

# Data Visualisation with R

## Workshop Day 1

Multiple layers, facetting and tidying your data

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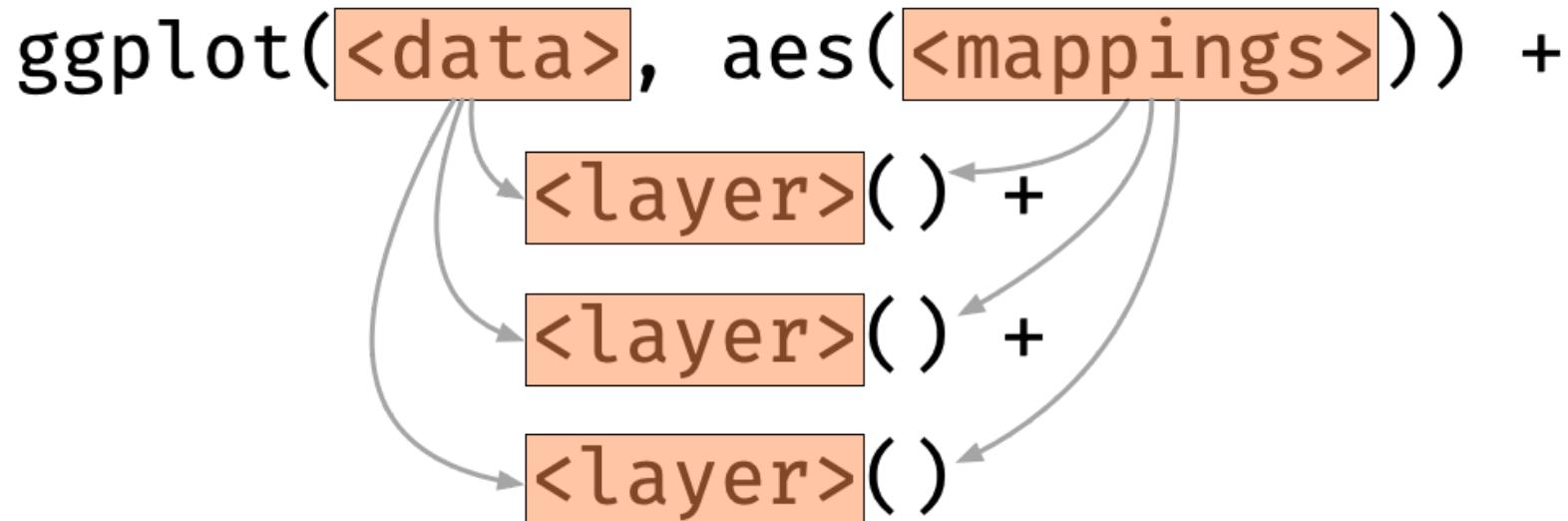
Department of Econometrics and Business Statistics



MONASH University

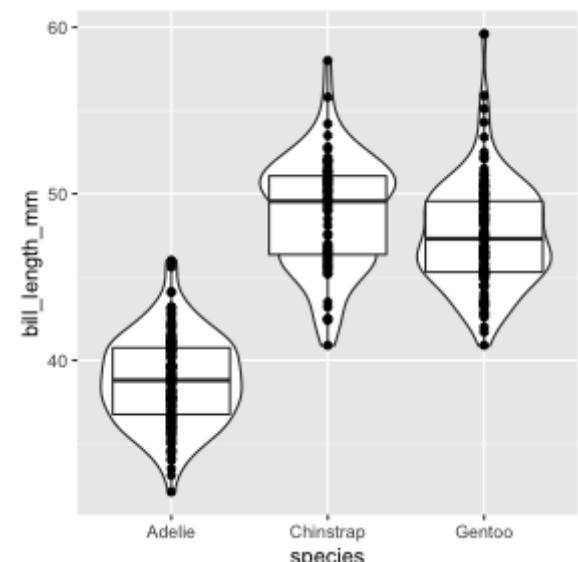
28th July 2020 @ Statistical Society of Australia | Online

# Add multiple layers



Each layer inherits mapping and data from ggplot by default.

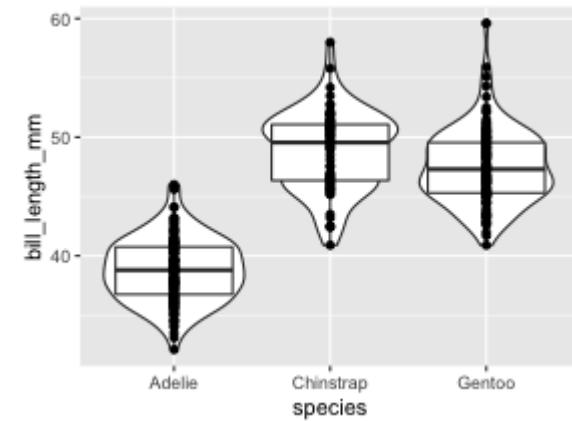
```
ggplot(penguins, aes(x = species, y = bill_length_mm)) +  
  geom_violin() +  
  geom_boxplot() +  
  geom_point()
```



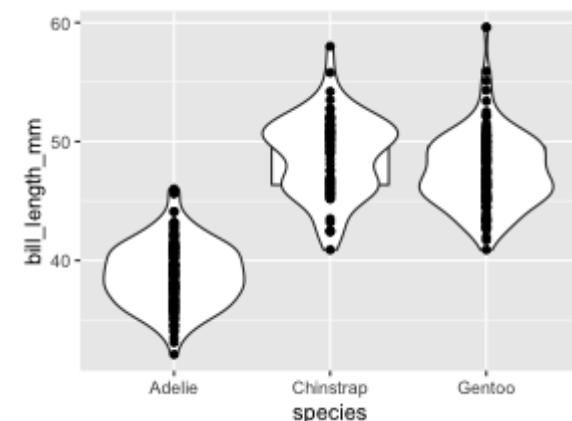
# Order of the layers matters!

Boxplot and violin plot order are switched around.

```
ggplot(penguins, aes(species, bill_length_mm)) +  
  geom_violin() +  
  geom_boxplot() +  
  geom_point()
```



```
ggplot(penguins, aes(species, bill_length_mm)) +  
  geom_boxplot() +  
  geom_violin() +  
  geom_point()
```

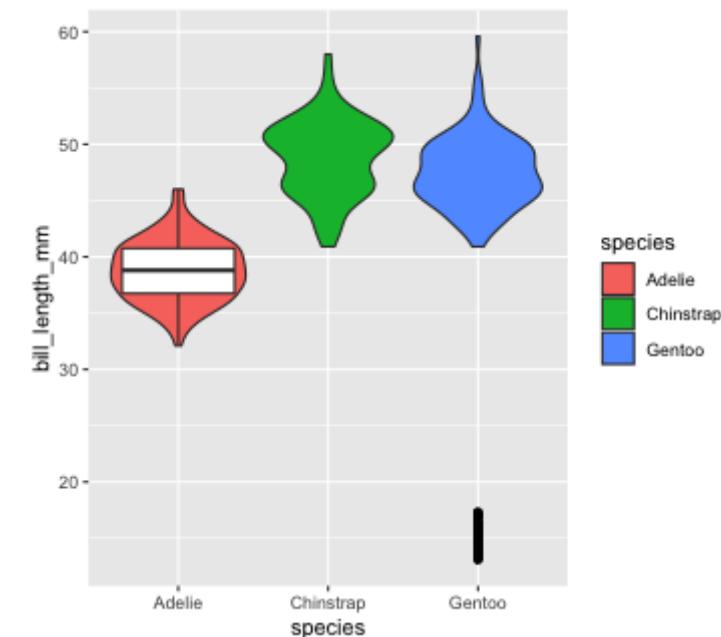


# Layer-specific data and aesthetic mappings

```
ggplot(<data>, aes(<mappings>)) +  
  <layer>(aes(<mappings>)) +  
  <layer>(data = <data>) +  
  <layer>(aes(<mappings>), <data>)
```

For each layer, aesthetic and/or data can be overwritten.

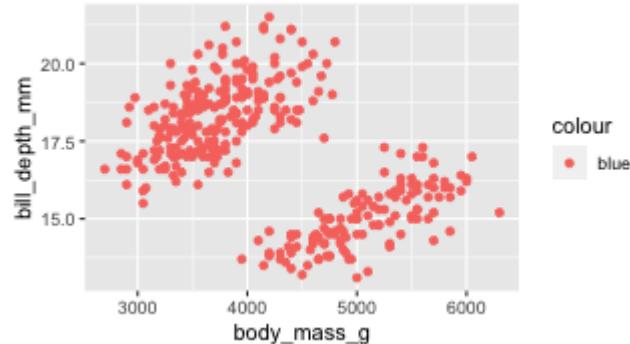
```
ggplot(penguins, aes(species, bill_length_mm)) +  
  geom_violin(aes(fill = species)) +  
  geom_boxplot(data = filter(penguins, species=="Adelie")) +  
  geom_point(data = filter(penguins, species=="Gentoo"),  
             aes(y = bill_depth_mm))
```



# Aesthetic or Attribute?

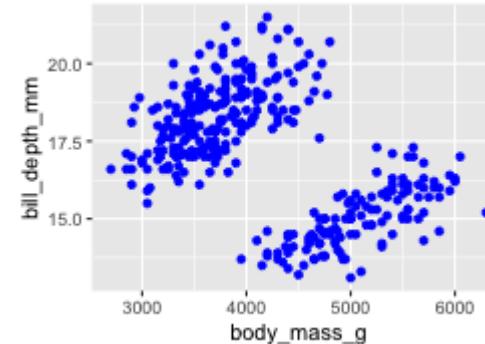
Not what you want

```
ggplot(penguins) +  
  geom_point(aes(body_mass_g,  
                 bill_depth_mm,  
                 color = "blue"))
```



What you want

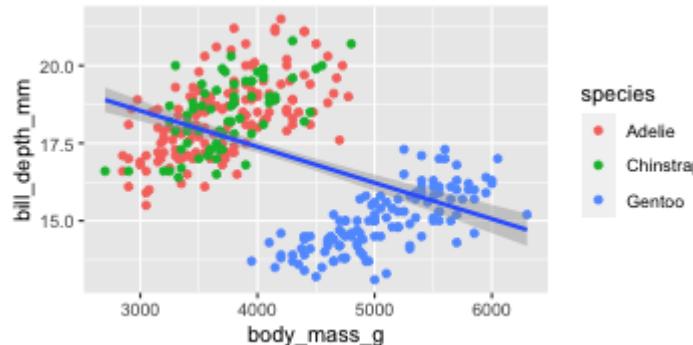
```
ggplot(penguins) +  
  geom_point(aes(body_mass_g,  
                 bill_depth_mm),  
             color = "blue")
```



```
ggplot(penguins) +  
  geom_point(aes(body_mass_g,  
                 bill_depth_mm,  
                 color = I("blue")))
```

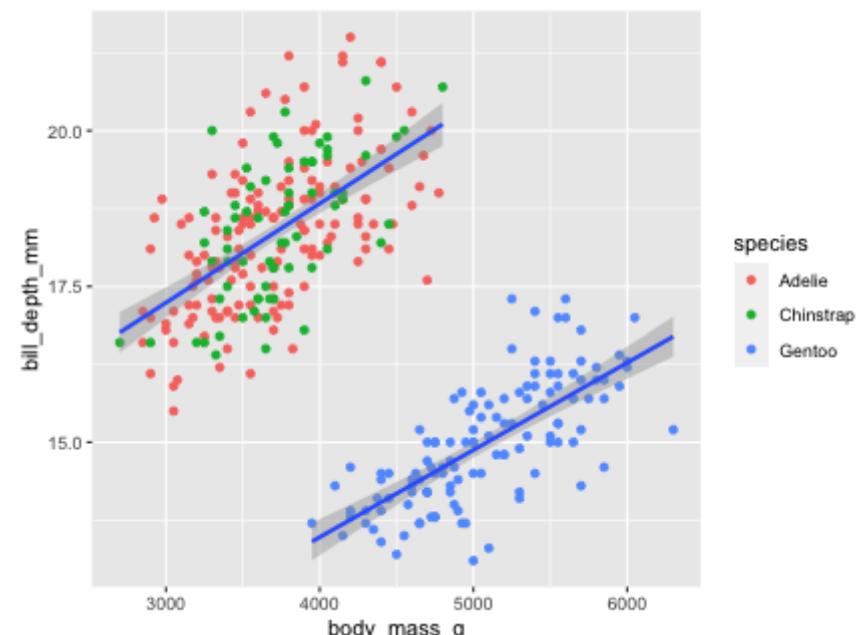
# group in ggplot

```
ggplot(penguins,  
       aes(body_mass_g,  
           bill_depth_mm)) +  
  geom_point(aes(color = species)) +  
  geom_smooth(method = "lm")
```



- This is an obvious case of Simpson's paradox.
- What if we wanted to draw the fit of a simple linear model for each cluster?

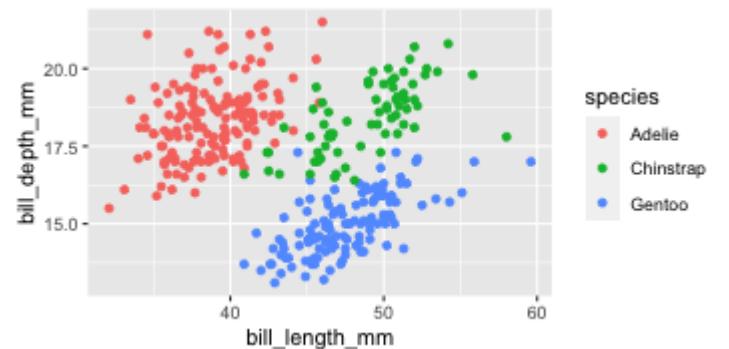
```
ggplot(penguins,  
       aes(body_mass_g,  
           bill_depth_mm)) +  
  geom_point(aes(color = species)) +  
  geom_smooth(method = "lm",  
             aes(group = species=="Gentoo"))
```



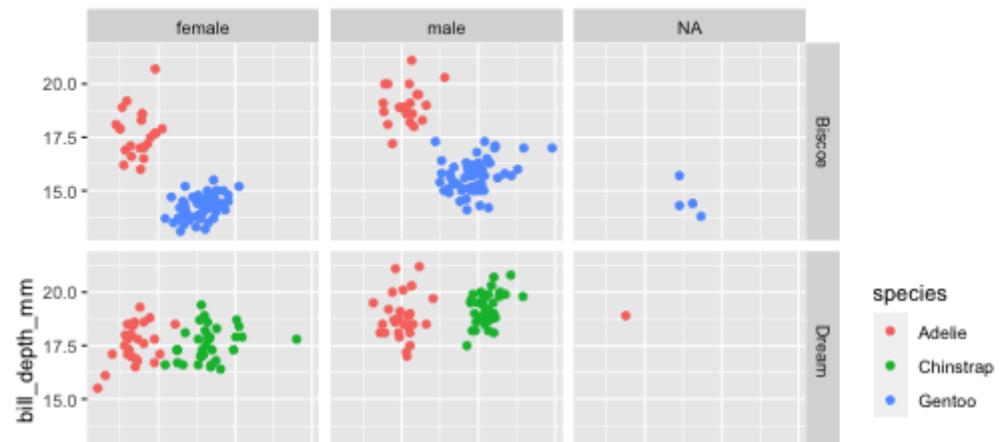
# Facetting

```
g <- ggplot(penguins, aes(bill_length_mm, bill_depth_mm, color = species)) + geom_point()
```

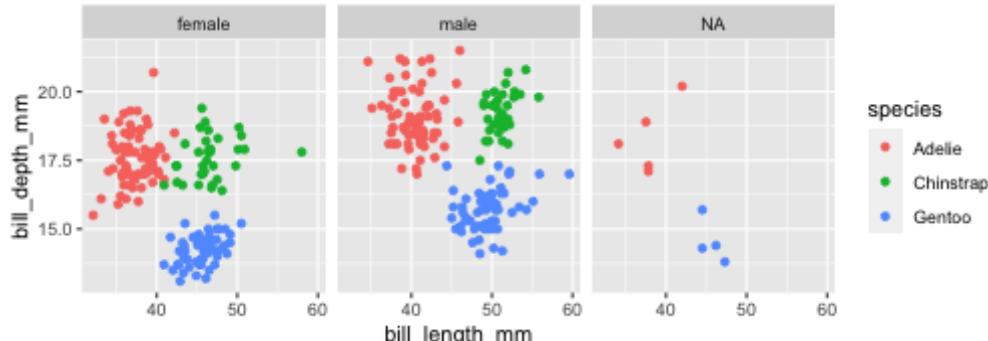
g



g + facet\_grid(island ~ sex)

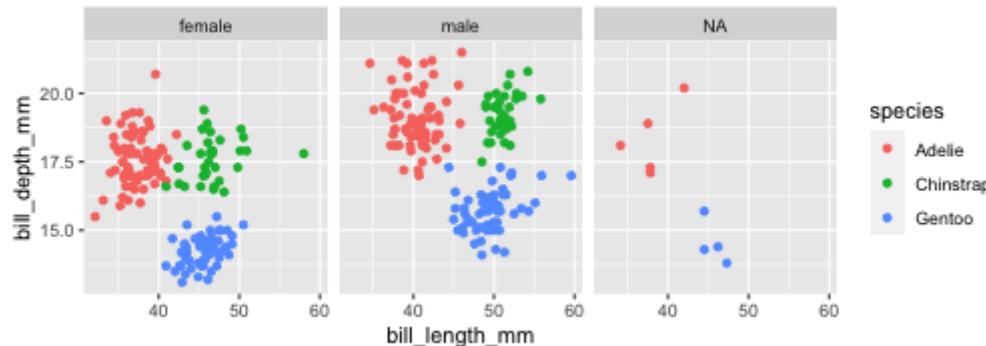


g + facet\_wrap(~sex)

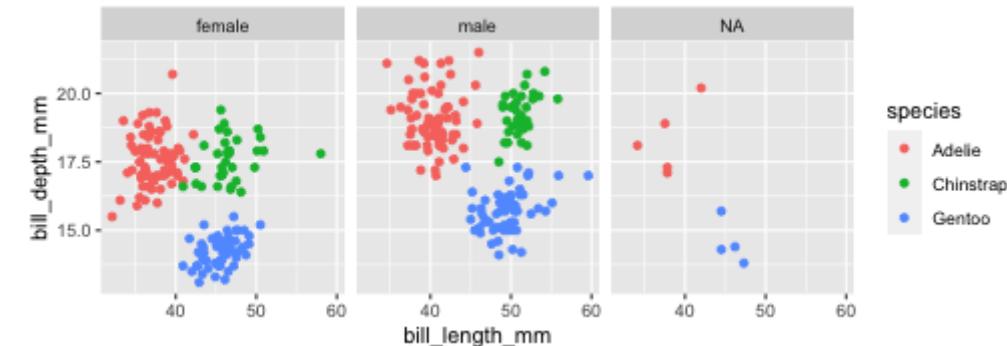


# facet\_wrap and facet\_grid

```
g + facet_wrap( ~ sex)
```



```
g + facet_grid(. ~ sex)
```



```
g + facet_wrap( ~ sex, ncol = 1)
```

```
g + facet_grid(sex ~ .)
```

# Data Visualization with ggplot2 :: CHEAT SHEET

## Basics

ggplot2 is based on the **grammar of graphics**, the idea that you can build every graph from the same components: a **data set**, a **coordinate system**, and geoms—visual marks that represent data points.



To display values, map variables in the data to visual properties of the geom (**aesthetics**) like **size**, **color**, and **y locations**.



Complete the template below to build a graph.

```
ggplot(data = <DATA>) +
  <GEO FUNCTION>(mapping = aes(<MAPPINGS>),
  stat = <STAT>, position = <POSITION>) +
  <COORDINATE FUNCTION> +
  <FACET FUNCTION> +
  <SCALE FUNCTION> +
  <THEME FUNCTION>
```

`ggplot(data = mpg, aes(x = cyl, y = hwy))` Begins a plot that you finish by adding layers to. Add one geom function per layer.

`aesthetic mappings` `data` `geom`

`qplot(x = cyl, y = hwy, data = mpg, geom = "point")` Creates a complete plot with given data, geom, and mappings. Supplies many useful defaults.

`last_plot()` Returns the last plot

`ggsave("plot.png", width = 5, height = 5)` Saves last plot as 5' x 5' file named "plot.png" in working directory. Matches file type to file extension.

## Geoms

Use a geom function to represent data points, use the geom's aesthetic properties to represent variables. Each function returns a layer.

### GRAPHICAL PRIMITIVES

```
a <- ggplot(economics, aes(date, unemployed))
b <- ggplot(seals, aes(x = long, y = lat))

a + geom_blank()
#(Useful for expanding limits)

b + geom_curve(aes(yend = lat + 1,
xend = long + 1, curvature = 0.5)) -> x, yend, y, yend,
alpha, angle, color, curvature, linetype, size

a + geom_path(linewidth = "butt", linejoin = "round",
linemetre = 1)
x, y, alpha, color, group, linetype, size

a + geom_polygon(aes(group = group))
x, y, alpha, color, fill, group, linetype, size

b + geom_rect(aes(xmin = long, ymin = lat, xmax =
long + 1, ymax = lat + 1)) -> xmin, ymin, xmax,
ymin, alpha, color, fill, linetype, size

a + geom_ribbon(aes(ymin = unemployed - 900,
ymax = unemployed + 900)) -> x, ymax, ymin,
alpha, color, fill, group, linetype, size
```

### LINE SEGMENTS

common aesthetics: x, y, alpha, color, linetype, size

```
b + geom_abline(aes(intercept = 0, slope = 1))
b + geom_hline(aes(yintercept = lat))
b + geom_vline(aes(xintercept = long))

b + geom_segment(aes(yend = lat + 1, xend = long + 1))
b + geom_spoke(aes(angle = 1:1155, radius = 1))
```

### ONE VARIABLE continuous

```
c <- ggplot(mpg, aes(hwy)); c2 <- ggplot(mpg)

c + geom_area(stat = "bin")
x, y, alpha, color, fill, linetype, size

c + geom_density(kernel = "gaussian")
x, y, alpha, color, fill, group, linetype, size, weight

c + geom_dotplot()
x, y, alpha, color, fill

c + geom_freqpoly()
x, y, alpha, color, group, size

c + geom_histogram(binwidth = 5)
x, y, alpha, color, fill, linetype, size, weight

c2 + geom_qq(aes(sample = hwy))
x, y, alpha, color, fill, group, linetype, size, weight
```

### discrete

```
d <- ggplot(mpg, aes(fl))
d + geom_bar()
x, alpha, color, fill, linetype, size, weight
```

### TWO VARIABLES

```
continuous x , continuous y
e <- ggplot(mpg, aes(cty, hwy))

e + geom_label(aes(label = cty, nudge_x = 1,
nudge_y = 1, check_overlap = TRUE)) -> x, y, label,
alpha, angle, color, family, fontface, hjust,
lineheight, size, vjust

e + geom_jitter(height = 2, width = 2)
x, y, alpha, color, fill, shape, size

e + geom_point(), x, y, alpha, color, fill, shape,
size, stroke

e + geom_quantile()
x, y, alpha, color, group, linetype, size, weight

e + geom_rug(sides = "bl")
x, y, alpha, color, fill, linetype, size

e + geom_smooth(method = lm)
x, y, alpha, color, fill, group, linetype, size, weight

e + geom_text(aes(label = cty, nudge_x = 1,
nudge_y = 1, check_overlap = TRUE)) -> x, y, label,
alpha, angle, color, family, fontface, hjust,
lineheight, size, vjust
```

### discrete x , continuous y

```
f <- ggplot(mpg, aes(class, hwy))

f + geom_col()
x, y, alpha, color, fill, group, linetype, size

f + geom_boxplot()
x, y, lower, middle, upper, ymin, ymax, alpha, color, fill, group, linetype, size, weight

f + geom_dotplot(binaxis = "y", stackdir =
"center")
x, y, alpha, color, fill, group

f + geom_violin(scale = "area")
x, y, alpha, color, fill, group, linetype, size, weight
```

### discrete x , discrete y

```
g <- ggplot(diamonds, aes(cut, color))

g + geom_count()
x, y, alpha, color, fill, shape, size, stroke
```

### THREE VARIABLES

```
sealsSz <- with(seals, sqrt(delta_long^2 + delta_lat^2))
l <- ggplot(seals, aes(long, lat))

l + geom_contour(aes(z = z))
x, y, z, alpha, colour, group, linetype, size, weight

l + geom_raster(aes(fill = z), hjust = 0.5, vjust = 0.5,
interpolate = FALSE)
x, y, alpha, fill

l + geom_tile(aes(fill = z))
x, y, alpha, color, fill, linetype, size, width
```



# HELP!

- RStudio > Help > Cheatsheets
- R4DS Community Slack
- Twitter with hashtag #rstats
- RStudio Community
- Stackoverflow

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# Tidying your data

# Weight gain in pigs for different treatments

The `crampton.pig` is from the `agridat` 

```
library(agridat)
glimpse(crampton.pig)

## Rows: 50
## Columns: 5
## $ treatment <fct> T1, T2, T2, T2, T2,
## $ rep       <fct> R1, R2, R3, R4, R5, R6, R7, R8, R9, R10, R1, R2, R3, R4, R5
## $ weight1   <int> 30, 21, 21, 33, 27, 24, 20, 29, 28, 26, 26, 24, 20, 35, 25,
## $ feed      <int> 674, 628, 661, 694, 713, 585, 575, 638, 632, 637, 699, 626,
## $ weight2   <int> 195, 177, 180, 200, 197, 170, 150, 180, 192, 184, 194, 204,
```

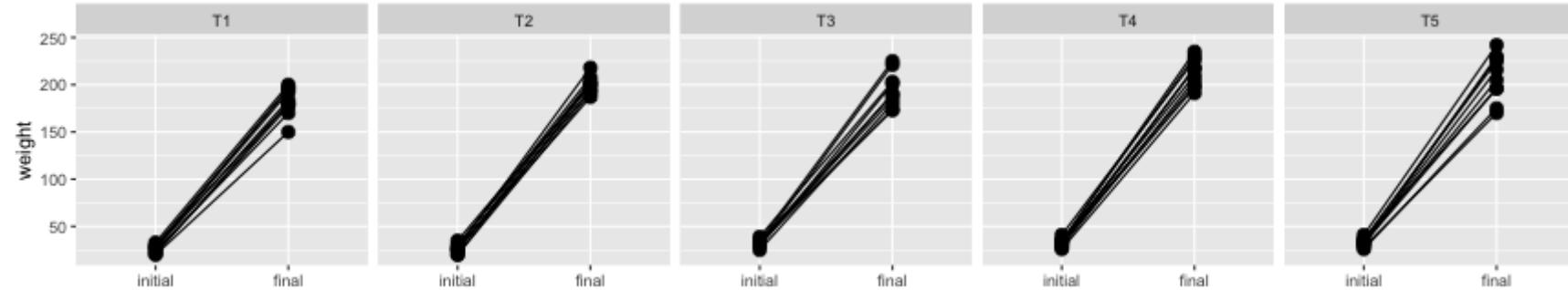
`weight1` is initial weight and `weight2` is final weight

Wright (2018). `agridat`: Agricultural Datasets. R package version 1.16. <https://CRAN.R-project.org/package=agridat>

Crampton and Hopkins (1934). The Use of the Method of Partial Regression in the Analysis of Comparative Feeding Trial Data, Part II. *The Journal of Nutrition* 8 113-123.

```
names(crampton.pig)
```

```
## [1] "treatment" "rep"      "weight1"    "feed"       "weight2"
```

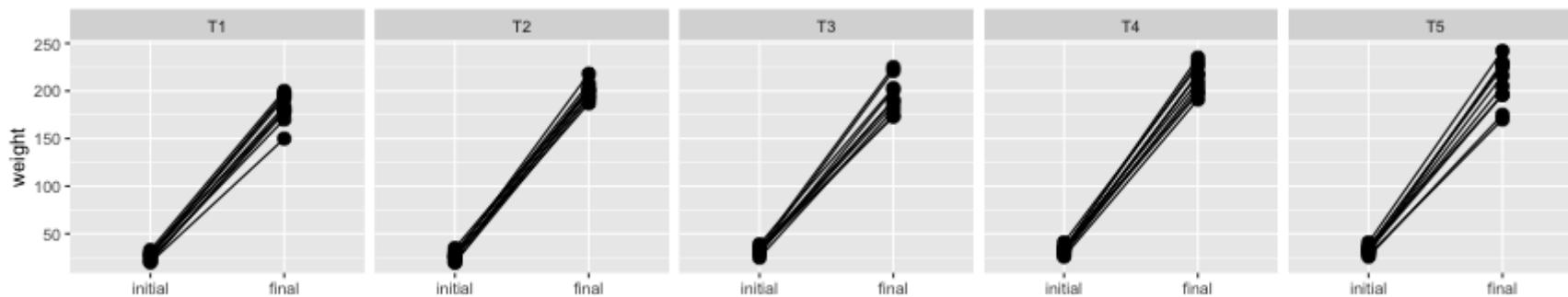


What are the mappings to get the above graph? 🤔

```
ggplot(crampton.pig, aes(x = ???, y = ???)) +  
  geom_point() +  
  geom_line() +  
  facet_grid(. ~ treatment)
```



# Getting the data in the right form



- The x-axis is the time when pig was weighed
- The y-axis is the weight
- The facetting is by treatment

```
## # A tibble: 100 x 5
##   treatment feed id    when     weight
##   <fct>      <int> <chr> <fct>     <int>
## 1 T1          674  pig1 initial     30
## 2 T1          674  pig1 final      195
## 3 T1          628  pig2 initial     21
## 4 T1          628  pig2 final      150
## 5 T2          675  pig3 initial     45
## 6 T2          675  pig3 final      205
## 7 T2          676  pig4 initial     40
## 8 T2          676  pig4 final      210
## 9 T3          677  pig5 initial     40
## 10 T3         677  pig5 final      220
## # ... with 90 more rows
```

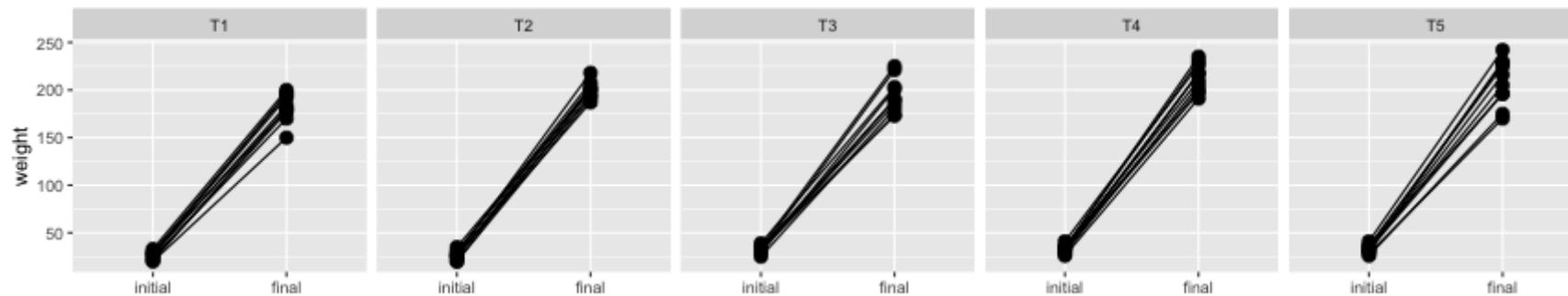
How I wrangled this data

```
pig_df <- crampton.pig %>%
  mutate(id = paste0("pig", 1:n())) %>%
  pivot_longer(c(weight1, weight2),
               names_to = "when",
               values_to = "weight") %>%
  mutate(when = factor(when,
                      levels = c("weight1", "weight2"),
                      labels = c("initial", "final")))
```

(note: teaching wrangling is not part of this workshop, please see [here](#) if you want to learn more or please request SSA you would like a workshop on data wrangling)

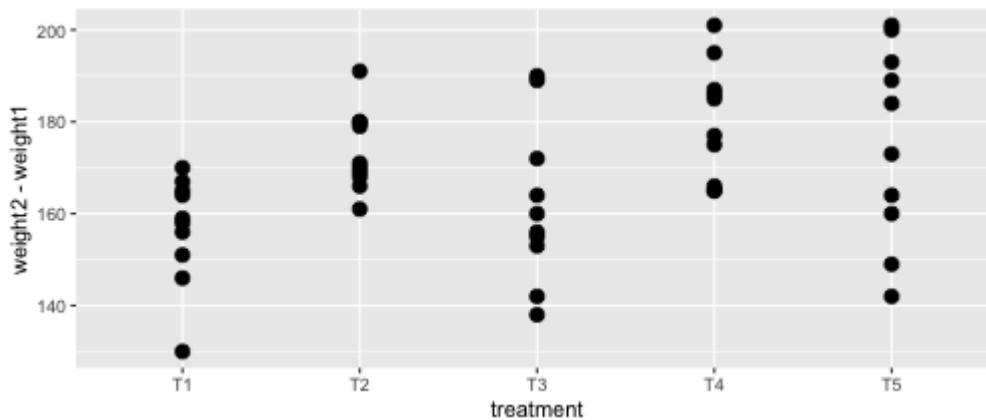
# Putting it all together

```
ggplot(pig_df, aes(when, weight)) + # tidying your data for plotting  
  geom_point(size = 3) + # attribute not aesthetic  
  geom_line(aes(group = id)) + # grouping  
  facet_grid(. ~ treatment) + # facetting  
  labs(x = "") # we'll learn this in the last session
```



# Meaningfully order categorical variables

```
ggplot(crampton.pig,  
       aes(treatment, weight2 - weight1)) +  
       geom_point(size = 3)
```

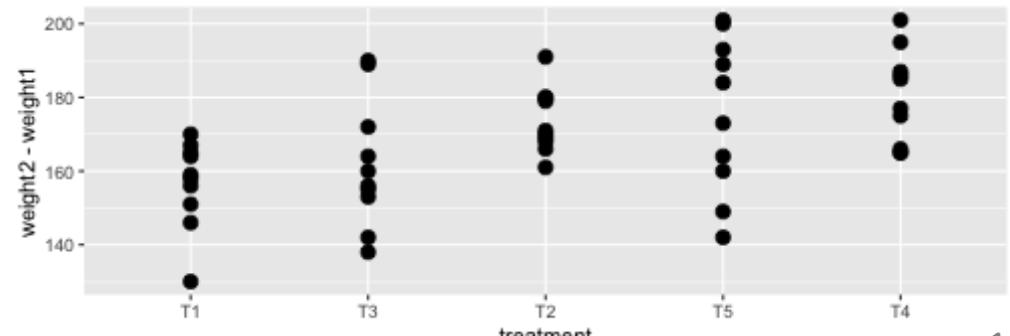


- Treatments are ordered alphabetically by default
- It's better to order categorical variables meaningfully

Order factor levels by the mean of the weight difference.

```
library(forcats) # for easy factor manipulation  
crampton.pig2 <- crampton.pig %>%  
  mutate(  
    treatment = fct_reorder(treatment,  
                            weight2 - weight1,  
                            mean))
```

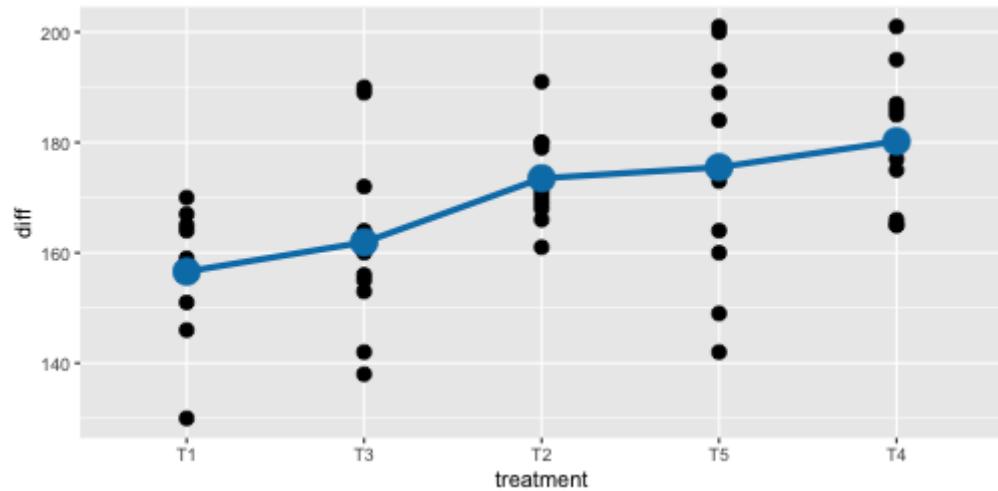
```
ggplot(crampton.pig2,  
       aes(treatment, weight2 - weight1)) +  
       geom_point(size = 3)
```



# Plotting auxilliary data

```
trtmean_df <- crampton.pig2 %>%  
  group_by(treatment) %>%  
  summarise(  
    diff = mean(weight2 - weight1))  
  
trtmean_df  
  
## # A tibble: 5 x 2  
##   treatment  diff  
## * <fct>     <dbl>  
## 1 T1         157.  
## 2 T3         162.  
## 3 T2         174.  
## 4 T5         176.  
## 5 T4         180.
```

Plot you may want:

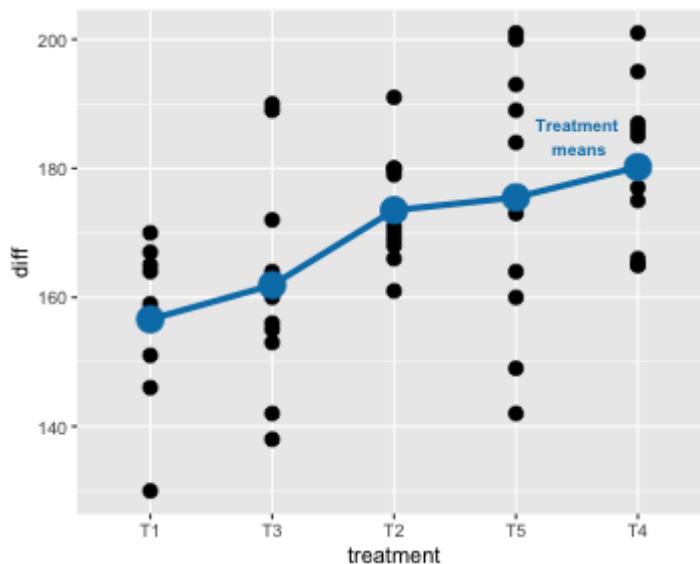


One way to do this:

```
fig <- ggplot(trtmean_df, aes(treatment, diff)) +  
  geom_point(data = crampton.pig2, size = 3,  
             aes(y = weight2 - weight1)) +  
  geom_point(color = "#027EB6", size = 6) +  
  geom_line(color = "#027EB6", size = 1.5,  
            group = 1)
```

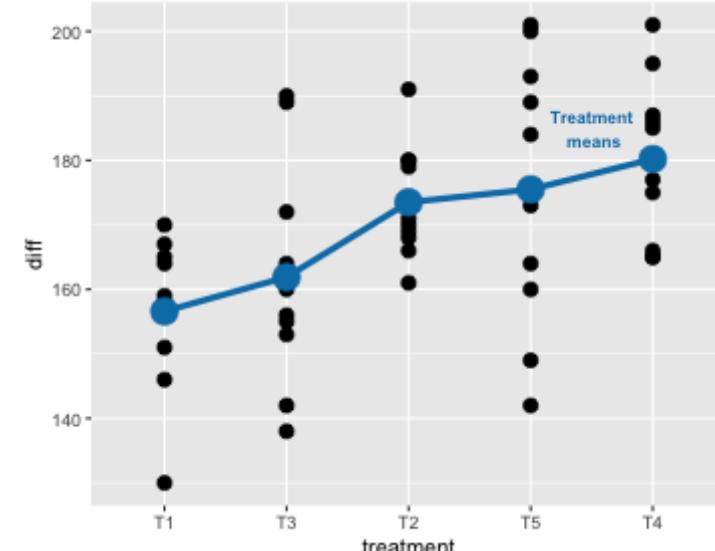
# Plotting annotations

```
fig +  
  geom_text(data = data.frame(treatment = 4.5,  
                               diff = 185),  
            aes(label = "Treatment\n means"),  
            size = 3,  
            color = "#027EB6",  
            fontface = "bold")
```



But it might be just easier to:

```
fig +  
  annotate("text",  
          x = 4.5, y = 185,  
          label = "Treatment\n means",  
          size = 3,  
          color = "#027EB6",  
          fontface = "bold")
```





</> Open day1-exercise-02.Rmd

15:00

# Session Information

```
devtools::session_info()
```

```
## - Session info --
##   setting  value
##   version  R version 3.6.3 (2020-02-29)
##   os        macOS Catalina 10.15.6
##   system   x86_64, darwin15.6.0
##   ui        X11
##   language (EN)
##   collate  en_AU.UTF-8
##   ctype    en_AU.UTF-8
##   tz       Australia/Melbourne
##   date     2020-07-25
##
## - Packages --
##   package      * version    date lib
## 
```

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