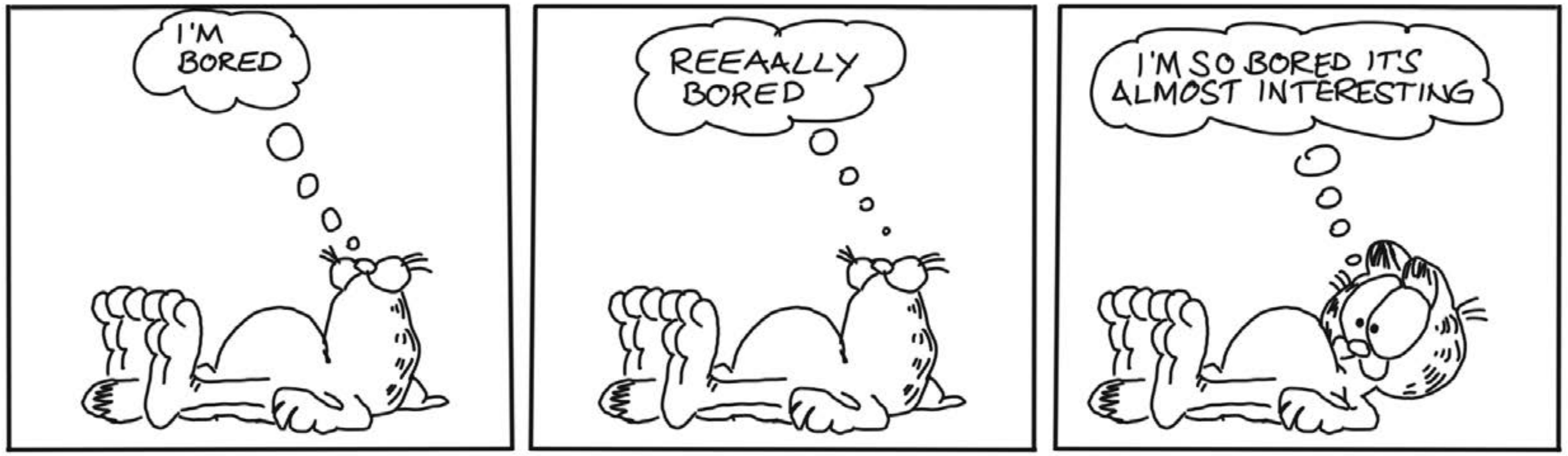
How do you feel now.....?

Totally confused?

23uzr8?! §€@@´´`§/;...€ hbfj,§%46;)9=.,§4`´ 7:@,9 RRR4RRR8RRR RRRROORRR§()

Practice on the exercise data and try out maybe all species or all years. Read chapter 15 on factors in 'R for Data Science'.

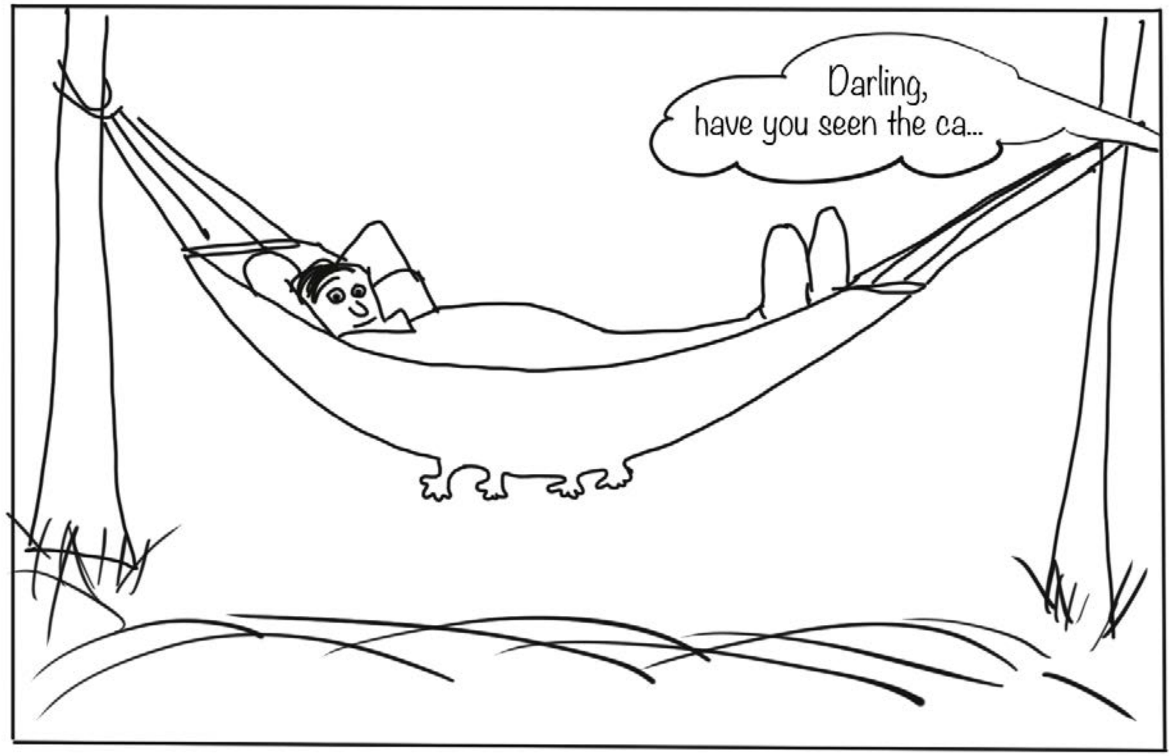
Totally bored?



Stay tuned for the next case study where you can play around as much as you want!

Totally content?

Then go grab a coffee, lean back and enjoy the rest of the day...!



Thank You

For more information contact me: saskia.otto@uni-hamburg.de

http://www.researchgate.net/profile/Saskia_Otto
http://www.github.com/saskiaotto

Solution

Solution for all 3 species, all Quarters and 2015

You could calculate your summary statistics such as **mean, standard deviation**, etc. by applying functions to margins of the dataframe such as `rowSums`, `rowMeans()` or `apply(x, MARGIN, FUN)` as I showed you in the previous examples. Alternatively, if you want to *aggregate both across columns AND rows* (because you have e.g. repeated entries) or you want to use later the *faceting option*, convert your data into a **long format**. If you keep quarters or years, however, you should calculate total CPUE (summed up across the different ages) separately for each quarter or year!

In this example I will use the long format as I want to facet later also my plots.

Solution for all 3 species, all Quarters and 2015 (cont)

1. Load data and convert variables into factors

```r
cpue <- read_csv("data/CPUE per age per area_2017-11-20 06_48_16.csv")
cpue$Area <- factor(cpue$Area,
  levels = c(21,22,23,24,25,26,27,28,29,30,31,32))
```

2. Create data subset

```r
cpue_sub <- cpue %>% filter(Year == 2015) %>%
  select(Area, Quarter, Species, contains("Age"))
```

3. Make data wide

```r
cpue_subl <- cpue_sub %>% gather(key = "age", value = "cpue", -Area, -Quarter, -Species)
# Same as
cpue_subl <- cpue_sub %>% gather(key = "age", value = "cpue", Age_0:Age_10)
```

4.Convert `Age` into a factor

```
cpue_subl$age <- factor(cpue_subl$age)
# this won't give the order you want (age 10 comes after age 1)
levels(cpue_subl$age)
```

```
##  [1] "Age_0"  "Age_1"  "Age_10" "Age_2"  "Age_3"  "Age_4"  "Age_5" 
##  [8] "Age_6"  "Age_7"  "Age_8"  "Age_9"
```

Uups, not a great order.

```
cpue_subl$age <- fct_relevel(cpue_subl$age, "Age_10", after = 10)
# check again
levels(cpue_subl$age)
```

```
##  [1] "Age_0"  "Age_1"  "Age_2"  "Age_3"  "Age_4"  "Age_5"  "Age_6" 
##  [8] "Age_7"  "Age_8"  "Age_9"  "Age_10"
```

5.Now calculate the summary statistics in one step

```
cpue_stats <- cpue_subl %>%
  group_by(Area, Quarter, Species) %>%
  summarise(
  total_cpue = sum(cpue),
  mean_cpue = mean(cpue),
  se_cpue = sd(cpue) / sqrt(n()) # n() has to be empty
  )
```

Create and save distribution plots per species

```
p_cod_tot <- cpue_stats %>% filter(Species == "Gadus morhua") %>%
  ggplot(aes(x = Area, y = total_cpue, fill = Area)) +
  geom_col() +
  guides(fill = "none") +
  facet_grid(. ~ Quarter, labeller = label_both)

p_cod_mean <- cpue_stats %>% filter(Species == "Gadus morhua") %>%
  ggplot(aes(x = Area, y = mean_cpue, fill = Area)) + # only y replaced
  geom_col() +
  guides(fill = "none") +
  geom_errorbar(aes(  # standard error will be added here
  ymin = mean_cpue - se_cpue,
  ymax = mean_cpue + se_cpue),
  width = .2) +
  facet_grid(. ~ Quarter, labeller = label_both)
```

Create and save distribution plots per species (cont)

```r
p_cod_age_q1 <- cpue_subl %>%
  filter(Species == "Gadus morhua", Quarter == 1) %>%
  ggplot(aes(x = Area, y = cpue, fill = Area)) + # y replaced again
  geom_col() +
  guides(fill = "none") +
  facet_wrap(~ age, labeller = label_both)  # ~month replaced with ~age
```

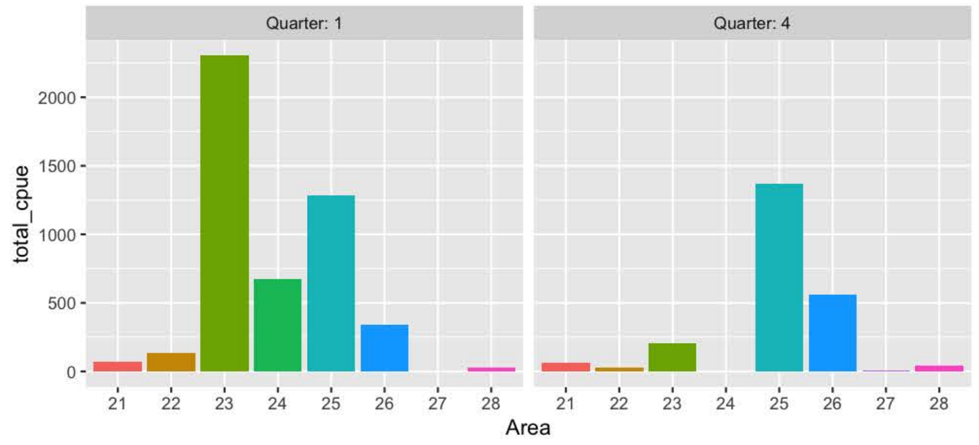
Show all 3 plots together

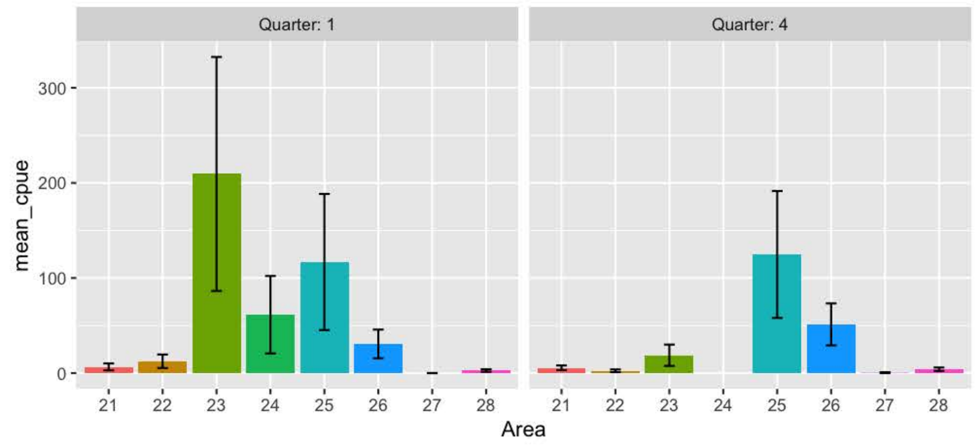
To show all these plots together we can use the `grid.arrange()` function in the **gridExtra** package where we can specify a *layout matrix*. Here, I created a 2x2 matrix where I show the total cpue plot (#1) in the left upper panel, the mean cpue plot (#2) in the lower left panel, and the age-specific plot (#3) in the upper and lower right panels combined. ALl 3 saved ggplot objects need to put together in a list for the 'grobs' argument:

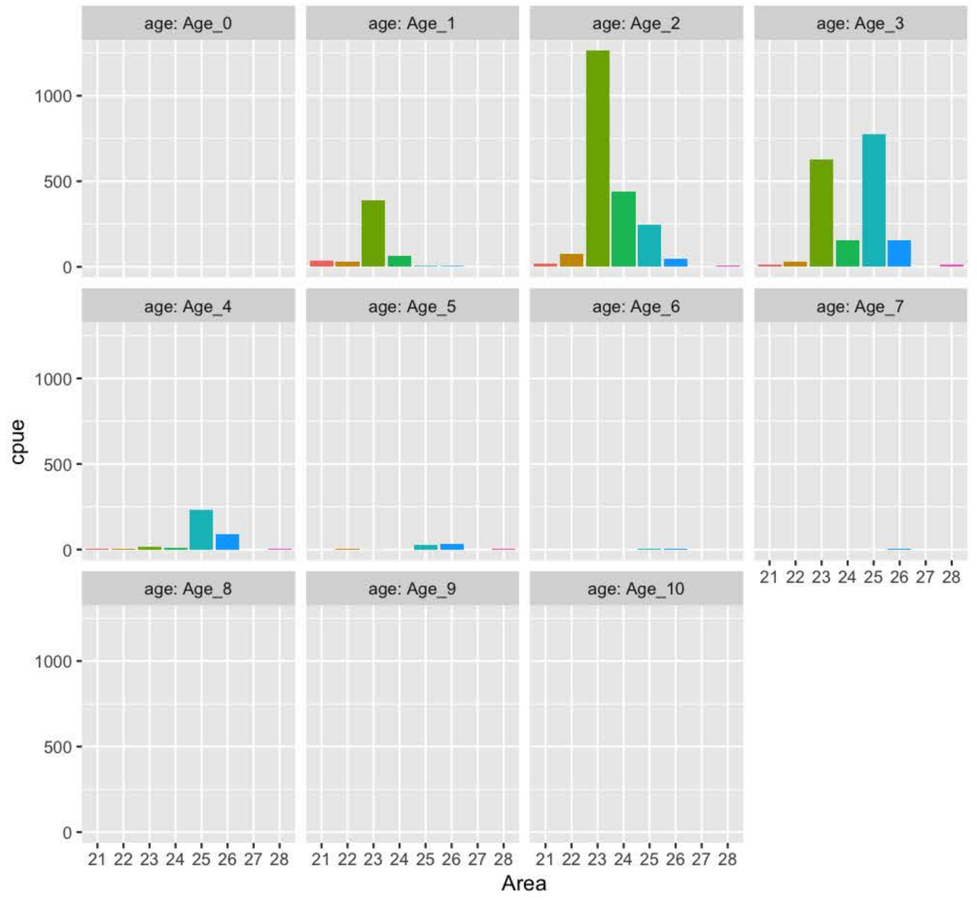
```r
gridExtra::grid.arrange(grobs = list(p_cod_tot, p_cod_mean, p_cod_age_q1),
  layout_matrix = matrix(c(1,3,2,3), byrow =TRUE, nrow = 2))
```

See on the next slide the plots

Gadus morhua results







Press 'p' for a conclusion.

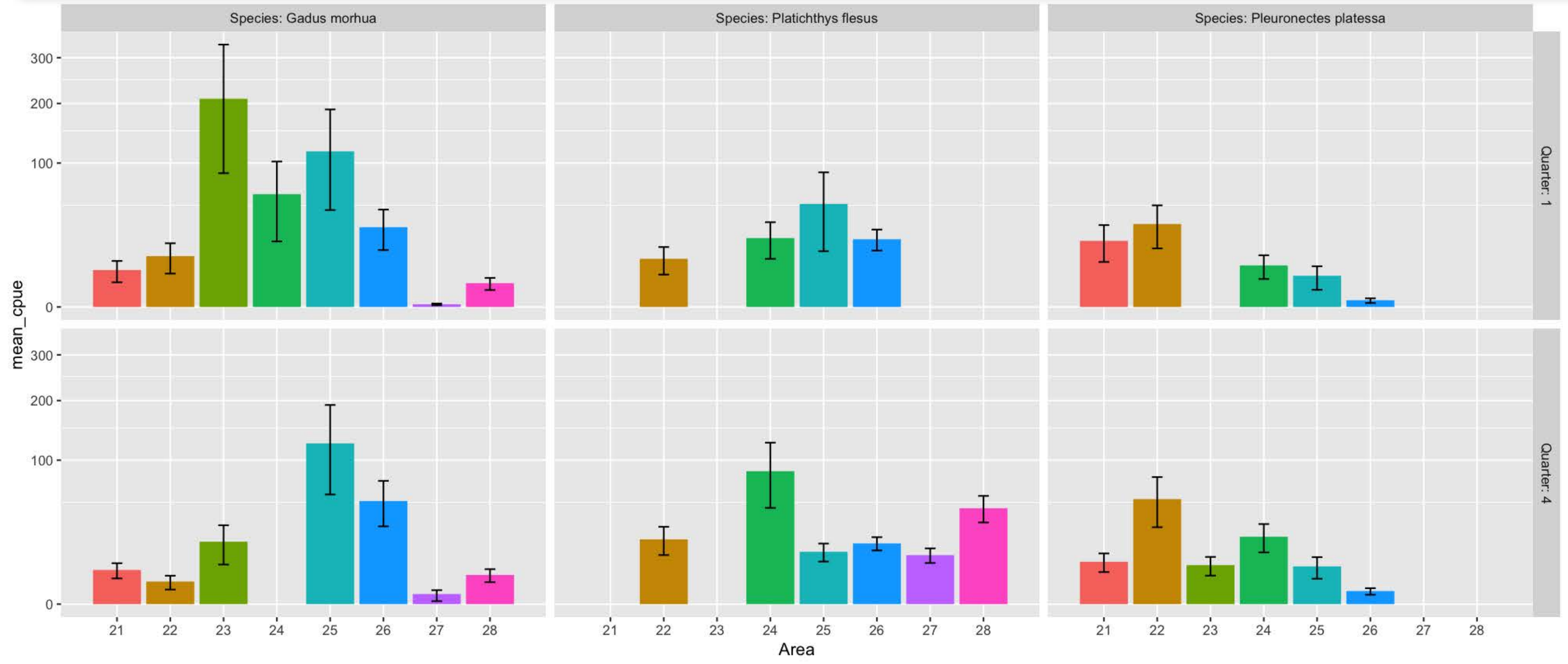
Plot mean CPUE of all species together

We can use almost the same code as for cod with the only difference that we do not filter any species. Instead, we include the species in the faceting:

```r
p_all_mean <- cpue_stats %>%
  ggplot(aes(x = Area, y = mean_cpue, fill = Area)) +
  geom_col() +
  guides(fill = "none") +
  geom_errorbar(aes(
  ymin = mean_cpue - se_cpue,
  ymax = mean_cpue + se_cpue),
  width = .2) +
  facet_grid(Quarter ~ Species, labeller = label_both) +
  coord_trans(y = "sqrt")
```

Plot mean CPUE of all species together

```
p_all_mean
```



Press 'p' for a conclusion.