Advanced R

(with Tidyverse)

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Babraham Bioinformatics

Course Content

- Expanding knowledge
  - More functions and operators
- Improving efficiency
  - More options for elegant code
- Awkward cases
  - Dealing with real data
- Tidyverse operations
  - Data Import
  - Filtering, selecting and sorting
  - Restructuring data
  - Grouping and Summarising
  - Extending and Merging
- Custom functions

Tidyverse Packages

- Tibble - data storage
- ReadR - reading data from files
- TidyR - Model data correctly
- DplyR - Manipulate and filter data
- Ggplot2 - Draw figures and graphs

Reading Files with readr

- Tidyverse functions for reading text files into tibbles
  - `read_delim("file.txt")`
    `read_csv("file.csv")`
    `read_tsv("file.tsv")`
  - `read_fwf("file.txt",col_positions=c(1,3,6))`
  - `read_excel("file.xlsx", sheet="Sheet1")`

The `read_excel` function isn't in core tidyverse. You need to install the `readxl` package to get it

Reading files with readr

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

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

Guesses the delimiter in the file

Guesses the data types for the columns

```
> 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
```

What do we do if it guesses wrong (or can't guess at all?)

Import Warnings

```
> read_delim("import_problems.txt") -> problem_data
Rows: 1042 Columns: 4
-- Column specification --------------------------------
Delimiter: "\t"
chr (2): Gene, Significance
dbl (2): Chr, Expression

Warning message:
One or more parsing issues, see `problems()` for details
```

Import Problems

```
> problems(problem_data)


# A tibble: 1 x 5
    row   col expected actual file
  <int> <int> <chr>    <chr>  <chr>
1  1042     1 a double Y      import_problems.txt
```

Which line in the file | Which column | What should be in there | What was actually there

Common Problems

- Not all of the data matches the guessed type
  - Only some rows are examined to guess the type

```
1 4 2 6 6 3 7 8 4 2 5 F 2 6 7 8 9 4 3 1 5 6 7 8
```

- Different number of fields on different lines

```
Name     Age
Simon    42
Dave     36   Check
Brian    23
```

Fixing guessed columns

```
# A tibble: 1,174 x 4
     Chr Gene     Expression Significance
   <dbl> <chr>         <dbl> <chr>
 1     1 Depdc2         9.19 NS
 2     1 Sulf1          9.66 NS
 3     1 Rpl7           8.75 0.050626416
 4     X Phf3           8.43 NS
 5     1 Khdrbs2        8.94 NS
 6     1 Prim2          9.64 NS
 7     1 Hs6st1         9.60 0.03441748
```

- `Chr` should be character
- `Significance` should be numeric

Fixing guessed columns

```
# A tibble: 1,174 x 4
   Chr   Chr Gene     Expression Significance
   <dbl> <chr>          <dbl>      <dbl>
 1 1     1 Depdc2         9.19 NA
 2 1     1 Sulf1          9.66 NA
 3 1     1 Rpl7           8.75 0.0506
 4 X     X Phf3           8.43 NA
 5 1     1 Khdrbs2        8.94 NA
 6 1     1 Prim2          9.64 NA
 7 1     1 Hs6st1         9.60 0.0344
```

```
read_delim(
  "problems.txt",
  col_types = "c??n"
)
```

- c = character
- i = integer
- n = number
- d = double
- l = logical
- f = factor
- D = date
- T = date time
- t = time
- ? = guess
- _ or - = skip

```
> problems()
# A tibble: 874 x 5
     row   col expected actual file
   <int> <int> <chr>    <chr>  <chr>
 1     2     4 a double NS     problems.txt
 2     3     4 a double NS     problems.txt
 3     5     4 a double NS     problems.txt
 4     6     4 a double NS     problems.txt
 5     7     4 a double NS     problems.txt
```

```
c("c","?","?","n")
c("character", "guess", "guess", "number")
c("Chr"="character","Significance"="number")
```

Single Column Files

```
read_delim("single.txt")
Error: Could not guess the delimiter.
```

```
Gene
ABC1
DEF1
HIJ1
```

```
read_tsv("single.txt")
```

```
# A tibble: 3 × 1
  Gene
  <chr>
1 ABC1
2 DEF1
3 HIJ1
```

Unwanted header lines

```
read_delim("broken.txt")
Error: Could not guess the delimiter.
```

```
# Format version 1.0
# Created 20/05/2020
Gene,Strand,Group_A,Group_B,Group_C
ABC1,+,5.30,4.69,4.84
DEF1,-,14.97,15.66,15.92
HIJ1,-,2.17,3.14,1.94
```

```
read_csv("broken.txt")

Delimiter: ","
chr (1): # Format version 1.0

# A tibble: 5 x 1
  `# Format version 1.0`
  <chr>
1 # Created 20/05/2020
2 Gene
3 ABC1
4 DEF1
5 HIJ1
```

```
> problems()
# A tibble: 4 x 5
    row   col expected  actual    file
  <int> <int> <chr>     <chr>     <chr>
1     3     5 1 columns 5 columns broken.txt
2     4     5 1 columns 5 columns broken.txt
3     5     5 1 columns 5 columns broken.txt
4     6     5 1 columns 5 columns broken.txt
```

Unwanted header lines

```
read_delim(
  "broken.txt",
  skip=2
)
```

```
read_delim(
  "broken.txt",
  comment="#"
)
```

```
# Format version 1.0
# Created 20/05/2020
Gene,Strand,Group_A,Group_B,Group_C
ABC1,+,5.30,4.69,4.84
DEF1,-,14.97,15.66,15.92
HIJ1,-,2.17,3.14,1.94
```

```
# A tibble: 3 x 5
  Gene  Strand Group_A Group_B Group_C
  <chr> <chr>    <dbl>   <dbl>   <dbl>
1 ABC1  +         5.3     4.69    4.84
2 DEF1  -        15.0    15.7    15.9
3 HIJ1  -         2.17    3.14    1.94
```

Exercise 1
Reading Data into Tibbles

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Filtering, Selecting, Sorting etc.

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Subsetting and Filtering

- `select` pick columns by name/position
- `filter` pick rows based on the data
- `slice` pick rows by position
- `arrange` sort rows
- `distinct` deduplicate rows

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` or `slice`

```
select(data,cols)
slice(data,rows)
```

```
trumpton %>%
    select(LastName,Age,Height)
```

```
# A tibble: 7 x 3
  LastName   Age Height
  <chr>    <dbl>  <dbl>
1 Hugh        26    175
2 Pew         32    183
3 Barney      18    168
4 McGrew      48    155
5 Cuthbert    28    188
6 Dibble      35    145
7 Grub        31    164
```

```
trumpton %>%
    slice(1,4,7)
```

```
# A tibble: 3 x 5
  LastName FirstName   Age Weight Height
  <chr>    <chr>     <dbl>  <dbl>  <dbl>
1 Hugh     Chris        26     90    175
2 McGrew   Chris        48     97    155
3 Grub     Doug         31     89    164
```

Using `select` and `slice`

```
trumpton %>%
  select(LastName, Age, Height) %>%
  slice(1,4,7)
```

```
# A tibble: 3 x 3
  LastName   Age Height
  <chr>    <dbl>  <dbl>
1 Hugh        26    175
2 McGrew      48    155
3 Grub        31    164
```

Functional row selection using `filter`

```
trumpton %>%
  filter(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
```

arrange (sorting)
distinct (deduplication)

```
trumpton %>%
  arrange(Height) %>%
  distinct(FirstName, .keep_all = TRUE)
```

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

You need **`.keep_all=TRUE`** if you want to see more than the distinct column. "**keep_all**" has a dot before it

arrange (sorting)
distinct (deduplication)

```
trumpton %>%
  arrange(desc(Height)) %>%
  distinct(FirstName, .keep_all = TRUE)
```

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

Defining Selected Columns

- Single definitions (name, position or function)

  Positive `weight, height, length, 1, 2, 3, last_col(), everything()`

  Negative `-chromosome, -start, -end, -1, -2, -3`

- Range selections

  `3:5` `-(3:5)` `height:length` `-(height:length)`

- Functional selections (positive or negative)

  `starts_with()` `-starts_with()`
  `ends_with()` `-ends_with()`
  `contains()` `-contains()`
  `matches()` `-matches()`

Using `select` helpers

```
colnames(child.variants)        CHR POS dbSNP REF ALT QUAL GENE ENST  MutantReads COVERAGE MutantReadPercent
child.variants %>%
 select(REF,COVERAGE)           REF COVERAGE
 select(REF,everything())       REF CHR POS dbSNP ALT QUAL GENE ENST  MutantReads COVERAGE MutantReadPercent
 select(-CHR, -ENST)            POS dbSNP REF ALT QUAL GENE MutantReads COVERAGE MutantReadPercent
 select(-REF,everything())      CHR POS dbSNP ALT QUAL GENE ENST  MutantReads COVERAGE MutantReadPercent REF
 select(5:last_col())           ALT QUAL GENE ENST MutantReads COVERAGE MutantReadPercent
 select(POS:GENE)               POS dbSNP REF ALT QUAL GENE
 select(-(POS:GENE))            CHR ENST MutantReads COVERAGE MutantReadPercent
 select(starts_with("Mut"))     MutantReads MutantReadPercent
 select(-ends_with("t",ignore.case = FALSE))
                                CHR POS dbSNP REF ALT QUAL GENE ENST MutantReads COVERAGE
 select(contains("Read"))       MutantReads MutantReadPercent
```

Exercise 2
Filtering and selecting

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More clever filtering

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Multi-condition `filter`

```
trumpton %>%
  filter(Height > 170) %>%
  filter(Age > 30)
```

& = logical AND
| = logical OR
! = logical NOT

```
# A tibble: 1 x 5
  LastName FirstName   Age Weight Height
  <chr>    <chr>     <dbl>  <dbl>  <dbl>
1 Pew      Adam         32    102    183
```

Multi-condition `filter`

```
trumpton %>%
  filter(Height > 170 & Age > 30)
```

```
# A tibble: 1 x 5
  LastName FirstName   Age Weight Height
  <chr>    <chr>     <dbl>  <dbl>  <dbl>
1 Pew      Adam         32    102    183
```

```
& = logical AND
| = logical OR
! = logical NOT
```

Multi-condition `filter`

```
trumpton %>%
  filter(Height > 170 | Age > 30)
```

```
# A tibble: 6 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 McGrew   Chris        48     97    155
4 Cuthbert Carl         28     91    188
5 Dibble   Liam         35     94    145
6 Grub     Doug         31     89    164
```

& = logical AND
| = logical OR
! = logical NOT

Multi-condition `filter`

```
trumpton %>%
  filter(!(Height > 170 | Age > 30))
```

```
# A tibble: 1 x 5
  LastName FirstName   Age Weight Height
  <chr>    <chr>     <dbl>  <dbl>  <dbl>
1 Barney   Daniel       18     88    168
```

& = logical AND
| = logical OR
! = logical NOT

Using `filter` with `%in%`

```
> hits
 [1] "FGFR1"  "RASAL1" "GLB1L2" "DNAH1"  "PTH1R"
```

```
child.variants %>%
  filter(GENE %in% hits)
```

```
# A tibble: 5 x 11
  CHR         POS dbSNP      REF   ALT    QUAL GENE   ENST           MutantReads COVERAGE MutantReadPerce~
  <chr>     <dbl> <chr>      <chr> <chr> <dbl> <chr>  <chr>                <dbl>    <dbl>            <dbl>
1 11    134226278 rs3802928  C     T       200 GLB1L2 ENST03898~          13       43               30
2 12    113539822 rs1674101  A     G       200 RASAL1 ENST05465~          19       22               86
3 3      46944274 rs1138518  T     C       200 PTH1R  ENST04495~          32       75               42
4 3      52430526 rs12163565 G     A       200 DNAH1  ENST04203~          38       50               76
5 8      38271182 .          TG    T       200 FGFR1  ENST04259~           9       31               29
```

Using `filter` with other string operations

```
child %>%
  select(REF,ALT) %>%
  filter(startsWith(REF,"GAT"))
```

```
# A tibble: 3 x 2
  REF   ALT
  <chr> <chr>
1 GATA  G
2 GATAT GAT
3 GAT   G
```

```
child %>%
  select(GENE,ENST) %>%
  filter(endsWith(ENST,"878"))
```

```
# A tibble: 4 x 2
  GENE     ENST
  <chr>    <chr>
1 CIB3     ENST0269878
2 KCTD18   ENST0359878
3 KIAA1407 ENST0295878
4 RBM33    ENST0401878
```

These are different to the select helpers **starts_with** and **ends_with** which are used for picking columns

Using `filter` with `str_detect`

```
child.variants %>%
  filter(str_detect(GENE,"ZFP"))
```

```
# A tibble: 9 x 11
  CHR         POS dbSNP     REF   ALT    QUAL GENE   ENST           MutantReads COVERAGE MutantReadPerce~
  <chr>     <dbl> <chr>     <chr> <chr> <dbl> <chr>  <chr>                <dbl>    <dbl>            <dbl>
1 16     68598007 rs1177648 A     G       200 ZFP90  ENST0398253             43      100               43
2 16     88552370 rs3751673 A     G        53 ZFPM1  ENST0319555              4       23               17
3 18      5292030 rs620652  A     G       200 ZFP161 ENST0357006             28       71               39
4 19     57065189 rs145011  T     C       200 ZFP28  ENST0301318             59      137               43
5 20     50768672 .         GT    G       200 ZFP64  ENST0216923             36       41               87
6 5     180276402 rs168726  C     T       200 ZFP62  ENST0502412             74       83               89
7 8     106814656 rs2920048 G     C       200 ZFPM2  ENST0407775             33       79               41
8 8     144332012 rs6558339 T     C       200 ZFP41  ENST0330701             32       37               86
9 9     115818949 rs2282076 A     T       200 ZFP37  ENST0374227             18       43               41
```

Using `filter` with `is` functions

```
> data.with.na
# A tibble: 8 x 2
  sample value
  <chr>  <dbl>
1 A       9.98
2 A       8.58
3 A      10.4
4 A      11.4
5 B       9.75
6 B      11.2
7 B      NA
8 B      NA
```

```
data.with.na %>%
  filter(!is.na(value))
```

```
# A tibble: 6 x 2
  sample value
  <chr>  <dbl>
1 A       9.98
2 A       8.58
3 A      10.4
4 A      11.4
5 B       9.75
6 B      11.2
```

```
is_finite
is_infinite
is.nan
```

Note that some functions have dots whilst others have an underscore.

Transforming data in a `filter`

```
trumpton %>%
  filter(log(Height)>5)
```

```
# A tibble: 6 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 Grub     Doug         31     89    164
```

log
abs
sqrt
nchar
substr
tolower
toupper
etc.

Transforming `filter` examples

```
trumpton %>%
  filter(str_detect(tolower(LastName),"h"))

trumpton %>%
  filter(Weight*0.16 > 15)

trumpton %>%
  filter(nchar(LastName) == nchar(FirstName))
```

Exercise 3
More clever filtering

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Restructuring Data

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'Tidy' Data Format

- Tibbles are a 2D data structure where each column has a fixed data type (character, number, logical etc)

- Tidy data principles
  1. Rows should represent “observations”
  2. Columns should represent “variables”
  3. Columns should only contain a single piece of data

- Where these are not met – we restructure the data

Restructuring Data

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

- “Observation” is a single gene expression measure
- “Variables” are
  - Gene
  - Genotype
  - Replicate
- Data needs to be restructured to be “longer”

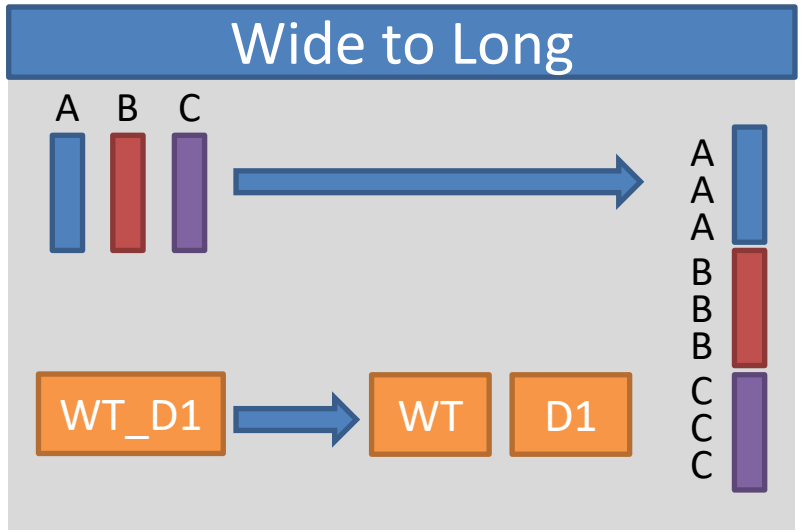
Restructuring Data

Gene	Genotype	Value
ABC1	WT	8.86
ABC1	KO	4.00
DEF1	WT	29.60
DEF1	KO	11.18
GHI1	WT	16.68
GHI1	KO	1.64

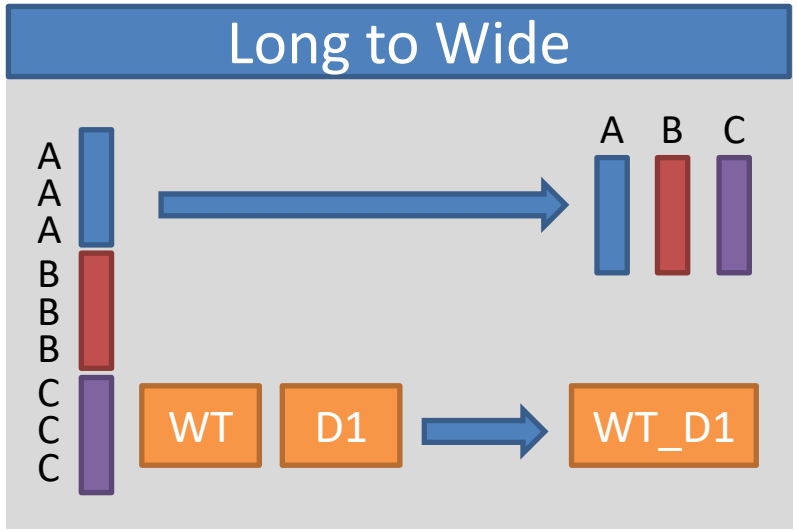
- Plot a GGPlot of WT vs KO
  - Need a WT and KO column
  - Can’t create aesthetic mappings
- Data needs to be restructured to be “wider”

Restructuring operations

- `pivot_longer`
  - Takes multiple columns of the same type and puts them into a pair of key-value columns
- `separate`
  - Splits a delimited column into multiple columns



- `pivot_wider`
  - Takes a key-value column pair and spreads them out to multiple columns of the same type
- `unite`
  - Combines multiple columns into one



Converting to "Tidy" format

```
# A tibble: 3 x 8
  Gene    Chr   Start     End  WT_1  WT_2  KO_1  KO_2
  <chr> <dbl>   <dbl>   <dbl> <dbl> <dbl> <dbl> <dbl>
1 Gnai3     2  163898  167465  9.39  10.9  33.5  81.9
2 Pbsn      5 4888573 4891351 91.7   59.6  45.3  82.3
3 Cdc45     7 1250084 1262669 69.2   36.1  54.4  38.1
```

- Do `pivot_longer` to put all measures into a column
  - Column names become a new column of values
- Use `separate` to split the new column of names into Genotype and Replicate

Converting to "Tidy" format

```
# A tibble: 12 x 7
   Gene    Chr   Start     End genotype replicate value
   <chr> <dbl>   <dbl>   <dbl> <chr>         <int> <dbl>
 1 Gnai3     2  163898  167465 WT                1  9.39
 2 Pbsn      5 4888573 4891351 WT                1 91.7
 3 Cdc45     7 1250084 1262669 WT                1 69.2
 4 Gnai3     2  163898  167465 WT                2 10.9
 5 Pbsn      5 4888573 4891351 WT                2 59.6
 6 Cdc45     7 1250084 1262669 WT                2 36.1
 7 Gnai3     2  163898  167465 KO                1 33.5
 8 Pbsn      5 4888573 4891351 KO                1 45.3
 9 Cdc45     7 1250084 1262669 KO                1 54.4
10 Gnai3     2  163898  167465 KO                2 81.9
11 Pbsn      5 4888573 4891351 KO                2 82.3
12 Cdc45     7 1250084 1262669 KO                2 38.1
```

Converting to "Tidy" format

```
non.normalised %>%

  pivot_longer(
    cols=WT_1:KO_2,
    names_to="sample",
    values_to="value"
  ) %>%

  separate(
    col=sample,
    into=c("genotype","replicate"),
    sep="_",
    convert = TRUE
  )
```

```
# A tibble: 3 x 8
  Gene    Chr   Start     End  WT_1  WT_2  KO_1  KO_2
  <chr> <dbl>   <dbl>   <dbl> <dbl> <dbl> <dbl> <dbl>
1 Gnai3     2  163898  167465  9.39  10.9  33.5  81.9
2 Pbsn      5 4888573 4891351 91.7   59.6  45.3  82.3
3 Cdc45     7 1250084 1262669 69.2   36.1  54.4  38.1
```

```
# A tibble: 12 x 6
   Gene    Chr   Start     End sample value
   <chr> <dbl>   <dbl>   <dbl> <chr>  <dbl>
 1 Gnai3     2  163898  167465 WT_1    9.39
 2 Gnai3     2  163898  167465 WT_2   10.9
 3 Gnai3     2  163898  167465 KO_1   33.5
 4 Gnai3     2  163898  167465 KO_2   81.9
 5 Pbsn      5 4888573 4891351 WT_1   91.7
 6 Pbsn      5 4888573 4891351 WT_2   59.6
```

`convert=TRUE` makes separate re-detect the type of the column, so replicate becomes a numeric value

Converting to "Tidy" format

```
# A tibble: 12 x 7
   Gene    Chr   Start     End genotype replicate value
   <chr> <dbl>   <dbl>   <dbl> <chr>         <int> <dbl>
 1 Gnai3     2  163898  167465 WT                1  9.39
 2 Pbsn      5 4888573 4891351 WT                1 91.7
 3 Cdc45     7 1250084 1262669 WT                1 69.2
 4 Gnai3     2  163898  167465 WT                2 10.9
 5 Pbsn      5 4888573 4891351 WT                2 59.6
 6 Cdc45     7 1250084 1262669 WT                2 36.1
 7 Gnai3     2  163898  167465 KO                1 33.5
 8 Pbsn      5 4888573 4891351 KO                1 45.3
 9 Cdc45     7 1250084 1262669 KO                1 54.4
10 Gnai3     2  163898  167465 KO                2 81.9
11 Pbsn      5 4888573 4891351 KO                2 82.3
12 Cdc45     7 1250084 1262669 KO                2 38.1
```

Pivoting Examples

```
> pivot.long
# A tibble: 8 x 3
  gene  Condition Count
  <chr> <chr>     <dbl>
1 ABC1  WT         14.2
2 ABC1  KO         12.9
3 DEF1  WT         15.0
4 DEF1  KO         15.8
5 GHI1  WT         12.9
6 GHI1  KO         16.5
7 JKL1  WT         16.6
8 JKL1  KO         15.5
```

```
pivot.long %>%
  pivot_wider(
    names_from = Condition,
    values_from = Count
  )
```

```
# A tibble: 4 x 3
  gene     WT    KO
  <chr> <dbl> <dbl>
1 ABC1   14.2  12.9
2 DEF1   15.0  15.8
3 GHI1   12.9  16.5
4 JKL1   16.6  15.5
```

- Plot WT vs KO
- Pivot wider
  - Which column of names?
  - Which column of values?

Splitting into multiple tibbles

Where you have a lot of annotation, you can split this into a separate tibble to reduce the amount of data duplication

```
# A tibble: 3 x 8
  Gene    Chr   Start     End  WT_1  WT_2  KO_1  KO_2
  <chr> <dbl>   <dbl>   <dbl> <dbl> <dbl> <dbl> <dbl>
1 Gnai3     2  163898  167465  9.39  10.9  33.5  81.9
2 Pbsn      5 4888573 4891351 91.7   59.6  45.3  82.3
3 Cdc45     7 1250084 1262669 69.2   36.1  54.4  38.1
```

Splitting into multiple tibbles

Annotation tibble

```
# A tibble: 3 x 4
  Gene    Chr   Start     End
  <chr> <dbl>   <dbl>   <dbl>
1 Gnai3     2  163898  167465
2 Pbsn      5 4888573 4891351
3 Cdc45     7 1250084 1262669
```

These can be recombined later on as needed using a join operation

Data tibble

```
# A tibble: 12 x 4
   Gene  genotype replicate value
   <chr> <chr>        <int> <dbl>
 1 Gnai3 WT               1  9.39
 2 Pbsn  WT               1 91.7
 3 Cdc45 WT               1 69.2
 4 Gnai3 WT               2 10.9
 5 Pbsn  WT               2 59.6
 6 Cdc45 WT               2 36.1
 7 Gnai3 KO               1 33.5
```

Exercise 4
Restructuring data into ‘tidy’ format

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Adding or creating new data

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Adding or creating data

- `add_row` adds a single new row
- `add_column` adds a column of new data
- `mutate` create a new column from existing columns

Adding new rows or columns

```
trumpton %>%
  add_row(
    FirstName="Simon",
    LastName="Andrews",
    Age=39,
    Weight=80,
    Height=185
  )
```

```
trumpton %>%
  add_column(
    vegetarian = c(T,F,F,T,F,F,T)
  )
```

```
trumpton %>%
  add_column(
    profession = "Fireman"
  )
```

Creating columns with `mutate`

```
trumpton %>%
  mutate(
    weight_stones=Weight*0.16,
    height_feet=Height*0.033
  )
```

```
# A tibble: 7 x 7
  LastName FirstName   Age Weight Height weight_stones height_feet
  <chr>    <chr>     <dbl>  <dbl>  <dbl>          <dbl>       <dbl>
1 Hugh     Chris        26     90    175           14.4        5.78
2 Pew      Adam         32    102    183           16.3        6.04
3 Barney   Daniel       18     88    168           14.1        5.54
4 McGrew   Chris        48     97    155           15.5        5.12
5 Cuthbert Carl         28     91    188           14.6        6.20
6 Dibble   Liam         35     94    145           15.0        4.78
7 Grub     Doug         31     89    164           14.2        5.41
```

Tricks with `mutate` – Creating categories

```
trumpton %>%
  mutate(Category = if_else(Height > 180, "Tall", "Short"))
```

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

More than 2 categories

```
trumpton %>%
  mutate(
    Category = case_when(
      Height > 180 ~ "Tall",
      Height > 160 ~ "Medium",
      TRUE ~ "Short"
    )
  )
```

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

The first condition to match is used.

Good to have TRUE as the last test to catch anything which hasn't yet matched.

Tricks with `mutate` – replacing values

```
data.with.na %>%
  mutate(value = replace(value,value>10, 10))
```

```
data.with.na %>%
  mutate(value = replace_na(value,0))
```

```
> data.with.na
# A tibble: 8 x 2
  sample value
  <chr>  <dbl>
1 A       9.98
2 A       8.58
3 A      16.4
4 A      18.4
5 B       9.75
6 B      17.2
7 B      NA
8 B      NA
```

```
# A tibble: 8 x 2
  sample value
  <chr>  <dbl>
1 A       9.98
2 A       8.58
3 A      10
4 A      10
5 B       9.75
6 B      10
7 B      NA
8 B      NA
```

```
# A tibble: 8 x 2
  sample value
  <chr>  <dbl>
1 A       9.98
2 A       8.58
3 A      16.4
4 A      18.4
5 B       9.75
6 B      17.2
7 B      0
8 B      0
```

Exercise 5
Adding or creating new data

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Grouping and Summarising

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Grouping and Summarising

- `group_by` sets groups for summarisation
- `ungroup` removes grouping information
- `summarise` collapse grouped variables
- `count` count grouped variables

Grouping and Summarising Workflow

1. Load a tibble with repeated values in one or more columns

2. Use `group_by` to select all of the categorical columns you want to combine to define your groups

3. Run `count` to see how many values are in each group, or `summarise` to quantitatively summarise groups

4. Run `ungroup` to remove any remaining group information

Grouping and Summarising Workflow

1. Load a tibble with repeated values in one or more columns

2. Use `group_by` to select all of the categorical columns you want to combine to define your groups

3. Run `count` to see how many values are in each group, or `summarise` to quantitatively summarise groups

4. Run `ungroup` to remove any remaining group information

Grouping and Summarising

```
> group.data

# A tibble: 8 x 5
  Sample Genotype Sex   Height Length
   <dbl> <chr>    <chr>  <dbl>  <dbl>
1      1 WT       M         15    200
2      2 WT       F         13    185
3      3 WT       F         14    221
4      4 WT       M         18    265
5      5 KO       M         26    120
6      6 KO       F         22    165
7      7 KO       F         19    143
8      8 KO       M         27    110
```

- Want to get the average Height and Length for each combination of sex and genotype

Grouping and Summarising Workflow

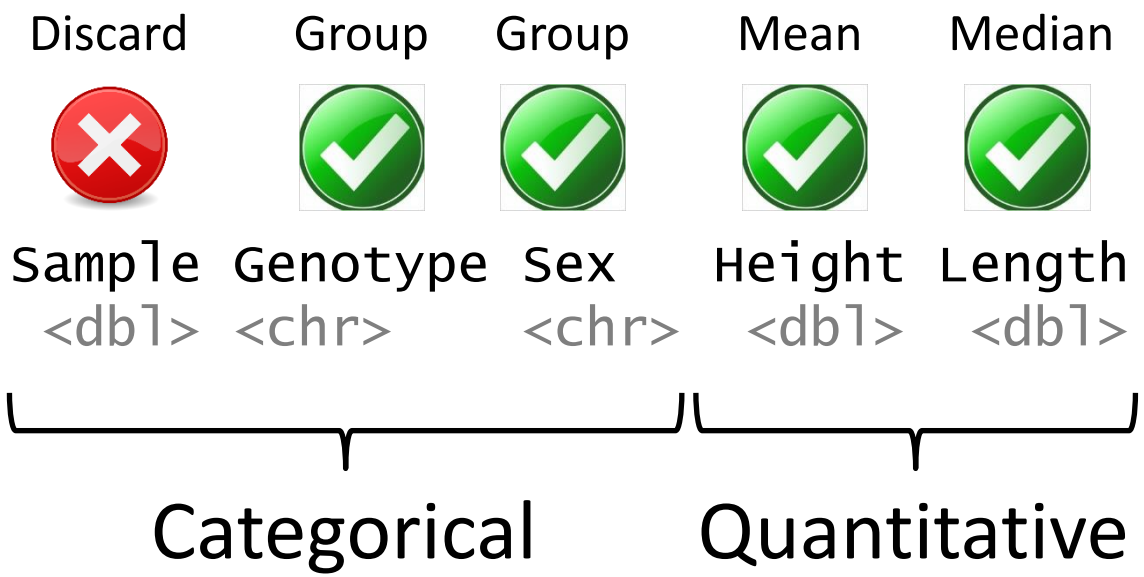
1. Load a tibble with repeated values in one or more columns

2. Use `group_by` to select all of the categorical columns you want to combine to define your groups

3. Run `count` to see how many values are in each group, or `summarise` to quantitatively summarise groups

4. Run `ungroup` to remove any remaining group information

Grouping and Summarising



- Want to get the average Height and Length for each combination of sex and genotype

Grouping and Summarising

```
group.data %>% group_by(Genotype,Sex)
```

```
# A tibble: 8 x 5
# Groups:   Genotype, Sex [4]
  Sample Genotype Sex   Height Length
   <dbl> <chr>    <chr>  <dbl>  <dbl>
1      1 WT       M         15    200
4      4 WT       M         18    265
2      2 WT       F         13    185
3      3 WT       F         14    221
5      5 KO       M         26    120
8      8 KO       M         27    110
6      6 KO       F         22    165
7      7 KO       F         19    143
```

Discard	Group	Group	Mean	Median
Sample	Genotype	Sex	Height	Length
<dbl>	<chr>	<chr>	<dbl>	<dbl>

Grouping and Summarising Workflow

1. Load a tibble with repeated values in one or more columns

2. Use `group_by` to select all of the categorical columns you want to combine to define your groups

3. Run `count` to see how many values are in each group, or `summarise` to quantitatively summarise groups

4. Run `ungroup` to remove any remaining group information

Grouping and Summarising

```
group.data %>%
  group_by(Genotype,Sex) %>%
  count()
```

```
# A tibble: 4 x 3
# Groups:   Genotype, Sex [4]
  Genotype Sex       n
  <chr>    <chr> <int>
1 KO       F         2
2 KO       M         2
3 WT       F         2
4 WT       M         2
```

Discard	Group	Group	Mean	Median
Sample	Genotype	Sex	Height	Length
<dbl>	<chr>	<chr>	<dbl>	<dbl>

Grouping and Summarising

```
group.data %>%
  group_by(Genotype,Sex) %>%
  summarise(
    Height2 = mean(Height),
    Length  = median(Length),
    Counts  = n()
  )
```

```
# A tibble: 4 × 5
# Groups:   Genotype [2]
  Genotype Sex   Height2 Length Counts
  <chr>    <chr>   <dbl>  <dbl>  <int>
1 KO       F        20.5   154      2
2 KO       M        26.5   115      2
3 WT       F        13.5   203      2
4 WT       M        16.5   232.     2
```

Discard	Group	Group	Mean	Median
Sample <dbl>	Genotype <chr>	Sex <chr>	Height <dbl>	Length <dbl>

If you want the count of values as part of a summarised result use the n() function

Grouping and Summarising Workflow

1. Load a tibble with repeated values in one or more columns

2. Use `group_by` to select all of the categorical columns you want to combine to define your groups

3. Run `count` to see how many values are in each group, or `summarise` to quantitatively summarise groups

4. Run `ungroup` to remove any remaining group information

Ungrouping

- A summarise operation removes the the last level of grouping (“Sex” in our worked example)

- Other levels of grouping (“Genotype”) remain annotated on the data, so you could do an additional summarisation if needed

- If you’re not going to use them it’s a good idea to use `ungroup` to remove remaining groups so they don’t interfere with other operations

Grouping affects lots of operations

Find the tallest member of each Sex

```
group.data %>%
  arrange(desc(Height)) %>%
  group_by(Sex) %>%
  slice(1) %>%
  ungroup()
```

```
# A tibble: 2 x 5
Sample Genotype Sex   Height Length
   <dbl> <chr>    <chr>  <dbl>  <dbl>
1      6 KO       F         22    165
2      8 KO       M         27    110
```

Grouping affects lots of operations

Normalise by mean centring the Length values

```
group.data %>%
  mutate(Diff=Length - mean(Length))
```

```
# A tibble: 8 x 6
  Sample Genotype Sex   Height Length  Diff
   <dbl> <chr>    <chr>  <dbl>  <dbl>  <dbl>
1      1 WT       M         15    200  23.9
2      2 WT       F         13    185  8.88
3      3 WT       F         14    221  44.9
4      4 WT       M         18    265  88.9
5      5 KO       M         26    120  -56.1
6      6 KO       F         22    165  -11.1
7      7 KO       F         19    143  -33.1
8      8 KO       M         27    110  -66.1
```

```
group.data %>%
  group_by(Genotype) %>%
  mutate(Diff=Length - mean(Length))
```

```
# A tibble: 8 x 6
# Groups:   Genotype [2]
  Sample Genotype Sex   Height Length   Diff
   <dbl> <chr>    <chr>  <dbl>  <dbl>  <dbl>
1      1 WT       M         15    200 -17.8
2      2 WT       F         13    185 -32.8
3      3 WT       F         14    221   3.25
4      4 WT       M         18    265  47.2
5      5 KO       M         26    120 -14.5
6      6 KO       F         22    165  30.5
7      7 KO       F         19    143   8.5
8      8 KO       M         27    110 -24.5
```

Exercise 6
Grouping and Summarising

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Joining Tibbles

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Simple joins

- `bind_rows` join tibbles by row
- `bind_cols` join tibbles by column
- `rename` rename a column

```
trumpton %>%
  rename(Surname=LastName)
```

Complex joins for tibbles x and y

- `left_join` join matching values from y into x
- `right_join` join matching values of x into y
- `inner_join` join x and y keeping only rows in both
- `full_join` join x and y keeping all values in both

Join types

```
> join1
  name   count
1 Simon      3
2 Laura      6
3 Felix      2
```

```
> join2
  name    percentage
1 Felix           10
2 Anne            25
3 Simon           36
```

left_join(join1,join2)

```
  name   count percentage
1 Simon      3         36
2 Laura      6         NA
3 Felix      2         10
```

right_join(join1,join2)

```
  name   count percentage
1 Felix      2         10
2 Anne      NA         25
3 Simon      3         36
```

inner_join(join1,join2)

```
  name   count percentage
1 Simon      3         36
2 Felix      2         10
```

full_join(join1,join2)

```
  name   count percentage
1 Simon      3         36
2 Laura      6         NA
3 Felix      2         10
4 Anne      NA         25
```

Rejoining split tables

Find the highest value for each genotype

```
> gathered.data
# A tibble: 12 x 4
   Gene  genotype replicate value
   <chr> <chr>        <int> <dbl>
 1 Gnai3 WT               1  9.39
 2 Pbsn  WT               1 91.7
 3 Cdc45 WT               1 69.2
 4 Gnai3 WT               2 10.9
 5 Pbsn  WT               2 59.6
 6 Cdc45 WT               2 36.1
 7 Gnai3 KO               1 33.5
 8 Pbsn  KO               1 45.3
 9 Cdc45 KO               1 54.4
10 Gnai3 KO               2 81.9
11 Pbsn  KO               2 82.3
12 Cdc45 KO               2 38.1
```

```
> gathered.annotation
# A tibble: 3 x 4
  Gene    Chr   Start     End
  <chr> <dbl>   <dbl>   <dbl>
1 Gnai3     2  163898  167465
2 Pbsn      5 4888573 4891351
3 Cdc45     7 1250084 1262669
```

Rejoining split tables

Find the highest value for each genotype

```
gathered.data %>%
  arrange(desc(value)) %>%
  group_by(genotype) %>%
  slice(1) %>%
  ungroup()
```

```
# A tibble: 2 x 4
  Gene  genotype replicate value
  <chr> <chr>        <int> <dbl>
1 Pbsn  KO               2  82.3
2 Pbsn  WT               1  91.7
```

```
gathered.data %>%
  arrange(desc(value)) %>%
  group_by(genotype) %>%
  slice(1) %>%
  ungroup() %>%
  left_join(gathered.annotation)
```

```
# A tibble: 2 x 7
  Gene  genotype replicate value   Chr   Start     End
  <chr> <chr>        <int> <dbl> <dbl>   <dbl>   <dbl>
1 Pbsn  KO               2  82.3     5 4888573 4891351
2 Pbsn  WT               1  91.7     5 4888573 4891351
```

Exercise 7
Joining Tibbles

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Custom Functions

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Custom Functions

Function name

Function Arguments

```
bmi <- function(weight, height) {
  height/100 -> height
  height^2 -> height
  return(weight/height)
}
```

Code Block

Return value

```
> bmi(90,175)
[1] 29.38776
```

```
> bmi(c(90,102), c(175,183))
[1] 29.38776 30.45776
```

Custom function with mutate

```
trumpton %>%
mutate(bodymass=Weight/(Height/100)^2)
```

```
trumpton %>%
    mutate(bodymass=bmi(Weight,Height))
```

```
bmi <- function(weight, height) {
  height/100 -> height
  height^2 -> height
  return(weight/height)
}
```

Custom Functions with Tidyverse

```
summarise.gene <- function(tbl, genename="NANOG") {
  tbl %>%
    filter(GENE==genename) %>%
    filter(nchar(REF) == 1, nchar(ALT) == 1) %>%
    group_by(REF, ALT) %>%
    count() %>%
    ungroup() %>%
    return()
}
```

```
child %>%
  summarise.gene("PLEC")
```

```
# A tibble: 6 x 3
  REF   ALT       n
  <chr> <chr> <int>
1 A     C         1
2 A     G         9
3 C     T         6
4 G     A         8
5 T     C         6
6 T     G         1
```

Custom Functions with Tidyverse

```
count_mutations <- function(tbl, col=REF) {
  tbl %>%
    group_by({{ col }}) %>%
    count() %>%
    ungroup() %>%
    arrange(desc(n)) %>%
    return()
}
```

```
child %>%
  count_mutations(col=ALT)
```

```
# A tibble: 257 x 2
   ALT       n
   <chr> <int>
 1 C      6480
 2 G      6404
 3 A      6275
 4 T      6103
 5 GA       43
 6 TA       37
 7 GC       33
 8 AG       24
 9 CT       22
10 CA       20
# ... with 247 more rows
```

Exercise 8
Custom Functions

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