Numeric Variable Graphs

Justin Post

Recap: `ggplot2`

A great plotting system!

To create plots:

- Create base object
- Add `geom` or `stat` layers
- Use `aes()` to map variables to attributes of the plot
- Add other layers to modify things

`ggplot2` Smoothed Histogram

Numeric variables - generally, describe distribution via a histogram or boxplot!

- For a single numeric variable, describe the distribution via
    - Shape: Histogram, Density plot, ...
    - Comparing across a categorical variable: Boxplot
- For two numeric variables, describe the distribution via
    - Shape: Scatter plot

Reading in Our Data

First, let's read in the appendicitis data from the previous lecture.

```
library(tidyverse)
library(readxl)
app_data <- read_excel("app_data.xlsx", sheet = 1)
app_data <- app_data |>
  mutate(BMI = as.numeric(BMI),
         US_Number = as.character(US_Number),
         SexF = factor(Sex, levels = c("female", "male"), labels = c("Female", "Male")),
         DiagnosisF = as.factor(Diagnosis),
         SeverityF = as.factor(Severity))
app_data
```

```
## # A tibble: 782 × 61
##     Age   BMI Sex    Height Weight Length_of_Stay Management   Severity
##   <dbl> <dbl> <chr>   <dbl>  <dbl>          <dbl> <chr>        <chr>
## 1  12.7  16.9 female    148   37                3 conservative uncomplicated
## 2  14.1  31.9 male      147   69.5              2 conservative uncomplicated
## 3  14.1  23.3 female    163   62                4 conservative uncomplicated
## 4  16.4  20.6 female    165   56                3 conservative uncomplicated
## 5  11.1  16.9 female    163   45                3 conservative uncomplicated
## # ℹ 777 more rows
## # ℹ 53 more variables: Diagnosis_Presumptive <chr>, Diagnosis <chr>,
## #   Alvarado_Score <dbl>, Paediatric_Appendicitis_Score <dbl>,
##                         ndix_Diameter <dbl>, Migratory_Pain <chr>,
##                         , Contralateral_Rebound_Tenderness <chr>,
##                         a <chr>, Loss_of_Appetite <chr>,
## #   Body_Temperature <dbl>, WBC_Count <dbl>, Neutrophil_Percentage <dbl>, …
```

Density Plot

- **Kernel Smoother** - Smoothed version of a histogram
- Common `aes` values (from cheat sheet):

```
c + geom_density(kernel = "gaussian")
```

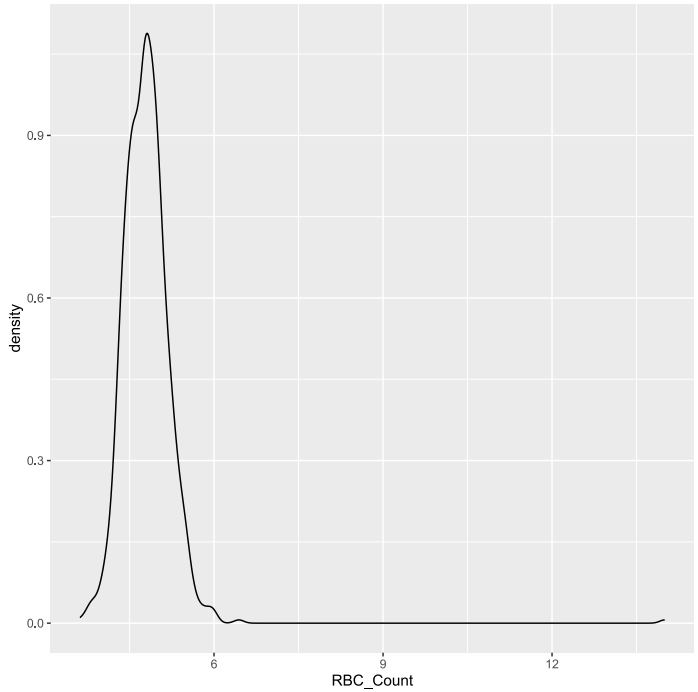
```
x, y, alpha, color, fill, group, linetype, size, weight
```

- Only `x =` is really needed

ggplot2 Smoothed Histogram

- **Kernel Smoother** - Smoothed version of a histogram

```
g <- ggplot(app_data |> drop_na(RBC_Count), aes(x = RBC_Count))
g + geom_density()
```



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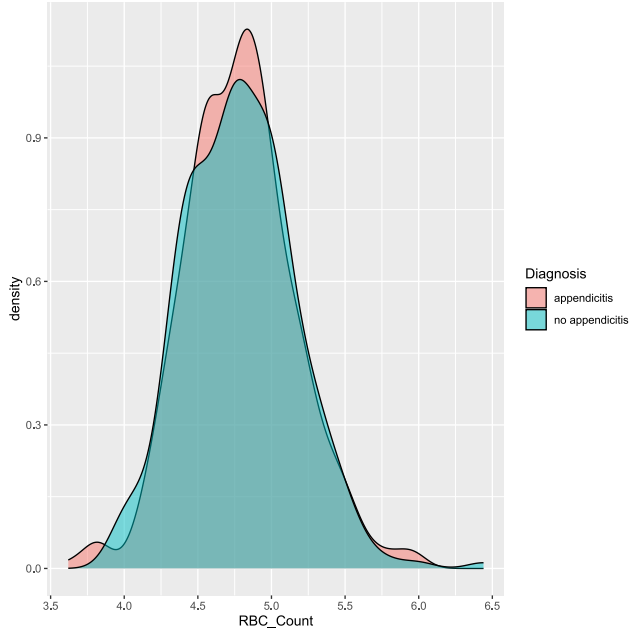
`ggplot2` Smoothed Histogram

- **Kernel Smoother** - Smoothed version of a histogram
- Remove really large value and use the `fill` aesthetic to compare groups!

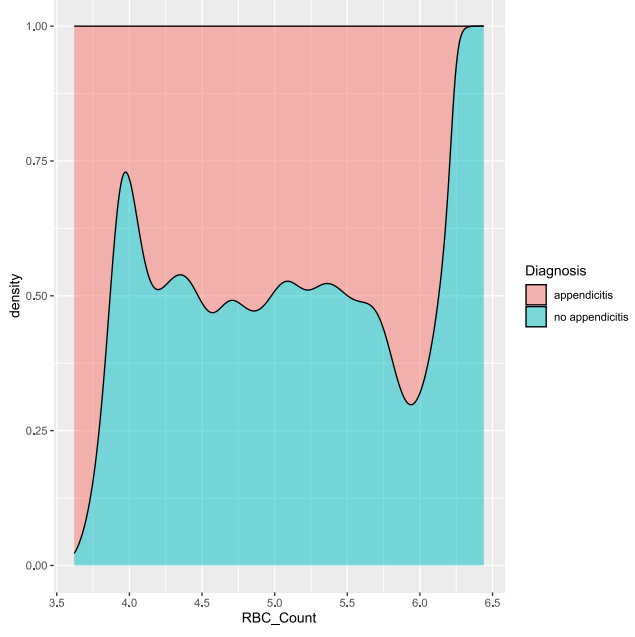
```
g <- ggplot(app_data |> drop_na(RBC_Count, Diagnosis) |> filter(RBC_Count < 8), aes(x = RBC_Count))
g + geom_density(alpha = 0.5, aes(fill = Diagnosis))
```



`ggplot2` Smoothed Histogram

- **Kernel Smoother** - Smoothed version of a histogram
- Recall `position` choices of `dodge`, `jitter`, `fill`, and `stack`

```
g <- ggplot(app_data |> drop_na(RBC_Count, Diagnosis) |> filter(RBC_Count < 8), aes(x = RBC_Count))
g + geom_density(alpha = 0.5, position = "fill", aes(fill = Diagnosis))
```



`ggplot2` Boxplots

- **Boxplot** - Provides the five number summary in a graph
- Common `aes` values (from cheat sheet):

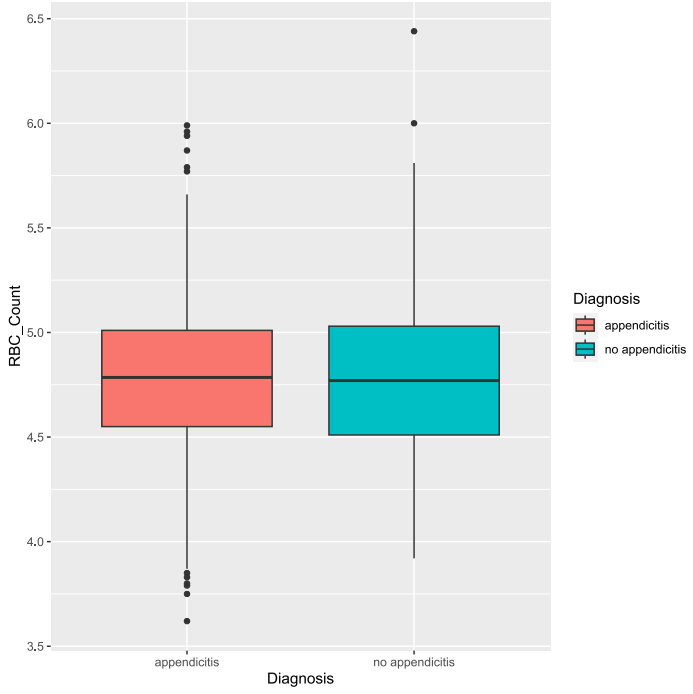
`f + geom_boxplot()`

`x, y, lower, middle, upper, ymax, ymin, alpha, color, fill, group, linetype, shape, size, weight`

- Only `x =, y =` are really needed

ggplot2 Boxplots

```
g <- ggplot(app_data |> drop_na(RBC_Count, Diagnosis) |> filter(RBC_Count < 8))
g + geom_boxplot(aes(x = Diagnosis, y = RBC_Count, fill = Diagnosis))
```



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`ggplot2` Boxplots with Points

- Can add data points (jittered) to see shape of data better (or use violin plot)

```
g <- ggplot(app_data |> drop_na(RBC_Count, Diagnosis) |> filter(RBC_Count < 8))
g + geom_boxplot(aes(x = Diagnosis, y = RBC_Count, fill = Diagnosis)) +
  geom_jitter(width = 0.1, alpha = 0.3)
```

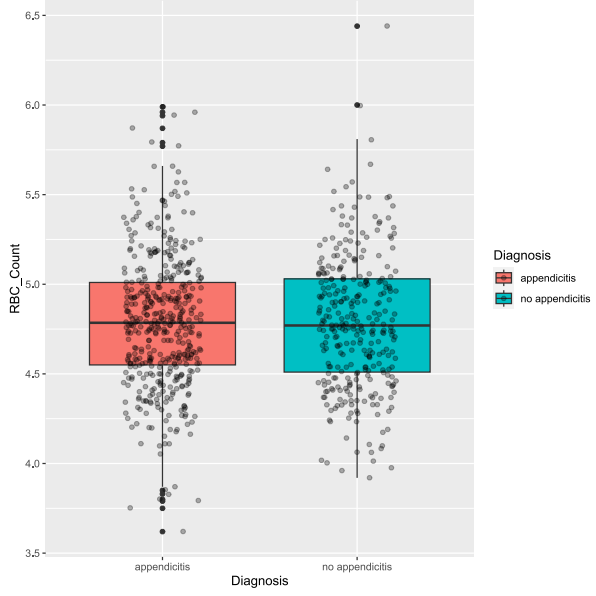
```
## Error in `geom_jitter()`:
## ! Problem while setting up geom.
## ℹ Error occurred in the 2nd layer.
## Caused by error in `compute_geom_1()`:
## ! `geom_point()` requires the following missing aesthetics: x and y
```

- Oh, global vs local `aes()`!

`ggplot2` Boxplots with Points

- Can add data points (jittered) to see shape of data better (or use violin plot)

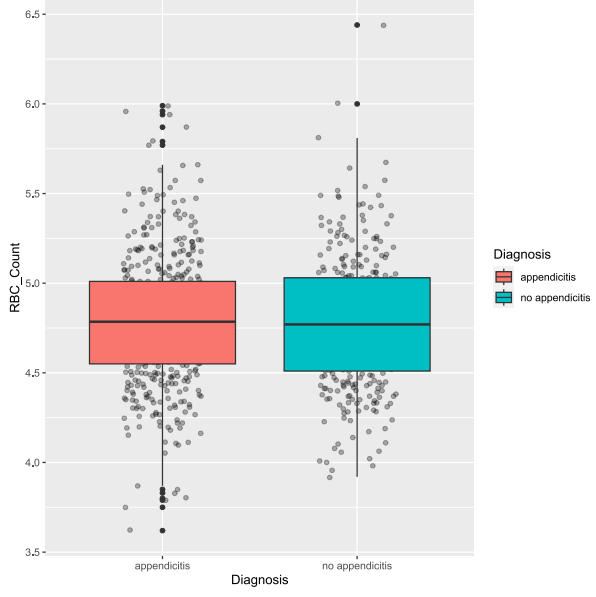
```
g <- ggplot(app_data |> drop_na(RBC_Count, Diagnosis) |> filter(RBC_Count < 8),
            aes(x = Diagnosis, y = RBC_Count, fill = Diagnosis))
g + geom_boxplot() +
  geom_jitter(width = 0.2, alpha = 0.3)
```



`ggplot2` Boxplots with Points

- Order of layers important!

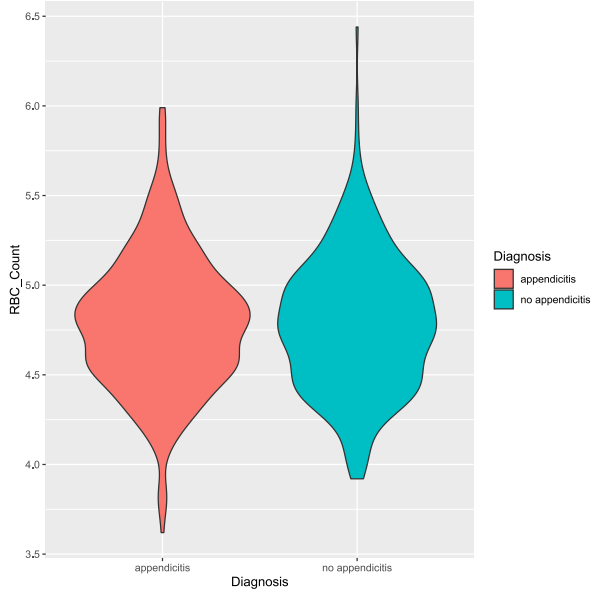
```
g <- ggplot(app_data |> drop_na(RBC_Count, Diagnosis) |> filter(RBC_Count < 8),
            aes(x = Diagnosis, y = RBC_Count, fill = Diagnosis))
g + geom_jitter(width = 0.2, alpha = 0.3) +
  geom_boxplot()
```



ggplot2 Violin Plots

- Violin plot similar to boxplot

```
g <- ggplot(app_data |> drop_na(RBC_Count, Diagnosis) |> filter(RBC_Count < 8),
            aes(x = Diagnosis, y = RBC_Count, fill = Diagnosis))
g + geom_violin()
```



`ggplot2` Scatter Plots

Two numerical variables

- **Scatter Plot** - graphs points corresponding to each observation
- Common `aes` values (from cheat sheet):

  `e + geom_point()`

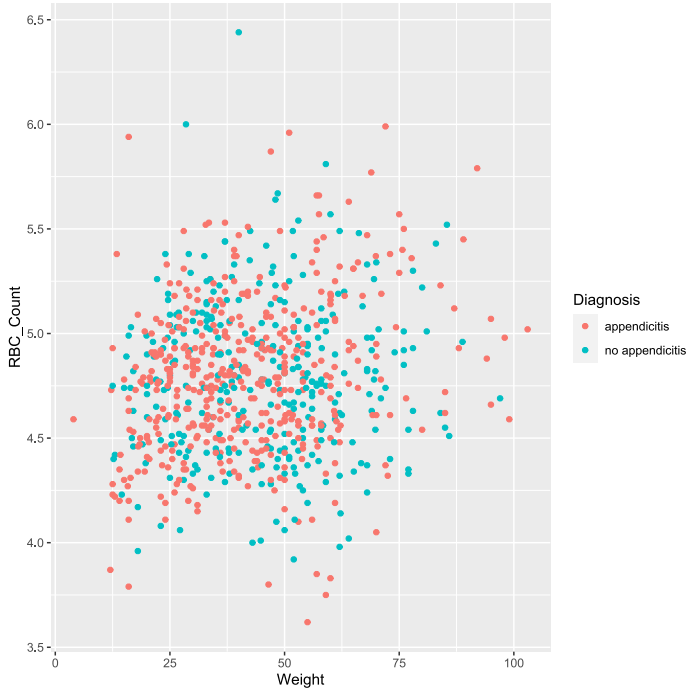
  `x, y, alpha, color, fill, shape, size, stroke`

- Only `x =, y =` are really needed

`ggplot2` Scatter Plots

- **Scatter Plot** - graphs points corresponding to each observation

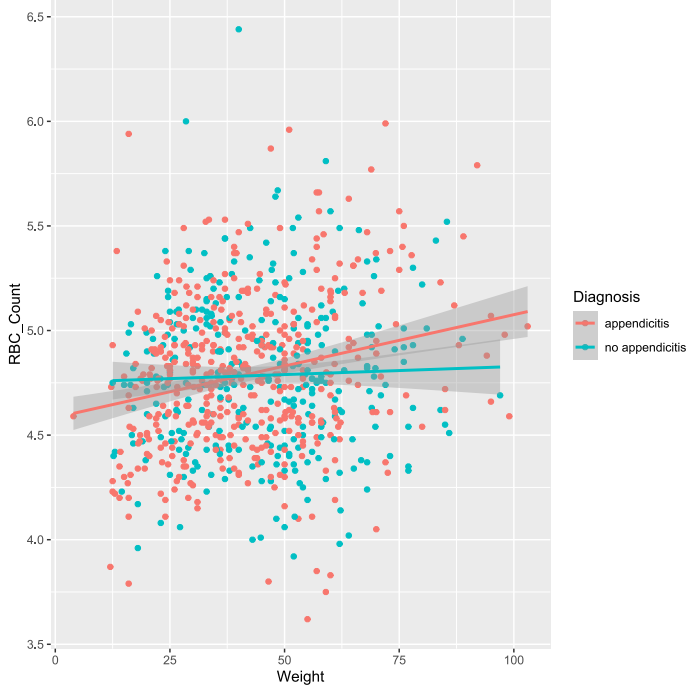
```
g <- ggplot(app_data |> drop_na(RBC_Count, Weight, Diagnosis) |> filter(RBC_Count < 8),
            aes(x = Weight, y = RBC_Count, color = Diagnosis))
g + geom_point()
```



`ggplot2` Scatter Plots with Trend Line

- Add trend lines easily with `geom_smooth()`

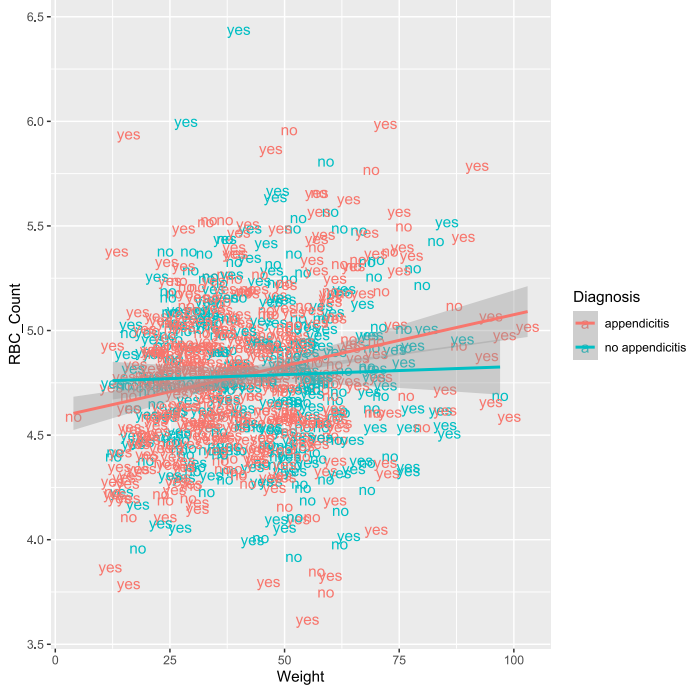
```
g <- ggplot(app_data |> drop_na(RBC_Count, Weight, Diagnosis) |> filter(RBC_Count < 8),
            aes(x = Weight, y = RBC_Count, color = Diagnosis))
g + geom_point() +
    geom_smooth(method = lm)
```



`ggplot2` Scatter Plots with Text Points

- Text for points with `geom_text()`

```
g <- ggplot(app_data |> drop_na(RBC_Count, Weight, Diagnosis) |> filter(RBC_Count < 8),
            aes(x = Weight, y = RBC_Count, color = Diagnosis))
g + geom_text(aes(label = Nausea)) +
    geom_smooth(method = lm)
```



`ggplot2` Scatter Plots with Text

- Can add a note to the plot with `geom_text()` too

```
correlation <- app_data |>
  drop_na(RBC_Count, Weight, Diagnosis) |>
  filter(RBC_Count < 8) |>
  group_by(Diagnosis) |>
  select(RBC_Count, Weight, Diagnosis) |>
  summarize(cor_vals = cor(RBC_Count, Weight, use = "complete.obs"))
correlation
```

```
## # A tibble: 2 × 2
##   Diagnosis       cor_vals
##   <chr>              <dbl>
## 1 appendicitis      0.233
## 2 no appendicitis   0.0353
```

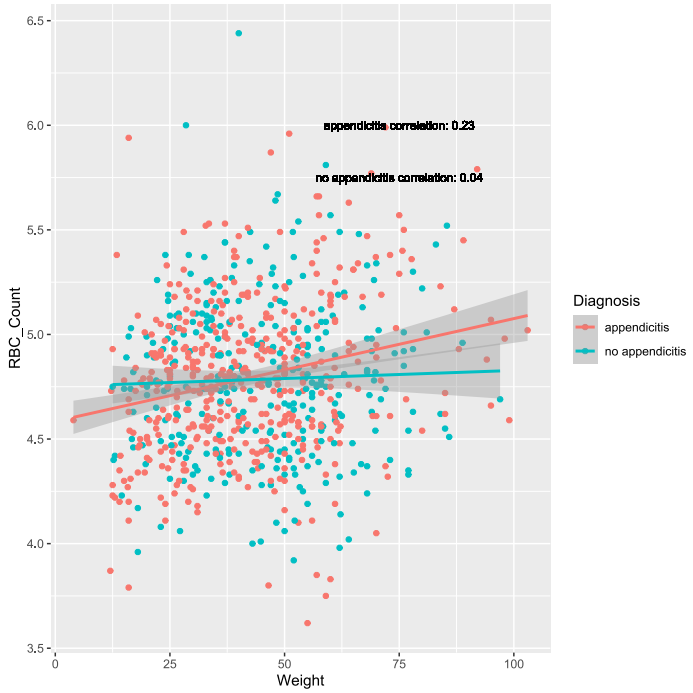
`ggplot2` Scatter Plots with Text

- Can add a note to the plot with `geom_text()` too

```
g <- ggplot(app_data |> drop_na(RBC_Count, Weight, Diagnosis) |> filter(RBC_Count < 8))
g + geom_point(aes(x = Weight, y = RBC_Count, color = Diagnosis)) +
    geom_smooth(method = lm, aes(x = Weight, y = RBC_Count, color = Diagnosis)) +
    geom_text(x = 75, y = 6, size = 3,
              label = paste0(correlation[1,1], " correlation: ", round(correlation[1,2], 2))) +
    geom_text(x = 75, y = 5.75, size = 3,
              label = paste0(correlation[2,1], " correlation: ", round(correlation[2,2], 2)))
```

`ggplot2` Scatter Plots with Text

- Can add a note to the plot with `geom_text()` too

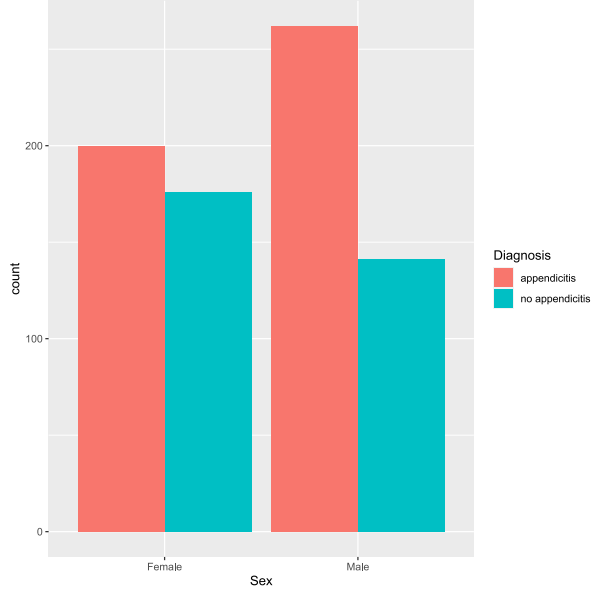


`ggplot2` Faceting

Suppose we want to take one of our plots and produce similar plots across another variable!

How to create this plot across each `Management` category? Use **faceting**!

```
ggplot(data = app_data |> drop_na(SexF, DiagnosisF), aes(x = SexF, fill = DiagnosisF)) +
  geom_bar(position = "dodge") +
  labs(x = "Sex")+
  scale_fill_discrete("Diagnosis")
```



`ggplot2` Faceting

`facet_wrap(~ var)` - creates a plot for each setting of `var`

- Can specify `nrow` and `ncol` or let R figure it out

`ggplot2` Faceting

`facet_wrap(~ var)` - creates a plot for each setting of `var`

- Can specify `nrow` and `ncol` or let R figure it out

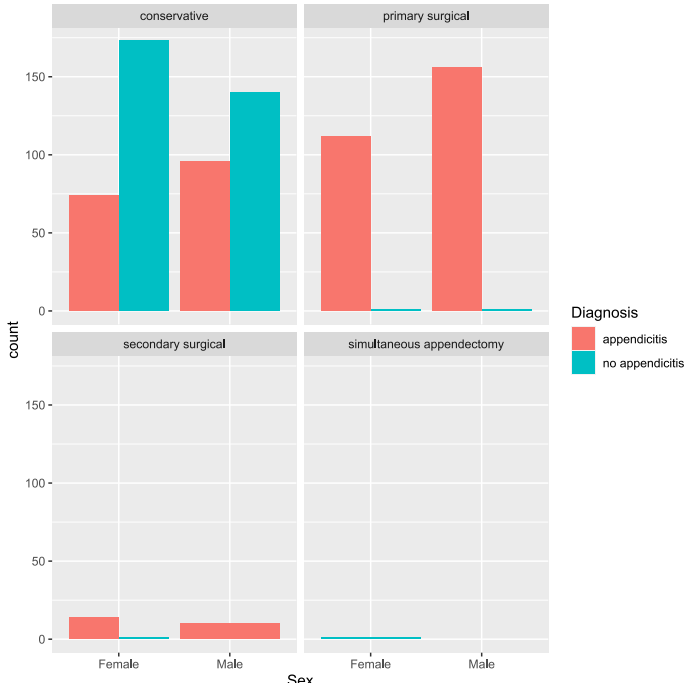
`facet_grid(var1 ~ var2)` - creats a plot for each combination of `var1` and `var2`

- `var1` values across rows
- `var2` values across columns
- Use `. ~ var2` or `var1 ~ .` to have only one row or column

`ggplot2` Faceting

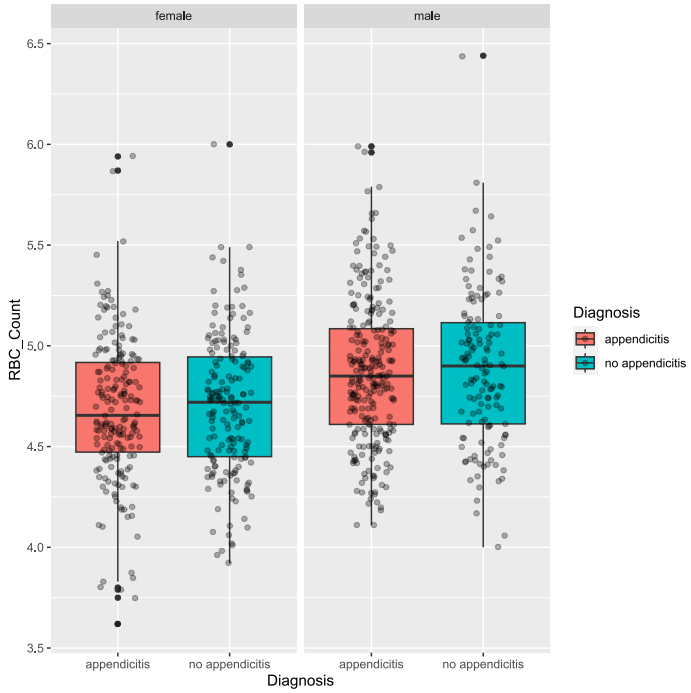
- `facet_wrap(~ var)` - creates a plot for each setting of `var`

```
ggplot(data = app_data |> drop_na(SexF, DiagnosisF, Management), aes(x = SexF, fill = DiagnosisF)) +
  geom_bar(position = "dodge") +
  labs(x = "Sex")+
  scale_fill_discrete("Diagnosis") +
  facet_wrap(~ Management)
```



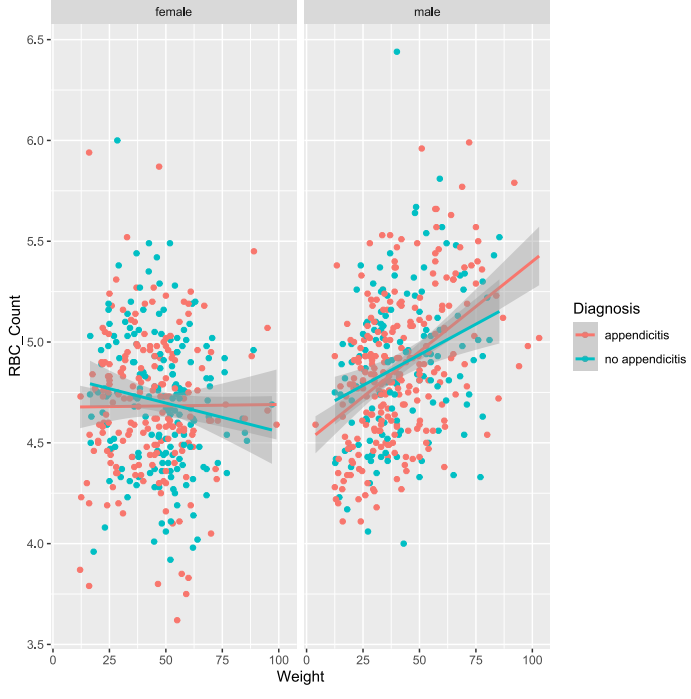
ggplot2 FacetingCan be Used with Any ggplot

```
g <- ggplot(app_data |> drop_na(RBC_Count, Diagnosis, Sex) |> filter(RBC_Count < 8),
            aes(x = Diagnosis, y = RBC_Count, fill = Diagnosis))
g + geom_boxplot() +
  geom_jitter(width = 0.2, alpha = 0.3) +
    facet_wrap(~ Sex)
```



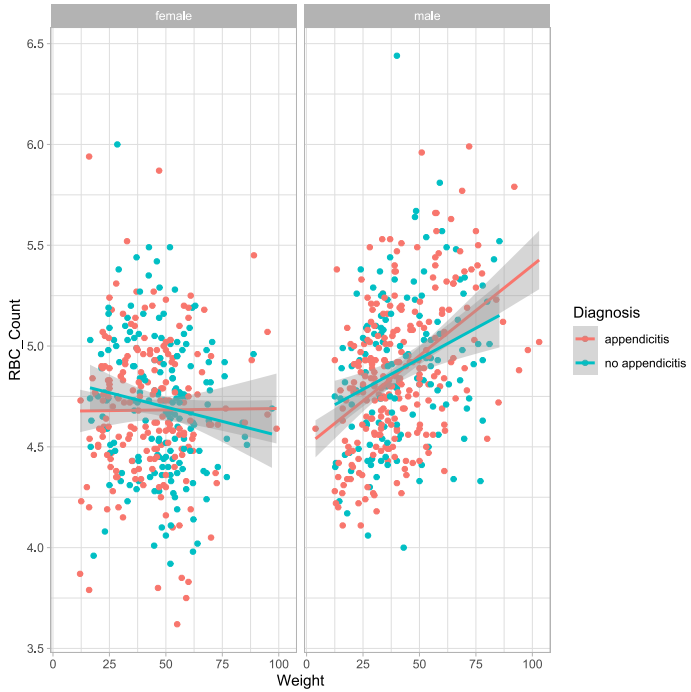
ggplot2 FacetingCan be Used with Any ggplot

```
g <- ggplot(app_data |> drop_na(RBC_Count, Weight, Diagnosis, Sex) |> filter(RBC_Count < 8),
            aes(x = Weight, y = RBC_Count, color = Diagnosis))
g + geom_point() +
    geom_smooth(method = lm) +
    facet_wrap(~ Sex)
```



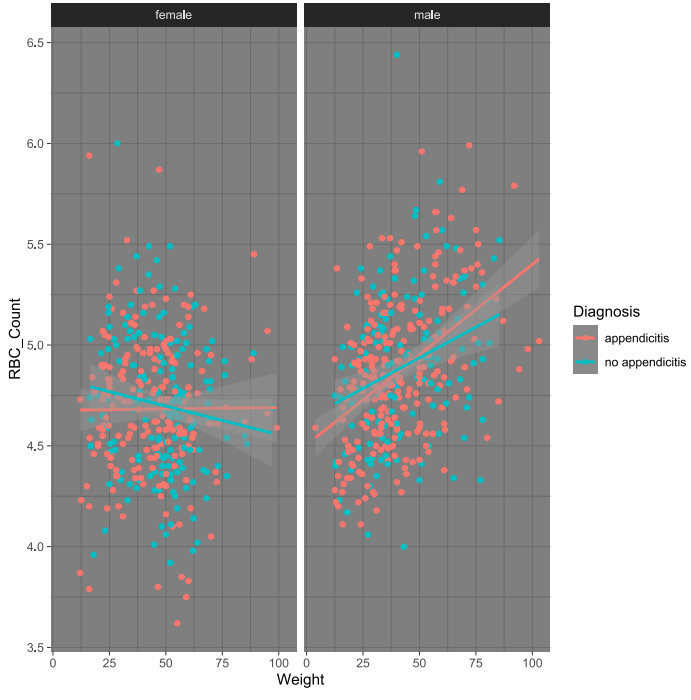
ggplot2 Themes

```
g <- ggplot(app_data |> drop_na(RBC_Count, Weight, Diagnosis, Sex) |> filter(RBC_Count < 8),
            aes(x = Weight, y = RBC_Count, color = Diagnosis))
g + geom_point() +
    geom_smooth(method = lm) +
    facet_wrap(~ Sex) +
    theme_light()
```



ggplot2 Themes

```
g <- ggplot(app_data |> drop_na(RBC_Count, Weight, Diagnosis, Sex) |> filter(RBC_Count < 8),
            aes(x = Weight, y = RBC_Count, color = Diagnosis))
g + geom_point() +
    geom_smooth(method = lm) +
    facet_wrap(~ Sex) +
    theme_dark()
```

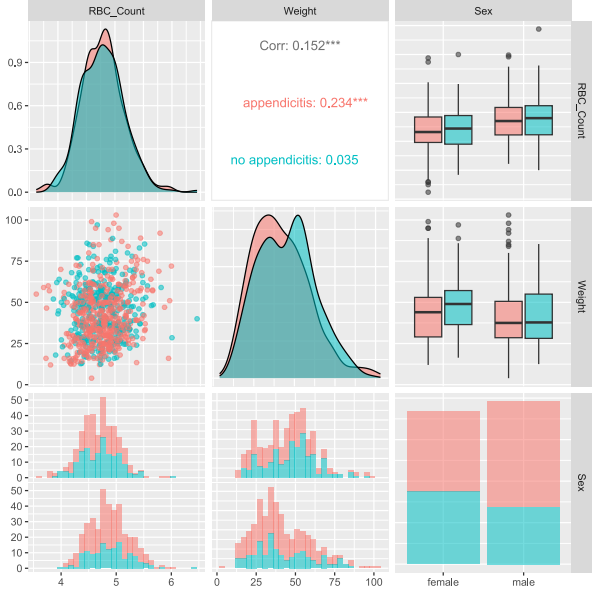


`ggplot2` Extensions

Many extension packages that do nice things!

- `GGally` package has the `ggpairs()` function

```
library(GGally) #install if needed
ggpairs(app_data |> drop_na(RBC_Count, Weight, Diagnosis, Sex) |> filter(RBC_Count < 8),
        aes(colour = Diagnosis, alpha = 0.4), columns = c("RBC_Count", "Weight", "Sex"))
```



`ggplot2` Extensions

Over 100 registered extensions at https://exts.ggplot2.tidyverse.org/!

- `gganimate` package allows for the creation of gifs

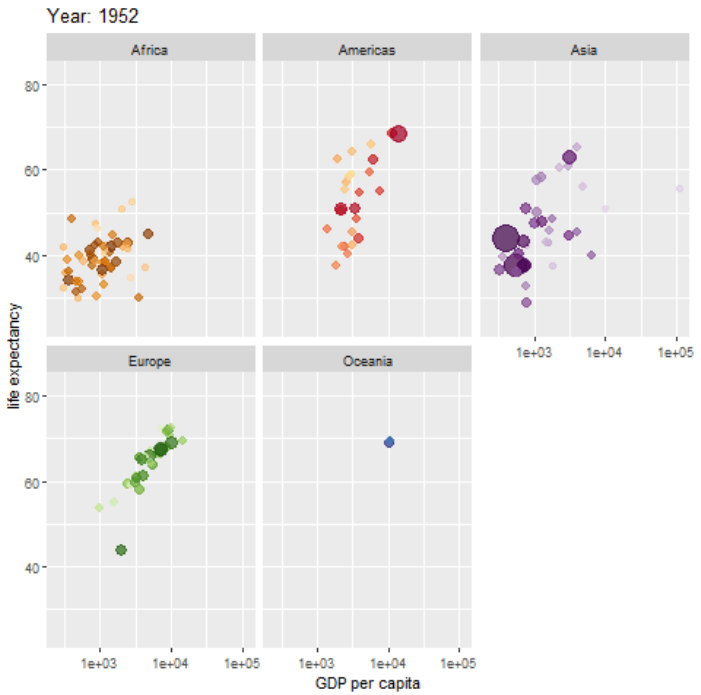
```
#install each if needed
library(gapminder)
library(gganimate)
library(gifski)

gif <- ggplot(gapminder, aes(gdpPercap, lifeExp, size = pop, colour = country)) +
          geom_point(alpha = 0.7, show.legend = FALSE) +
          scale_colour_manual(values = country_colors) +
          scale_size(range = c(2, 12)) +
          scale_x_log10() +
          facet_wrap(~continent) +
          # Here comes the gganimate specific bits
          labs(title = 'Year: {frame_time}', x = 'GDP per capita', y = 'life expectancy') +
          transition_time(year) +
          ease_aes('linear')
anim_save(filename = "img/myGif.gif", animation = gif, renderer = gifski_renderer())
```

`ggplot2` Extensions

Over 100 registered extensions at https://exts.ggplot2.tidyverse.org/!

- `gganimate` package allows for the creation of gifs



Recap!

General `ggplot2` things:

- Can set local or global `aes()`
  - Generally, only need `aes()` if setting a mapping value that is dependent on the data
- Modify titles/labels by adding more layers
- Use either `stat` or `geom` layer
- Faceting (multiple plots) via `facet_grid()` or `facet_wrap()`
- `esquisse` is a great package for exploring ggplot2!

Big Recap!

Goal: Understand types of data and their distributions

- Numerical summaries (across subgroups)
    - Contingency Tables
    - Mean/Median
    - Standard Deviation/Variance/IQR
    - Quantiles/Percentiles
- Graphical summaries (across subgroups)
    - Bar plots
    - Histograms
    - Box plots
    - Scatter plots