Data exploration with `tidyverse`

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S0: Prior to lecture

Preparing for this lecture

- All materials are on Ed and https://github.com/kevinwang09/2017_STAT3914.
- Please run these codes on your laptop,

```
## Might be a while...
install.packages(c("ggplot2","dplyr", "readr","tidyr","janitor","plotly",
                   "devtools","learnr","gapminder", "e1071"))

library(devtools)
install_github("kevinwang09/2017_STAT3914", subdir = "learnr3914")
```

- Familiar yourself with the `iris` dataset. Typing `iris` into `R` console should load this data. Pay attention to its column, row names, summary statistics and structure of each column.

S1: Necessary of Applied Statistics

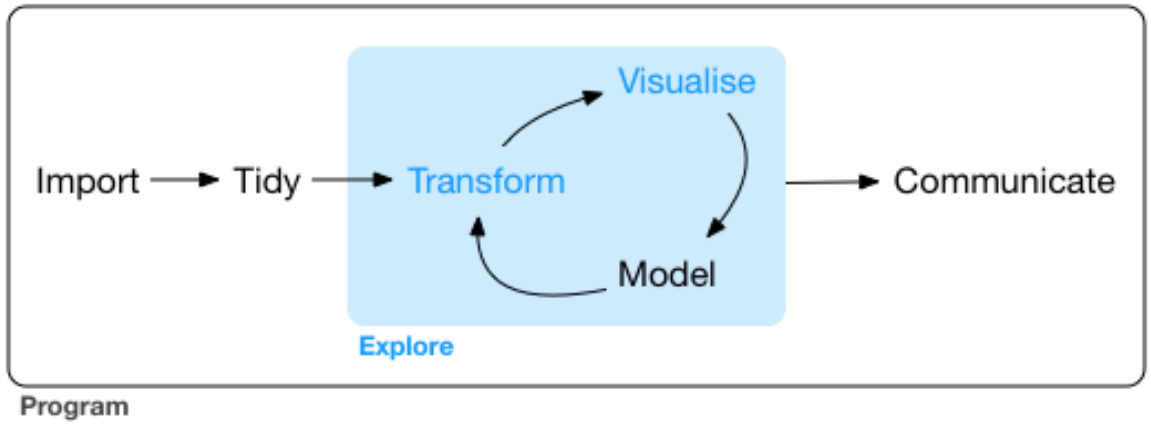
Good statistical discoveries don't fall out from the sky

- Statisticians are great at many things:
  1. Understanding data characteristics
  2. Building statistical/mathematical models
  3. Repeat 1 and 2…like…a lot…
  4. Extract insights
- But the mother of all these, i.e. **preparing data** is not trivial. (e.g. STAT2xxx lab exams)

Let X be the thing I want…

- The real problem is not applying fancy shampoo for your cat. It is getting your cat into the bathtub.

Hidden side of being a statistician



- Assume we have data
- Assume we have data that can answer our questions
- Assume we have cleaned data
- Assume we interrogated the right aspects of the data using appropriate statistics
- Assume we did everything right, communicate insights with others

Aim: effectively clean your data (1)

- "Your statistical model is only ever going to be as good as your data quality" — Kevin Wang.
- There will be no recipe, there will be a lot of back and forth exploration.
- Computational and visualisation tools.

SepAl....LeNgth	Sepal.? Width	petal.Length(*&^	petal.$%^&Width	species^
6.2	2.8	4.8	1.8	virginica
6.8	2.8	4.8	1.4	versicolor
7.6	3	6.6	2.1	virginica
NA	NA	NA	NA	NA
5.4	3.4	1.7	0.2	setosa

- Corrupted column names, 100% missing column, 100% missing rows, rows with at least 1 missing value.
- Most severe problem: rows with random values.

Aim: effectively clean your data (2)

- The classical `iris` data is known to be well-separated.
- Running Support Vector Machine (SVM) classification algorithm on the cleaned `iris` data has very low number of classifications.
- True `iris` data

	setosa	versicolor	virginica
setosa	50	0	0
versicolor	0	48	2
virginica	0	2	48

Aim: effectively clean your data (3)

- Not so much when you have corruptions.
- In addition of introduce missing values, I also created non-sense rows in the data, they corrupted classification results.

	setosa	versicolor	virginica
setosa	89	25	27
versicolor	0	47	4
virginica	0	3	46

Summary of this lecture

- Passive learning is not going to work.
- S1: Introduction
- S2: Reading in data using `readr` and `readxl`
- S3: Basic data cleaning using `janitor`
- S4: Clean coding using `magrittr`
- S5: Data filtering using `dplyr`
- S6: Data visualisation using `ggplot2`
- S7: Conclusion

S2: Reading data

Better read/write data

- `base` R functions are not sufficient for modern uses.
- `readr` functions are superior in data import warnings, column type handling, speed, scalability and consistency.

```
library(readr)
```

Reading data using (1)

```
dirtyIris = readr::read_csv("dirtyIris.csv")
```

```
## Parsed with column specification:
## cols(
##   SepAl....LeNgth = col_double(),
##   `Sepal.?    Width` = col_double(),
##   `petal.Length(*&^` = col_double(),
##   `petal.$#^&Width` = col_double(),
##   `SPECIES^` = col_character(),
##   allEmpty = col_character()
## )
```

```
class(dirtyIris) ## `tibble` is a `data.frame` with better formatting.
```

```
## [1] "tbl_df"     "tbl"        "data.frame"
```

- `readxl` and `haven` (for SAS, SPSS etc) packages work similarly.

Reading data using (2)

```
dirtyIris
```

```
## # A tibble: 650 x 6
##   SepAl....LeNgth `Sepal.?    Width` `petal.Length(*&^` `petal.$#^&Width`
##             <dbl>               <dbl>               <dbl>              <dbl>
## 1       7.7000000                 3.8                 6.7          2.200000
## 2      -0.1842525                  NA                  NA          1.099848
## 3       7.2000000                 3.6                 6.1          2.500000
## 4       6.3000000                 2.3                 4.4          1.300000
## 5       5.6000000                 2.9                 3.6          1.300000
## # ... with 645 more rows, and 2 more variables: `SPECIES^` <chr>,
## #   allEmpty <chr>
```

- We now proceed to data cleaning on the `dirtyIris` dataset.

Too trivial? Here is a short homework

Here is a dataset. Click here.

1. Write 2 sentences about what is a `.gmt` file and who publishes this format?
2. Which packages can read in `.gmt` files?
3. How to download this package?
4. What class is this data once read into `R`? Is it a `data.frame`?
5. The data contains 50 different gene-sets. What is the size of each gene-set?
6. What is the mostly frequent mentioned 6 genes?

S3: Cleaned data

What is clean data?

Clean data is a data set that allows you to do statistical modelling without extra processing

1. Good documentation on the entire data.
2. Each column is a **variable**. The name should be informative, and:
   - No bad characters/formatting @KevinWang009
   - No inconsistent capitalisation or separators (`Cricket_australia` vs `cricket.Australia`)
3. Each row is an **observation**:
   - No bad characters
   - No poorly designed row names (3, 2, 5, …)
   - No repeated row names (a, a.1, b, b.1, …)

Data cleaning in

- Clean data is a well-designed `data.frame`.
- Column type (esp. dates and factors) handling was the primary reason we used `readr` instead of `base` R when importing data.
- Our goal: clean the `dirtyIris` data to be exactly the same as the original `iris` data.
    - Basic data cleaning using `janitor` package.
    - More advanced data manipulation through `dplyr`.

: basic data cleaning

- Clean up the bad column names

```
library(janitor)
library(dplyr)
glimpse(dirtyIris)
```

```
## Observations: 650
## Variables: 6
## $ SepAl....LeNgth  <dbl> 7.70000000, -0.18425254, 7.20000000, 6.300000...
## $ Sepal.?    Width <dbl> 3.8000000, NA, 3.6000000, 2.3000000, 2.900000...
## $ petal.Length(*&^ <dbl> 6.7000000, NA, 6.1000000, 4.4000000, 3.600000...
## $ petal.$#^&Width  <dbl> 2.2000000, 1.0998477, 2.5000000, 1.3000000, 1...
## $ SPECIES^         <chr> "virginica", "setosa", "virginica", "versicol...
## $ allEmpty         <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, N...
```

```
## Clean up column names
better = clean_names(dirtyIris)
glimpse(better)
```

```
## Observations: 650
## Variables: 6
## $ sepal_length <dbl> 7.70000000, -0.18425254, 7.20000000, 6.30000000, ...
## $ sepal_width  <dbl> 3.8000000, NA, 3.6000000, 2.3000000, 2.9000000, -...
## $ petal_length <dbl> 6.7000000, NA, 6.1000000, 4.4000000, 3.6000000, 0...
## $ petal_width  <dbl> 2.2000000, 1.0998477, 2.5000000, 1.3000000, 1.300...
```

: removal of empty rows and columns

- Purely empty rows/columns are non-informative.

```
## Removing empty rows/columns
evenBetter = remove_empty_rows(better)
evenBetter = remove_empty_cols(evenBetter)

glimpse(evenBetter)
```

```
## Observations: 650
## Variables: 5
## $ sepal_length <dbl> 7.70000000, -0.18425254, 7.20000000, 6.30000000, ...
## $ sepal_width  <dbl> 3.8000000, NA, 3.6000000, 2.3000000, 2.9000000, -...
## $ petal_length <dbl> 6.7000000, NA, 6.1000000, 4.4000000, 3.6000000, 0...
## $ petal_width  <dbl> 2.2000000, 1.0998477, 2.5000000, 1.3000000, 1.300...
## $ species      <chr> "virginica", "setosa", "virginica", "versicolor",...
```

: removal of rows with NA

- Genuinely missing values should be retained, but in this case, the NA's were added. Only use `na.omit` when you 100% certain of the structure of your data.

```
evenBetterBetter = na.omit(evenBetter)
almostIris = evenBetterBetter
```

```
glimpse(almostIris)
```

```
## Observations: 241
## Variables: 5
## $ sepal_length <dbl> 7.70000000, 7.20000000, 6.30000000, 5.60000000, 6...
## $ sepal_width  <dbl> 3.8000000, 3.6000000, 2.3000000, 2.9000000, 2.500...
## $ petal_length <dbl> 6.7000000, 6.1000000, 4.4000000, 3.6000000, 4.900...
## $ petal_width  <dbl> 2.2000000, 2.5000000, 1.3000000, 1.3000000, 1.500...
## $ species      <chr> "virginica", "virginica", "versicolor", "versicol...
```

```
glimpse(iris)
```

```
## Observations: 150
## Variables: 5
## $ Sepal.Length <dbl> 5.1, 4.9, 4.7, 4.6, 5.0, 5.4, 4.6, 5.0, 4.4, 4.9,...
## $ Sepal.Width  <dbl> 3.5, 3.0, 3.2, 3.1, 3.6, 3.9, 3.4, 3.4, 2.9, 3.1,...
## $ Petal.Length <dbl> 1.4, 1.4, 1.3, 1.5, 1.4, 1.7, 1.4, 1.5, 1.4, 1.5,...
## $ Petal.Width  <dbl> 0.2, 0.2, 0.2, 0.2, 0.2, 0.4, 0.3, 0.2, 0.2, 0.1,...
## $ Species      <fct> setosa, setosa, setosa, setosa, setosa, setosa,...
```

S4: Clean coding

Coding complexity increases with the number of brackets

- The "inside out" structure of coding isn't great for human reading.

```
mean(almostIris$sepal_length)
```

```
## [1] 3.602734
```

```
plot(density(almostIris$sepal_length), col = "red", lwd = 2)
```

Piping: read code from left to right

- We introduce a new notation: " x %>% f " means "f(x)". We call this operation as "x pipe f".
- Compounded operations are possible. Keyboard shortcut is Cmd+shift+M.

```
almostIris$sepal_length %>% mean
```

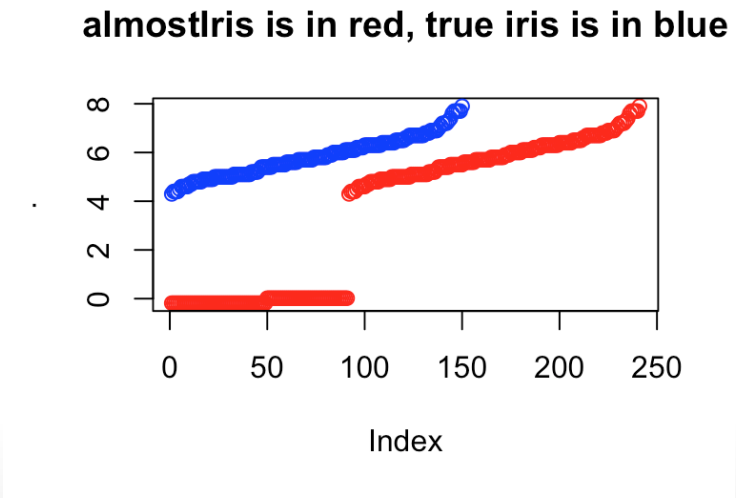
```
## [1] 3.602734
```

```
almostIris$sepal_length %>%
  density %>%
  plot(col = "red", lwd = 2)
```

Using an informative variable (Sepal.Length) in `iris` to guide cleaning

```
almostIris$sepal_length %>%
  sort %>%
  plot(col = "red", main = "almostIris is in red, true iris is in blue")

iris$Sepal.Length %>%
  sort %>%
  points(col = "blue")
```



S5: `dplyr`: data subsetting master

Traditional way of subsetting data in R (1)

- If I want remove all observations with `sepal_length` less than 2:

```
cleanIris = almostIris[almostIris[, "sepal_length"] > 2, ]
glimpse(cleanIris)
```

```
## Observations: 150
## Variables: 5
## $ sepal_length <dbl> 7.7, 7.2, 6.3, 5.6, 6.3, 5.5, 5.0, 6.4, 6.2, 6.7,...
## $ sepal_width  <dbl> 3.8, 3.6, 2.3, 2.9, 2.5, 2.4, 3.3, 2.7, 3.4, 3.1,...
## $ petal_length <dbl> 6.7, 6.1, 4.4, 3.6, 4.9, 3.7, 1.4, 5.3, 5.4, 4.4,...
## $ petal_width  <dbl> 2.2, 2.5, 1.3, 1.3, 1.5, 1.0, 0.2, 1.9, 2.3, 1.4,...
## $ species      <chr> "virginica", "virginica", "versicolor", "versicol...
```

- We now have agreement over the size of the two data!
- But this subsetting code is a bit cumbersome!

Traditional way of subsetting data in R (2)

- Subsetting data in base R might not be the most concise solution.
- Suppose we wish to extract first two rows of column `sepal_length` and `sepal_width` in the `cleanIris` data:

```
## Assuming you know the position of column names.
## But what if you resample your data?
cleanIris[1:2, c(1, 2)]

## Assuming you know the position of column names.
## Also assuming the first two columns satisfy certain properties.
cleanIris[1:2, c(T, T, F, F, F)]

## Much better!
## What if you can't type out all the column names
## due to the size of your data?
cleanIris[1:2, c("sepal_length", "sepal_width")]
```

Traditional way of subsetting data in R (3)

- Even more complex subsetting: we want to extract rows based on some compounded criteria and select columns based on special keywords.

```
cleanIris[(cleanIris[,"sepal_length"] < 5) &
            (cleanIris[,"sepal_width"] < 3), c("petal_length", "sepal_length")]
```

```
## # A tibble: 4 x 2
##   petal_length sepal_length
##          <dbl>        <dbl>
## 1          1.3          4.5
## 2          3.3          4.9
## 3          1.4          4.4
## 4          4.5          4.9
```

- (Optional) A pro `R` user might know about the `subset` function, but it suffers the same problem of not able to have multiple subsetting criteria without predefined variables.

Subsetting data using

- Think of subsetting rows and columns as two **separate different procedures**:
- `select` columns are operations on variables, and
- `filter` rows are operations on observations
- See dplyr cheatsheet.

```
library(dplyr)

cleanIris %>%
  filter(sepal_length < 5,
         sepal_width < 3) %>%
  select(contains("length"))
```

```
## # A tibble: 4 x 2
##   sepal_length petal_length
##          <dbl>        <dbl>
## 1          4.5          1.3
## 2          4.9          3.3
## 3          4.4          1.4
## 4          4.9          4.5
```

`arrange` for ordering rows

```
arrangeCleanIris = cleanIris %>%
  arrange(sepal_length, sepal_width, petal_length, petal_width)

## The true iris data
arrangeIris = iris %>%
  clean_names() %>%
  arrange(sepal_length, sepal_width, petal_length, petal_width)
```

Checking if we cleaned the data properly

- We sorted both the processed `dirtyIris` data and the arranged `iris` data.

```
## The `Species` column is character or factor
all.equal(arrangeCleanIris, arrangeIris)
```

```
## [1] "Incompatible type for column `species`: x character, y factor"
```

```
arrangeIris = arrangeIris %>%
  mutate(species = as.character(species))

## Great!
all.equal(arrangeCleanIris, arrangeIris)
```

```
## [1] TRUE
```

Job done!


EXCELLENT, MY LORD
I SHALL PREPARE THE GRANDEST
OF FEASTS IN CELEBRATION
quickmeme.com

But what about the modelling?

- Cleaned data is one thing, but again, we need to extract insights about the data.
- This can be done via summary statistics, visualisation or running statistical models.
- "Your statistical insights is only going to be as good as the question you ask" — Kevin Wang.

: **mutate** create new columns

```
iris_mutated = mutate(cleanIris,
      V1 = sepal_length - sepal_width,
      V2 = V1 + sepal_width
      )

iris_mutated
```

```
## # A tibble: 150 x 7
##   sepal_length sepal_width petal_length petal_width    species    V1    V2
##          <dbl>       <dbl>        <dbl>       <dbl>      <chr> <dbl> <dbl>
## 1          7.7         3.8          6.7         2.2  virginica   3.9   7.7
## 2          7.2         3.6          6.1         2.5  virginica   3.6   7.2
## 3          6.3         2.3          4.4         1.3 versicolor   4.0   6.3
## 4          5.6         2.9          3.6         1.3 versicolor   2.7   5.6
## 5          6.3         2.5          4.9         1.5 versicolor   3.8   6.3
## # ... with 145 more rows
```

`group_by` + `summarise` will create summary statistics for grouped variables

```
bySpecies = cleanIris %>%
  group_by(species)

bySpecies
```

```
## # A tibble: 150 x 5
## # Groups:   species [3]
##   sepal_length sepal_width petal_length petal_width    species
##          <dbl>       <dbl>        <dbl>       <dbl>      <chr>
## 1          7.7         3.8          6.7         2.2  virginica
## 2          7.2         3.6          6.1         2.5  virginica
## 3          6.3         2.3          4.4         1.3 versicolor
## 4          5.6         2.9          3.6         1.3 versicolor
## 5          6.3         2.5          4.9         1.5 versicolor
## # ... with 145 more rows
```

special select functions (advanced)

- `select` only if a column satisfy a certain condition

```
bySpecies %>%
  summarise_if(is.numeric,
               funs(m = mean))
```

```
## # A tibble: 3 x 5
##      species sepal_length_m sepal_width_m petal_length_m petal_width_m
##        <chr>          <dbl>         <dbl>          <dbl>         <dbl>
## 1     setosa          5.006         3.428          1.462         0.246
## 2 versicolor          5.936         2.770          4.260         1.326
## 3  virginica          6.588         2.974          5.552         2.026
```

```
cleanIris %>%
  select(starts_with("sepal")) %>%
  top_n(3, sepal_width)
```

```
## # A tibble: 3 x 2
##   sepal_length sepal_width
##          <dbl>       <dbl>
## 1          5.2         4.1
## 2          5.5         4.2
## 3          5.7         4.4
```

`left_join` for merging data

```
flowers = data.frame(species = c("setosa", "versicolor", "virginica"),
                     comments = c("meh", "kinda_okay", "love_it!"))

## cleanIris has the priority in this join operation
iris_comments = left_join(cleanIris, flowers, by = "species")
```

```
## Warning: Column `species` joining character vector and factor, coercing
## into character vector
```

```
## Randomly sampling 6 rows
sample_n(iris_comments, 6)
```

```
## # A tibble: 6 x 6
##   sepal_length sepal_width petal_length petal_width    species   comments
##          <dbl>       <dbl>        <dbl>       <dbl>      <chr>     <fctr>
## 1          7.2         3.2          6.0         1.8  virginica   love_it!
## 2          5.6         2.9          3.6         1.3 versicolor kinda_okay
## 3          5.1         3.4          1.5         0.2     setosa        meh
## 4          6.8         3.0          5.5         2.1  virginica   love_it!
```

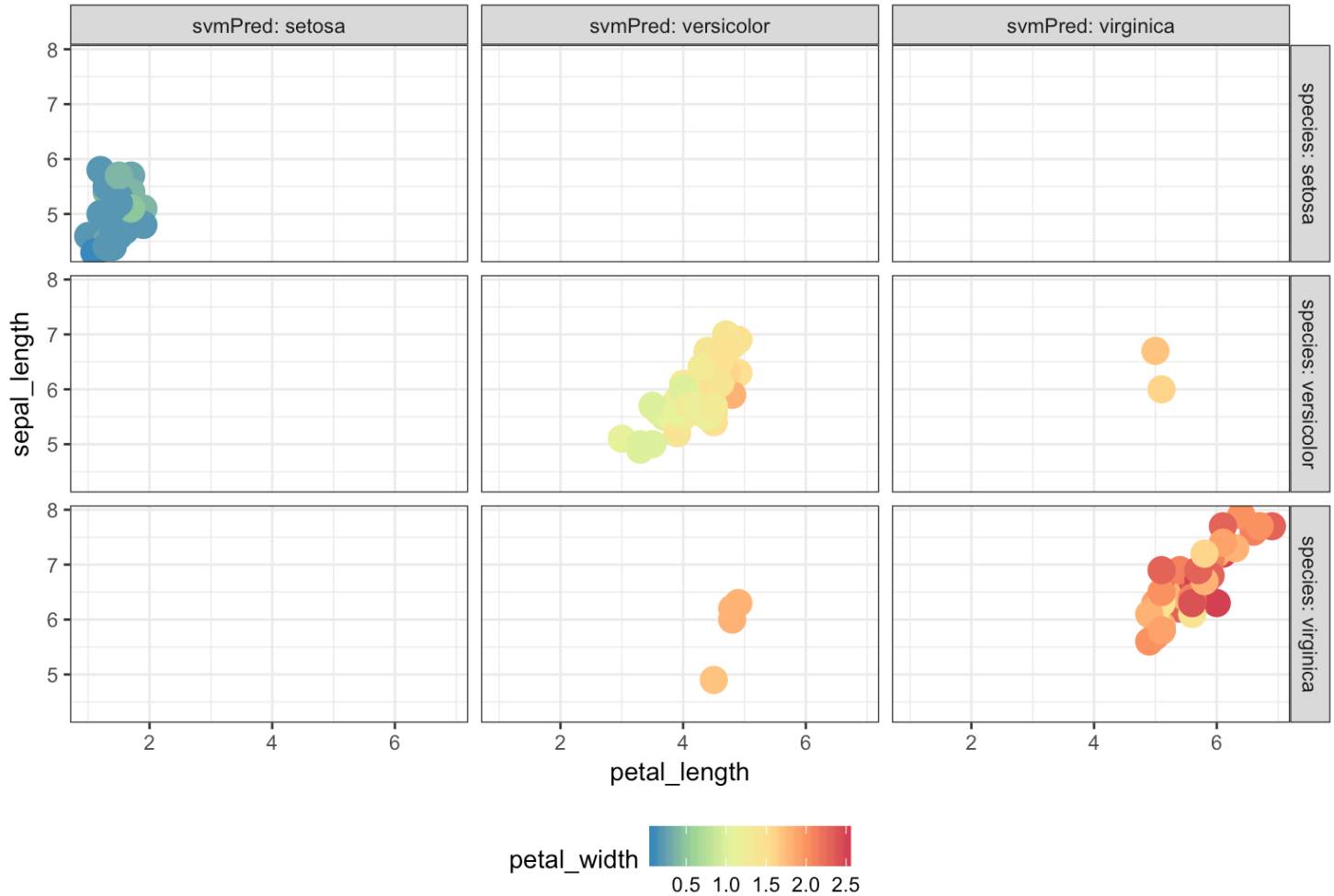
S6: `ggplot2`: the best visualisation package

Why do we visualise? (1)

- `datasaurus`: all statistics describe the data in some limited ways.
- Plots usually give more dimensions to our analysis.
- Suppose in our `cleanIris` data, we will use `sepal_length` and `petal_length` as SVM predictors for the classes of iris flowers.

	setosa	versicolor	virginica
setosa	50	0	0
versicolor	0	48	2
virginica	0	4	46

Why do we visualise? (2)



: the philosophy

- Di Cook - the real reason that you should use `ggplot2` is that, its design will force you to use a certain **grammar** when producing a plot.
- $\frac{1}{n}\sum_{i=1}^{n} X_i$ is a transformation of random variables, i.e., a statistic which provides insights into a data.
- Similarly, ggplot is also a statistic, because we take components of the data and presented it in an informative way.
- Publishing quality, rigourous syntax and design, flexible customisations, facetting.

tutorial sheet

- If you managed to install all packages successfully, you should be able to run the following to get an interactive tutorial sheet.

```
library(learnr3914)
learnggplot2()
```

- Otherwise, please download and compile the "ggplot2_basic_tutorial.Rmd" from Ed or here
- If all fails, try https://gauss17gon.shinyapps.io/ggplot2_basic_tutorial or https://garthtarr.shinyapps.io/ggplot2_basic_tutorial

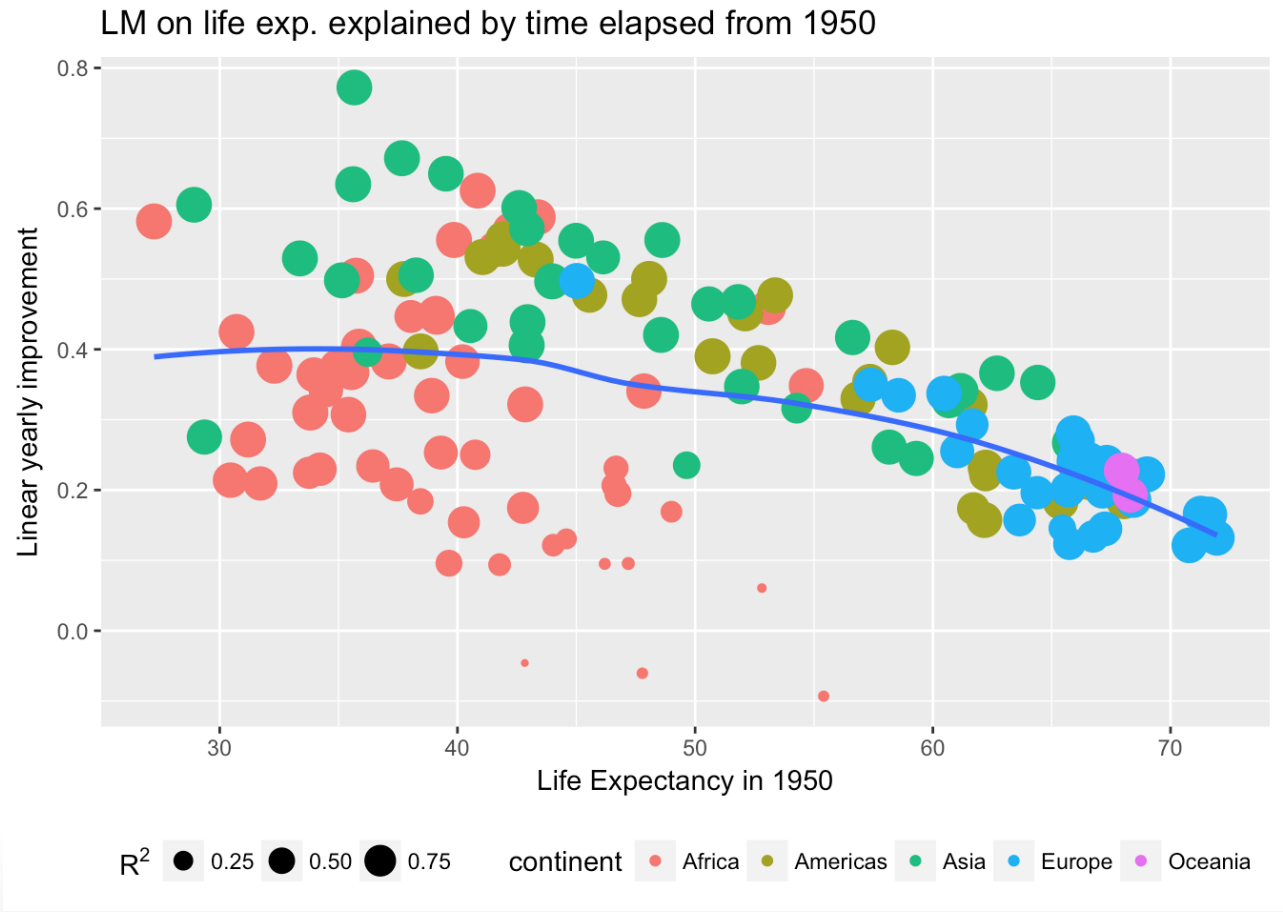
S7: Conclusion

tidy data, coding, modelling and reporting

- `tidyverse` is a collection of 20+ packages built on the philosophy of being organised for the purpose of collaboration.
- These functions:
  - Well designed programming and data science solutions.
  - They will always throw errors at you if you don't have a thorough understanding of your data.
  - Capable for functional programming.

Peek at the

http://edinbr.org/edinbr/2016/05/11/may-Hadley-Update2-PostingTalk.html



Interactive plotting from ggplot

```
library(plotly)
ggplotly(p2)
```

Advice in the future

- Use RStudio + RMarkdown to document your codes.
- Learn some computational tools. They are not statistics, but not learning them could inhibit your career aspects.
- Find "cool" components and adapt those into your work routine. (Hint: start with all RStudio cheatsheets and build up gradually.)
- Take time to re-analyse an old dataset.
- Learn core functions and vignette.
- Don't forget the theories and interpretations! This is a course about statistics after all, not Cranking-Out-Numbers-Less-Than-0.05-And-Reject-Null-Hypothesis-101.

Session Info and References

- Dr. Garth Tarr
- tidyverse.org
- github.com/sfirke/janitor
- gapminder.org
- rstudio.com