Introduction to R

(with Tidyverse)

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Babraham Bioinformatics

R can just be a calculator

```
> 3+2
[1] 5

> 2/7
[1] 0.2857143

> 5^10
[1] 9765625
```

Storing numerical data in variables

```
x <- 10
20 -> y

x
[1] 10

x+y
[1] 30

z <- x+y
```

Variable names

- The rules
  - Can't start with a number
  - Made up of letters, numbers dots and underscores

- The guidelines
  - Make the name mean something (`x` = bad, `weight` = good)
  - Keep variables all lower case
  - Separate words with dots or underscores

    `gene_name` or `gene.name` are the preferred options

Storing text in variables

```
height <- 167

my_name <- "laura"

my_other_name <- 'biggins'
```

Running a simple function

```
sqrt(10)
[1] 3.162278
```

Looking up help

```
?sqrt
```

MathFun {base} R Documentation

Miscellaneous Mathematical Functions

Description

`abs(x)` computes the absolute value of x, `sqrt(x)` computes the (principal) square root of x, $\sqrt{x}$.

The naming follows the standard for computer languages such as C or Fortran.

Usage

```
abs(x)
sqrt(x)
```

Arguments

`x`	a numeric or `complex` vector or array.

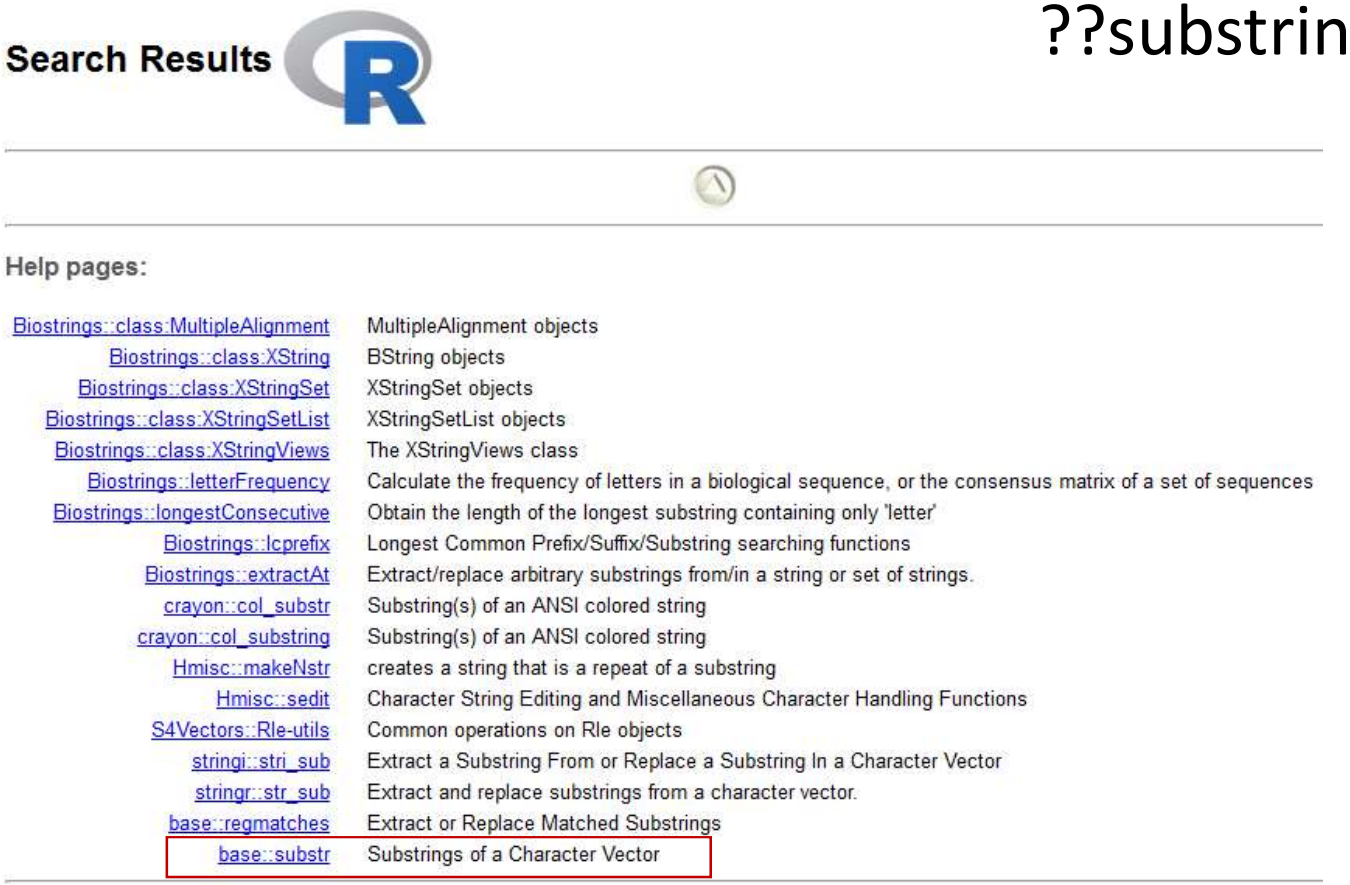
Details

These are internal generic primitive functions: methods can be defined for them individually or via the `Math` group generic. For complex arguments (and the default method), `z`, `abs(z) == Mod(z)` and `sqrt(z) == z^0.5`.

`abs(x)` returns an `integer` vector when `x` is `integer` or `logical`.

Searching Help

??substring



Search Results

Help pages:

Biostrings::class:MultipleAlignment	MultipleAlignment objects
Biostrings::class:XString	BString objects
Biostrings::class:XStringSet	XStringSet objects
Biostrings::class:XStringSetList	XStringSetList objects
Biostrings::class:XStringViews	The XStringViews class
Biostrings::letterFrequency	Calculate the frequency of letters in a biological sequence, or the consensus matrix of a set of sequences
Biostrings::longestConsecutive	Obtain the length of the longest substring containing only 'letter'
Biostrings::lcprefix	Longest Common Prefix/Suffix/Substring searching functions
Biostrings::extractAt	Extract/replace arbitrary substrings from/in a string or set of strings.
crayon::col_substr	Substring(s) of an ANSI colored string
crayon::col_substring	Substring(s) of an ANSI colored string
Hmisc::makeNstr	creates a string that is a repeat of a substring
Hmisc::sedit	Character String Editing and Miscellaneous Character Handling Functions
S4Vectors::Rle-utils	Common operations on Rle objects
stringi::stri_sub	Extract a Substring From or Replace a Substring In a Character Vector
stringr::str_sub	Extract and replace substrings from a character vector.
base::regmatches	Extract or Replace Matched Substrings
base::substr	Substrings of a Character Vector

Searching Help

substr {base} R Documentation

Substrings of a Character Vector

Description

Extract or replace substrings in a character vector.

Usage

```
substr(x, start, stop)
substring(text, first, last = 1000000L)
substr(x, start, stop) <- value
substring(text, first, last = 1000000L) <- value
```

Arguments

`x, text`	a character vector.
`start, first`	integer. The first element to be replaced.
`stop, last`	integer. The last element to be replaced.
`value`	a character vector, recycled if necessary.

Passing arguments to functions

```
my.name <- "simon"

substr(my.name, 2, 4)
[1] "imo"

substr(x=my.name, start=2, stop=4)
[1] "imo"

substr(
  start = 2,
  stop = 4,
  x = my.name
)
[1] "imo"
```

Exercise 1

Everything is a vector

- Vectors are the most basic unit of storage in R

- Vectors are ordered sets of values of the same type
  - Numeric
  - Character (text)
  - Factor (repeated text values)
  - Logical (TRUE or FALSE)
  - Date etc…

```
x <- 10
```

x is a vector of length 1 with 10 as its first value

Creating vectors manually

- Use the **`c`** (combine) function

```
simple_vector <- c(1,2,4,6,3)
some_names <- c("simon","laura",“hayley","jo",“sarah")
```

- Data must be of the same type

```
c(1,2,3,"fred")
[1] "1"    "2"    "3"    "fred"
```

Functions for creating vectors

- `rep` - repeat values

```
rep(2,times=10)
 [1] 2 2 2 2 2 2 2 2 2 2

rep("hello",times=5)
[1] "hello" "hello" "hello" "hello" "hello"

rep(c("dog","cat"),times=3)
[1] "dog" "cat" "dog" "cat" "dog" "cat"

rep(c("dog","cat"),each=3)
[1] "dog" "dog" "dog" "cat" "cat" "cat"
```

Functions for creating vectors

- `seq` - create numerical sequences
  - No required arguments!
    - `from`
    - `to`
    - `by`
    - `length.out`
  - Specify enough that the series is unique

Functions for creating vectors

- `seq` - create numerical sequences

```
seq(from=2,by=3,to=14)
[1]  2  5  8 11 14

seq(from=3,by=10,to=40)
[1]  3 13 23 33

seq(from=5,by=3.6,length.out=5)
[1]  5.0  8.6 12.2 15.8 19.4
```

Functions for creating vectors

- Sampling from statistical distributions
  - `rnorm`
  - `runif`
  - `rpois`
  - `rbeta`
  - `rbinom`

```
rnorm(10000)
```

- Statistically testing vectors
  - `t.test`
  - `lm`
  - `cor.test`
  - `aov`

```
t.test(
  c(1,5,3),
  c(10,15,30)
)
```

Language shortcuts for vector creation

- Single elements

```
c("simon")
```

```
"simon"
```

- Integer series

```
seq(from=4,to=20,by=1)
```

```
4:20
```

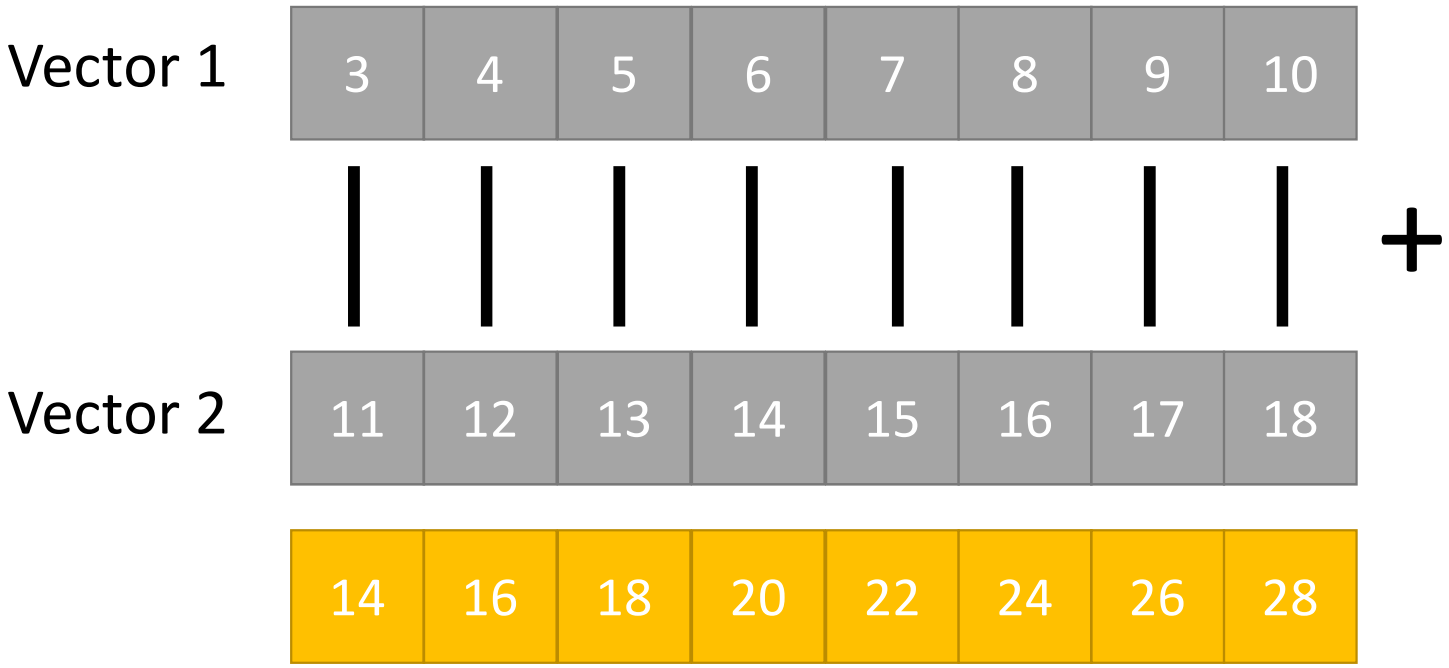
```
[1]  4  5  6  7  8  9 10 11 12 13 14 15 16 17 18 19 20
```

Vectorised Operations

```
2+3
[1] 5

c(2,4) + c(3,5)
[1] 5 9

simple_vector
     1      2      4      6      3

simple_vector * 100
   100    200    400    600    300
```

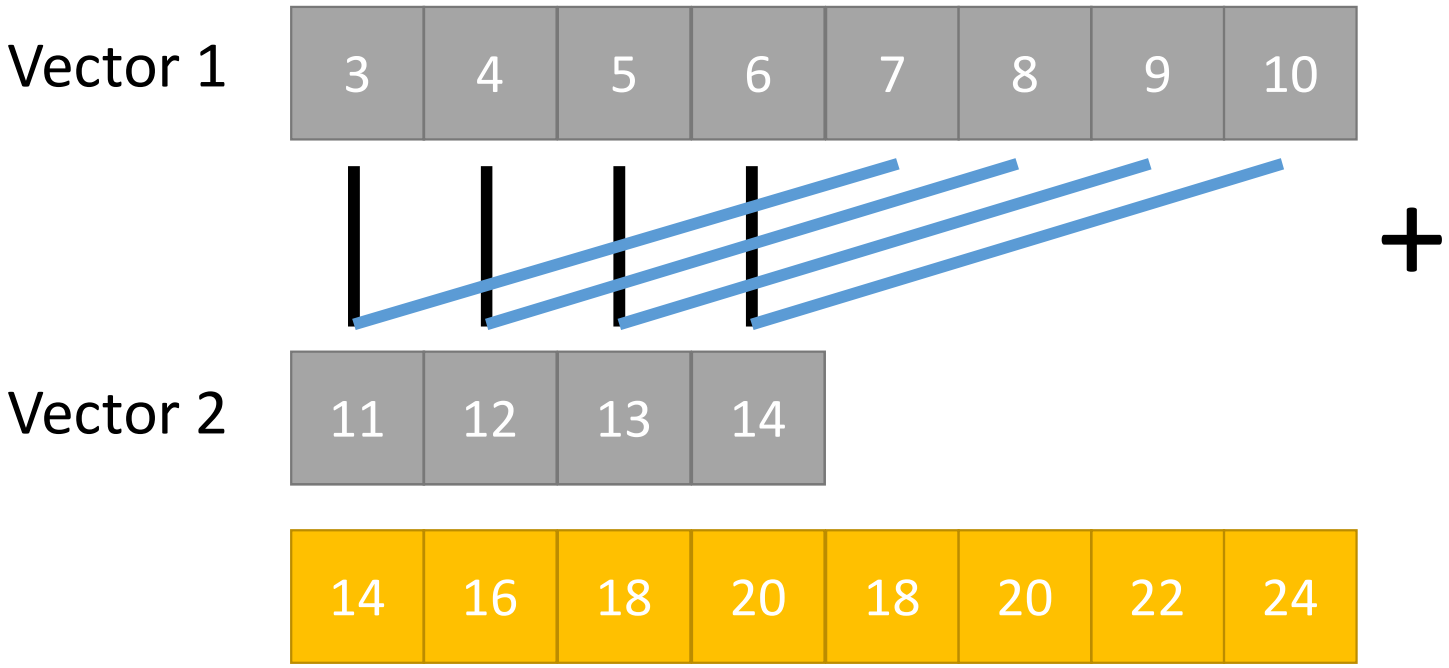
Rules for vectorised operations

- Equivalent positions are matched



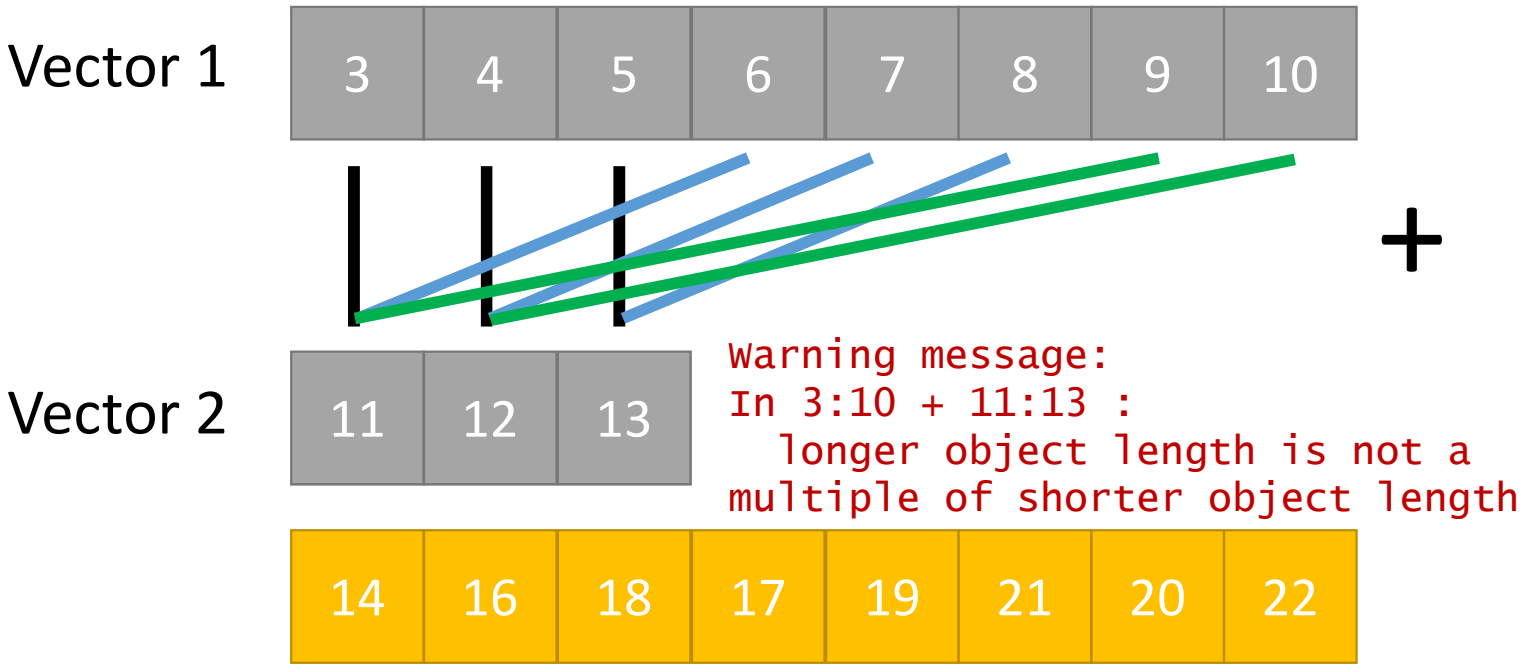
Rules for vectorised operations

- Shorter vectors are recycled



Rules for vectorised operations

- Incomplete vectors generate a warning



Vectorised Operations

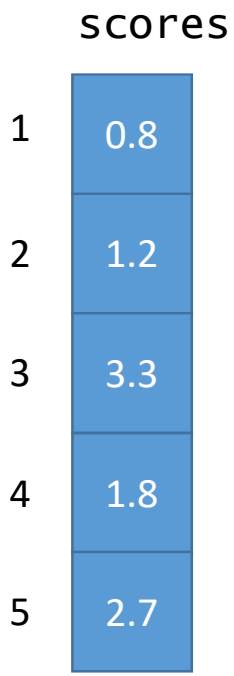
```
c(2,4) + c(3,5)
[1] 5 9

simple_vector
     1      2      4      6      3

simple_vector * 100
   100    200    400    600    300
```

Exercise 2

R Data Structures

Vector

- 1D Data Structure of fixed type

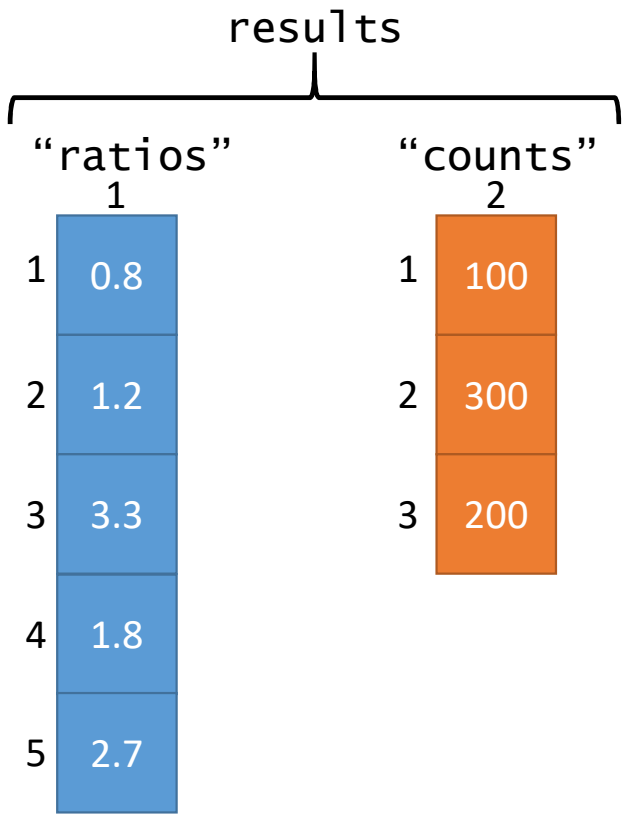



```
mean(scores)
sd(scores)
```

List

- Collection of vectors

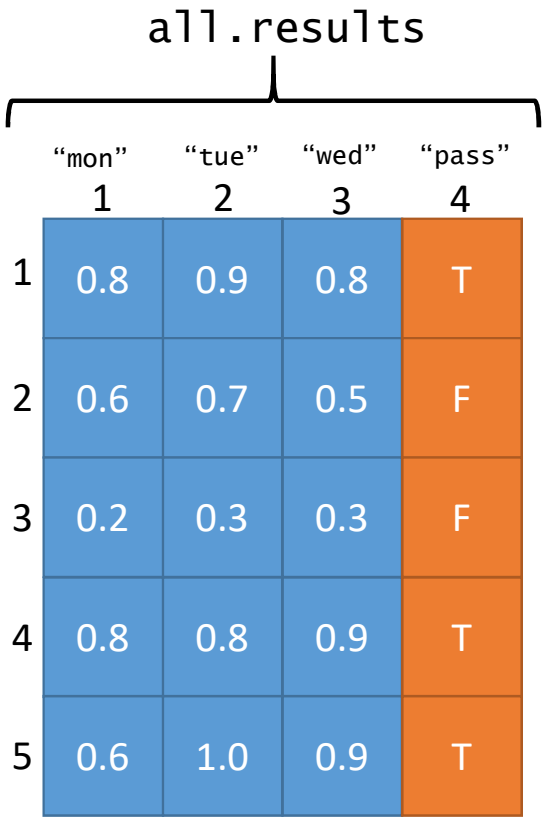
```
results$counts
mean(results$counts)
```



Data Frame

- Collection of vectors with same lengths
- Gain the concept of 'rows'

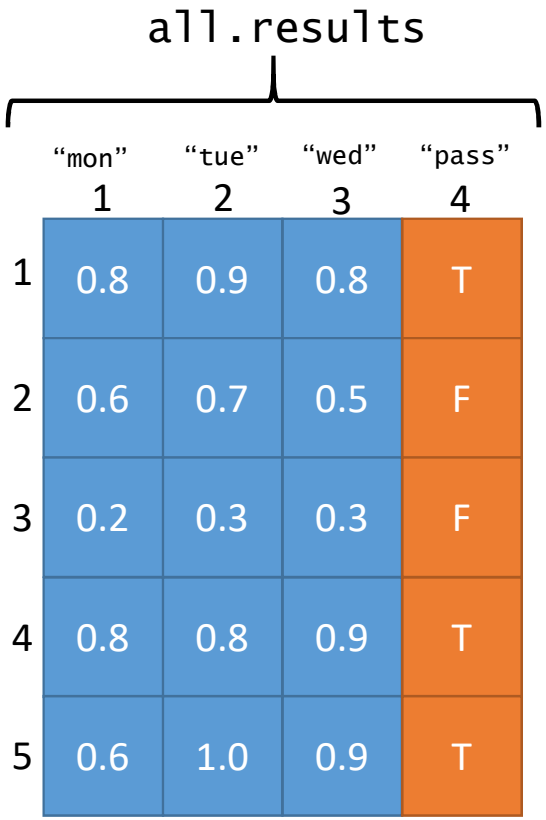
```
all.results$mon
mean(all.results$mon)
```



Tibble

- Collection of vectors with same lengths
- Gain the concept of 'rows'

```
all.results$mon
mean(all.results$mon)
```



Tibbles are nicer dataframes

```
> head(as.data.frame(data))
       Probe Chromosome    Start      End Probe Strand    Feature
1 AL645608.2          1   911435   914948            + AL645608.2
2  LINC02593          1   916865   921016            -  LINC02593
3     SAMD11          1   923928   944581            +     SAMD11
4 TMEM51-AS1          1 15111815 15153618            - TMEM51-AS1
5     TMEM51          1 15152532 15220478            +     TMEM51
6      FHAD1          1 15247272 15400283            +      FHAD1
                                                                Description
1                                                             novel transcript
2         long intergenic non-protein coding RNA 2593 [Source:HGNC Symbol;Acc:HGNC:53933]
3            sterile alpha motif domain containing 11 [Source:HGNC Symbol;Acc:HGNC:28706]
4                              TMEM51 antisense RNA 1 [Source:HGNC Symbol;Acc:HGNC:26301]
5                           transmembrane protein 51 [Source:HGNC Symbol;Acc:HGNC:25488]
6 forkhead associated phosphopeptide binding domain 1 [Source:HGNC Symbol;Acc:HGN
```

Tibbles are nicer dataframes

```
> head(as_tibble(data))
# A tibble: 6 x 12
  Probe Chromosome  Start    End `Probe Strand` Feature ID    Description
  <chr>      <dbl>  <dbl>  <dbl> <chr>          <chr>   <chr> <chr>
1 AL64~          1 9.11e5 9.15e5 +              AL6456~ ENSG~ novel tran~
2 LINC~          1 9.17e5 9.21e5 -              LINC02~ ENSG~ long inter~
3 SAMD~          1 9.24e5 9.45e5 +              SAMD11  ENSG~ sterile al~
4 TMEM~          1 1.51e7 1.52e7 -              TMEM51~ ENSG~ TMEM51 ant~
5 TMEM~          1 1.52e7 1.52e7 +              TMEM51  ENSG~ transmembr~
6 FHAD1          1 1.52e7 1.54e7 +              FHAD1   ENSG~ forkhead a~
# ... with 4 more variables: `Feature Strand` <chr>, Type <chr>, `Feature
#   Orientation` <chr>, Distance <dbl>
```

Tidyverse

https://www.tidyverse.org/

- Collection of R packages
  - Aims to fix many of core R's structural problems
  - Common design and data philosophy
  - Designed to work together, but integrate seamlessly with other parts of R

Tidyverse Packages

- Tibble - data storage

- ReadR - reading data from files

- TidyR - Model data correctly

- DplyR - Manipulate and filter data

- Ggplot2 - Draw figures and graphs

Installation and calling

- Once per machine (don't include in script)
  - `install.packages("tidyverse")`

- Once per R session (DO include in script)
  - `library(tidyverse)`

```
-- Attaching packages ------- tidyverse 1.3.1 --
v ggplot2 3.3.3     v purrr   0.3.4
v tibble  3.1.2     v dplyr   1.0.6
v tidyr   1.1.3     v stringr 1.4.0
v readr   2.0.0     v forcats 0.5.1

-- Conflicts ------------- tidyverse_conflicts()
x dplyr::filter() masks stats::filter()
x dplyr::lag() masks stats::lag()
```

Reading and Writing Files with readr

- Provides functions to read from text files into tibbles or write from tibbles to text files

  - `data <- read_delim("file.txt")`

    ```
    data <- read_csv("file.csv")
    data <- read_tsv("file.tsv")
    ```

  - `write_csv(data,"file.csv")`

  - `write_tsv(data,"file.tsv")`

Specifying file paths

- You can use full file paths, but it's a pain

```
read_delim("O:/Training/R_tidyverse_intro_data/neutrophils.csv")
```

- Just set the 'working directory' and then just provide a file name
  - `setwd(`*path*`)`
  - Session > Set Working Directory > Choose Directory

- Use [Tab] to fill in file paths in the editor
  - `read_delim("")` – put the cursor in the quotes and press tab

Reading files with readr


```
> trumpton <- read_delim("trumpton.txt")
Rows: 7 Columns: 5

-- Column specification --------------------------------
Delimiter: "\t"
chr (2): LastName, FirstName
dbl (3): Age, Weight, Height

> trumpton
   # A tibble: 7 x 5
     LastName FirstName   Age Weight Height
     <chr>    <chr>     <dbl>  <dbl>  <dbl>
   1 Hugh     Chris        26     90    175
   2 Pew      Adam         32    102    183
   3 Barney   Daniel       18     88    168
   4 McGrew   Chris        48     97    155
   5 Cuthbert Carl         28     91    188
   6 Dibble   Liam         35     94    145
   7 Grub     Doug         31     89    164
```

Exercise 3

'Tidy' Data Format

- Tibbles give you a 2D data structure where each column must be of a fixed data type
- Often data can be put into this sort of structure in more than one way
- Is there a right / wrong way to structure your data?

- Tidyverse has an opinion!

Journal of Statistical Software
August 2014, Volume 59, Issue 10. http://www.jstatsoft.org/

Tidy Data

Hadley Wickham
RStudio

Long vs Wide Data Modelling

- Consider a simple experiment:

- Two genes tested (ABC1 and DEF1)
- Two conditions (WT and KO)
- Three replicates for each condition

Wide Format

Gene	WT_1	WT_2	WT_3	KO_1	KO_2	KO_3
ABC1	8.86	4.18	8.90	4.00	14.52	13.39
DEF1	29.60	41.22	36.15	11.18	16.68	1.64

- Compact
- Easy to read
- Shows linkage for genes

- No explicit genotype or replicate
- Values spread out over multiple rows and columns
- Not extensible to more metadata

Long Format

Gene	Genotype	Replicate	Value
ABC1	WT	1	8.86
ABC1	WT	2	4.18
ABC1	WT	3	8.90
ABC1	KO	1	4.00
ABC1	KO	2	14.52
ABC1	KO	3	13.39
DEF1	WT	1	29.60
DEF1	WT	2	41.22
DEF1	WT	3	36.15
DEF1	KO	1	11.18
DEF1	KO	2	16.68
DEF1	KO	3	1.64

- More verbose (repeated values)
- Explicit genotype and replicate
- All values in a single column
- Extensible to more metadata

Filtering and subsetting

- Tidyverse (specifically dplyr) comes with functions to manipulate your data.

- All functions take a tibble as their first argument
- All functions return a modified tibble
  - Selecting columns
  - Logical subsetting

The data we're starting with

```
> trumpton
   # A tibble: 7 x 5
     LastName FirstName   Age Weight Height
     <chr>    <chr>     <dbl>  <dbl>  <dbl>
   1 Hugh     Chris        26     90    175
   2 Pew      Adam         32    102    183
   3 Barney   Daniel       18     88    168
   4 McGrew   Chris        48     97    155
   5 Cuthbert Carl         28     91    188
   6 Dibble   Liam         35     94    145
   7 Grub     Doug         31     89    164
```

Using select to pick columns

```
> select(trumpton,FirstName,LastName, Weight)
# A tibble: 7 x 3
  FirstName LastName Weight
  <chr>     <chr>     <dbl>
1 Chris     Hugh         90
2 Adam      Pew         102
3 Daniel    Barney       88
4 Chris     McGrew       97
5 Carl      Cuthbert     91
6 Liam      Dibble       94
7 Doug      Grub         89
```

You can use positions instead of names

```
> select(trumpton, 2,4)
# A tibble: 7 x 2
  FirstName Weight
  <chr>      <dbl>
1 Chris         90
2 Adam         102
3 Daniel        88
4 Chris         97
5 Carl          91
6 Liam          94
7 Doug          89
```

You can use negative selections

```
> select(trumpton, -LastName)
# A tibble: 7 x 4
  FirstName   Age Weight Height
  <chr>     <dbl>  <dbl>  <dbl>
1 Chris        26     90    175
2 Adam         32    102    183
3 Daniel       18     88    168
4 Chris        48     97    155
5 Carl         28     91    188
6 Liam         35     94    145
7 Doug         31     89    164
```

Functional selections using filter

```
> filter(trumpton, Height>=170)
# A tibble: 3 x 5
  LastName FirstName   Age Weight Height
  <chr>    <chr>     <dbl>  <dbl>  <dbl>
1 Hugh     Chris        26     90    175
2 Pew      Adam         32    102    183
3 Cuthbert Carl         28     91    188
```

Types of filter you can use

- Greater than
  - weight > 20
  - weight >= 30
- Less than
  - height < 170
  - height <= 180
- Equal to (or not)
  - value == 5
  - name == "simon"
  - name != "simon"

```
> filter(trumpton, FirstName == "Chris")
# A tibble: 2 x 5
  LastName FirstName   Age Weight Height
  <chr>    <chr>     <dbl>  <dbl>  <dbl>
1 Hugh     Chris        26     90    175
2 McGrew   Chris        48     97    155
```

You can transform data in a filter

Select rows where the difference (in either direction) is more than 5

```
> transform.data
# A tibble: 10 x 3
       WT      KO difference
    <dbl>   <dbl>      <dbl>
 1 -5.11   -3.29       1.81
 2  1.12   -1.85      -2.97
 3 -3.99   -3.77       0.222
 4 -4.18   -2.46       1.72
 5 -1.93  -10.0       -8.10
 6 -8.69   -2.38       6.31
 7 -0.670   2.73       3.40
 8 -1.15   -2.59      -1.43
 9 -1.98    1.83       3.80
10 -1.06    0.372      1.43
```

```
> filter(transform.data, difference > 5)
# A tibble: 1 x 3
     WT    KO difference
  <dbl> <dbl>      <dbl>
1 -8.69 -2.38       6.31

> filter(transform.data, difference < -5)
# A tibble: 1 x 3
     WT    KO difference
  <dbl> <dbl>      <dbl>
1 -1.93 -10.0      -8.10
```

```
> filter(transform.data, abs(difference) > 5)
# A tibble: 2 x 3
     WT      KO difference
  <dbl>  <dbl>      <dbl>
1 -1.93 -10.0       -8.10
2 -8.69  -2.38       6.31
```

Exercise 4

Combining Multiple Operations

- Find people who are:
  1. Taller than 170cm
  2. Called Chris

- Then report only their age and weight

Combining multiple operations

- The long winded way…
- Three separate operations with two intermediate variables
- Works, but is ugly!

```
> filter(trumpton, Height >= 170) -> answer1
> filter(answer1, FirstName == "Chris") -> answer2
> select(answer2, Age, Weight)

# A tibble: 1 x 2
    Age Weight
  <dbl>  <dbl>
1    26     90
```

Pipes to the rescue

- All tidyverse functions take a tibble as their first argument
- All tidyverse functions return a tibble
- You can therefore chain operations together, passing the output of one function as the first input to another

Data → Filter 1 → Filter 2 → Selection

The pipe operator: %>%

- Takes the data on its left and makes it the first argument to a function on its right.

```
> select(trumpton,-LastName)
# A tibble: 7 x 4
  FirstName   Age Weight Height
  <chr>     <dbl>  <dbl>  <dbl>
1 Chris        26     90    175
2 Adam         32    102    183
3 Daniel       18     88    168
4 Chris        48     97    155
5 Carl         28     91    188
6 Liam         35     94    145
7 Doug         31     89    164
```

```
> trumpton %>% select(-LastName)
# A tibble: 7 x 4
  FirstName   Age Weight Height
  <chr>     <dbl>  <dbl>  <dbl>
1 Chris        26     90    175
2 Adam         32    102    183
3 Daniel       18     88    168
4 Chris        48     97    155
5 Carl         28     91    188
6 Liam         35     94    145
7 Doug         31     89    164
```

Combining Multiple Operations with Pipes

- Give the age and weight for people who are taller than 170cm and called Chris

```
trumpton %>% filter(Height>=170) %>% filter(FirstName=="Chris") %>% select(Age,Weight)
```

```
trumpton %>%
  filter(Height>=170) %>%
  filter(FirstName=="Chris") %>%
  select(Age,Weight)

# A tibble: 1 x 2
    Age Weight
  <dbl>  <dbl>
1    26     90
```

Exercise 5

Plotting figures and graphs with ggplot

- ggplot is the plotting library for tidyverse
  - Powerful
  - Flexible

- Follows the same conventions as the rest of tidyverse
  - Data stored in tibbles
  - Data is arranged in 'tidy' format
  - Tibble is the first argument to each function

Code structure of a ggplot graph

- Start with a call to ggplot()
  - Pass the tibble of data
  - Say which columns you want to use
- Say which graphical representation you want to use
  - Points, lines, barplots etc
- Customise labels, colours annotations etc.

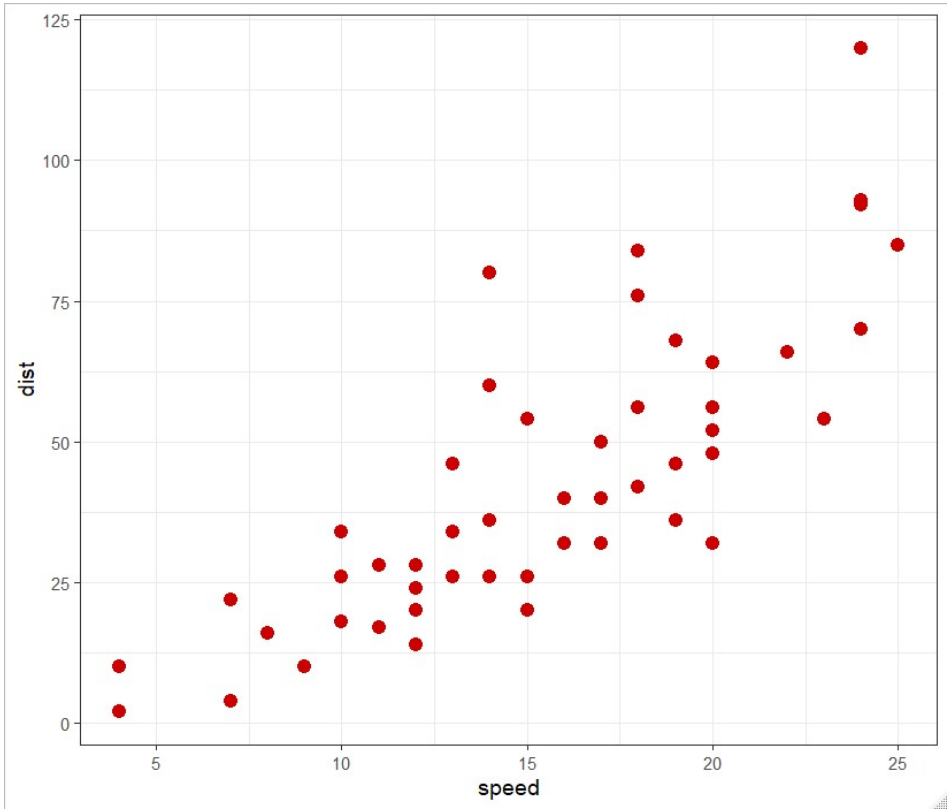
Geometries and Aesthetics

- Geometries are types of plot

`geom_point()`	Point geometry, (x/y plots, stripcharts etc)
`geom_line()`	Line graphs
`geom_boxplot()`	Box plots
`geom_bar()`	Barplots
`geom_histogram()`	Histogram plots

- Aesthetics are graphical parameters which can be adjusted in a given geometry

Aesthetics for `geom_point()`

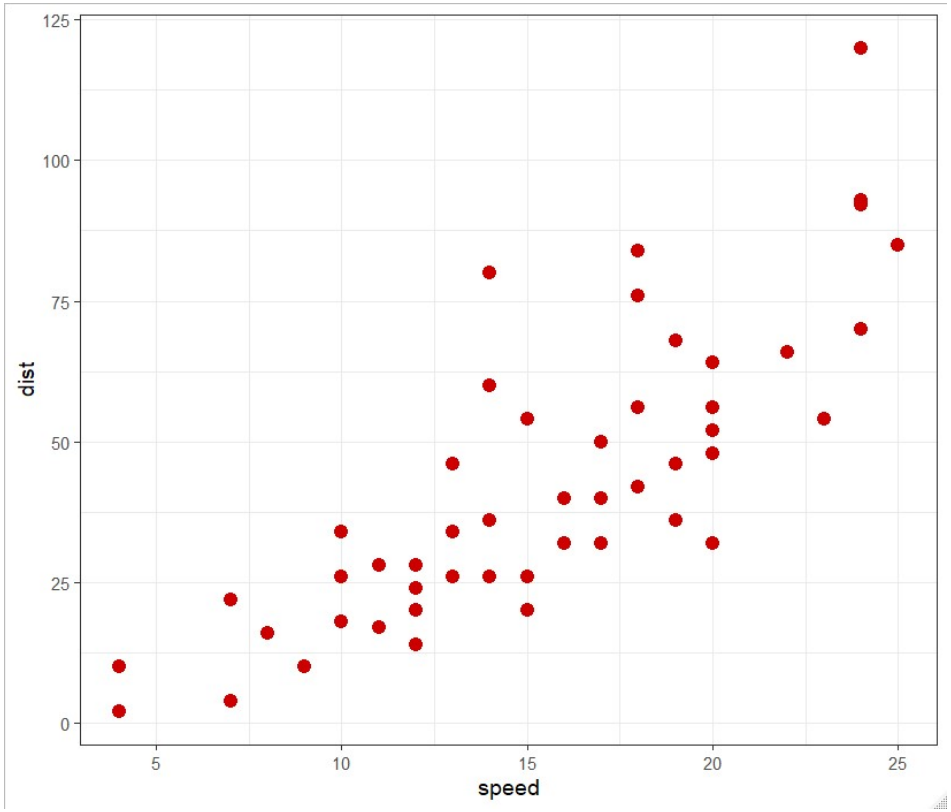


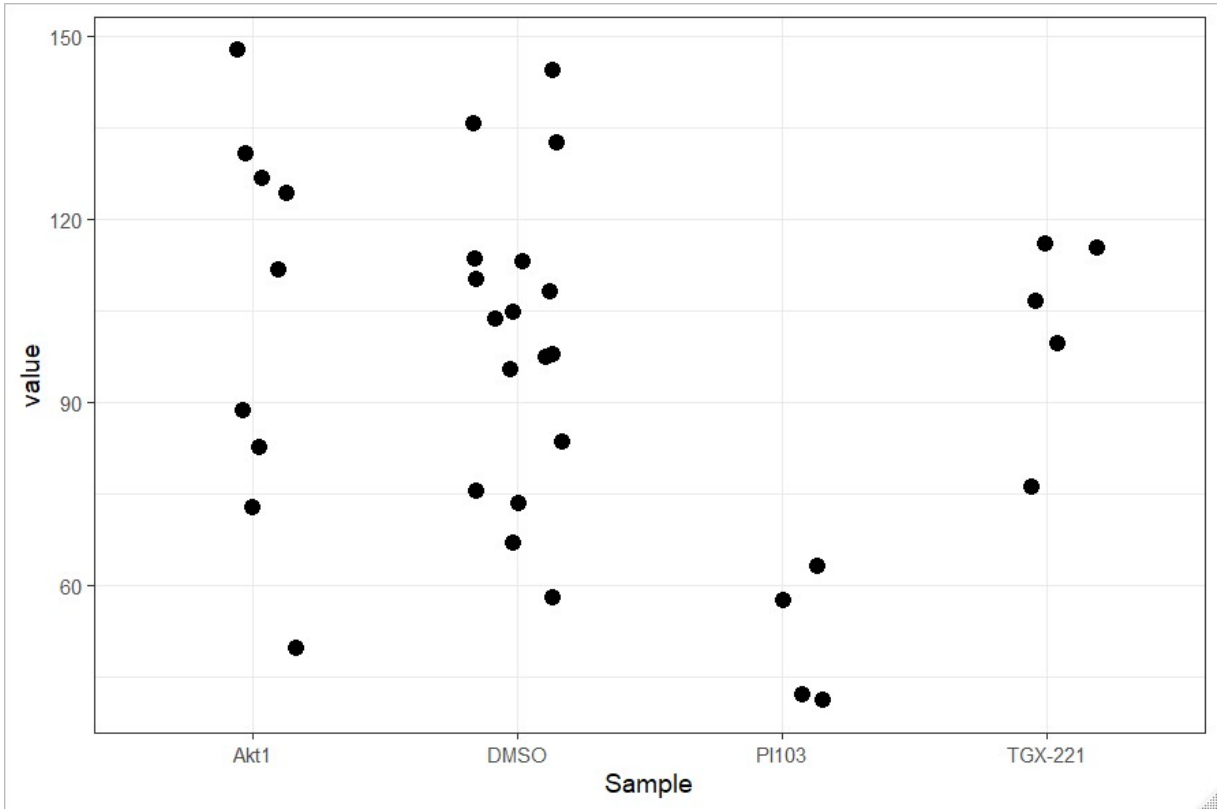
Aesthetics

`geom_point()` understands the following aesthetics (required aesthetics are in bold):

- **`x`**
- **`y`**
- `alpha`
- `colour`
- `fill`
- `group`
- `shape`
- `size`
- `stroke`

Mappings can be quantitative or categorical





How do you define aesthetics

- Fixed values
  - Colour all points red
  - Make the points size 4

- Encoded from your data – called an *aesthetic mapping*
  - Colour according to genotype
  - Size based on the number of observations

- Aesthetic mappings are set using the `aes()` function, normally as an argument to the `ggplot` function

```
data %>% ggplot(aes(x=weight, y=height, colour=genotype))
```

Putting things together

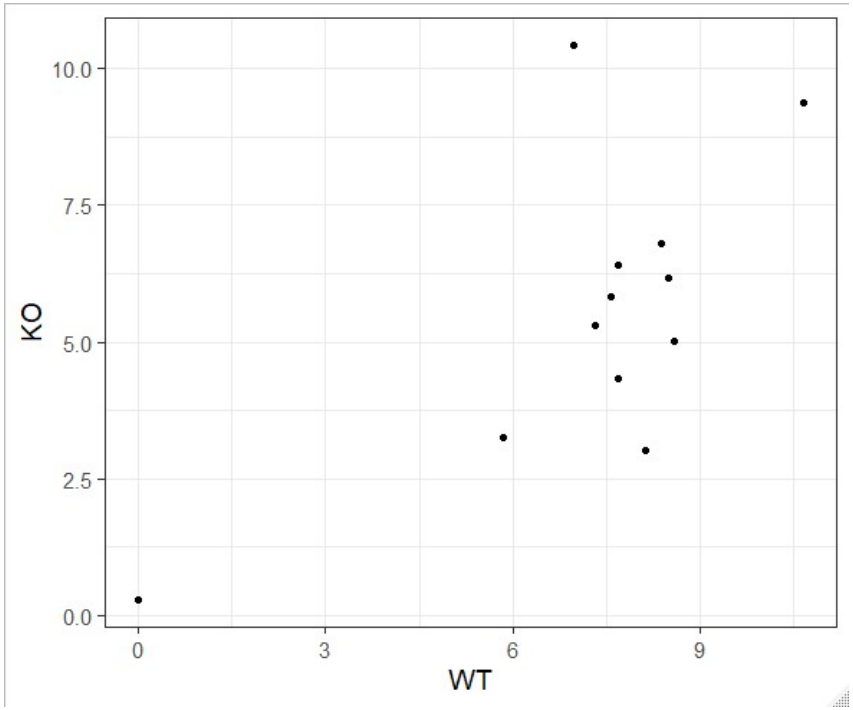
- Identify the tibble with the data you want to plot
- Decide on the geometry (plot type) you want to use
- Decide which columns will modify which aesthetic

- Call `ggplot(aes(...))`
- Add a `geom_xxx` function call

Our first plot…

`ggplot(expression, aes(x=WT, y=KO)) + geom_point()`

```
> expression
# A tibble: 12 x 4
   Gene        WT     KO pValue
   <chr>    <dbl>  <dbl>  <dbl>
 1 Mia1      5.83  3.24   0.1
 2 Snrpa     8.59  5.02   0.001
 3 Itpkc     8.49  6.16   0.04
 4 Adck4     7.69  6.41   0.2
 5 Numbl     8.37  6.81   0.1
 6 Ltbp4     6.96 10.4    0.001
 7 Shkbp1    7.57  5.83   0.1
 8 Spnb4    10.7   9.38   0.2
 9 Blvrb     7.32  5.29   0.05
10 Pgam1     0     0.285  0.5
11 Sertad3   8.13  3.02   0.0001
12 Sertad1   7.69  4.34   0.01
```



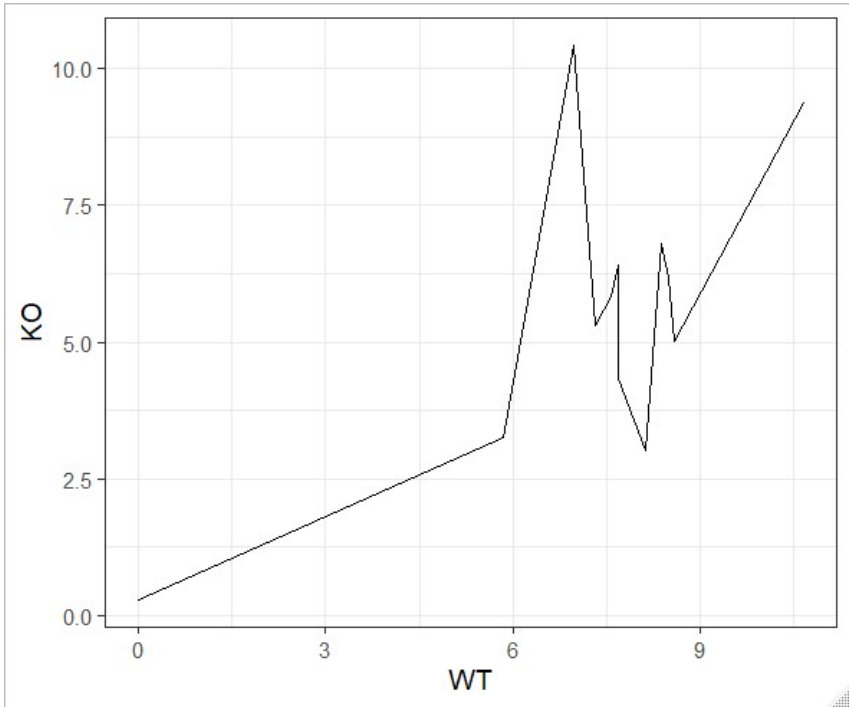
- Identify the tibble with the data you want to plot
- Decide on the geometry (plot type) you want to use
- Decide which columns will modify which aesthetic

- Call `ggplot(aes(...))`
- Add a `geom_xxx` function call

Our second plot…

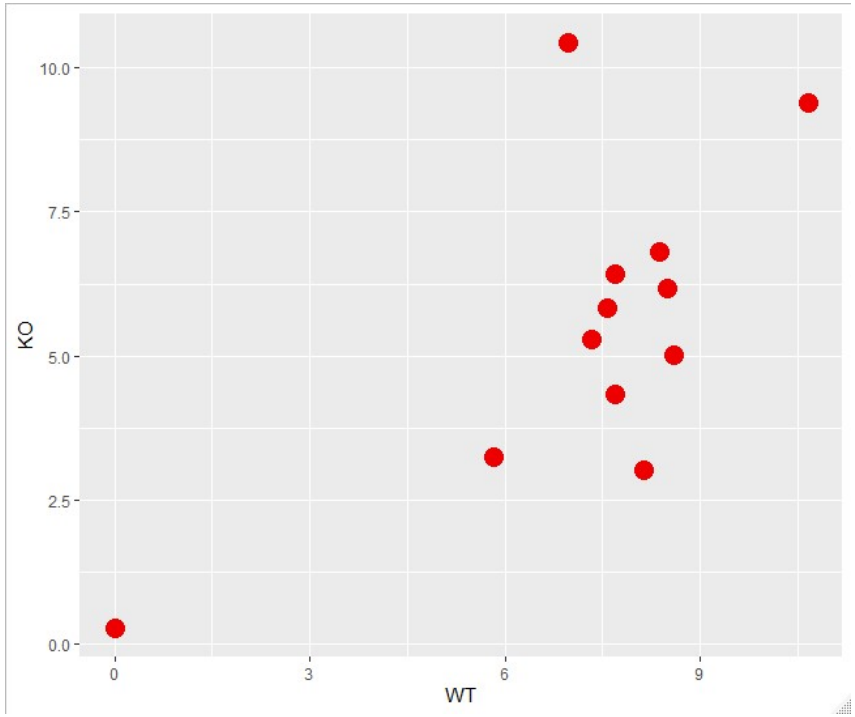
```
ggplot(expression, aes(x=WT, y=KO)) + geom_line()
```

```
> expression
# A tibble: 12 x 4
   Gene        WT     KO pValue
   <chr>    <dbl>  <dbl>  <dbl>
 1 Mia1      5.83  3.24   0.1
 2 Snrpa     8.59  5.02   0.001
 3 Itpkc     8.49  6.16   0.04
 4 Adck4     7.69  6.41   0.2
 5 Numbl     8.37  6.81   0.1
 6 Ltbp4     6.96 10.4    0.001
 7 Shkbp1    7.57  5.83   0.1
 8 Spnb4    10.7   9.38   0.2
 9 Blvrb     7.32  5.29   0.05
10 Pgam1     0     0.285  0.5
11 Sertad3   8.13  3.02   0.0001
12 Sertad1   7.69  4.34   0.01
```



Our third plot…

```
expression %>%
  ggplot (aes(x=WT, y=KO)) +
  geom_point(color="red2", size=5)
```



Colour recap

- Encoded from your data – called an *aesthetic mapping,* set using the `aes()` function

```
data %>%
   ggplot(aes(x=weight, y=height, colour=genotype)) +
   geom_point()
```

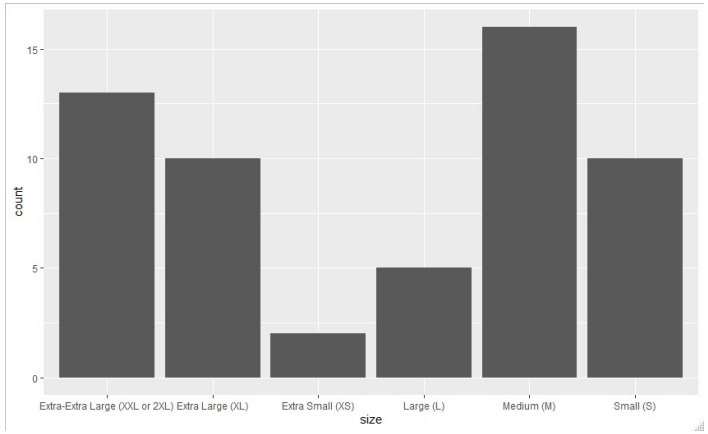
- Fixed values – all points the same colour

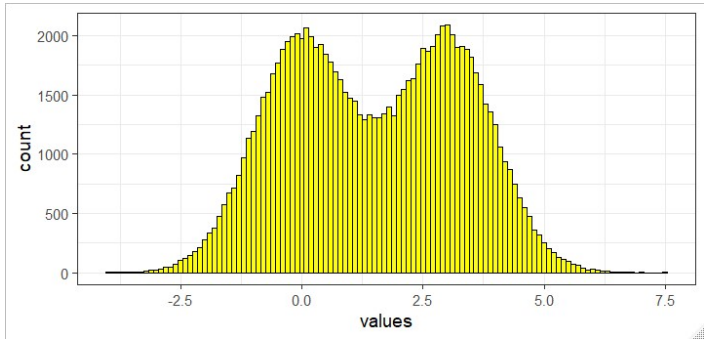
```
data %>%
   ggplot(aes(x=weight, y=height)) +
   geom_point(colour="blue2")
```

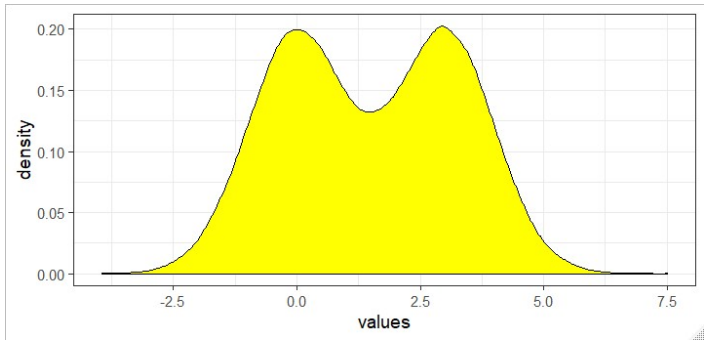
Exercise 6

Other plot types

- Barplots
  - geom_bar
  - geom_col
- Distribution Plots
  - geom_histogram
  - geom_density







Drawing a barplot (`geom_col()`)

Aesthetics

`geom_bar()` understands the following aesthetics (required aesthetics are in bold):

- **x**
- **y**
- alpha
- colour
- fill
- group
- linetype
- size

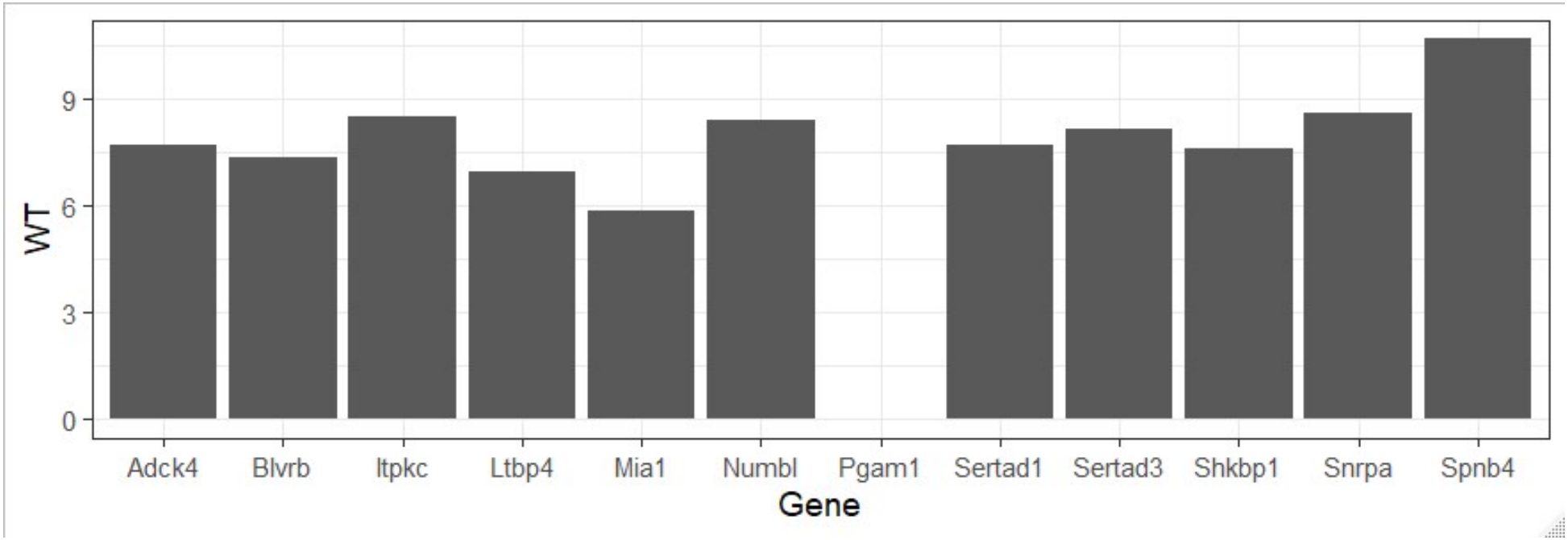
- Plot the expression values for the WT samples for all genes

- What is your X?
- What is your Y?

```
> expression
# A tibble: 12 x 4
   Gene        WT      KO pValue
   <chr>    <dbl>   <dbl>  <dbl>
 1 Mia1      5.83   3.24   0.1
 2 Snrpa     8.59   5.02   0.001
```

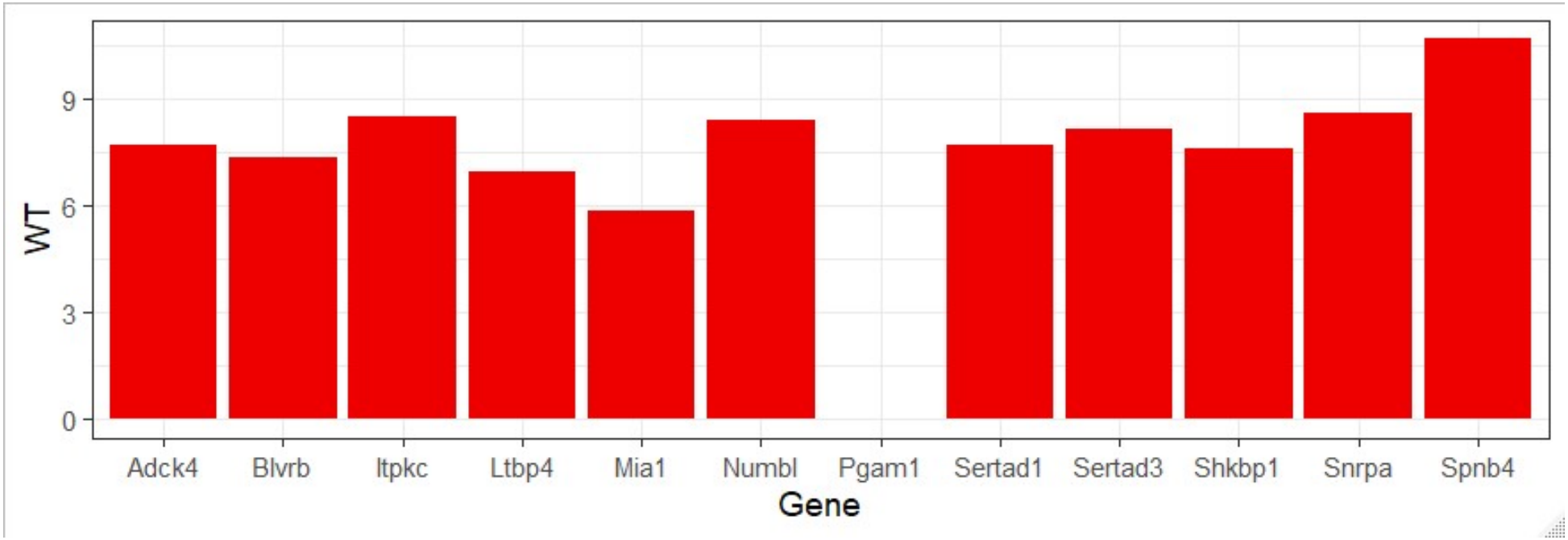
Our bar plot…

```
expression %>%
  ggplot(aes(x=Gene, y=WT)) +
  geom_col()
```



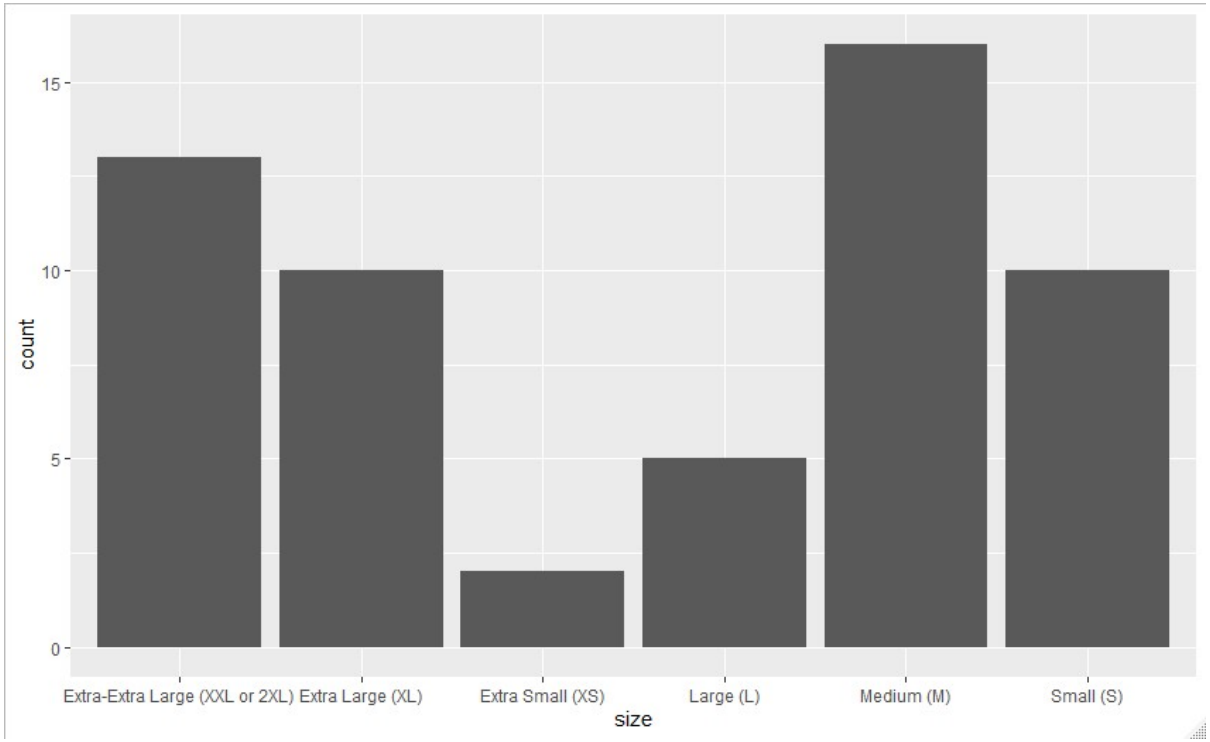
Our bar plot…

```
expression %>%
  ggplot(aes(x=Gene, y=WT)) +
  geom_col(fill="red2")
```



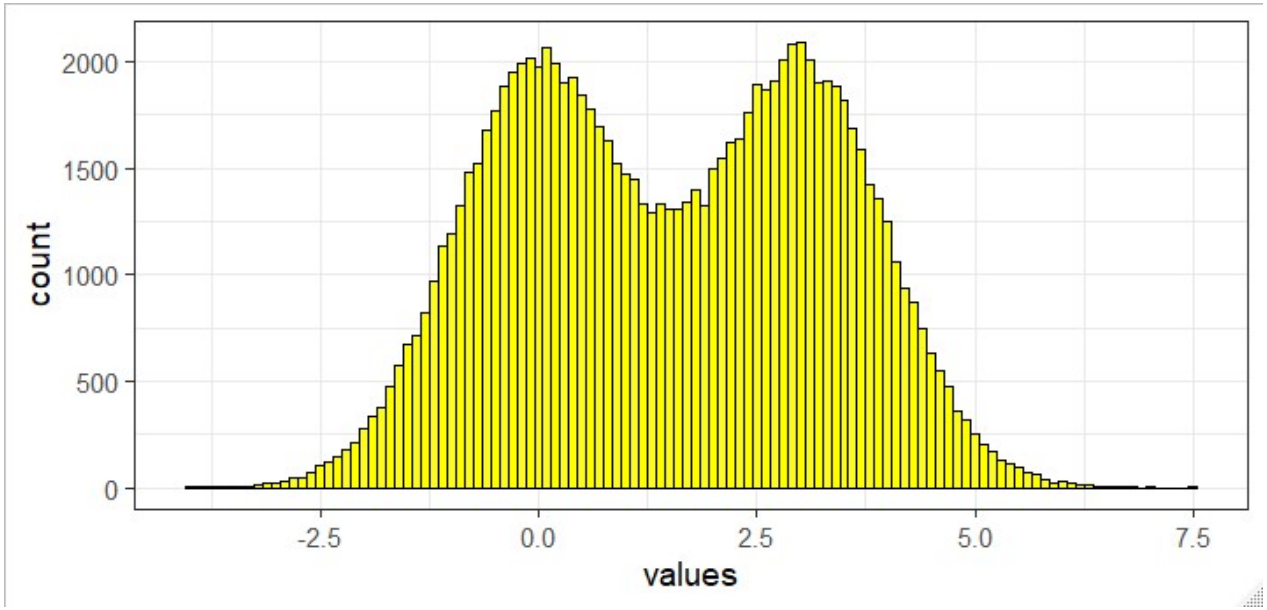
Counting bar plot…

```
dogs %>%
  ggplot(aes(x=size)) +
  geom_bar()
```




```
> dogs
# A tibble: 56 x 2
   size                          breed
   <chr>                         <chr>
 1 Extra Large (XL)              Airedale Terrier
 2 Extra-Extra Large (XXL or 2XL) Akita
 3 Extra Large (XL)              American Foxhound
 4 Extra Large (XL)              Australian Shepherd
 5 Extra Large (XL)              Bassett Hound
 6 Medium (M)                    Beagle
 7 Extra-Extra Large (XXL or 2XL) Bernese Mountain Dog
 8 Medium (M)                    Bichon Frise
 9 Small (S)                     Boston Terrier
10 Medium (M)                    Boston Terrier
# ... with 46 more rows
```

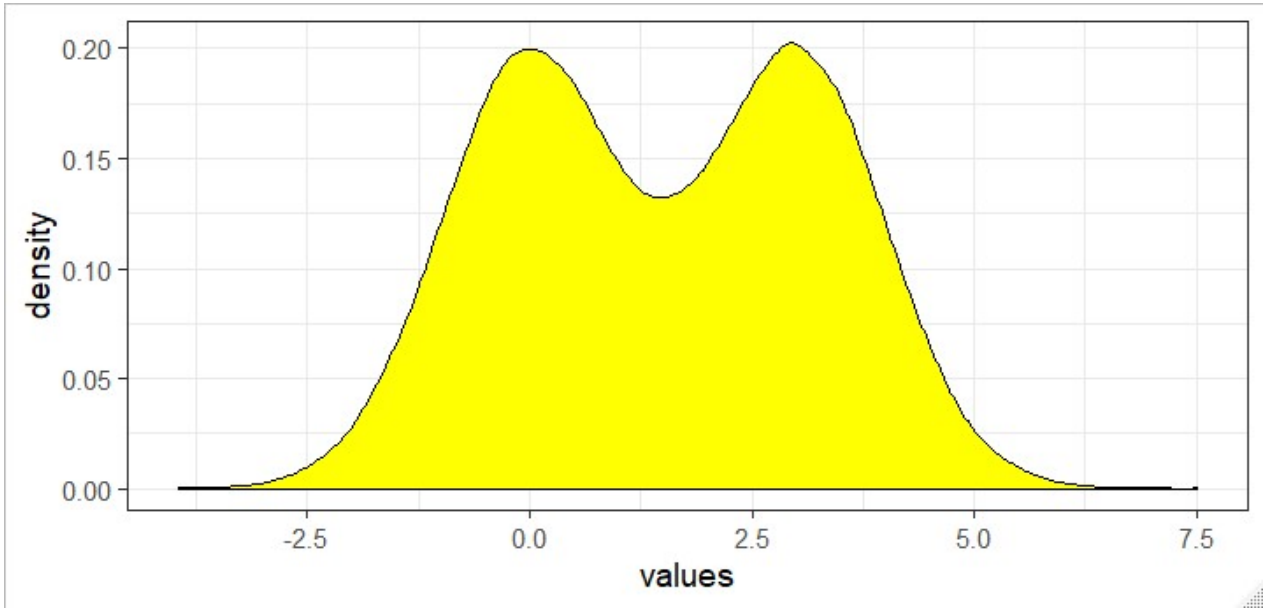
Plotting distributions - histograms




```
> many.values
# A tibble: 100,000 x 2
   values genotype
    <dbl> <chr>
 1  1.90  KO
 2  2.39  WT
 3  4.32  KO
 4  2.94  KO
 5  0.728 WT
 6 -0.280 WT
 7  0.337 WT
 8 -1.31  WT
 9  1.55  WT
10  1.86  KO
```

```
many.values %>%
  ggplot(aes(values)) +
  geom_histogram(binwidth = 0.1, fill="yellow", colour="black")
```

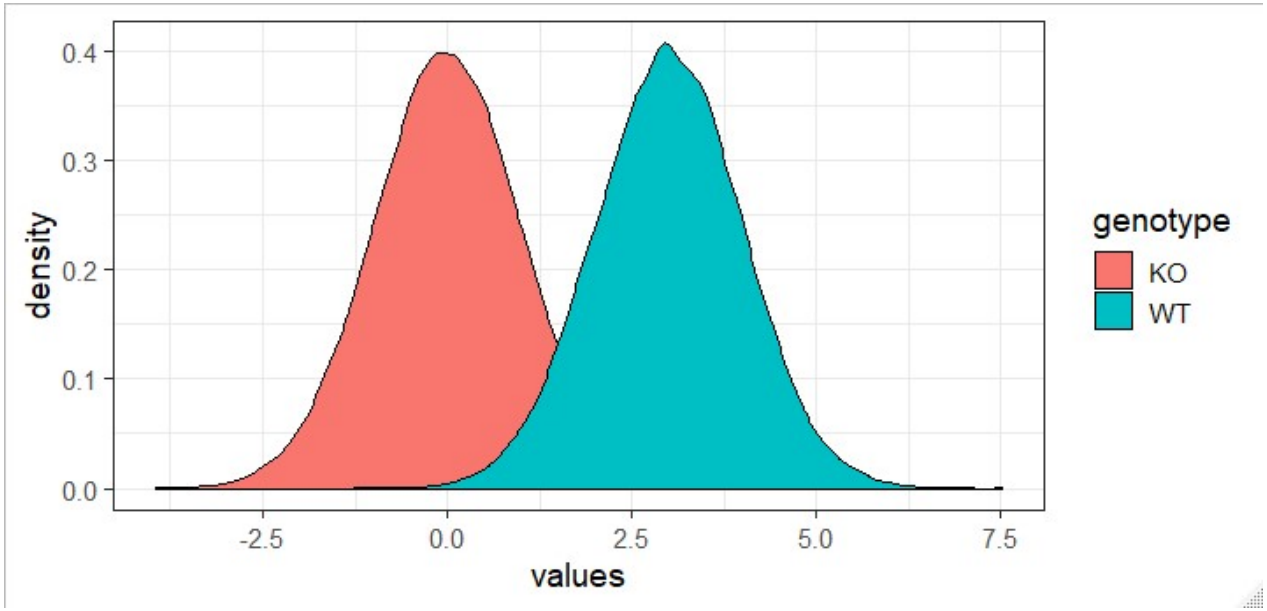
Plotting distributions - density




```
> many.values
# A tibble: 100,000 x 2
   values genotype
    <dbl> <chr>
 1  1.90  KO
 2  2.39  WT
 3  4.32  KO
 4  2.94  KO
 5  0.728 WT
 6 -0.280 WT
 7  0.337 WT
 8 -1.31  WT
 9  1.55  WT
10  1.86  KO
```

```
many.values %>%
  ggplot(aes(values)) +
  geom_density(fill="yellow", colour="black")
```

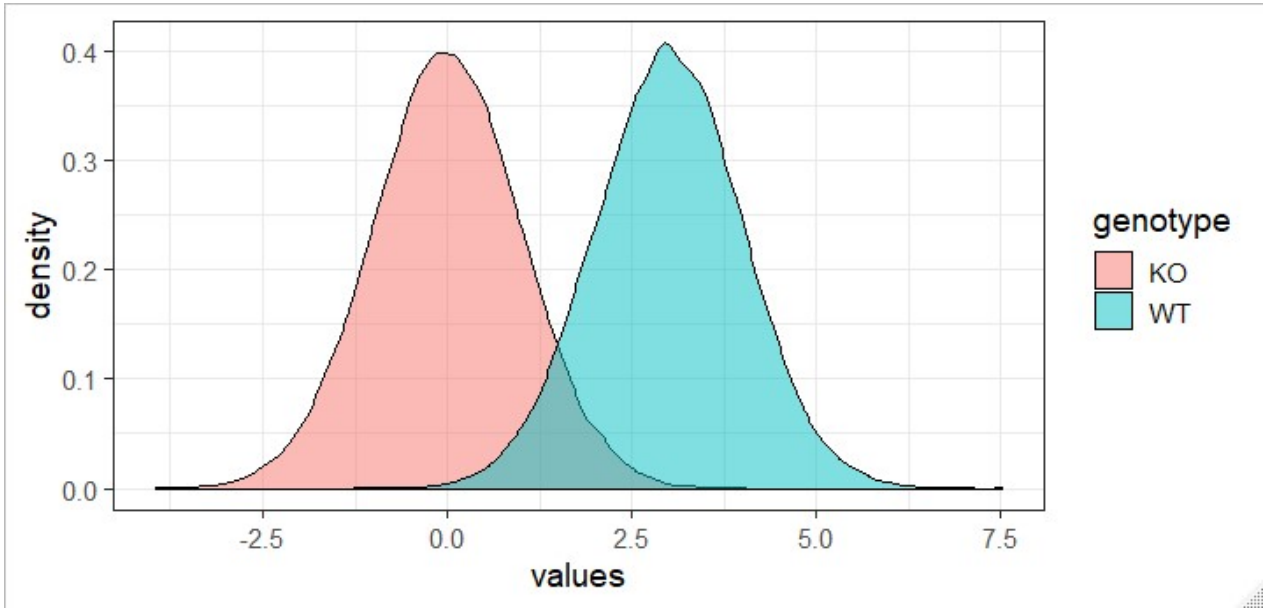
Plotting distributions - density




```
> many.values
# A tibble: 100,000 x 2
   values genotype
    <dbl> <chr>
 1  1.90  KO
 2  2.39  WT
 3  4.32  KO
 4  2.94  KO
 5  0.728 WT
 6 -0.280 WT
 7  0.337 WT
 8 -1.31  WT
 9  1.55  WT
10  1.86  KO
```

```
many.values %>%
  ggplot(aes(x=values, fill=genotype)) +
  geom_density(colour="black")
```

Plotting distributions - density




```
> many.values
# A tibble: 100,000 x 2
   values genotype
    <dbl> <chr>
 1  1.90  KO
 2  2.39  WT
 3  4.32  KO
 4  2.94  KO
 5  0.728 WT
 6 -0.280 WT
 7  0.337 WT
 8 -1.31  WT
 9  1.55  WT
10  1.86  KO
```

```
many.values %>%
  ggplot(aes(x=values, fill=genotype)) +
  geom_density(colour="black", alpha=0.5)
```

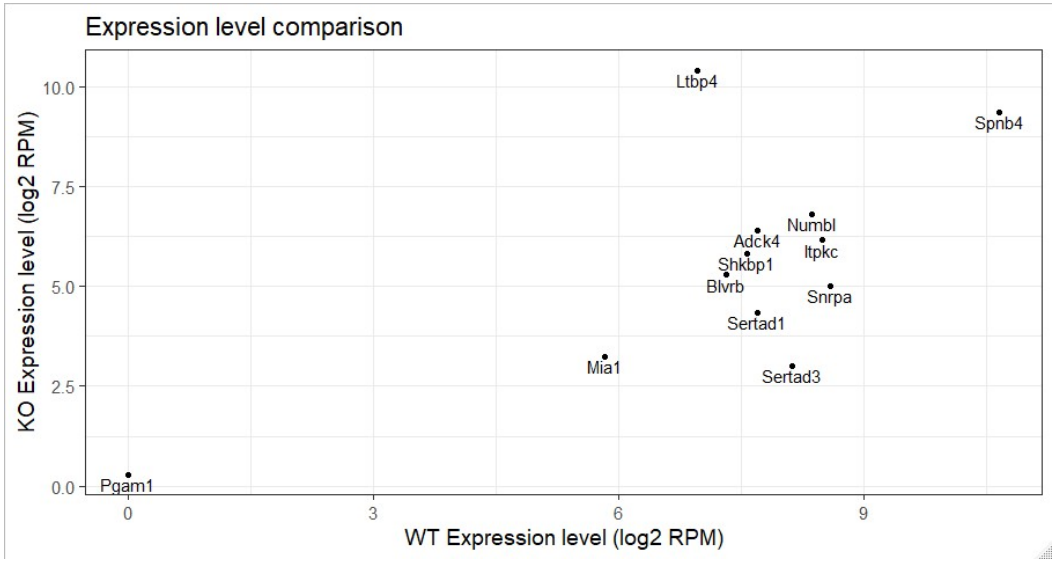
Other annotation geometries

```
expression %>%
  ggplot(aes(x=WT, y=KO, label=Gene)) +
  geom_point() +
  ggtitle("Expression level comparison") +
  xlab("WT Expression level (log2 RPM)") +
  ylab("KO Expression level (log2 RPM)") +
  geom_text(vjust=1.2)
```

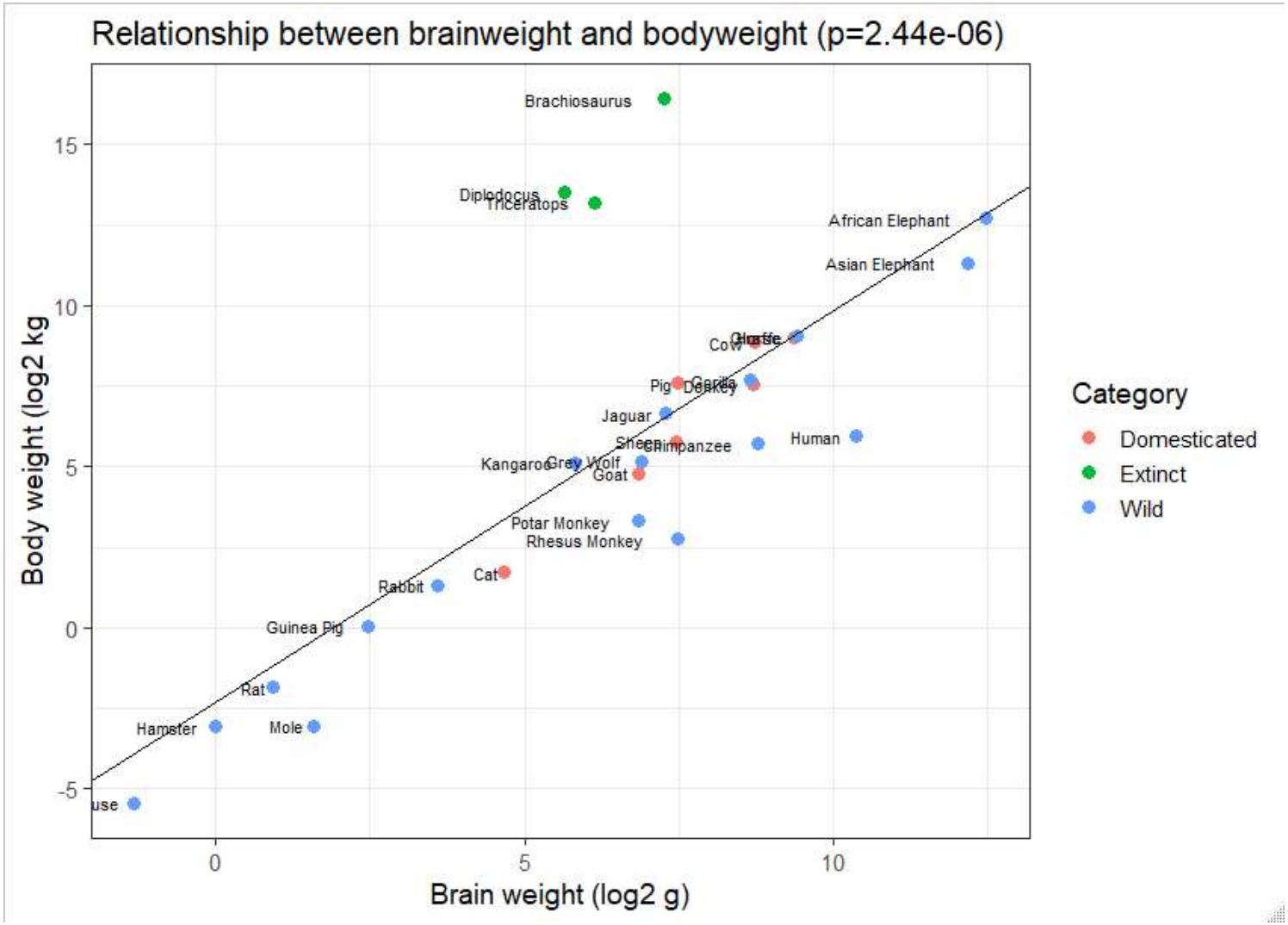
Aesthetics

`geom_text()` understands the following aesthetics (required aesthetics are in bold):

- **x**
- **y**
- **label**



Exercise 7


Relationship between brainweight and bodyweight (p=2.44e-06)
Body weight (log2 kg)
Brain weight (log2 g)
15
10
5
0
-5
0
5
10
Brachiosaurus
Diplodocus
Triceratops
African Elephant
Asian Elephant
Cow
Horse
Pig
Donkey
Jaguar
Sheep
Chimpanzee
Human
Kangaroo
Grey Wolf
Goat
Potar Monkey
Rhesus Monkey
Cat
Rabbit
Guinea Pig
Rat
Hamster
Mole
use
Category
Domesticated
Extinct
Wild

Viewing large variables

- In the console

  ```
  head(data)
  tail(data, n=10)
  ```

- Graphically

  ```
  View(data)
  ```
  [Note capital V!]

  Click in Environment tab