```r
library(tidyverse)

library(ggExtra)
library(ragg)
library(ggalluvial)
library(treemapify)
library(ggalt)

library(palmerpenguins)
```

Dataset

```r
head(penguins)
## # A tibble: 6 x 8
##   species island bill_length_mm bill_depth_mm flipper_length_…
body_mass_g sex
##
## 1 Adelie  Torge…           39.1          18.7              181
3750 male
## 2 Adelie  Torge…           39.5          17.4              186
3800 fema…
## 3 Adelie  Torge…           40.3          18                195
3250 fema…
## 4 Adelie  Torge…           NA            NA                 NA
NA
## 5 Adelie  Torge…           36.7          19.3              193
3450 fema…
## 6 Adelie  Torge…           39.3          20.6              190
3650 male
## # … with 1 more variable: year
#head(penguins_raw)
```

Colors

- set colorblind-friendly palettes

```r
# The palette with grey:
cbp1 <- c("#999999", "#E69F00", "#56B4E9", "#009E73",
          "#F0E442", "#0072B2", "#D55E00", "#CC79A7")

# The palette with black:
cbp2 <- c("#000000", "#E69F00", "#56B4E9", "#009E73",
          "#F0E442", "#0072B2", "#D55E00", "#CC79A7")

library(plotrix)
sliceValues <- rep(10, 8) # each slice value=10 for proportionate
slices
(
  p <- pie3D(sliceValues,
      explode=0,
      theta = 1.2,
```
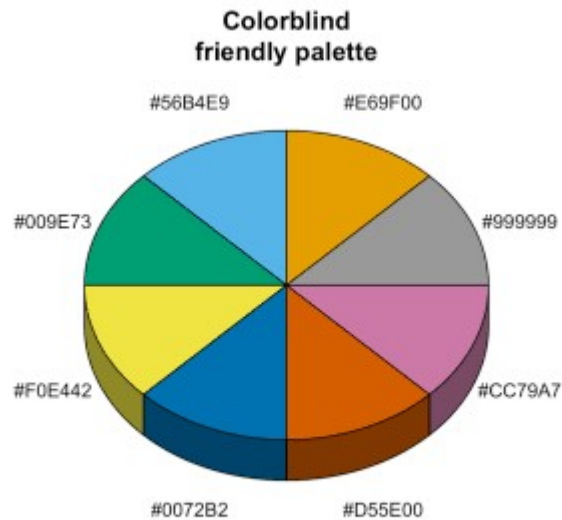
```
        col = cbp1,
        labels = cbp1,
        labelcex = 0.9,
        shade = 0.6,
        main = "Colorblind\nfriendly palette")
)
```



```
## [1] 0.3926991 1.1780972 1.9634954 2.7488936 3.5342917 4.3196899
5.1050881
## [8] 5.8904862
ggplot <- function(...) ggplot2::ggplot(...) +
  scale_color_manual(values = cbp1) +
  scale_fill_manual(values = cbp1) + # note: needs to be overridden
when using continuous color scales
  theme_bw()
```

Main diagram types

https://rstudio.com/wp-content/uploads/2015/03/ggplot2-cheatsheet.pdf
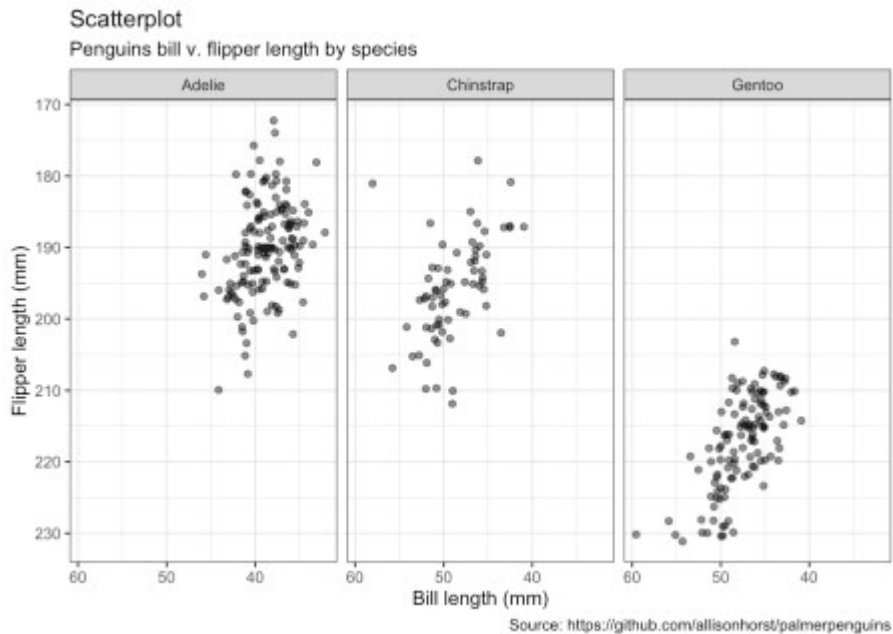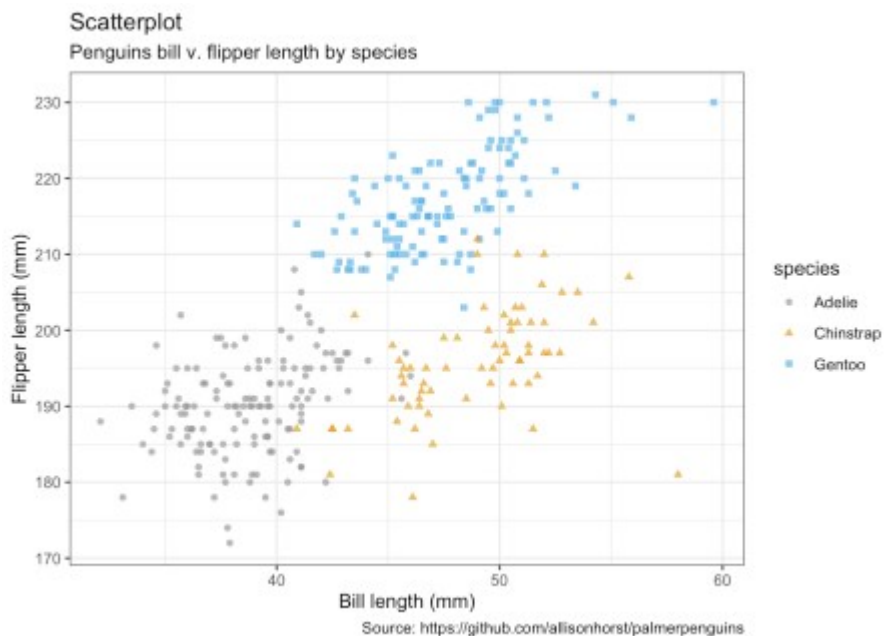
Pointcharts

```
penguins %>%
    remove_missing() %>%
    ggplot(aes(x = bill_length_mm, y = flipper_length_mm)) +
    geom_jitter(alpha = 0.5) +
    facet_wrap(vars(species), ncol = 3) +
    scale_x_reverse() +
    scale_y_reverse() +
    labs(x = "Bill length (mm)",
         y = "Flipper length (mm)",
         size = "body mass (g)",
        title = "Scatterplot",
        subtitle = "Penguins bill v. flipper length by species",
        caption = "Source: https://github.com/allisonhorst/palmerpenguins")
```

Scatterplot
Penguins bill v. flipper length by species

Source: https://github.com/allisonhorst/palmerpenguins

```
penguins %>%
    remove_missing() %>%
    ggplot(aes(x = bill_length_mm, y = flipper_length_mm,
            color = species, shape = species)) +
    geom_point(alpha = 0.7) +
    labs(x = "Bill length (mm)",
        y = "Flipper length (mm)",
        title = "Scatterplot",
        subtitle = "Penguins bill v. flipper length by species",
        caption = "Source: https://github.com/allisonhorst/palmerpenguins")
```


Scatterplot
Penguins bill v. flipper length by species

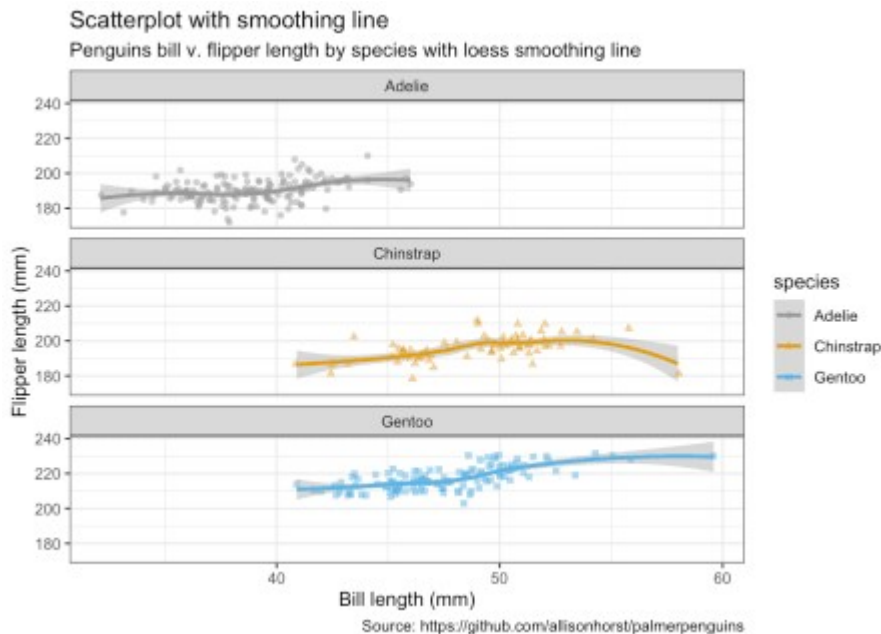Source: https://github.com/allisonhorst/palmerpenguins

- Jitter with smoothing line

```
penguins %>%
    remove_missing() %>%
    ggplot(aes(x = bill_length_mm, y = flipper_length_mm,
            color = species, shape = species)) +
```

```
        geom_jitter(alpha = 0.5) +
        geom_smooth(method = "loess", se = TRUE) +
        facet_wrap(vars(species), nrow = 3) +
        labs(x = "Bill length (mm)",
             y = "Flipper length (mm)",
             title = "Scatterplot with smoothing line",
             subtitle = "Penguins bill v. flipper length by species with
loess smoothing line",
             caption = "Source: https://github.com/allisonhorst/palmerpenguins")
```
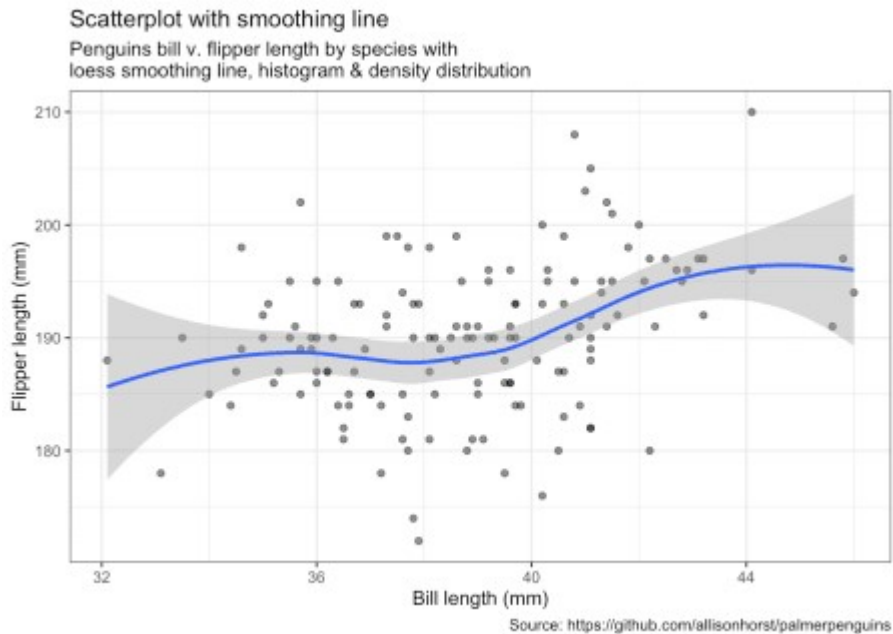

Scatterplot with smoothing line
Penguins bill v. flipper length by species with loess smoothing line

```
penguins %>%
  remove_missing() %>%
  filter(species == "Adelie") %>%
  ggplot(aes(x = bill_length_mm, y = flipper_length_mm)) +
  geom_point(alpha = 0.5) +
  geom_smooth(method = "loess", se = TRUE) +
    labs(x = "Bill length (mm)",
         y = "Flipper length (mm)",
         title = "Scatterplot with smoothing line",
         subtitle = "Penguins bill v. flipper length by species
with\nloess smoothing line, histogram & density distribution",
         caption = "Source: https://github.com/allisonhorst/palmerpenguins")
```

Scatterplot with smoothing line

Penguins bill v. flipper length by species with loess smoothing line, histogram & density distribution

```
#(ggMarginal(p, type = "densigram", fill = "transparent"))
```

Bubblecharts

```
penguins %>%
    remove_missing() %>%
    ggplot(aes(x = bill_length_mm, y = flipper_length_mm,
            color = species, shape = species, size = body_mass_g)) +
    geom_point(alpha = 0.5) +
    labs(x = "Bill length (mm)",
        y = "Flipper length (mm)",
       title = "Bubble plot",
       size = "body mass (g)",
       subtitle = "Penguins bill v. flipper length by species;\nsize
indicates body mass in grams",
       caption = "Source: https://github.com/allisonhorst/palmerpenguins")
```


Bubble plot

Penguins bill v. flipper length by species; size indicates body mass in grams
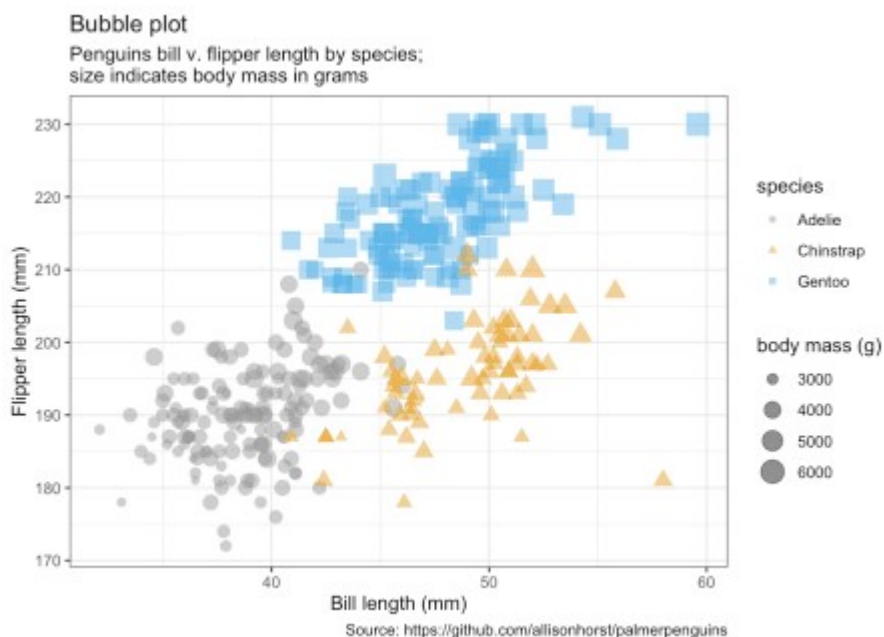
Linecharts

```
penguins %>%
    remove_missing() %>%
    filter(species == "Adelie") %>%
    ggplot(aes(x = bill_length_mm, y = flipper_length_mm,
               color = sex)) +
    geom_line() +
    geom_point() +
    labs(x = "Bill length (mm)",
         y = "Flipper length (mm)",
        title = "Line plot",
        subtitle = "Penguins bill v. flipper length by species and
sex",
        caption = "Source: https://github.com/allisonhorst/palmerpenguins")
```


Line plot
Penguins bill v. flipper length by species and sex
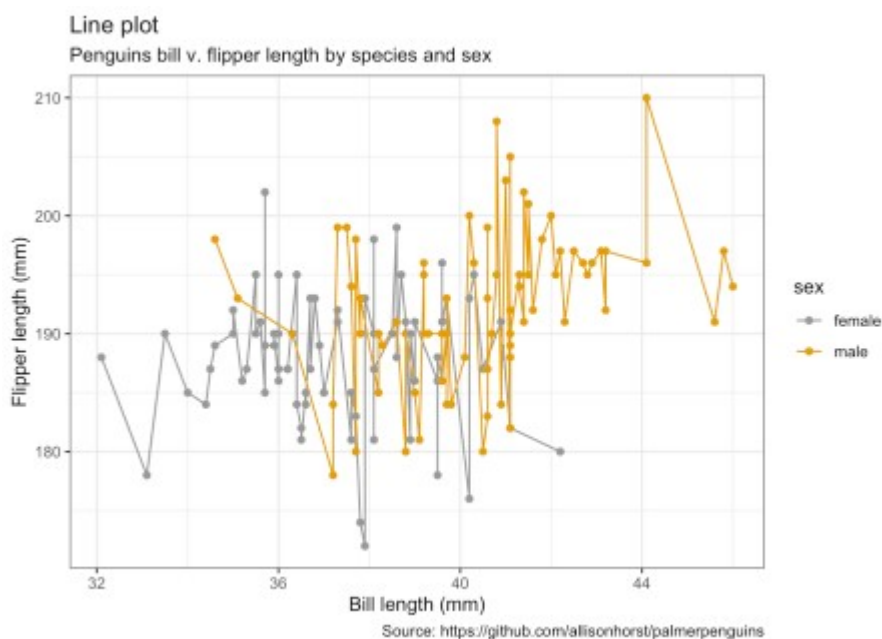
Correlation plots / heatmaps

```
mat <- penguins %>%
  remove_missing() %>%
  select(bill_depth_mm, bill_length_mm, body_mass_g, flipper_length_mm)

cormat <- round(cor(mat), 2)
cormat[upper.tri(cormat)] <- NA

cormat <- cormat %>%
  as_data_frame() %>%
  mutate(x = colnames(mat)) %>%
  gather(key = "y", value = "value", bill_depth_mm:flipper_length_mm)

cormat %>%
    remove_missing() %>%
    arrange(x, y) %>%
    ggplot(aes(x = x, y = y, fill = value)) +
    geom_tile() +
```
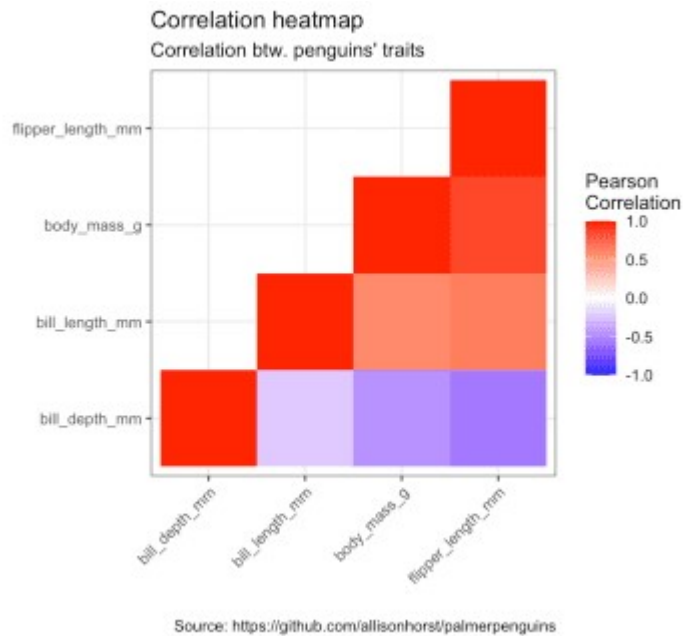
```
      scale_fill_gradient2(low = "blue", high = "red", mid = "white",
       midpoint = 0, limit = c(-1,1), space = "Lab",
       name = "Pearson\nCorrelation") +
      theme(axis.text.x = element_text(angle = 45, vjust = 1, hjust = 1))
+
      coord_fixed() +
        labs(x = "",
             y = "",
            title = "Correlation heatmap",
            subtitle = "Correlation btw. penguins' traits",
            caption = "Source: https://github.com/allisonhorst/palmerpenguins")
```


Correlation heatmap
Correlation btw. penguins' traits
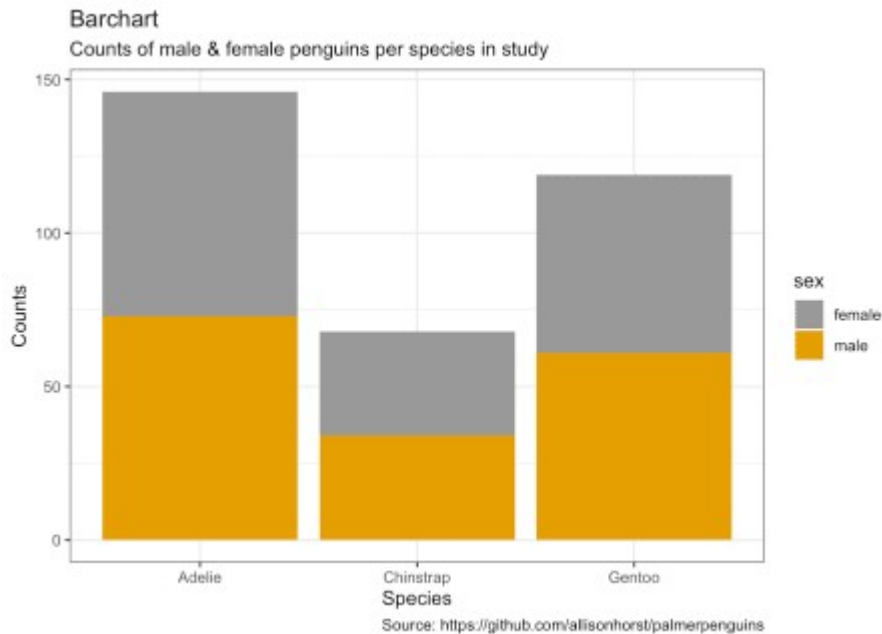
Barcharts

- per default: counts
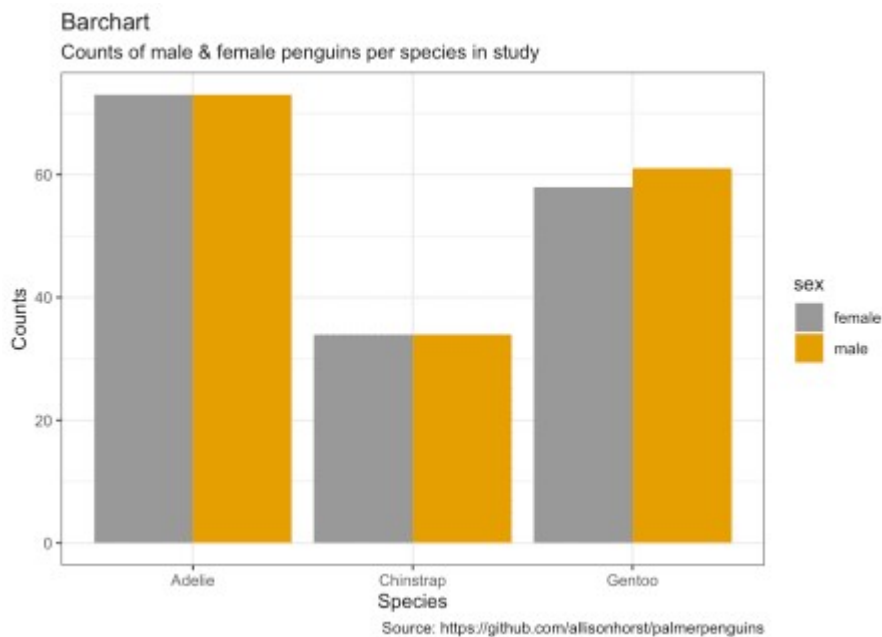
```
penguins %>%
    remove_missing() %>%
    ggplot(aes(x = species,
               fill = sex)) +
    geom_bar() +
      labs(x = "Species",
           y = "Counts",
          title = "Barchart",
          subtitle = "Counts of male & female penguins per species in
study",
          caption = "Source: https://github.com/allisonhorst/palmerpenguins")
```

Barchart
Counts of male & female penguins per species in study

```
penguins %>%
    remove_missing() %>%
    ggplot(aes(x = species,
               fill = sex)) +
    geom_bar(position = 'dodge') +
      labs(x = "Species",
           y = "Counts",
         title = "Barchart",
         subtitle = "Counts of male & female penguins per species in
study",
         caption = "Source: https://github.com/allisonhorst/palmerpenguins")
```


Barchart
Counts of male & female penguins per species in study

- alternative: set y-values

```
penguins %>%
    remove_missing() %>%
    group_by(species, sex) %>%
```

```
       summarise(mean_bmg = mean(body_mass_g),
                 sd_bmg = sd(body_mass_g)) %>%
    ggplot(aes(x = species, y = mean_bmg,
               fill = sex)) +
    geom_bar(stat = "identity", position = "dodge") +
    geom_errorbar(aes(ymin = mean_bmg - sd_bmg,
                      ymax = mean_bmg + sd_bmg),
                  width = 0.2,
                  position = position_dodge(0.9)) +
      labs(x = "Species",
           y = "Mean body mass (in g)",
           title = "Barchart",
           subtitle = "Mean body mass of male & female penguins per
species\nwith standard deviation",
           caption = "Source: https://github.com/allisonhorst/palmerpenguins")
```
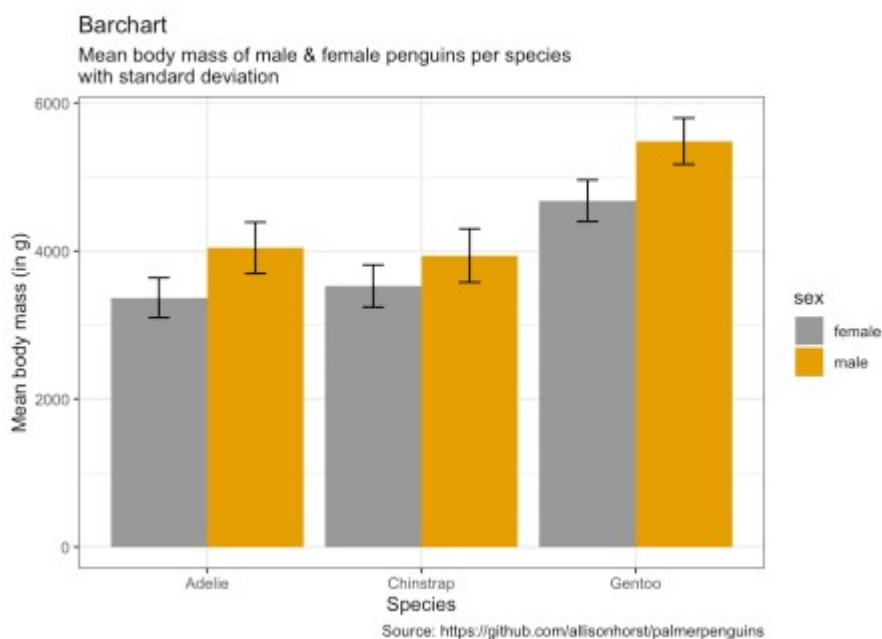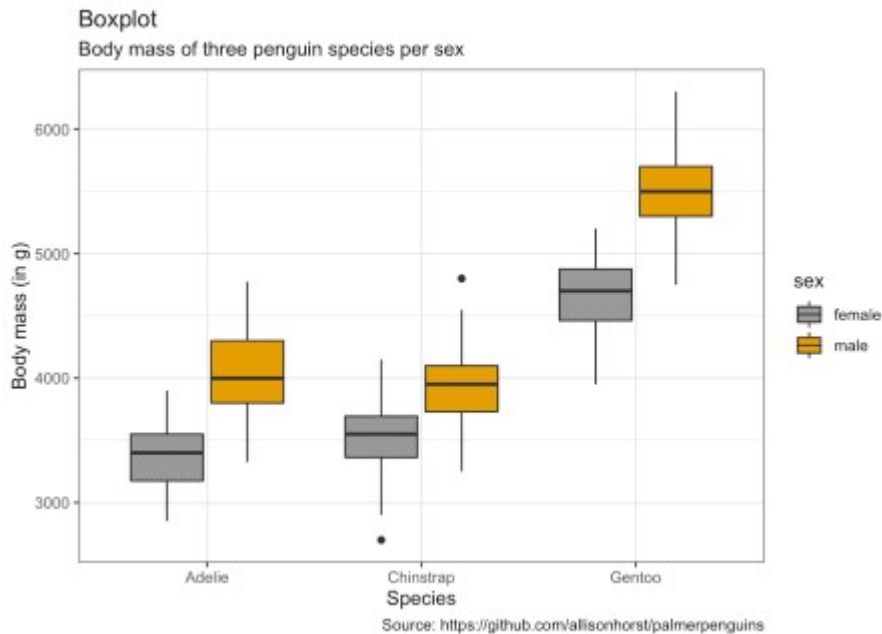

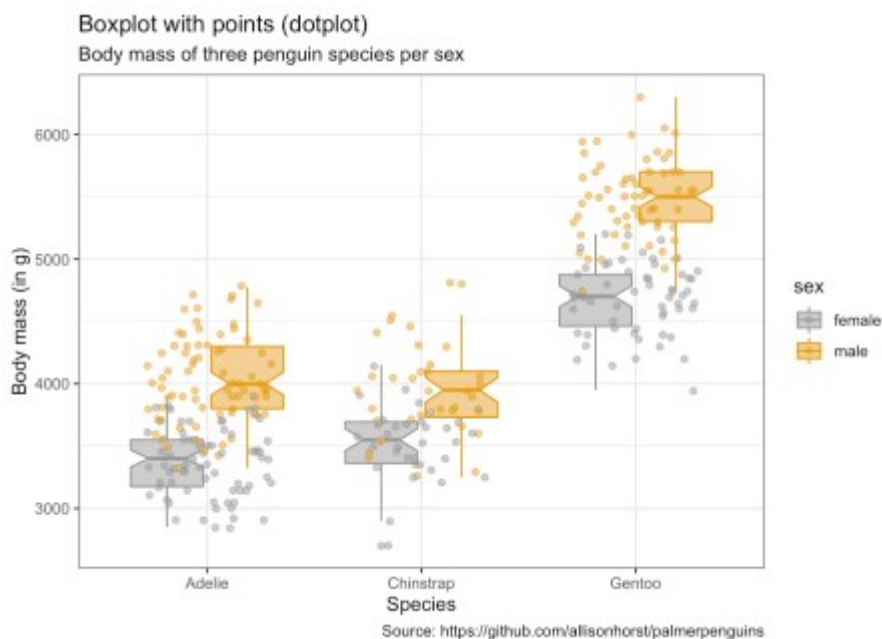## Boxplots

```
penguins %>%
    remove_missing() %>%
    ggplot(aes(x = species, y = body_mass_g,
               fill = sex)) +
    geom_boxplot() +
      labs(x = "Species",
           y = "Body mass (in g)",
           title = "Boxplot",
           subtitle = "Body mass of three penguin species per sex",
           caption = "Source: https://github.com/allisonhorst/palmerpenguins")
```

Boxplot
Body mass of three penguin species per sex

- with points

```
penguins %>%
    remove_missing() %>%
    ggplot(aes(x = species, y = body_mass_g,
               fill = sex, color = sex)) +
    geom_boxplot(alpha = 0.5, notch = TRUE) +
    geom_jitter(alpha = 0.5, position=position_jitter(0.3)) +
      labs(x = "Species",
            y = "Body mass (in g)",
          title = "Boxplot with points (dotplot)",
          subtitle = "Body mass of three penguin species per sex",
          caption = "Source: https://github.com/allisonhorst/palmerpenguins")
```


Boxplot with points (dotplot)
Body mass of three penguin species per sex

Violinplots

```
penguins %>%
    remove_missing() %>%
```

```
ggplot(aes(x = species, y = body_mass_g,
           fill = sex)) +
geom_violin(scale = "area") +
  labs(x = "Species",
       y = "Body mass (in g)",
       title = "Violinplot",
       subtitle = "Body mass of three penguin species per sex",
       caption = "Source: https://github.com/allisonhorst/palmerpenguins")
```
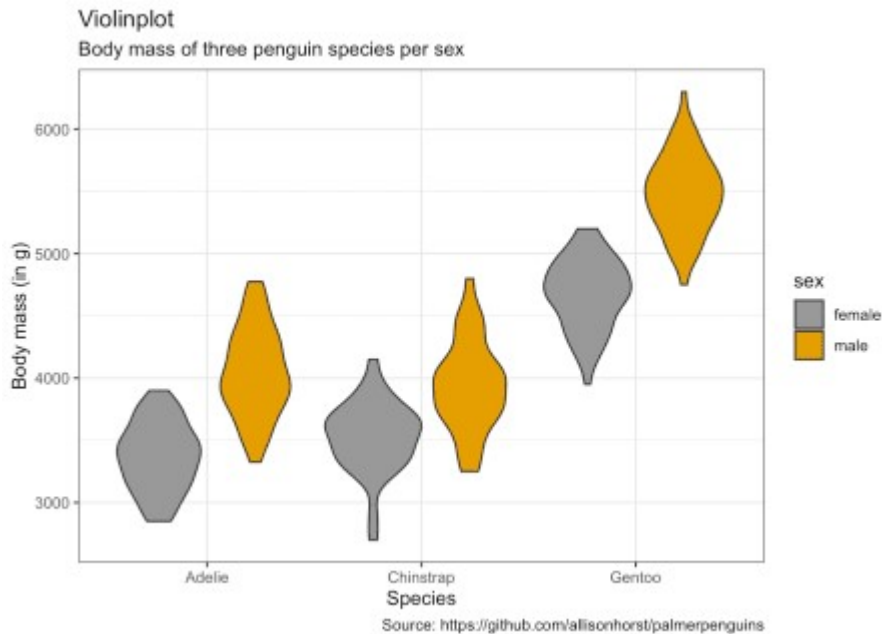

Violinplot
Body mass of three penguin species per sex

- with dots (sina-plots)

```
penguins %>%
    remove_missing() %>%
    ggplot(aes(x = species, y = body_mass_g,
               fill = sex, color = sex)) +
    geom_dotplot(method = "dotdensity", alpha = 0.7,
                 binaxis = 'y', stackdir = 'center',
                 position = position_dodge(1)) +
      labs(x = "Species",
           y = "Body mass (in g)",
           title = "Violinplot with points (dotplot)",
           subtitle = "Body mass of three penguin species per sex",
           caption = "Source: https://github.com/allisonhorst/palmerpenguins")
```

Violinplot with points (dotplot)
Body mass of three penguin species per sex

Source: https://github.com/allisonhorst/palmerpenguins
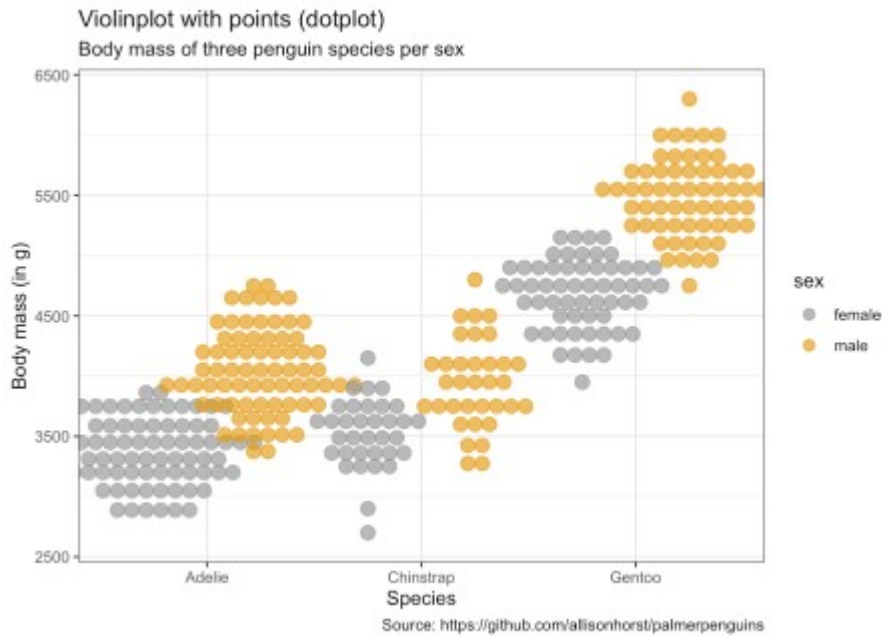
Piecharts

```
penguins %>%
    remove_missing() %>%
    group_by(species, sex) %>%
    summarise(n = n()) %>%
    mutate(freq = n / sum(n),
           percentage = freq * 100) %>%
    ggplot(aes(x = "", y = percentage,
               fill = sex)) +
    facet_wrap(vars(species), nrow = 1) +
    geom_bar(stat = "identity", alpha = 0.8) +
    coord_polar("y", start = 0) +
      labs(x = "",
           y = "Percentage",
           title = "Piechart",
           subtitle = "Percentage of male v. female penguins per species
in study",
           caption = "Source: https://github.com/allisonhorst/palmerpenguins")
```

Piechart

Percentage of male v. female penguins per species in study

Source: https://github.com/allisonhorst/palmerpenguins
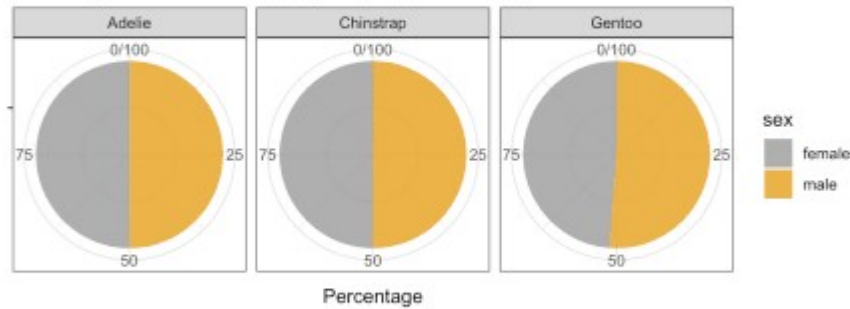
Alluvial charts

```
as.data.frame(UCBAdmissions) %>%
    ggplot(aes(y = Freq, axis1 = Gender, axis2 = Dept)) +
    geom_alluvium(aes(fill = Admit), width = 1/12) +
    geom_stratum(width = 1/12, fill = "black", color = "grey") +
    geom_label(stat = "stratum", aes(label = after_stat(stratum))) +
    scale_x_discrete(limits = c("Gender", "Dept"), expand = c(.05,
.05)) +
      labs(x = "",
           y = "Frequency",
          title = "Alluvial chart",
          subtitle = "UC Berkeley admissions and rejections, by sex and
department",
          caption = "Source: Bickel et al. (1975)\nSex bias in graduate
admissions: Data from Berkeley. Science, 187, 398-403.")
```


Alluvial chart

UC Berkeley admissions and rejections, by sex and department
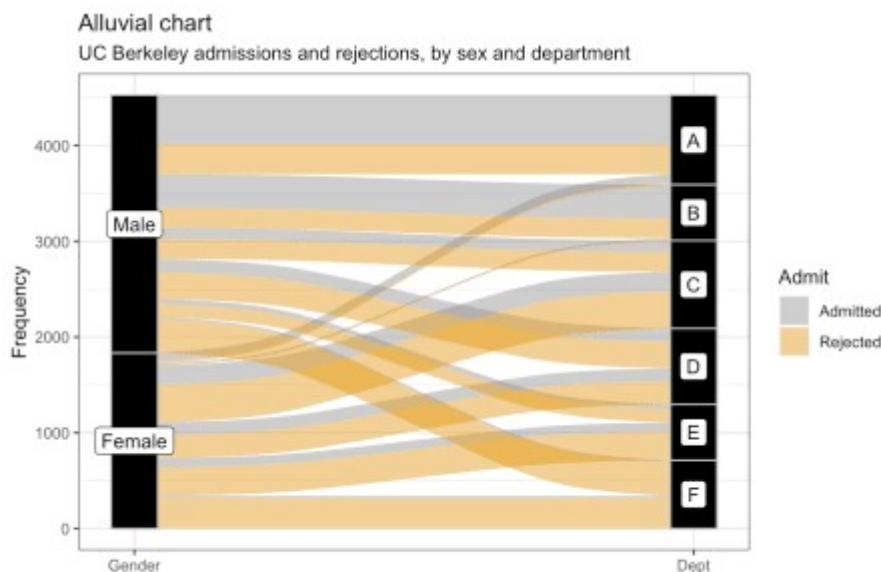
Source: Bickel et al. (1975)
Sex bias in graduate admissions: Data from Berkeley. Science, 187, 398–403.

Treemaps

```
as.data.frame(UCBAdmissions) %>%
    group_by(Admit, Gender) %>%
    summarise(sum_freq = sum(Freq)) %>%
    ggplot(aes(area = sum_freq, fill = sum_freq, label = Gender,
               subgroup = Admit)) +
    geom_treemap() +
    geom_treemap_subgroup_border() +
    geom_treemap_subgroup_text(place = "centre", grow = T, alpha = 0.5,
colour =
                                "black", fontface = "italic", min.size =
0) +
    geom_treemap_text(colour = "white", place = "centre", reflow = T) +
    scale_fill_gradient2(low = "#999999", high = "#E69F00", mid =
"white", midpoint = 1000, space = "Lab",
      name = "Sum of\nfrequencies") +
      labs(x = "",
           y = "",
          title = "Treemap",
          subtitle = "UC Berkeley admissions and rejections by sex",
          caption = "Source: Bickel et al. (1975)\nSex bias in graduate
admissions: Data from Berkeley. Science, 187, 398-403.")
```


Treemap
UC Berkeley admissions and rejections by sex

Source: Bickel et al. (1975)
Sex bias in graduate admissions: Data from Berkeley. Science, 187, 398–403.
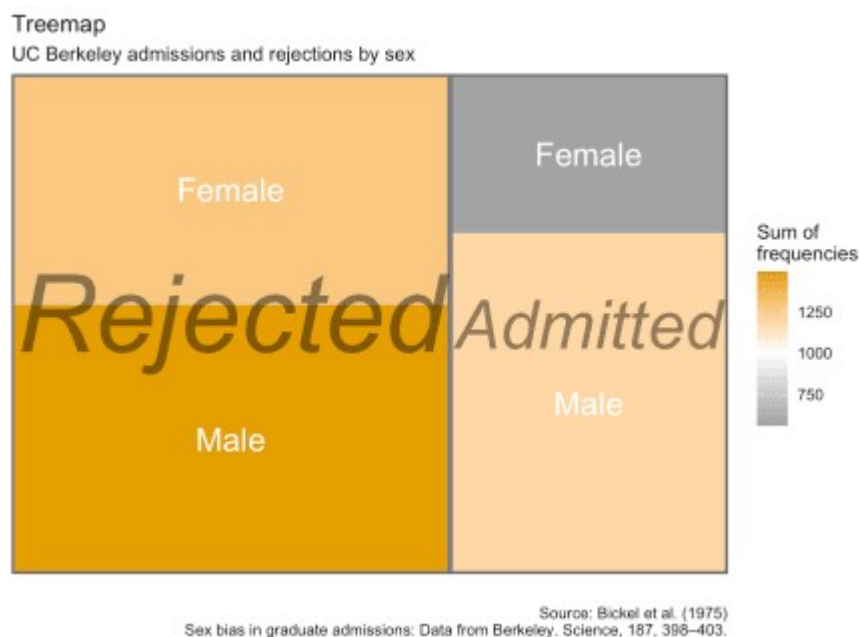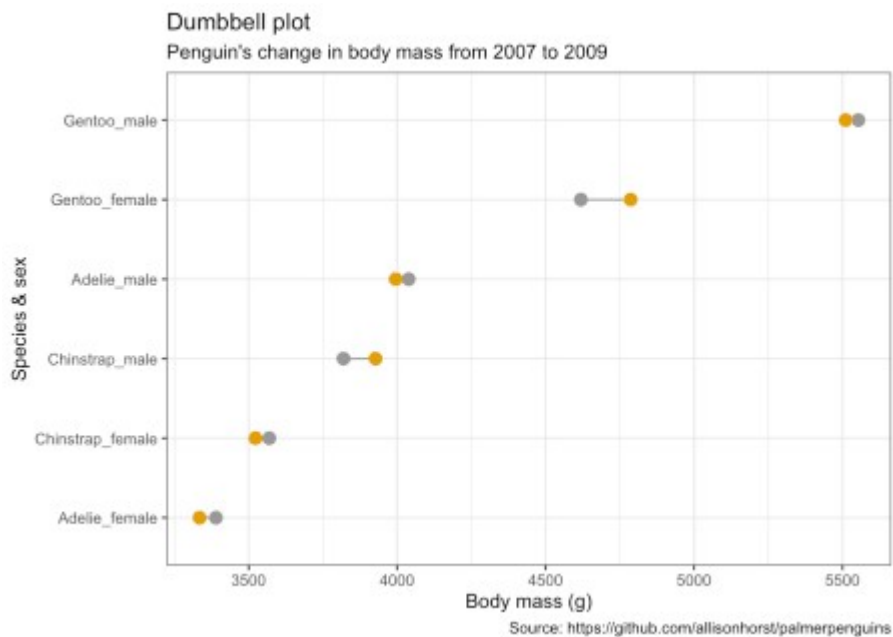
Dumbbell plots

```
penguins %>%
    remove_missing() %>%
    group_by(year, species, sex) %>%
    summarise(mean_bmg = mean(body_mass_g)) %>%
    mutate(species_sex = paste(species, sex, sep = "_"),
          year = paste0("year_", year)) %>%
    spread(year, mean_bmg) %>%
    ggplot(aes(x = year_2007, xend = year_2009,
               y = reorder(species_sex, year_2009))) +
```

```
        geom_dumbbell(color = "#999999",
                      size_x = 3,
                      size_xend = 3,
                      #Note: there is no US:'color' for UK:'colour'
                      # in geom_dumbbel unlike standard geoms in
ggplot()
                      colour_x = "#999999",
                      colour_xend = "#E69F00") +
        labs(x = "Body mass (g)",
             y = "Species & sex",
           title = "Dumbbell plot",
           subtitle = "Penguin's change in body mass from 2007 to 2009",
           caption = "Source: https://github.com/allisonhorst/palmerpenguins")
```


Dumbbell plot
Penguin's change in body mass from 2007 to 2009

Source: https://github.com/allisonhorst/palmerpenguins

Slope charts

```
penguins %>%
    remove_missing() %>%
    group_by(year, species, sex) %>%
    summarise(mean_bmg = mean(body_mass_g)) %>%
    ggplot(aes(x = year, y = mean_bmg, group = sex,
               color = sex)) +
    facet_wrap(vars(species), nrow = 3) +
    geom_line(alpha = 0.6, size = 2) +
    geom_point(alpha = 1, size = 3) +
    scale_x_continuous(breaks=c(2007, 2008, 2009)) +
      labs(x = "Year",
           y = "Body mass (g)",
           color = "Sex",
         title = "Slope chart",
         subtitle = "Penguin's change in body mass from 2007 to 2009",
         caption = "Source: https://github.com/allisonhorst/palmerpenguins")
```

Slope chart
Penguin's change in body mass from 2007 to 2009

Stacked area charts
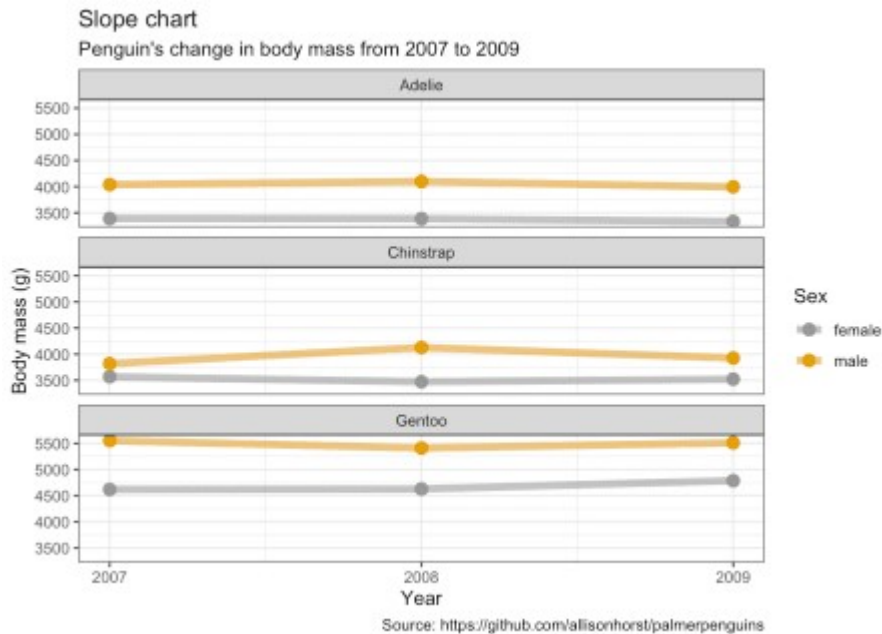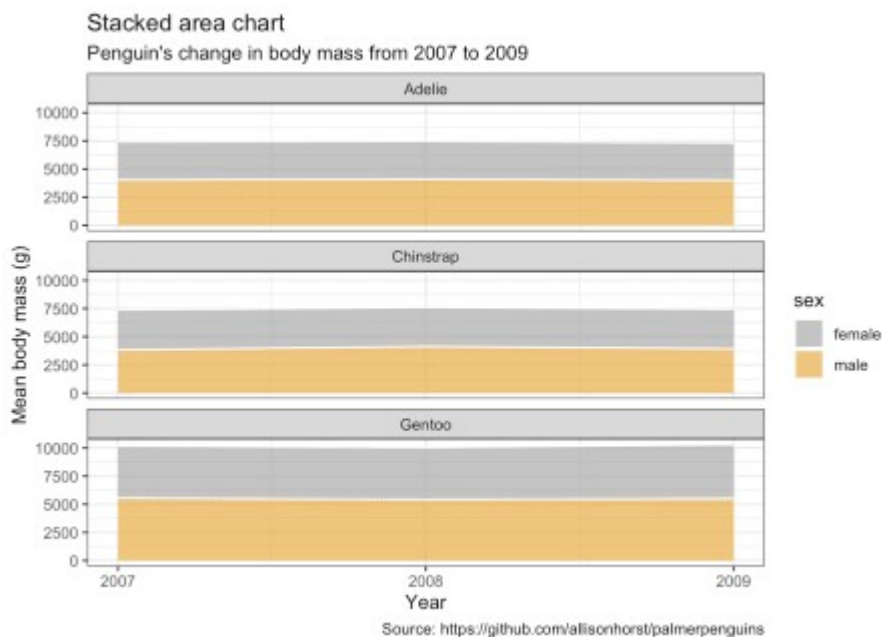
```
penguins %>%
    remove_missing() %>%
    group_by(year, species, sex) %>%
    summarise(mean_bmg = mean(body_mass_g)) %>%
    ggplot(aes(x = year, y = mean_bmg, fill = sex)) +
    facet_wrap(vars(species), nrow = 3) +
    geom_area(alpha = 0.6, size=.5, color = "white") +
    scale_x_continuous(breaks=c(2007, 2008, 2009)) +
      labs(x = "Year",
           y = "Mean body mass (g)",
           color = "Sex",
          title = "Stacked area chart",
          subtitle = "Penguin's change in body mass from 2007 to 2009",
          caption = "Source: https://github.com/allisonhorst/palmerpenguins")
```

Lolliplot chart

```
penguins %>%
    remove_missing() %>%
    group_by(year, species, sex) %>%
    summarise(mean_bmg = mean(body_mass_g)) %>%
    mutate(species_sex = paste(species, sex, sep = "_"),
        year = paste0("year_", year)) %>%
    spread(year, mean_bmg) %>%
    ggplot() +
    geom_segment(aes(x = reorder(species_sex, -year_2009), xend =
reorder(species_sex, -year_2009),
                y = 0, yend = year_2009),
            color = "#999999", size = 1) +
    geom_point(aes(x = reorder(species_sex, -year_2009), y =
year_2009),
            size = 4, color = "#E69F00") +
    coord_flip() +
        labs(x = "Species & sex",
            y = "Body mass (g)",
        title = "Lollipop chart",
        subtitle = "Penguin's body mass in 2009",
        caption = "Source: https://github.com/allisonhorst/palmerpenguins")
```
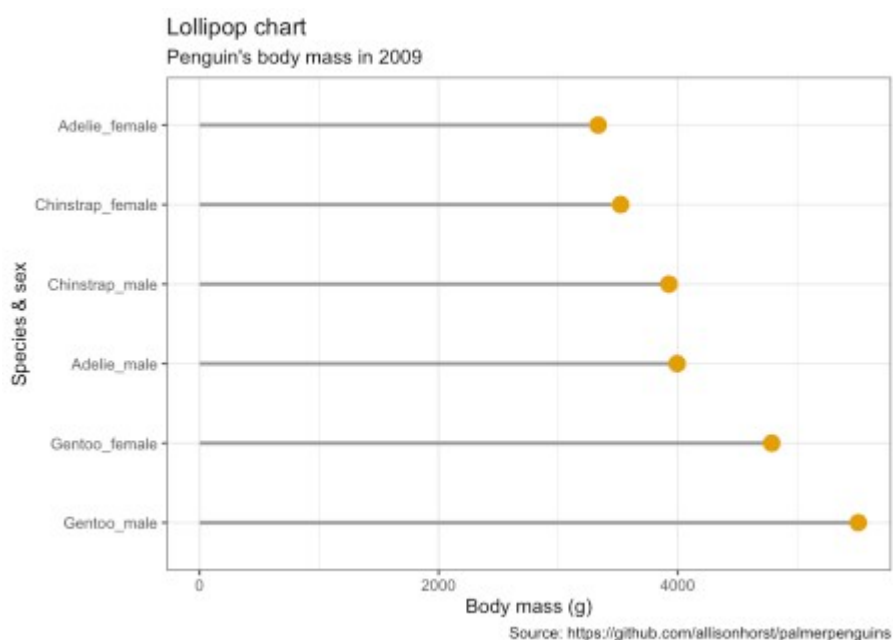

Dendrograms

```
library(ggdendro)
library(dendextend)
penguins_hist <- penguins %>%
  filter(sex == "male") %>%
  select(species, bill_length_mm, bill_depth_mm, flipper_length_mm,
body_mass_g) %>%
  group_by(species) %>%
  sample_n(10) %>%
  as.data.frame()
```

```r
rownames(penguins_hist) <- paste(penguins_hist$species,
seq_len(nrow(penguins_hist)), sep = "_")

penguins_hist <- penguins_hist %>%
  select(-species) %>%
  remove_missing()
#hc <- hclust(dist(penguins_hist, method = "euclidean"), method =
"ward.D2")
#ggdendrogram(hc)

# Create a dendrogram and plot it
penguins_hist %>%
  scale %>%
  dist(method = "euclidean") %>%
  hclust(method = "ward.D2") %>%
  as.dendrogram
## 'dendrogram' with 2 branches and 30 members total, at height
11.94105
```

Waterfall charts

```r
library(waterfall)
jaquith %>%
    arrange(score) %>%
    add_row(factor = "Total", score = sum(jaquith$score)) %>%
    mutate(factor = factor(factor, levels = factor),
                          id = seq_along(score)) %>%
    mutate(end = cumsum(score),
           start = c(0, end[-length(end)]),
           start = c(start[-length(start)], 0),
           end = c(end[-length(end)], score[length(score)]),
           gr_col = ifelse(factor == "Total", "Total", "Part")) %>%
    ggplot(aes(x = factor, fill = gr_col)) +
      geom_rect(aes(x = factor,
                    xmin = id - 0.45, xmax = id + 0.45,
                    ymin = end, ymax = start)) +
      theme(axis.text.x = element_text(angle = 60, vjust = 1, hjust =
1),
            legend.position = "none") +
        labs(x = "",
             y = "Amount",
             title = "Waterfall chart",
             subtitle = "Sample business-adjusted risk from Security
Metrics",
             caption = "Andrew Jaquith, Security Metrics: Replacing
Fear, Uncertainty, and Doubt\n(Boston: Addison-Wesley Professional,
2007), 170-171.")
```

Waterfall chart
Sample business-adjusted risk from Security Metrics
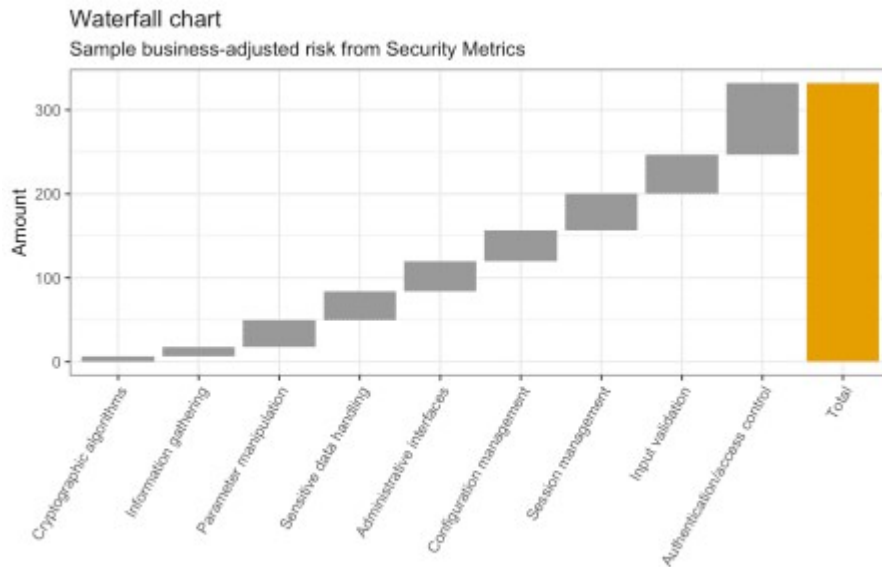
Andrew Jaquith, Security Metrics: Replacing Fear, Uncertainty, and Doubt
(Boston: Addison-Wesley Professional, 2007), 170-171.

Biplots

```r
library(ggfortify)
penguins_prep <- penguins %>%
  remove_missing() %>%
  select(bill_length_mm:body_mass_g)

penguins_pca <- penguins_prep %>%
  prcomp(scale. = TRUE)
penguins_km <- penguins_prep %>%
  kmeans(3)
autoplot(penguins_pca,
             data = penguins %>% remove_missing(),
             colour = 'species',
             shape = 'species',
             loadings = TRUE,
             loadings.colour = 'blue',
             loadings.label = TRUE,
             loadings.label.size = 3) +
    scale_color_manual(values = cbp1) +
  scale_fill_manual(values = cbp1) +
  theme_bw() +
          labs(
          title = "Biplot PCA",
          caption = "Source: https://github.com/allisonhorst/palmerpenguins")
```
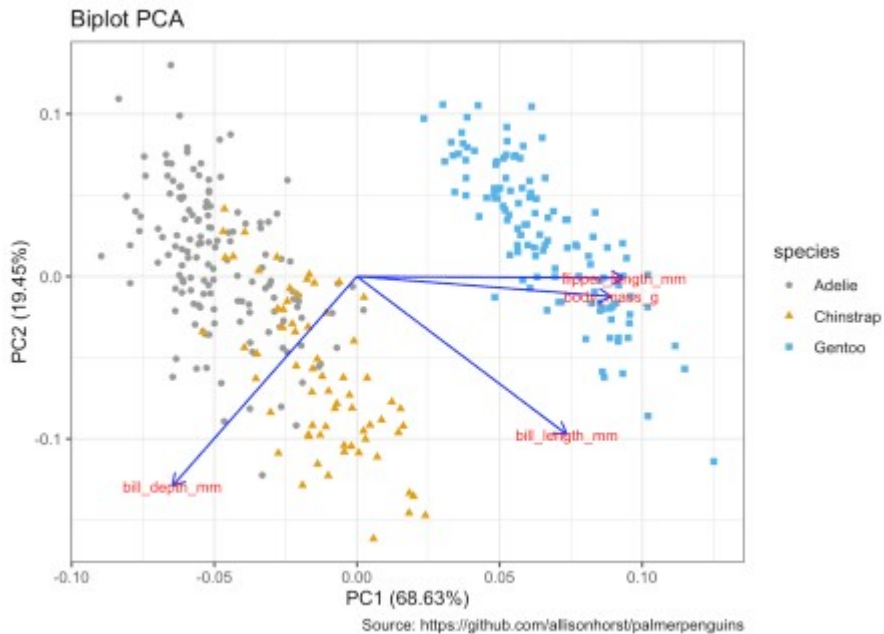
Biplot PCA

```
autoplot(penguins_km,
                data = penguins %>% remove_missing(),
                colour = 'species',
                shape = 'species',
                frame = TRUE, frame.type = 'norm') +
    scale_color_manual(values = cbp1) +
  scale_fill_manual(values = cbp1) +
  theme_bw() +
        labs(
        title = "Biplot k-Means clustering",
        caption = "Source: https://github.com/allisonhorst/palmerpenguins")
```


Biplot k-Means clustering
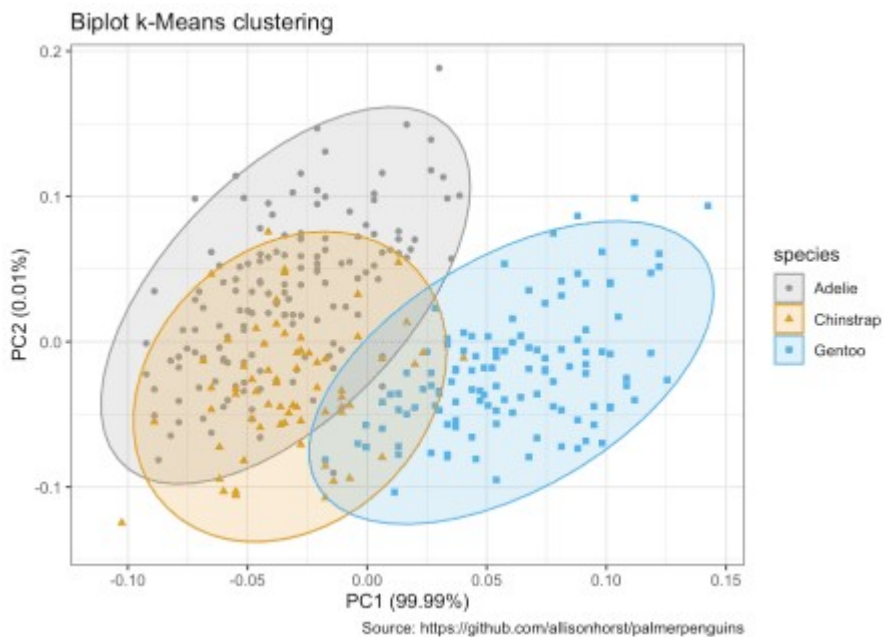
Radar charts, aka star chart, aka spider plot

https://www.data-to-viz.com/caveat/spider.html

```
library(ggiraphExtra)
penguins %>%
```

```
    remove_missing() %>%
    select(-island, -year) %>%
    ggRadar(aes(x = c(bill_length_mm, bill_depth_mm, flipper_length_mm,
body_mass_g),
                group = species,
                colour = sex, facet = sex),
            rescale = TRUE,
            size = 1, interactive = FALSE,
            use.label = TRUE) +
    scale_color_manual(values = cbp1) +
    scale_fill_manual(values = cbp1) +
    theme_bw() +
    scale_y_discrete(breaks = NULL) + # don't show ticks
      labs(
          title = "Radar/spider/star chart",
          subtitle = "Body mass of male & female penguins per species",
          caption = "Source: https://github.com/allisonhorst/palmerpenguins")
```


Radar/spider/star chart
Body mass of male & female penguins per species

Source: https://github.com/allisonhorst/palmerpenguins
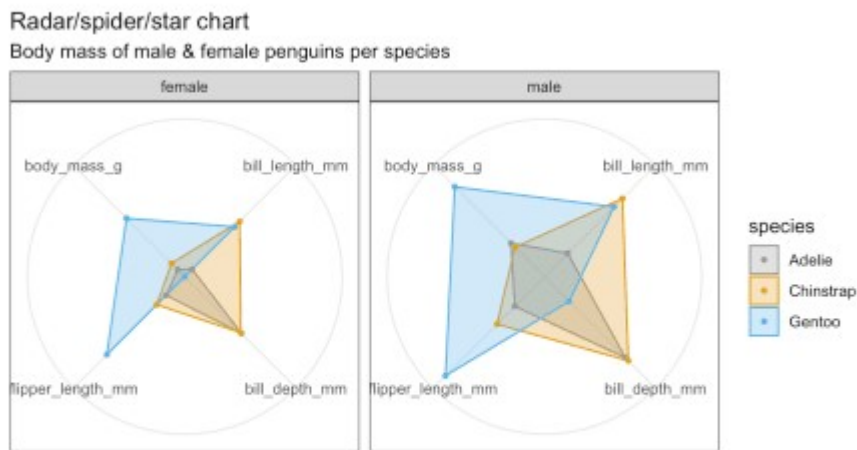
```
devtools::session_info()
## — Session info —————————————————————————————————
——————————————————————————————
##  setting  value
##  version  R version 4.0.2 (2020-06-22)
##  os       macOS Catalina 10.15.7
##  system   x86_64, darwin17.0
##  ui       X11
##  language (EN)
##  collate  en_US.UTF-8
##  ctype    en_US.UTF-8
##  tz       Europe/Berlin
##  date     2020-10-20
##
## — Packages ——————————————————————————————
———————————————————————————
```

```
##   package       * version date       lib source
##   ash             1.0-15  2015-09-01 [1] CRAN (R 4.0.2)
##   assertthat      0.2.1   2019-03-21 [1] CRAN (R 4.0.0)
##   backports       1.1.10  2020-09-15 [1] CRAN (R 4.0.2)
##   blob            1.2.1   2020-01-20 [1] CRAN (R 4.0.2)
##   blogdown        0.20.1  2020-09-09 [1] Github
(rstudio/blogdown@d96fe78)
##   bookdown        0.20    2020-06-23 [1] CRAN (R 4.0.2)
##   broom           0.7.0   2020-07-09 [1] CRAN (R 4.0.2)
##   callr           3.4.4   2020-09-07 [1] CRAN (R 4.0.2)
##   cellranger      1.1.0   2016-07-27 [1] CRAN (R 4.0.0)
##   cli             2.0.2   2020-02-28 [1] CRAN (R 4.0.0)
##   colorspace      1.4-1   2019-03-18 [1] CRAN (R 4.0.0)
##   crayon          1.3.4   2017-09-16 [1] CRAN (R 4.0.0)
##   DBI             1.1.0   2019-12-15 [1] CRAN (R 4.0.0)
##   dbplyr          1.4.4   2020-05-27 [1] CRAN (R 4.0.2)
##   dendextend    * 1.14.0  2020-08-26 [1] CRAN (R 4.0.2)
##   desc            1.2.0   2018-05-01 [1] CRAN (R 4.0.0)
##   devtools        2.3.2   2020-09-18 [1] CRAN (R 4.0.2)
##   digest          0.6.25  2020-02-23 [1] CRAN (R 4.0.0)
##   dplyr         * 1.0.2   2020-08-18 [1] CRAN (R 4.0.2)
##   ellipsis        0.3.1   2020-05-15 [1] CRAN (R 4.0.0)
##   evaluate        0.14    2019-05-28 [1] CRAN (R 4.0.1)
##   extrafont       0.17    2014-12-08 [1] CRAN (R 4.0.2)
##   extrafontdb     1.0     2012-06-11 [1] CRAN (R 4.0.2)
##   fansi           0.4.1   2020-01-08 [1] CRAN (R 4.0.0)
##   farver          2.0.3   2020-01-16 [1] CRAN (R 4.0.0)
##   fastmap         1.0.1   2019-10-08 [1] CRAN (R 4.0.0)
##   forcats       * 0.5.0   2020-03-01 [1] CRAN (R 4.0.0)
##   fs              1.5.0   2020-07-31 [1] CRAN (R 4.0.2)
##   gdtools         0.2.2   2020-04-03 [1] CRAN (R 4.0.2)
##   generics        0.0.2   2018-11-29 [1] CRAN (R 4.0.0)
##   ggalluvial    * 0.12.2  2020-08-30 [1] CRAN (R 4.0.2)
##   ggalt         * 0.4.0   2017-02-15 [1] CRAN (R 4.0.2)
##   ggdendro      * 0.1.22  2020-09-13 [1] CRAN (R 4.0.2)
##   ggExtra       * 0.9     2019-08-27 [1] CRAN (R 4.0.2)
##   ggfittext       0.9.0   2020-06-14 [1] CRAN (R 4.0.2)
##   ggfortify     * 0.4.10  2020-04-26 [1] CRAN (R 4.0.2)
##   ggiraph         0.7.8   2020-07-01 [1] CRAN (R 4.0.2)
##   ggiraphExtra  * 0.2.9   2018-07-22 [1] CRAN (R 4.0.2)
##   ggplot2       * 3.3.2   2020-06-19 [1] CRAN (R 4.0.2)
##   glue            1.4.2   2020-08-27 [1] CRAN (R 4.0.2)
##   gridExtra       2.3     2017-09-09 [1] CRAN (R 4.0.2)
##   gtable          0.3.0   2019-03-25 [1] CRAN (R 4.0.0)
##   haven           2.3.1   2020-06-01 [1] CRAN (R 4.0.2)
##   hms             0.5.3   2020-01-08 [1] CRAN (R 4.0.0)
##   htmltools       0.5.0   2020-06-16 [1] CRAN (R 4.0.2)
##   htmlwidgets     1.5.1   2019-10-08 [1] CRAN (R 4.0.0)
##   httpuv          1.5.4   2020-06-06 [1] CRAN (R 4.0.2)
##   httr            1.4.2   2020-07-20 [1] CRAN (R 4.0.2)
##   insight         0.9.6   2020-09-20 [1] CRAN (R 4.0.2)
##   jsonlite        1.7.1   2020-09-07 [1] CRAN (R 4.0.2)
```

```
##   KernSmooth      2.23-17 2020-04-26 [1] CRAN (R 4.0.2)
##   knitr           1.30    2020-09-22 [1] CRAN (R 4.0.2)
##   labeling        0.3     2014-08-23 [1] CRAN (R 4.0.0)
##   later           1.1.0.1 2020-06-05 [1] CRAN (R 4.0.2)
##   lattice       * 0.20-41 2020-04-02 [1] CRAN (R 4.0.2)
##   lifecycle       0.2.0   2020-03-06 [1] CRAN (R 4.0.0)
##   lubridate       1.7.9   2020-06-08 [1] CRAN (R 4.0.2)
##   magrittr        1.5     2014-11-22 [1] CRAN (R 4.0.0)
##   maps            3.3.0   2018-04-03 [1] CRAN (R 4.0.2)
##   MASS            7.3-53  2020-09-09 [1] CRAN (R 4.0.2)
##   Matrix          1.2-18  2019-11-27 [1] CRAN (R 4.0.2)
##   memoise         1.1.0   2017-04-21 [1] CRAN (R 4.0.0)
##   mgcv            1.8-33  2020-08-27 [1] CRAN (R 4.0.2)
##   mime            0.9     2020-02-04 [1] CRAN (R 4.0.0)
##   miniUI          0.1.1.1 2018-05-18 [1] CRAN (R 4.0.0)
##   modelr          0.1.8   2020-05-19 [1] CRAN (R 4.0.2)
##   munsell         0.5.0   2018-06-12 [1] CRAN (R 4.0.0)
##   mycor           0.1.1   2018-04-10 [1] CRAN (R 4.0.2)
##   nlme            3.1-149 2020-08-23 [1] CRAN (R 4.0.2)
##   palmerpenguins * 0.1.0  2020-07-23 [1] CRAN (R 4.0.2)
##   pillar          1.4.6   2020-07-10 [1] CRAN (R 4.0.2)
##   pkgbuild        1.1.0   2020-07-13 [1] CRAN (R 4.0.2)
##   pkgconfig       2.0.3   2019-09-22 [1] CRAN (R 4.0.0)
##   pkgload         1.1.0   2020-05-29 [1] CRAN (R 4.0.2)
##   plotrix       * 3.7-8   2020-04-16 [1] CRAN (R 4.0.2)
##   plyr            1.8.6   2020-03-03 [1] CRAN (R 4.0.0)
##   ppcor           1.1     2015-12-03 [1] CRAN (R 4.0.2)
##   prettyunits     1.1.1   2020-01-24 [1] CRAN (R 4.0.0)
##   processx        3.4.4   2020-09-03 [1] CRAN (R 4.0.2)
##   proj4           1.0-10  2020-03-02 [1] CRAN (R 4.0.1)
##   promises        1.1.1   2020-06-09 [1] CRAN (R 4.0.2)
##   ps              1.3.4   2020-08-11 [1] CRAN (R 4.0.2)
##   purrr         * 0.3.4   2020-04-17 [1] CRAN (R 4.0.0)
##   R6              2.4.1   2019-11-12 [1] CRAN (R 4.0.0)
##   ragg          * 0.3.1   2020-07-03 [1] CRAN (R 4.0.2)
##   RColorBrewer    1.1-2   2014-12-07 [1] CRAN (R 4.0.0)
##   Rcpp            1.0.5   2020-07-06 [1] CRAN (R 4.0.2)
##   readr         * 1.3.1   2018-12-21 [1] CRAN (R 4.0.0)
##   readxl          1.3.1   2019-03-13 [1] CRAN (R 4.0.0)
##   remotes         2.2.0   2020-07-21 [1] CRAN (R 4.0.2)
##   reprex          0.3.0   2019-05-16 [1] CRAN (R 4.0.0)
##   reshape2        1.4.4   2020-04-09 [1] CRAN (R 4.0.0)
##   rlang           0.4.7   2020-07-09 [1] CRAN (R 4.0.2)
##   rmarkdown       2.3     2020-06-18 [1] CRAN (R 4.0.2)
##   rprojroot       1.3-2   2018-01-03 [1] CRAN (R 4.0.0)
##   rstudioapi      0.11    2020-02-07 [1] CRAN (R 4.0.0)
##   Rttf2pt1        1.3.8   2020-01-10 [1] CRAN (R 4.0.2)
##   rvest           0.3.6   2020-07-25 [1] CRAN (R 4.0.2)
##   scales          1.1.1   2020-05-11 [1] CRAN (R 4.0.0)
##   sessioninfo     1.1.1   2018-11-05 [1] CRAN (R 4.0.0)
##   shiny           1.5.0   2020-06-23 [1] CRAN (R 4.0.2)
##   sjlabelled      1.1.7   2020-09-24 [1] CRAN (R 4.0.2)
```

```
##   sjmisc          2.8.5   2020-05-28 [1] CRAN (R 4.0.2)
##   stringi         1.5.3   2020-09-09 [1] CRAN (R 4.0.2)
##   stringr       * 1.4.0   2019-02-10 [1] CRAN (R 4.0.0)
##   systemfonts     0.3.2   2020-09-29 [1] CRAN (R 4.0.2)
##   testthat        2.3.2   2020-03-02 [1] CRAN (R 4.0.0)
##   tibble        * 3.0.3   2020-07-10 [1] CRAN (R 4.0.2)
##   tidyr         * 1.1.2   2020-08-27 [1] CRAN (R 4.0.2)
##   tidyselect      1.1.0   2020-05-11 [1] CRAN (R 4.0.0)
##   tidyverse     * 1.3.0   2019-11-21 [1] CRAN (R 4.0.0)
##   treemapify    * 2.5.3   2019-01-30 [1] CRAN (R 4.0.2)
##   usethis         1.6.3   2020-09-17 [1] CRAN (R 4.0.2)
##   utf8            1.1.4   2018-05-24 [1] CRAN (R 4.0.0)
##   uuid            0.1-4   2020-02-26 [1] CRAN (R 4.0.2)
##   vctrs           0.3.4   2020-08-29 [1] CRAN (R 4.0.2)
##   viridis         0.5.1   2018-03-29 [1] CRAN (R 4.0.2)
##   viridisLite     0.3.0   2018-02-01 [1] CRAN (R 4.0.0)
##   waterfall     * 1.0.2   2016-04-03 [1] CRAN (R 4.0.2)
##   withr           2.3.0   2020-09-22 [1] CRAN (R 4.0.2)
##   xfun            0.18    2020-09-29 [1] CRAN (R 4.0.2)
##   xml2            1.3.2   2020-04-23 [1] CRAN (R 4.0.0)
##   xtable          1.8-4   2019-04-21 [1] CRAN (R 4.0.0)
##   yaml            2.2.1   2020-02-01 [1] CRAN (R 4.0.0)
##
## [1] /Library/Frameworks/R.framework/Versions/4.0/Resources/library
```