R introduction using tidyverse

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References

A lot of this materials was based on material from:

- Hadley Wickham
- Michael Levy

Tidyverse and R

When we do data analysis the usual steps we follow are:
1. Import data
2. Tidy up
3. Transform data (select, filter, transform)
4. Visualize / Analyze
5. Model
6. Export and/or communicate

All the steps above need to be done in a consistent and reproducible way

The very beginning

1. What is R / Rstudio

2. Explanation of the window panes in R studio

3. R code
4. An R package is a collection of functions, data, and documentation that extends the capabilities of base R: **install.packages(tidyverse)**

5. In the begining of every session use the **library("tidyverse")**

What is the tidyverse?

~~Hadleyverse~~ **Hadley Wickam**

The tidyverse is a suite of R tools that follow a tidy philosophy:

Tidy data

Put data in data frames

- Each type of observation gets a data frame
- Each variable gets a column
- Each observation gets a row

Suite of ~20 packages that provide consistent, user-friendly, smart-default tools to do most of what most people do in R.

- Core packages: ggplot2, dplyr, tidyr, readr, purrr, tibble
- Specialized data manipulation: hms, stringr, lubridate, forcats
- Data import: DBI, haven, httr, jsonlite, readxl, rvest, xml2

- Modeling: modelr, broom

Bioconductor

```
if (!requireNamespace("BiocManager", quietly = TRUE))
    install.packages("BiocManager")
library("limma")
```

```
##Load the necessary packages

if (!require("tidyverse",quietly = TRUE))
  install.packages("tidyverse")
```

```
## -- Attaching packages ---------- tidyverse 1.2.1 --
```

```
## v ggplot2 3.1.0     v purrr   0.2.5
## v tibble  1.4.2     v dplyr   0.7.8
## v tidyr   0.8.2     v stringr 1.3.1
## v readr   1.2.1     v forcats 0.3.0
```

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

```
library("tidyverse")

if (!require("readxl",quietly = TRUE))
  install.packages("readxl")
library("readxl") ## Package for importing xls and xlsx files
```

Coding Basics

R operators

Arithmetic

Operator	Description
+	addition
-	subtraction
	multiplication
/	division
^ or **	exponentiation
x %% y	modulus (x mod y) 5%%2 is 1
x %/% y	integer division 5%/%2 is 2

Logical

Operator	Description
<	less than
<=	less than or equal to
>	greater than
>=	greater than or equal to
==	exactly equal to
!=	not equal to

Operator	Description
!x	Not x
x | y	x OR y
x & y	x AND y
isTRUE(x)	test if X is TRUE

```
2^3
```

```
## [1] 8
```

```
cos(45)^2 + sin(45)^2
```

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

```
x <- log2(8) ; y <- "R introduction" ## Assign value to a variable
#(in RStudio use Alt and - to create the assign symbol)

x ; y ## Print the x and y  values
```

```
## [1] 3
```

```
## [1] "R introduction"
```

```
d <- rnorm(10,mean = 0, sd = 1) # Almost everything in R is a function

d <- c(d,5,20)

d <- c(d,"Karim")
```

Data Structures in R

Homogeneous	Heterogenous
vectors	data frames (or tibbles)
matrix	lists
array	

```
v1 <- c(5,10,20) ; v1 # Vector 1
```

```
## [1]  5 10 20
```

```
v2 <- c(30,40,50) ;v2 # Vector 2
```

```
## [1] 30 40 50
```

```
m1 <- matrix(data = c(v1,v2),nrow=3,ncol = 4,byrow = F) # What will happen if I define byrow=True ?
m1
```

```
##      [,1] [,2] [,3] [,4]
## [1,]    5   30    5   30
## [2,]   10   40   10   40
## [3,]   20   50   20   50
```

```
dat1 <- data.frame(v1,v2)

daf <- as_tibble(diamonds)
```

```
### Transposable tibble

tribble(
~x, ~y, ~z,
#--/--/----
"a", 2, 3.6,
"b", 1, 8.5
)
```

```
## # A tibble: 2 x 3
##   x         y     z
##   <chr> <dbl> <dbl>
## 1 a         2   3.6
## 2 b         1   8.5
```

```
### You can store everything in a list
List1 <- list(c("a,b,c"),dat1,daf)
```

Subsetting using base R

```
diamonds[1:3,5:7] ## We will focus later on this using dplyr package
```

```
## # A tibble: 3 x 3
##   depth table price
##   <dbl> <dbl> <int>
## 1  61.5    55   326
## 2  59.8    61   326
## 3  56.9    65   327
```

One pipe to rule them all %>% magrittr

Sends the output of the LHS function to the first argument of the RHS function.

```
sum(1:8) %>%
  sqrt()
```

```
## [1] 6
```

```
cos(log10(rnorm(n = 100,mean = 5,10))) # Syntax with base R without using the pipe operator
```

```
## Warning: NaNs produced
```

```
##   [1] 0.82966917 0.77235270 0.87886532 0.88060333 0.26731887        NaN
##   [7] 0.44501725 0.41985509 0.27569410 0.38963974 0.39313783 0.27490747
##  [13]        NaN        NaN        NaN 0.91149950        NaN 0.65164585
##  [19]        NaN        NaN 0.72354954        NaN 0.21336326 0.40404567
##  [25]        NaN 0.99190508        NaN        NaN 0.29313019 0.60556058
##  [31] 0.35642351 0.45943322 0.43224837 0.54471722 0.98658794 0.47099767
##  [37]        NaN        NaN 0.31703929 0.09937456 0.49824081        NaN
##  [43] 0.36609238        NaN 0.95621902 0.79074137 0.47647315        NaN
##  [49] 0.37892115        NaN 0.48808468 0.99114351        NaN        NaN
##  [55]        NaN 0.57454676        NaN 0.99120064        NaN        NaN
##  [61] 0.27464174 0.31337954 0.63666495 0.53716322 0.65418149 0.34921358
##  [67] 0.38674326 0.99222355 0.48868194 0.60659908 0.16952137        NaN
##  [73] 0.66726383 0.36283898 0.96501964        NaN 0.45018365 0.45543474
##  [79] 0.38594150        NaN        NaN 0.77928292 0.93736934        NaN
```

```
##  [85] 0.64074218        NaN 0.42705454 0.29776128        NaN 0.18204934
##  [91] 0.39052601        NaN 0.46219785 0.45318893 0.70488715 0.55128993
##  [97]        NaN 0.86997309 0.12313992        NaN
```

```
rnorm(n = 100,mean = 5,10) %>% log10 %>% cos()
```

```
## Warning in function_list[[i]](value): NaNs produced
```

```
##   [1]       NaN       NaN 0.6465152 0.5683669       NaN 0.1805776       NaN
##   [8]       NaN       NaN 0.7309611 0.3137573 0.8724206       NaN 0.6606644
##  [15] 0.6469654 0.8818210 0.8082375 0.8393382       NaN 0.5452523 0.4790926
##  [22] 0.9849281 0.9439202 0.6514918 0.3797931       NaN       NaN 0.9880421
##  [29] 0.3253074 0.8548854       NaN 0.3623505 0.7165511 0.3130600 0.7039961
##  [36] 0.8520086       NaN 0.5322978 0.4545624       NaN       NaN       NaN
##  [43] 0.3401266 0.5047294 0.9971492       NaN       NaN 0.9228125 0.8711228
##  [50]       NaN       NaN 0.6945257 0.7735845 0.3678466 0.7243544 0.8368254
##  [57]       NaN 0.5114831 0.7450163 0.2737860       NaN 0.2422307       NaN
##  [64] 0.9447519       NaN 0.2237590       NaN 0.6675313 0.9325462 0.7707834
##  [71]       NaN 0.4710709 0.7677117       NaN 0.9227577       NaN       NaN
##  [78] 0.2694803       NaN 0.4627828 0.7805921 0.7249190 0.3611613       NaN
##  [85] 0.6548501 0.3792875       NaN 0.2612633 0.6463555       NaN 0.4793726
##  [92] 0.7690765 0.5234508       NaN       NaN 0.8827757       NaN 0.9953647
##  [99] 0.7970821 0.7334931
```

```
### How is the pipe incorporated for functions with multiple arguments

sum(1:8) %>% sqrt() %>% rnorm(n=20,mean=.,sd=.) ### Just subsitute the dot in the argument
```

```
##  [1] -1.5513296  5.0154524  9.0713736 -3.2694693 -5.5549385 -0.3333255
##  [7]  9.2954943  8.5512526 20.6119710  6.7740767  4.0322661  6.2461081
## [13]  0.4937288  9.9913776 -3.0971779  6.3683259  4.5275097  9.1558241
## [19]  7.6755823 12.4431486
```

Set seed function

Set the seed of R's random number generator, which is useful for creating simulations or random objects that can be reproduced.

```
rnorm(5) ## Gives random numbers everytime it is executed
```

```
## [1] -0.13664273  0.64638740 -1.16293092 -0.04888993 -0.01600302
```

```
## Set seed produces the same random numbers all the time ##
set.seed(123)
rnorm (5)
```

```
## [1] -0.56047565 -0.23017749  1.55870831  0.07050839  0.12928774
```

```
## If you run the rnorm only you get the same sequence of random numbers when the seed is set.

## If you want to reset the seed just

set.seed(Sys.time()) ## everytime it gets a different number
rnorm (5)
```

```
## [1] -0.9981179  0.4017049  0.1168478 -1.5823714 -1.4935367
```

Importing data into R

We will depend on **readr** and **readxl** instead of the base R functions instead of using the base R code

- ** read_csv() ** reads comma-delimited files
- ** read_csv2() ** reads semicolon-separated files
- ** read_tsv() ** reads tab-delimited files
- ** read_delim() ** read_delim()
- ** read_xls() ** "old excel files" **AVOID IMPORTING EXCEL FILES**

- ** read_xlsx() ** "newer excel files"

Maxquant output files

Irrespectively of the MQ version the output files are all in txt format.

```
## Using base R

#prot <- read.table(choose.files(), header=TRUE, sep="\t") ## Why this is bad ??


### Select the location in your computer of where your file is located

prot <- read.table("C:/Users/jimpa/Documents/R_projects/R_introduction_B230/proteinGroups_Kar_081118.tx


system.time(prot <- read.table(
"C:/Users/jimpa/Documents/R_projects/R_introduction_B230/proteinGroups_Kar_081118.txt", header=TRUE, se
```

```
##    user  system elapsed
##    1.64    0.00    1.68
```

```
#prot <- read_tsv(choose.files(),na = "NaN")

#system.time(prot <- read_tsv(file = "C:/Users/papageor/OneDrive/R_files/proteinGroups_Kar_081118.txt")

### Select the location in your computer of where your file is located

system.time(prot <- read_tsv(file = "C:/Users/jimpa/Documents/R_projects/R_introduction_B230_v2.0/prote
```

```
##    user  system elapsed
##    0.30    0.09    0.47
```

In the new version of readr 1.2.1 for some reason the Reversed column is not parsed (read) properly. In the older versions it was read as character but in this one it is read as logical. For this reason we need to manually define how to parse this column by including the argument col_types = cols(Reverse = col_character()))

Tidy Data

- **The first step is always to figure out what the variables and observations are**
- **Solve two usual problems:**
  - **One variable might be spread across multiple columns**
  - **One observation might be scattered across multiple rows**

Is proteingroups.txt from MQ in a tidy data format ?

Tidy proteingroups.txt

```
colnames(prot) <- str_replace_all(colnames(prot), "\\s",replacement = "_")

## Makes our life for later easier (Replaces space in the column names with _)

colnames(prot)
```

```
##   [1] "Protein_IDs"
##   [2] "Majority_protein_IDs"
##   [3] "Peptide_counts_(all)"
##   [4] "Peptide_counts_(razor+unique)"
##   [5] "Peptide_counts_(unique)"
##   [6] "Protein_names"
##   [7] "Gene_names"
##   [8] "Fasta_headers"
##   [9] "Number_of_proteins"
##  [10] "Peptides"
##  [11] "Razor_+_unique_peptides"
##  [12] "Unique_peptides"
##  [13] "Peptides_KRAS_1xIC50_R1"
##  [14] "Peptides_KRAS_1xIC50_R2"
##  [15] "Peptides_KRAS_5xIC50_R1"
##  [16] "Peptides_KRAS_5xIC50_R2"
##  [17] "Peptides_PIK3CA_1xIC50_R1"
##  [18] "Peptides_PIK3CA_1xIC50_R2"
##  [19] "Peptides_PIK3CA_5xIC50_R1"
##  [20] "Peptides_PIK3CA_5xIC50_R2"
##  [21] "Razor_+_unique_peptides_KRAS_1xIC50_R1"
##  [22] "Razor_+_unique_peptides_KRAS_1xIC50_R2"
##  [23] "Razor_+_unique_peptides_KRAS_5xIC50_R1"
##  [24] "Razor_+_unique_peptides_KRAS_5xIC50_R2"
##  [25] "Razor_+_unique_peptides_PIK3CA_1xIC50_R1"
##  [26] "Razor_+_unique_peptides_PIK3CA_1xIC50_R2"
##  [27] "Razor_+_unique_peptides_PIK3CA_5xIC50_R1"
##  [28] "Razor_+_unique_peptides_PIK3CA_5xIC50_R2"
##  [29] "Unique_peptides_KRAS_1xIC50_R1"
##  [30] "Unique_peptides_KRAS_1xIC50_R2"
##  [31] "Unique_peptides_KRAS_5xIC50_R1"
##  [32] "Unique_peptides_KRAS_5xIC50_R2"
##  [33] "Unique_peptides_PIK3CA_1xIC50_R1"
##  [34] "Unique_peptides_PIK3CA_1xIC50_R2"
##  [35] "Unique_peptides_PIK3CA_5xIC50_R1"
##  [36] "Unique_peptides_PIK3CA_5xIC50_R2"
##  [37] "Sequence_coverage_[%]"
##  [38] "Unique_+_razor_sequence_coverage_[%]"
##  [39] "Unique_sequence_coverage_[%]"
##  [40] "Mol._weight_[kDa]"
##  [41] "Sequence_length"
##  [42] "Sequence_lengths"
##  [43] "Q-value"
##  [44] "Identification_type_KRAS_1xIC50_R1"
##  [45] "Identification_type_KRAS_1xIC50_R2"
##  [46] "Identification_type_KRAS_5xIC50_R1"
```

```
##  [47] "Identification_type_KRAS_5xIC50_R2"
##  [48] "Identification_type_PIK3CA_1xIC50_R1"
##  [49] "Identification_type_PIK3CA_1xIC50_R2"
##  [50] "Identification_type_PIK3CA_5xIC50_R1"
##  [51] "Identification_type_PIK3CA_5xIC50_R2"
##  [52] "Ratio_M/L"
##  [53] "Ratio_M/L_normalized"
##  [54] "Ratio_M/L_variability_[%]"
##  [55] "Ratio_M/L_count"
##  [56] "Ratio_M/L_iso-count"
##  [57] "Ratio_M/L_type"
##  [58] "Ratio_H/L"
##  [59] "Ratio_H/L_normalized"
##  [60] "Ratio_H/L_variability_[%]"
##  [61] "Ratio_H/L_count"
##  [62] "Ratio_H/L_iso-count"
##  [63] "Ratio_H/L_type"
##  [64] "Ratio_H/M"
##  [65] "Ratio_H/M_normalized"
##  [66] "Ratio_H/M_variability_[%]"
##  [67] "Ratio_H/M_count"
##  [68] "Ratio_H/M_iso-count"
##  [69] "Ratio_H/M_type"
##  [70] "Ratio_M/L_KRAS_1xIC50_R1"
##  [71] "Ratio_M/L_normalized_KRAS_1xIC50_R1"
##  [72] "Ratio_M/L_variability_[%]_KRAS_1xIC50_R1"
##  [73] "Ratio_M/L_count_KRAS_1xIC50_R1"
##  [74] "Ratio_M/L_iso-count_KRAS_1xIC50_R1"
##  [75] "Ratio_M/L_type_KRAS_1xIC50_R1"
##  [76] "Ratio_H/L_KRAS_1xIC50_R1"
##  [77] "Ratio_H/L_normalized_KRAS_1xIC50_R1"
##  [78] "Ratio_H/L_variability_[%]_KRAS_1xIC50_R1"
##  [79] "Ratio_H/L_count_KRAS_1xIC50_R1"
##  [80] "Ratio_H/L_iso-count_KRAS_1xIC50_R1"
##  [81] "Ratio_H/L_type_KRAS_1xIC50_R1"
##  [82] "Ratio_H/M_KRAS_1xIC50_R1"
##  [83] "Ratio_H/M_normalized_KRAS_1xIC50_R1"
##  [84] "Ratio_H/M_variability_[%]_KRAS_1xIC50_R1"
##  [85] "Ratio_H/M_count_KRAS_1xIC50_R1"
##  [86] "Ratio_H/M_iso-count_KRAS_1xIC50_R1"
##  [87] "Ratio_H/M_type_KRAS_1xIC50_R1"
##  [88] "Ratio_M/L_KRAS_1xIC50_R2"
##  [89] "Ratio_M/L_normalized_KRAS_1xIC50_R2"
##  [90] "Ratio_M/L_variability_[%]_KRAS_1xIC50_R2"
##  [91] "Ratio_M/L_count_KRAS_1xIC50_R2"
##  [92] "Ratio_M/L_iso-count_KRAS_1xIC50_R2"
##  [93] "Ratio_M/L_type_KRAS_1xIC50_R2"
##  [94] "Ratio_H/L_KRAS_1xIC50_R2"
##  [95] "Ratio_H/L_normalized_KRAS_1xIC50_R2"
##  [96] "Ratio_H/L_variability_[%]_KRAS_1xIC50_R2"
##  [97] "Ratio_H/L_count_KRAS_1xIC50_R2"
##  [98] "Ratio_H/L_iso-count_KRAS_1xIC50_R2"
##  [99] "Ratio_H/L_type_KRAS_1xIC50_R2"
## [100] "Ratio_H/M_KRAS_1xIC50_R2"
```

```
## [101] "Ratio_H/M_normalized_KRAS_1xIC50_R2"
## [102] "Ratio_H/M_variability_[%]_KRAS_1xIC50_R2"
## [103] "Ratio_H/M_count_KRAS_1xIC50_R2"
## [104] "Ratio_H/M_iso-count_KRAS_1xIC50_R2"
## [105] "Ratio_H/M_type_KRAS_1xIC50_R2"
## [106] "Ratio_M/L_KRAS_5xIC50_R1"
## [107] "Ratio_M/L_normalized_KRAS_5xIC50_R1"
## [108] "Ratio_M/L_variability_[%]_KRAS_5xIC50_R1"
## [109] "Ratio_M/L_count_KRAS_5xIC50_R1"
## [110] "Ratio_M/L_iso-count_KRAS_5xIC50_R1"
## [111] "Ratio_M/L_type_KRAS_5xIC50_R1"
## [112] "Ratio_H/L_KRAS_5xIC50_R1"
## [113] "Ratio_H/L_normalized_KRAS_5xIC50_R1"
## [114] "Ratio_H/L_variability_[%]_KRAS_5xIC50_R1"
## [115] "Ratio_H/L_count_KRAS_5xIC50_R1"
## [116] "Ratio_H/L_iso-count_KRAS_5xIC50_R1"
## [117] "Ratio_H/L_type_KRAS_5xIC50_R1"
## [118] "Ratio_H/M_KRAS_5xIC50_R1"
## [119] "Ratio_H/M_normalized_KRAS_5xIC50_R1"
## [120] "Ratio_H/M_variability_[%]_KRAS_5xIC50_R1"
## [121] "Ratio_H/M_count_KRAS_5xIC50_R1"
## [122] "Ratio_H/M_iso-count_KRAS_5xIC50_R1"
## [123] "Ratio_H/M_type_KRAS_5xIC50_R1"
## [124] "Ratio_M/L_KRAS_5xIC50_R2"
## [125] "Ratio_M/L_normalized_KRAS_5xIC50_R2"
## [126] "Ratio_M/L_variability_[%]_KRAS_5xIC50_R2"
## [127] "Ratio_M/L_count_KRAS_5xIC50_R2"
## [128] "Ratio_M/L_iso-count_KRAS_5xIC50_R2"
## [129] "Ratio_M/L_type_KRAS_5xIC50_R2"
## [130] "Ratio_H/L_KRAS_5xIC50_R2"
## [131] "Ratio_H/L_normalized_KRAS_5xIC50_R2"
## [132] "Ratio_H/L_variability_[%]_KRAS_5xIC50_R2"
## [133] "Ratio_H/L_count_KRAS_5xIC50_R2"
## [134] "Ratio_H/L_iso-count_KRAS_5xIC50_R2"
## [135] "Ratio_H/L_type_KRAS_5xIC50_R2"
## [136] "Ratio_H/M_KRAS_5xIC50_R2"
## [137] "Ratio_H/M_normalized_KRAS_5xIC50_R2"
## [138] "Ratio_H/M_variability_[%]_KRAS_5xIC50_R2"
## [139] "Ratio_H/M_count_KRAS_5xIC50_R2"
## [140] "Ratio_H/M_iso-count_KRAS_5xIC50_R2"
## [141] "Ratio_H/M_type_KRAS_5xIC50_R2"
## [142] "Ratio_M/L_PIK3CA_1xIC50_R1"
## [143] "Ratio_M/L_normalized_PIK3CA_1xIC50_R1"
## [144] "Ratio_M/L_variability_[%]_PIK3CA_1xIC50_R1"
## [145] "Ratio_M/L_count_PIK3CA_1xIC50_R1"
## [146] "Ratio_M/L_iso-count_PIK3CA_1xIC50_R1"
## [147] "Ratio_M/L_type_PIK3CA_1xIC50_R1"
## [148] "Ratio_H/L_PIK3CA_1xIC50_R1"
## [149] "Ratio_H/L_normalized_PIK3CA_1xIC50_R1"
## [150] "Ratio_H/L_variability_[%]_PIK3CA_1xIC50_R1"
## [151] "Ratio_H/L_count_PIK3CA_1xIC50_R1"
## [152] "Ratio_H/L_iso-count_PIK3CA_1xIC50_R1"
## [153] "Ratio_H/L_type_PIK3CA_1xIC50_R1"
## [154] "Ratio_H/M_PIK3CA_1xIC50_R1"
```

```
## [155] "Ratio_H/M_normalized_PIK3CA_1xIC50_R1"
## [156] "Ratio_H/M_variability_[%]_PIK3CA_1xIC50_R1"
## [157] "Ratio_H/M_count_PIK3CA_1xIC50_R1"
## [158] "Ratio_H/M_iso-count_PIK3CA_1xIC50_R1"
## [159] "Ratio_H/M_type_PIK3CA_1xIC50_R1"
## [160] "Ratio_M/L_PIK3CA_1xIC50_R2"
## [161] "Ratio_M/L_normalized_PIK3CA_1xIC50_R2"
## [162] "Ratio_M/L_variability_[%]_PIK3CA_1xIC50_R2"
## [163] "Ratio_M/L_count_PIK3CA_1xIC50_R2"
## [164] "Ratio_M/L_iso-count_PIK3CA_1xIC50_R2"
## [165] "Ratio_M/L_type_PIK3CA_1xIC50_R2"
## [166] "Ratio_H/L_PIK3CA_1xIC50_R2"
## [167] "Ratio_H/L_normalized_PIK3CA_1xIC50_R2"
## [168] "Ratio_H/L_variability_[%]_PIK3CA_1xIC50_R2"
## [169] "Ratio_H/L_count_PIK3CA_1xIC50_R2"
## [170] "Ratio_H/L_iso-count_PIK3CA_1xIC50_R2"
## [171] "Ratio_H/L_type_PIK3CA_1xIC50_R2"
## [172] "Ratio_H/M_PIK3CA_1xIC50_R2"
## [173] "Ratio_H/M_normalized_PIK3CA_1xIC50_R2"
## [174] "Ratio_H/M_variability_[%]_PIK3CA_1xIC50_R2"
## [175] "Ratio_H/M_count_PIK3CA_1xIC50_R2"
## [176] "Ratio_H/M_iso-count_PIK3CA_1xIC50_R2"
## [177] "Ratio_H/M_type_PIK3CA_1xIC50_R2"
## [178] "Ratio_M/L_PIK3CA_5xIC50_R1"
## [179] "Ratio_M/L_normalized_PIK3CA_5xIC50_R1"
## [180] "Ratio_M/L_variability_[%]_PIK3CA_5xIC50_R1"
## [181] "Ratio_M/L_count_PIK3CA_5xIC50_R1"
## [182] "Ratio_M/L_iso-count_PIK3CA_5xIC50_R1"
## [183] "Ratio_M/L_type_PIK3CA_5xIC50_R1"
## [184] "Ratio_H/L_PIK3CA_5xIC50_R1"
## [185] "Ratio_H/L_normalized_PIK3CA_5xIC50_R1"
## [186] "Ratio_H/L_variability_[%]_PIK3CA_5xIC50_R1"
## [187] "Ratio_H/L_count_PIK3CA_5xIC50_R1"
## [188] "Ratio_H/L_iso-count_PIK3CA_5xIC50_R1"
## [189] "Ratio_H/L_type_PIK3CA_5xIC50_R1"
## [190] "Ratio_H/M_PIK3CA_5xIC50_R1"
## [191] "Ratio_H/M_normalized_PIK3CA_5xIC50_R1"
## [192] "Ratio_H/M_variability_[%]_PIK3CA_5xIC50_R1"
## [193] "Ratio_H/M_count_PIK3CA_5xIC50_R1"
## [194] "Ratio_H/M_iso-count_PIK3CA_5xIC50_R1"
## [195] "Ratio_H/M_type_PIK3CA_5xIC50_R1"
## [196] "Ratio_M/L_PIK3CA_5xIC50_R2"
## [197] "Ratio_M/L_normalized_PIK3CA_5xIC50_R2"
## [198] "Ratio_M/L_variability_[%]_PIK3CA_5xIC50_R2"
## [199] "Ratio_M/L_count_PIK3CA_5xIC50_R2"
## [200] "Ratio_M/L_iso-count_PIK3CA_5xIC50_R2"
## [201] "Ratio_M/L_type_PIK3CA_5xIC50_R2"
## [202] "Ratio_H/L_PIK3CA_5xIC50_R2"
## [203] "Ratio_H/L_normalized_PIK3CA_5xIC50_R2"
## [204] "Ratio_H/L_variability_[%]_PIK3CA_5xIC50_R2"
## [205] "Ratio_H/L_count_PIK3CA_5xIC50_R2"
## [206] "Ratio_H/L_iso-count_PIK3CA_5xIC50_R2"
## [207] "Ratio_H/L_type_PIK3CA_5xIC50_R2"
## [208] "Ratio_H/M_PIK3CA_5xIC50_R2"
```

```
## [209] "Ratio_H/M_normalized_PIK3CA_5xIC50_R2"
## [210] "Ratio_H/M_variability_[%]_PIK3CA_5xIC50_R2"
## [211] "Ratio_H/M_count_PIK3CA_5xIC50_R2"
## [212] "Ratio_H/M_iso-count_PIK3CA_5xIC50_R2"
## [213] "Ratio_H/M_type_PIK3CA_5xIC50_R2"
## [214] "Sequence_coverage_KRAS_1xIC50_R1_[%]"
## [215] "Sequence_coverage_KRAS_1xIC50_R2_[%]"
## [216] "Sequence_coverage_KRAS_5xIC50_R1_[%]"
## [217] "Sequence_coverage_KRAS_5xIC50_R2_[%]"
## [218] "Sequence_coverage_PIK3CA_1xIC50_R1_[%]"
## [219] "Sequence_coverage_PIK3CA_1xIC50_R2_[%]"
## [220] "Sequence_coverage_PIK3CA_5xIC50_R1_[%]"
## [221] "Sequence_coverage_PIK3CA_5xIC50_R2_[%]"
## [222] "Intensity"
## [223] "Intensity_L"
## [224] "Intensity_M"
## [225] "Intensity_H"
## [226] "Intensity_KRAS_1xIC50_R1"
## [227] "Intensity_L_KRAS_1xIC50_R1"
## [228] "Intensity_M_KRAS_1xIC50_R1"
## [229] "Intensity_H_KRAS_1xIC50_R1"
## [230] "Intensity_KRAS_1xIC50_R2"
## [231] "Intensity_L_KRAS_1xIC50_R2"
## [232] "Intensity_M_KRAS_1xIC50_R2"
## [233] "Intensity_H_KRAS_1xIC50_R2"
## [234] "Intensity_KRAS_5xIC50_R1"
## [235] "Intensity_L_KRAS_5xIC50_R1"
## [236] "Intensity_M_KRAS_5xIC50_R1"
## [237] "Intensity_H_KRAS_5xIC50_R1"
## [238] "Intensity_KRAS_5xIC50_R2"
## [239] "Intensity_L_KRAS_5xIC50_R2"
## [240] "Intensity_M_KRAS_5xIC50_R2"
## [241] "Intensity_H_KRAS_5xIC50_R2"
## [242] "Intensity_PIK3CA_1xIC50_R1"
## [243] "Intensity_L_PIK3CA_1xIC50_R1"
## [244] "Intensity_M_PIK3CA_1xIC50_R1"
## [245] "Intensity_H_PIK3CA_1xIC50_R1"
## [246] "Intensity_PIK3CA_1xIC50_R2"
## [247] "Intensity_L_PIK3CA_1xIC50_R2"
## [248] "Intensity_M_PIK3CA_1xIC50_R2"
## [249] "Intensity_H_PIK3CA_1xIC50_R2"
## [250] "Intensity_PIK3CA_5xIC50_R1"
## [251] "Intensity_L_PIK3CA_5xIC50_R1"
## [252] "Intensity_M_PIK3CA_5xIC50_R1"
## [253] "Intensity_H_PIK3CA_5xIC50_R1"
## [254] "Intensity_PIK3CA_5xIC50_R2"
## [255] "Intensity_L_PIK3CA_5xIC50_R2"
## [256] "Intensity_M_PIK3CA_5xIC50_R2"
## [257] "Intensity_H_PIK3CA_5xIC50_R2"
## [258] "Only_identified_by_site"
## [259] "Reverse"
## [260] "Potential_contaminant"
## [261] "id"
## [262] "Peptide_IDs"
```

```
## [263] "Peptide_is_razor"
## [264] "Mod._peptide_IDs"
## [265] "Evidence_IDs"
## [266] "MS/MS_IDs"
## [267] "Best_MS/MS"
## [268] "AHA->DAB_site_IDs"
## [269] "AHA->HS_site_IDs"
## [270] "Met->AHA_site_IDs"
## [271] "Oxidation_(M)_site_IDs"
## [272] "AHA->DAB_site_positions"
## [273] "AHA->HS_site_positions"
## [274] "Met->AHA_site_positions"
## [275] "Oxidation_(M)_site_positions"
```

dplyr

Common data(frame) manipulation tasks.

Four core "verbs": filter, select, arrange, group_by + summarize, plus many more convenience functions.

Filter

```
# Remove contaminants, reverse hits and only identified by site

prot_f <- prot %>%

  filter(Only_identified_by_site != "+",Reverse != "+",Potential_contaminant != "+")

prot_f
```

```
## # A tibble: 3,804 x 275
##    Protein_IDs Majority_protei~ `Peptide_counts~ `Peptide_counts~
##    <chr>       <chr>            <chr>            <chr>
##  1 A0A096LP01  A0A096LP01       2                2
##  2 A0FGR8      A0FGR8           28               28
##  3 A1L0T0      A1L0T0           13               13
##  4 A2A288      A2A288           2                2
##  5 A2A3N6      A2A3N6           7                2
##  6 A2RRP1      A2RRP1           5                5
##  7 A3KMH1      A3KMH1           27               27
##  8 A4D1E9      A4D1E9           7                7
##  9 A5PLL7      A5PLL7           3                3
## 10 A5YKK6      A5YKK6           9                9
## # ... with 3,794 more rows, and 271 more variables:
## #   `Peptide_counts_(unique)` <chr>, Protein_names <chr>,
## #   Gene_names <chr>, Fasta_headers <chr>, Number_of_proteins <dbl>,
## #   Peptides <dbl>, `Razor_+_unique_peptides` <dbl>,
## #   Unique_peptides <dbl>, Peptides_KRAS_1xIC50_R1 <dbl>,
## #   Peptides_KRAS_1xIC50_R2 <dbl>, Peptides_KRAS_5xIC50_R1 <dbl>,
## #   Peptides_KRAS_5xIC50_R2 <dbl>, Peptides_PIK3CA_1xIC50_R1 <dbl>,
## #   Peptides_PIK3CA_1xIC50_R2 <dbl>, Peptides_PIK3CA_5xIC50_R1 <dbl>,
## #   Peptides_PIK3CA_5xIC50_R2 <dbl>,
## #   `Razor_+_unique_peptides_KRAS_1xIC50_R1` <dbl>,
## #   `Razor_+_unique_peptides_KRAS_1xIC50_R2` <dbl>,
## #   `Razor_+_unique_peptides_KRAS_5xIC50_R1` <dbl>,
```

```
## #   `Razor_+_unique_peptides_KRAS_5xIC50_R2` <dbl>,
## #   `Razor_+_unique_peptides_PIK3CA_1xIC50_R1` <dbl>,
## #   `Razor_+_unique_peptides_PIK3CA_1xIC50_R2` <dbl>,
## #   `Razor_+_unique_peptides_PIK3CA_5xIC50_R1` <dbl>,
## #   `Razor_+_unique_peptides_PIK3CA_5xIC50_R2` <dbl>,
## #   Unique_peptides_KRAS_1xIC50_R1 <dbl>,
## #   Unique_peptides_KRAS_1xIC50_R2 <dbl>,
## #   Unique_peptides_KRAS_5xIC50_R1 <dbl>,
## #   Unique_peptides_KRAS_5xIC50_R2 <dbl>,
## #   Unique_peptides_PIK3CA_1xIC50_R1 <dbl>,
## #   Unique_peptides_PIK3CA_1xIC50_R2 <dbl>,
## #   Unique_peptides_PIK3CA_5xIC50_R1 <dbl>,
## #   Unique_peptides_PIK3CA_5xIC50_R2 <dbl>, `Sequence_coverage_[%]` <dbl>,
## #   `Unique_+_razor_sequence_coverage_[%]` <dbl>,
## #   `Unique_sequence_coverage_[%]` <dbl>, `Mol._weight_[kDa]` <dbl>,
## #   Sequence_length <dbl>, Sequence_lengths <chr>, `Q-value` <dbl>,
## #   Identification_type_KRAS_1xIC50_R1 <chr>,
## #   Identification_type_KRAS_1xIC50_R2 <chr>,
## #   Identification_type_KRAS_5xIC50_R1 <chr>,
## #   Identification_type_KRAS_5xIC50_R2 <chr>,
## #   Identification_type_PIK3CA_1xIC50_R1 <chr>,
## #   Identification_type_PIK3CA_1xIC50_R2 <chr>,
## #   Identification_type_PIK3CA_5xIC50_R1 <chr>,
## #   Identification_type_PIK3CA_5xIC50_R2 <chr>, `Ratio_M/L` <dbl>,
## #   `Ratio_M/L_normalized` <dbl>, `Ratio_M/L_variability_[%]` <dbl>,
## #   `Ratio_M/L_count` <dbl>, `Ratio_M/L_iso-count` <dbl>,
## #   `Ratio_M/L_type` <chr>, `Ratio_H/L` <dbl>,
## #   `Ratio_H/L_normalized` <dbl>, `Ratio_H/L_variability_[%]` <dbl>,
## #   `Ratio_H/L_count` <dbl>, `Ratio_H/L_iso-count` <dbl>,
## #   `Ratio_H/L_type` <chr>, `Ratio_H/M` <dbl>,
## #   `Ratio_H/M_normalized` <dbl>, `Ratio_H/M_variability_[%]` <dbl>,
## #   `Ratio_H/M_count` <dbl>, `Ratio_H/M_iso-count` <dbl>,
## #   `Ratio_H/M_type` <chr>, `Ratio_M/L_KRAS_1xIC50_R1` <dbl>,
## #   `Ratio_M/L_normalized_KRAS_1xIC50_R1` <dbl>,
## #   `Ratio_M/L_variability_[%]_KRAS_1xIC50_R1` <dbl>,
## #   `Ratio_M/L_count_KRAS_1xIC50_R1` <dbl>,
## #   `Ratio_M/L_iso-count_KRAS_1xIC50_R1` <dbl>,
## #   `Ratio_M/L_type_KRAS_1xIC50_R1` <chr>,
## #   `Ratio_H/L_KRAS_1xIC50_R1` <dbl>,
## #   `Ratio_H/L_normalized_KRAS_1xIC50_R1` <dbl>,
## #   `Ratio_H/L_variability_[%]_KRAS_1xIC50_R1` <dbl>,
## #   `Ratio_H/L_count_KRAS_1xIC50_R1` <dbl>,
## #   `Ratio_H/L_iso-count_KRAS_1xIC50_R1` <dbl>,
## #   `Ratio_H/L_type_KRAS_1xIC50_R1` <chr>,
## #   `Ratio_H/M_KRAS_1xIC50_R1` <dbl>,
## #   `Ratio_H/M_normalized_KRAS_1xIC50_R1` <dbl>,
## #   `Ratio_H/M_variability_[%]_KRAS_1xIC50_R1` <dbl>,
## #   `Ratio_H/M_count_KRAS_1xIC50_R1` <dbl>,
## #   `Ratio_H/M_iso-count_KRAS_1xIC50_R1` <dbl>,
## #   `Ratio_H/M_type_KRAS_1xIC50_R1` <chr>,
## #   `Ratio_M/L_KRAS_1xIC50_R2` <dbl>,
## #   `Ratio_M/L_normalized_KRAS_1xIC50_R2` <dbl>,
## #   `Ratio_M/L_variability_[%]_KRAS_1xIC50_R2` <dbl>,
## #   `Ratio_M/L_count_KRAS_1xIC50_R2` <dbl>,
```

```
## #   `Ratio_M/L_iso-count_KRAS_1xIC50_R2` <dbl>,
## #   `Ratio_M/L_type_KRAS_1xIC50_R2` <chr>,
## #   `Ratio_H/L_KRAS_1xIC50_R2` <dbl>,
## #   `Ratio_H/L_normalized_KRAS_1xIC50_R2` <dbl>,
## #   `Ratio_H/L_variability_[%]_KRAS_1xIC50_R2` <dbl>,
## #   `Ratio_H/L_count_KRAS_1xIC50_R2` <dbl>,
## #   `Ratio_H/L_iso-count_KRAS_1xIC50_R2` <dbl>,
## #   `Ratio_H/L_type_KRAS_1xIC50_R2` <chr>,
## #   `Ratio_H/M_KRAS_1xIC50_R2` <dbl>,
## #   `Ratio_H/M_normalized_KRAS_1xIC50_R2` <dbl>,
## #   `Ratio_H/M_variability_[%]_KRAS_1xIC50_R2` <dbl>,
## #   `Ratio_H/M_count_KRAS_1xIC50_R2` <dbl>,
## #   `Ratio_H/M_iso-count_KRAS_1xIC50_R2` <dbl>, ...
```

Select

- starts_with("abc") matches names that begin with "abc"
- ends_with("xyz") matches names that end with "xyz"
- contains("ijk") matches names that contain "ijk"
- matches("(.)\1") selects variables that match a regular expression.
- num_range("x", 1:3) matches x1 , x2 , and x3

```
# Select columns that we will need for further processing

prot_f1 <- prot_f %>% select(Protein_IDs,Majority_protein_IDs,

                             Protein_names,Gene_names,

                             Fasta_headers,Number_of_proteins)

# Isn't there a faster way ?

prot_f1 <- prot_f %>%

  select(contains("Protein"),Gene_names:Number_of_proteins,

                             starts_with("Peptides_"),

                             matches("^Sequence_coverage_[^[]"), `Mol._weight_[kDa]`,

                             starts_with("Identification"),

         matches("Ratio_./._[^vit]"),

                             matches("^Intensity_._."))
```

Split Protein IDs and Gene names

```
prot_f1 <- prot_f1 %>%

  mutate(Protein_IDs = str_split(Protein_IDs,";",simplify = TRUE)[,1],

                              Gene_names = str_split(Gene_names,";",simplify = T)[,1])
```

```
##prot_f1$Protein_IDs <- str_split(string = prot_f1$Protein_IDs, pattern = ";",simplify = T)[,1]
#prot_f1$Gene_names <- str_split(string = prot_f1$Gene_names, pattern = ";",simplify = T)[,1]
```

Tidying up the variables

We observe that variables (both categorical and numerical are spread across the table)

```
Peptides_tb <- prot_f1 %>% select(Protein_IDs:Peptides_PIK3CA_5xIC50_R2) %>%

  gather(Peptides_KRAS_1xIC50_R1:Peptides_PIK3CA_5xIC50_R2 ,key = "Experiment",
         value = "Peptide_Number") %>%

  mutate(Experiment = str_remove_all(Experiment,pattern = "Peptides_"))


Seq_cov_tb <- prot_f1 %>% select(Protein_IDs:Fasta_headers,starts_with("Seq")) %>%

  gather(starts_with("Seq") ,key = "Experiment", value = "Seq_cov_[%]") %>%

  mutate(Experiment = str_remove_all(Experiment,pattern = "Sequence_coverage_")) %>%

  mutate(Experiment = str_remove_all(Experiment,pattern ="_\\[%]"))

Id_type_tb <- prot_f1 %>% select(Protein_IDs:Fasta_headers,starts_with("Ident")) %>%

  gather(starts_with("Ident") ,key = "Experiment", value = "Ident_type") %>%

  mutate(Experiment = str_remove_all(Experiment,pattern = "Identification_type_"))

## Gather the intensities

Intensity_tb_L <- prot_f1 %>% select(Protein_IDs:Fasta_headers,starts_with("Intensity")) %>%

  gather(starts_with("Intensity_L") ,key = "Experiment", value = "Intensity_L") %>%

  mutate(Experiment = str_remove_all(Experiment,pattern = "Intensity_L_")) %>%

  select(Protein_IDs:Fasta_headers,Experiment:Intensity_L)


Intensity_tb_M <-  prot_f1 %>% select(Protein_IDs:Fasta_headers,starts_with("Intensity")) %>%

  gather(starts_with("Intensity_M") ,key = "Experiment", value = "Intensity_M") %>%

  mutate(Experiment = str_remove_all(Experiment,pattern = "Intensity_M_")) %>%

    select(Protein_IDs:Fasta_headers,Experiment:Intensity_M)


 Intensity_tb_H <- prot_f1 %>% select(Protein_IDs:Fasta_headers,starts_with("Intensity")) %>%

   gather(starts_with("Intensity_H") ,key = "Experiment", value = "Intensity_H") %>%
```

```
  mutate(Experiment = str_remove_all(Experiment,pattern = "Intensity_H_")) %>%

  select(Protein_IDs:Fasta_headers,Experiment:Intensity_H)


 Intensity_tb <- left_join(Intensity_tb_L,Intensity_tb_M) %>% left_join(Intensity_tb_H)
```

```
## Joining, by = c("Protein_IDs", "Majority_protein_IDs", "Protein_names", "Number_of_proteins", "Gene_n
## Joining, by = c("Protein_IDs", "Majority_protein_IDs", "Protein_names", "Number_of_proteins", "Gene_n
```

```
#%>%
  #mutate(Channel = if_else(str_detect(Experiment,"\\_L_")==TRUE,"Light",
   #                      if_else(str_detect(Experiment,"\\_M_")==TRUE,"Medium","Heavy")),
    #  Experiment = str_remove_all(Experiment,pattern = "Intensity_._"))



##Intensity_tb <- prot_f1 %>% select(Protein_IDs:Fasta_headers,starts_with("Intensity")) %>%
  ##gather(starts_with("Intensity") ,key = "Experiment", value = "Intensity") %>%
  ##mutate(Channel = if_else(str_detect(Experiment,"\\_L_")==TRUE,"Light",
    ##                     if_else(str_detect(Experiment,"\\_M_")==TRUE,"Medium","Heavy")),
      ## Experiment = str_remove_all(Experiment,pattern = "Intensity_._"))


######## Normalized Silac Ratios ##################
#### H/L

Silac_tb_norm_HL <- prot_f1 %>% select(Protein_IDs:Fasta_headers,starts_with("Ratio"),-("Ratio_M/L_norma

  gather(contains("H/L_normalized"),key = "Experiment",value = "Ratio_norm_H/L") %>%


  mutate(Experiment = str_remove_all(Experiment,pattern = "Ratio_H/L_normalized_")) %>%

  select(Protein_IDs:Fasta_headers,Experiment:"Ratio_norm_H/L")

## M/L

Silac_tb_norm_ML <- prot_f1 %>%

  select(Protein_IDs:Fasta_headers,starts_with("Ratio"),-("Ratio_M/L_normalized":"Ratio_H/M_count")) %>%

  gather(contains("M/L_normalized"),key = "Experiment",value = "Ratio_norm_M/L") %>%


  mutate(Experiment = str_remove_all(Experiment,pattern = "Ratio_M/L_normalized_")) %>%

  select(Protein_IDs:Fasta_headers,Experiment:"Ratio_norm_M/L")

## H/M

Silac_tb_norm_HM <- prot_f1 %>% select(Protein_IDs:Fasta_headers,starts_with("Ratio"),-("Ratio_M/L_norma

  gather(contains("H/M_normalized"),key = "Experiment",value = "Ratio_norm_H/M") %>%
```

```
  mutate(Experiment = str_remove_all(Experiment,pattern = "Ratio_H/M_normalized_")) %>%

  select(Protein_IDs:Fasta_headers,Experiment:"Ratio_norm_H/M")

### Gather the Silac_ratios

Silac_tb_norm <- left_join(Silac_tb_norm_HL,Silac_tb_norm_ML) %>%

  left_join(Silac_tb_norm_HM)
```

```
## Joining, by = c("Protein_IDs", "Majority_protein_IDs", "Protein_names", "Number_of_proteins", "Gene_n
## Joining, by = c("Protein_IDs", "Majority_protein_IDs", "Protein_names", "Number_of_proteins", "Gene_n
```

Speed up the tidying up of the variables with gather and spread

```
### Fix the counts

Silac_tb_count <- prot_f1 %>% select(Protein_IDs:Fasta_headers,starts_with("Ratio"),-("Ratio_M/L_normali

  gather(contains("count"),key = "Experiment",value = "Ratio_count") %>%

 ### mutate(Ratio_type = if_else(str_detect(Experiment,"\\_H/L_")==TRUE,"H/L",
                             ### if_else(str_detect(Experiment,"\\_M/L_")==TRUE,"M/L","H/M"))) %>%

  select(Protein_IDs:Fasta_headers,Experiment:Ratio_count) %>%

  extract(Experiment, c("Ratio_type","Experiment"),"([^.].{15})(.*)") %>%

  spread(Ratio_type,value = Ratio_count)


### Tidy the not normalized value

Silac_tb_unnorm <- prot_f1 %>% select(Protein_IDs:Fasta_headers,starts_with("Ratio"),-("Ratio_M/L_normal
  gather(seq(from = 7,to = 76, by = 3),key = "Experiment",value = "Ratio_unnorm") %>%

  select(Protein_IDs:Fasta_headers,Experiment:Ratio_unnorm) %>%

   extract(Experiment, c("Ratio_type","Experiment"),"([^.].{9})(.*)") %>%

  spread(Ratio_type,value = Ratio_unnorm)

### Create our final table

table_merg <- left_join(Silac_tb_norm,Silac_tb_count) %>%
  left_join(Silac_tb_unnorm) %>% left_join(Intensity_tb) %>% left_join(Peptides_tb) %>%
  left_join(Id_type_tb) %>% left_join(Seq_cov_tb)
```

```
## Joining, by = c("Protein_IDs", "Majority_protein_IDs", "Protein_names", "Number_of_proteins", "Gene_n
## Joining, by = c("Protein_IDs", "Majority_protein_IDs", "Protein_names", "Number_of_proteins", "Gene_n
## Joining, by = c("Protein_IDs", "Majority_protein_IDs", "Protein_names", "Number_of_proteins", "Gene_n
## Joining, by = c("Protein_IDs", "Majority_protein_IDs", "Protein_names", "Number_of_proteins", "Gene_n
```

```
## Joining, by = c("Protein_IDs", "Majority_protein_IDs", "Protein_names", "Number_of_proteins", "Gene_
## Joining, by = c("Protein_IDs", "Majority_protein_IDs", "Protein_names", "Number_of_proteins", "Gene_
```

Data exploration

Excel Comparison

```
table_merg %>% group_by(Experiment) %>%  summarize(Peptides = sum(Peptide_Number))
```

```
## # A tibble: 8 x 2
##   Experiment       Peptides
##   <chr>               <dbl>
## 1 KRAS_1xIC50_R1      18746
## 2 KRAS_1xIC50_R2      18414
## 3 KRAS_5xIC50_R1      18384
## 4 KRAS_5xIC50_R2      18018
## 5 PIK3CA_1xIC50_R1    17945
## 6 PIK3CA_1xIC50_R2    14852
## 7 PIK3CA_5xIC50_R1    18224
## 8 PIK3CA_5xIC50_R2    17719
```

```
### Why the petide numbers are completely off ??

table_merg %>% filter(Gene_names == "CTCF") %>%

  group_by(Experiment,Gene_names,Ident_type)  %>%

  summarize(Peptides = sum(Peptide_Number)) %>%

  arrange(desc(Peptides))
```

```
## # A tibble: 8 x 4
## # Groups:   Experiment, Gene_names [8]
##   Experiment       Gene_names Ident_type  Peptides
##   <chr>            <chr>      <chr>          <dbl>
## 1 PIK3CA_1xIC50_R1 CTCF       By MS/MS           4
## 2 PIK3CA_1xIC50_R2 CTCF       By MS/MS           2
## 3 PIK3CA_5xIC50_R1 CTCF       By MS/MS           1
## 4 PIK3CA_5xIC50_R2 CTCF       By MS/MS           1
## 5 KRAS_1xIC50_R1   CTCF       By matching        0
## 6 KRAS_1xIC50_R2   CTCF       By matching        0
## 7 KRAS_5xIC50_R1   CTCF       By matching        0
## 8 KRAS_5xIC50_R2   CTCF       By matching        0
```

```
 table_merg %>%
   group_by(Gene_names,Experiment,Ident_type,Intensity_L,Intensity_M,Intensity_H) %>%

   filter(Ident_type == "By matching",Gene_names == "DDX39A") %>%

   summarize(Peptides = sum(Peptide_Number)) %>%

   arrange(desc(Peptides))
```

```
## # A tibble: 4 x 7
## # Groups:   Gene_names, Experiment, Ident_type, Intensity_L, Intensity_M
## #   [4]
```

```
##   Gene_names Experiment Ident_type Intensity_L Intensity_M Intensity_H
##   <chr>      <chr>      <chr>            <dbl>       <dbl>       <dbl>
## 1 DDX39A     KRAS_5xIC~ By matchi~     6897000    11349000     8359400
## 2 DDX39A     PIK3CA_1x~ By matchi~           0           0           0
## 3 DDX39A     PIK3CA_5x~ By matchi~           0           0           0
## 4 DDX39A     PIK3CA_5x~ By matchi~    15783000    30887000    27892000
## # ... with 1 more variable: Peptides <dbl>
```

```
table_merg %>% group_by(Gene_names,Experiment) %>% filter (Gene_names == "SUZ12") %>% select (`Seq_cov_
```

```
## Adding missing grouping variables: `Gene_names`, `Experiment`
```

```
## # A tibble: 8 x 3
## # Groups:   Gene_names, Experiment [8]
##   Gene_names Experiment       `Seq_cov_[%]`
##   <chr>      <chr>                    <dbl>
## 1 SUZ12      KRAS_5xIC50_R2             3
## 2 SUZ12      KRAS_1xIC50_R1             2.7
## 3 SUZ12      KRAS_5xIC50_R1             2.7
## 4 SUZ12      PIK3CA_1xIC50_R2           2.3
## 5 SUZ12      KRAS_1xIC50_R2             1.4
## 6 SUZ12      PIK3CA_1xIC50_R1           1.4
## 7 SUZ12      PIK3CA_5xIC50_R1           1.4
## 8 SUZ12      PIK3CA_5xIC50_R2           1.4
```

```
write_tsv(table_merg,"table_merg.txt",na = "NA")
```

You can also save to clipboard

Instead of specifying a path just add "clipboard"

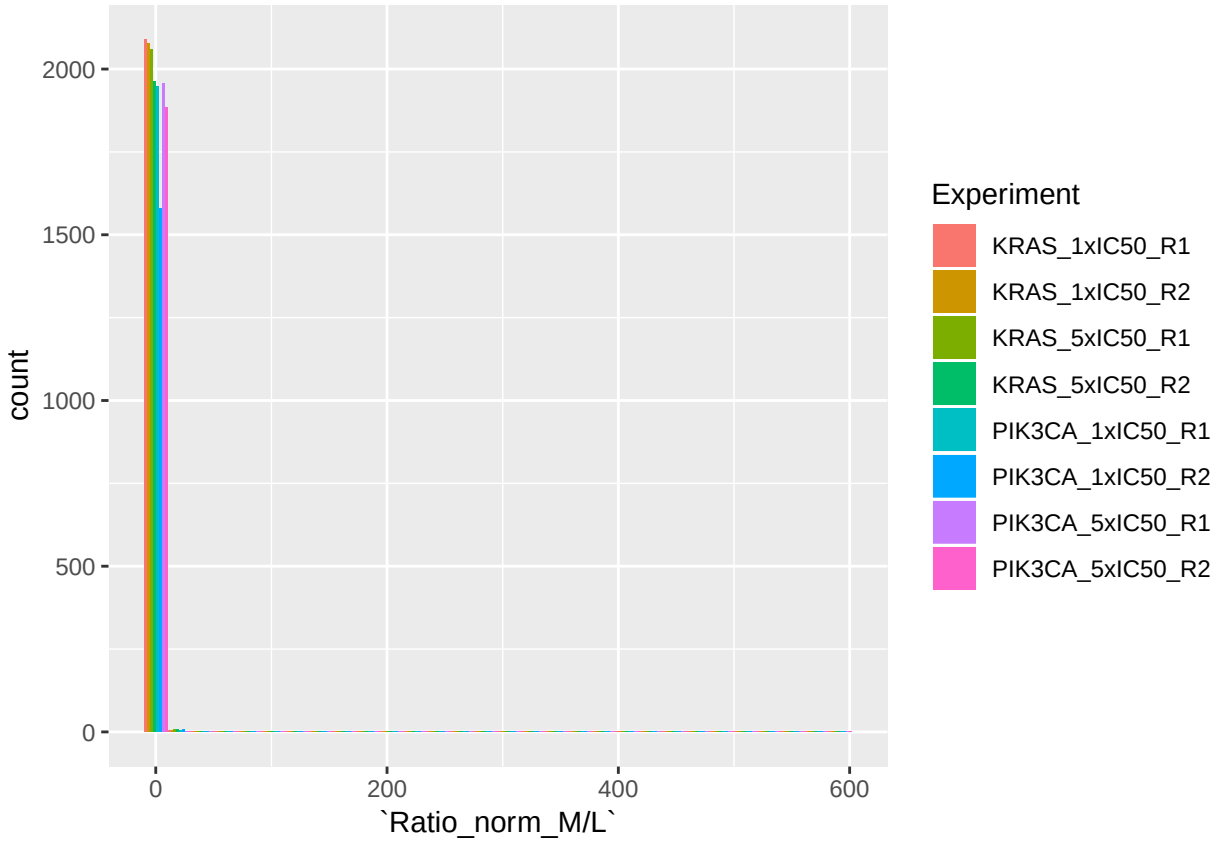
Introduction to ggplot2

Basic concepts of ggplot:

```
ggplot(data = table_merg) +
  geom_histogram(mapping = aes(x = `Ratio_norm_M/L`,fill = Experiment),position = "dodge")
```

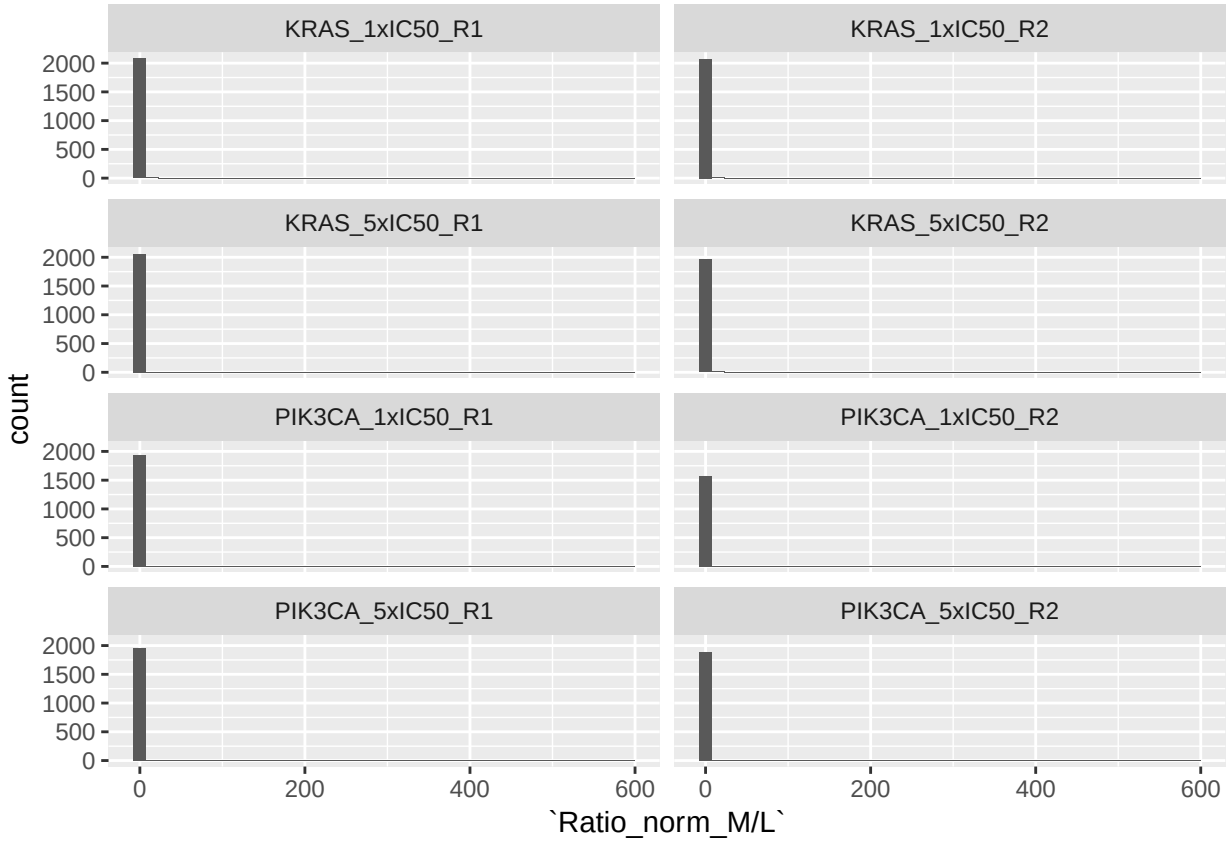
```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

```
## Warning: Removed 14818 rows containing non-finite values (stat_bin).
```




```
ggplot(data = table_merg) +
  geom_histogram(mapping = aes(x = `Ratio_norm_M/L`),bins = 40)+
  facet_wrap(~Experiment,ncol = 2)
```

```
## Warning: Removed 14818 rows containing non-finite values (stat_bin).
```

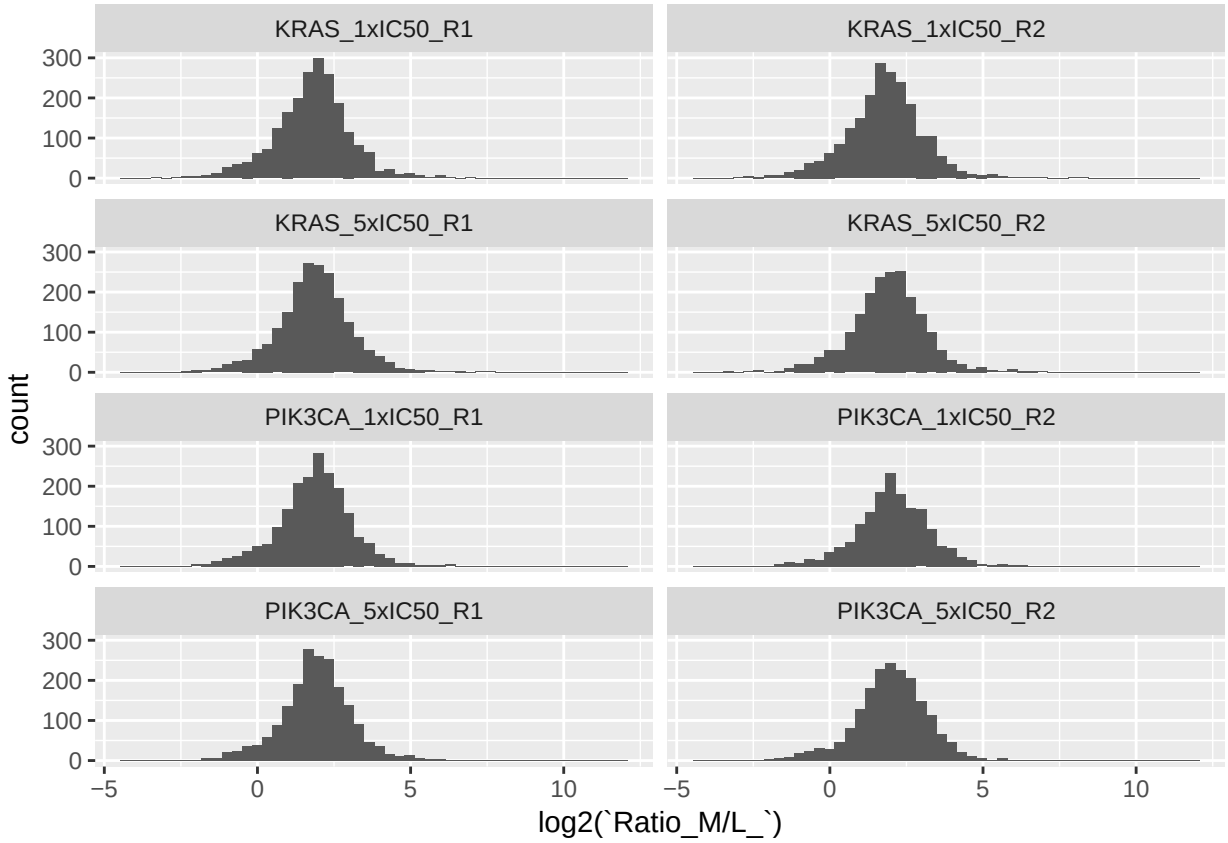



```
## ggplot can handle missing values
```

Appears that our data are not following a normal distribution. Log transform

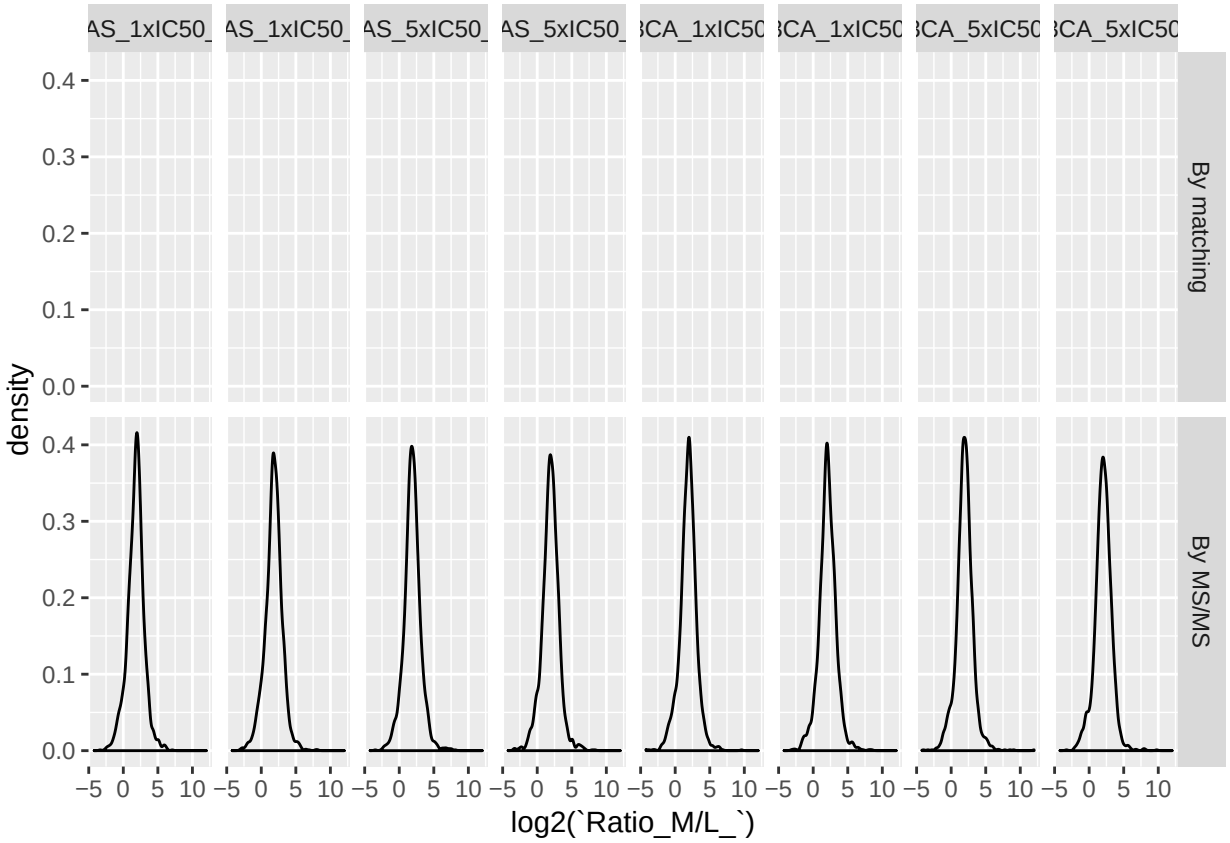
```
ggplot(data = table_merg) +
  geom_histogram(mapping = aes(x = log2(`Ratio_M/L_`)),bins = 50) +
  facet_wrap(~Experiment,ncol = 2)
```

```
## Warning: Removed 14818 rows containing non-finite values (stat_bin).
```




```
ggplot(data = table_merg) +
  geom_density(mapping = aes(x = log2(`Ratio_M/L_`))) +
  facet_grid(Ident_type ~ Experiment)
```

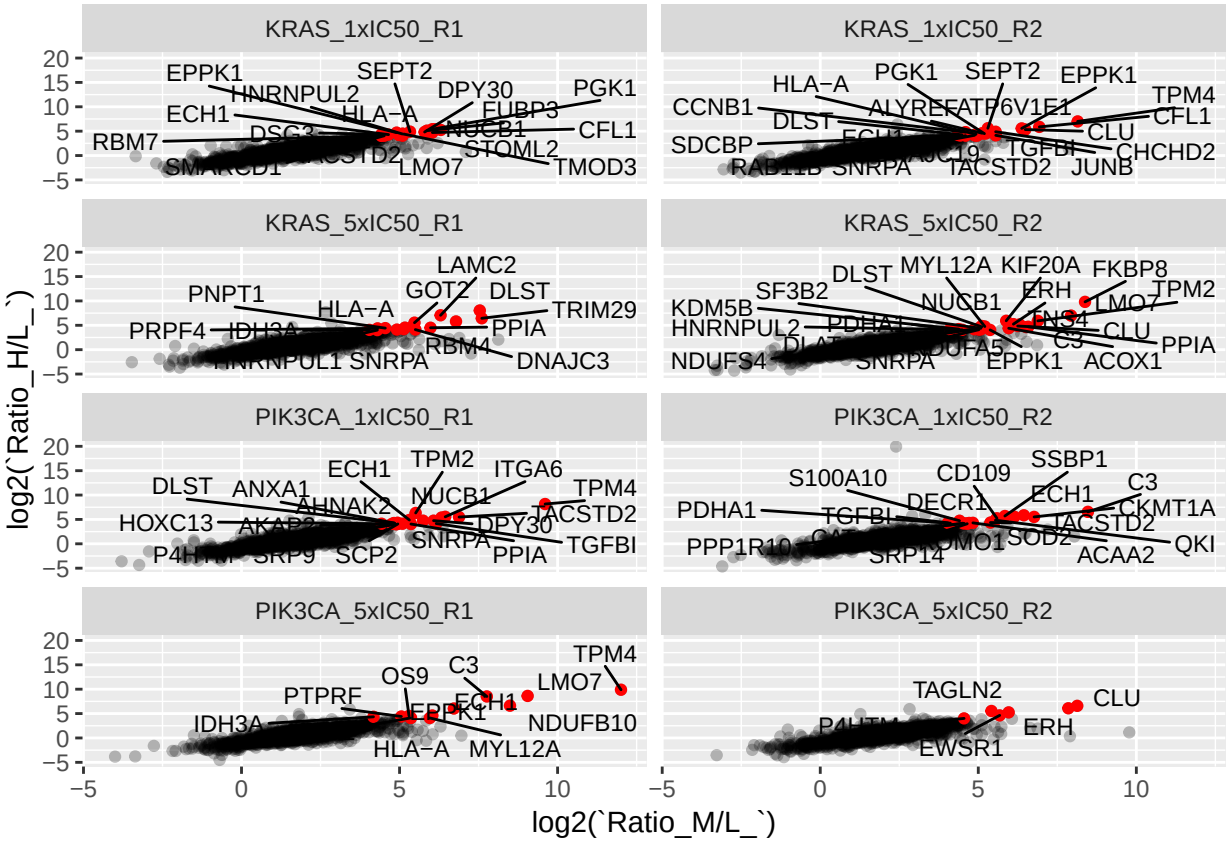
```
## Warning: Removed 14818 rows containing non-finite values (stat_density).
```




```
library("ggrepel") ### Quick way of adding labels to plots

ggplot(data = table_merg,aes(x = log2(`Ratio_M/L_`) , y = log2(`Ratio_H/L_`))) +

  geom_point(alpha = 0.25) +

    geom_point(data = table_merg %>% filter(log2(`Ratio_M/L_`)>4 & log2(`Ratio_H/L_`) >4), color = "red

  geom_text_repel(data = table_merg %>% filter(log2(`Ratio_M/L_`)>4 & log2(`Ratio_H/L_`) >4), mapping =
facet_wrap(~Experiment,ncol = 2.5)
```

```
## Warning: Coercing `ncol` to be an integer.
```

```
## Warning: Removed 14940 rows containing missing values (geom_point).
```



Loops

```
means <- vector ("double",ncol(table_merg %>% group_by(Experiment)))
for (i in seq_along(table_merg)) {
  means[[i]] <- mean(table_merg[[i]], na.rm = T)
}
```

```
## Warning in mean.default(table_merg[[i]], na.rm = T): argument is not
## numeric or logical: returning NA

## Warning in mean.default(table_merg[[i]], na.rm = T): argument is not
## numeric or logical: returning NA

## Warning in mean.default(table_merg[[i]], na.rm = T): argument is not
## numeric or logical: returning NA

## Warning in mean.default(table_merg[[i]], na.rm = T): argument is not
## numeric or logical: returning NA

## Warning in mean.default(table_merg[[i]], na.rm = T): argument is not
## numeric or logical: returning NA

## Warning in mean.default(table_merg[[i]], na.rm = T): argument is not
## numeric or logical: returning NA

## Warning in mean.default(table_merg[[i]], na.rm = T): argument is not
```

```
## numeric or logical: returning NA
```

```
print(means)
```

```
##  [1]           NA           NA           NA 1.128549e+00           NA
##  [6]           NA           NA 1.806581e+02 1.167639e+00 1.150466e+00
## [11] 3.377760e+00 3.378187e+00 3.409273e+00 6.854368e+01 5.651591e-01
## [16] 6.035793e+00 1.531941e+08 6.834835e+08 3.438022e+08 4.676065e+00
## [21]           NA 1.322201e+01
```

```
medians <- vector ("double",ncol(table_merg))
for (i in seq_along(table_merg)) {
  medians[[i]] <- median(table_merg[[i]], na.rm = T)
}
```

```
## Warning in mean.default(sort(x, partial = half + 0L:1L)[half + 0L:1L]):
## argument is not numeric or logical: returning NA
```

```
## Warning in mean.default(sort(x, partial = half + 0L:1L)[half + 0L:1L]):
## argument is not numeric or logical: returning NA

## Warning in mean.default(sort(x, partial = half + 0L:1L)[half + 0L:1L]):
## argument is not numeric or logical: returning NA

## Warning in mean.default(sort(x, partial = half + 0L:1L)[half + 0L:1L]):
## argument is not numeric or logical: returning NA

## Warning in mean.default(sort(x, partial = half + 0L:1L)[half + 0L:1L]):
## argument is not numeric or logical: returning NA

## Warning in mean.default(sort(x, partial = half + 0L:1L)[half + 0L:1L]):
## argument is not numeric or logical: returning NA

## Warning in mean.default(sort(x, partial = half + 0L:1L)[half + 0L:1L]):
## argument is not numeric or logical: returning NA
```

```
print(medians)
```

```
##  [1]           NA           NA           NA 1.00000e+00           NA
##  [6]           NA           NA 8.95470e-01 8.76840e-01 1.03600e+00
## [11] 2.00000e+00 2.00000e+00 2.00000e+00 1.94980e+00 5.09410e-01
## [16] 3.79555e+00 1.34770e+07 4.53315e+07 2.17575e+07 2.00000e+00
## [21]           NA 7.50000e+00
```

** Avoid using for loops **

Use the Purrr package instead

purrr is kind of like dplyr for lists. It helps you repeatedly apply functions.

```
library("purrr")
```

map is a slightly improved version of lapply and it is quite powerfull and only returns a list

```
map(1:4, log)
```

```
## [[1]]
## [1] 0
##
```

```
## [[2]]
## [1] 0.6931472
##
## [[3]]
## [1] 1.098612
##
## [[4]]
## [1] 1.386294
```

```
map(1:4, log, base = 2) # Argument
```

```
## [[1]]
## [1] 0
##
## [[2]]
## [1] 1
##
## [[3]]
## [1] 1.584963
##
## [[4]]
## [1] 2
```

```
map(1:4, ~ log(4, base = .x)) # formula, map(1:4, function(x) log(4, base = x))
```

```
## [[1]]
## [1] Inf
##
## [[2]]
## [1] 2
##
## [[3]]
## [1] 1.26186
##
## [[4]]
## [1] 1
```

```
map_dbl(c(1:4,0), log, base = 2)
```

```
## [1] 0.000000 1.000000 1.584963 2.000000     -Inf
```

```
means <- map_dbl(mtcars,mean)
medians <- map_dbl(mtcars,median)
```

Transform the data frame filter missing values

```
table_merg_f <- table_merg %>% mutate_at(vars(`Ratio_norm_H/L`:`Ratio_norm_H/M`,`Ratio_H/L_`:`Ratio_M/L_
  mutate_at(vars(Intensity_L:Intensity_H),log10)

## Change NaN and -Inf to NAs

#install.packages("naniar")
library("naniar")

table_merg_f <- table_merg_f %>% replace_with_na_all(condition = ~.x == -Inf)
### Easy to do but quite slow
```

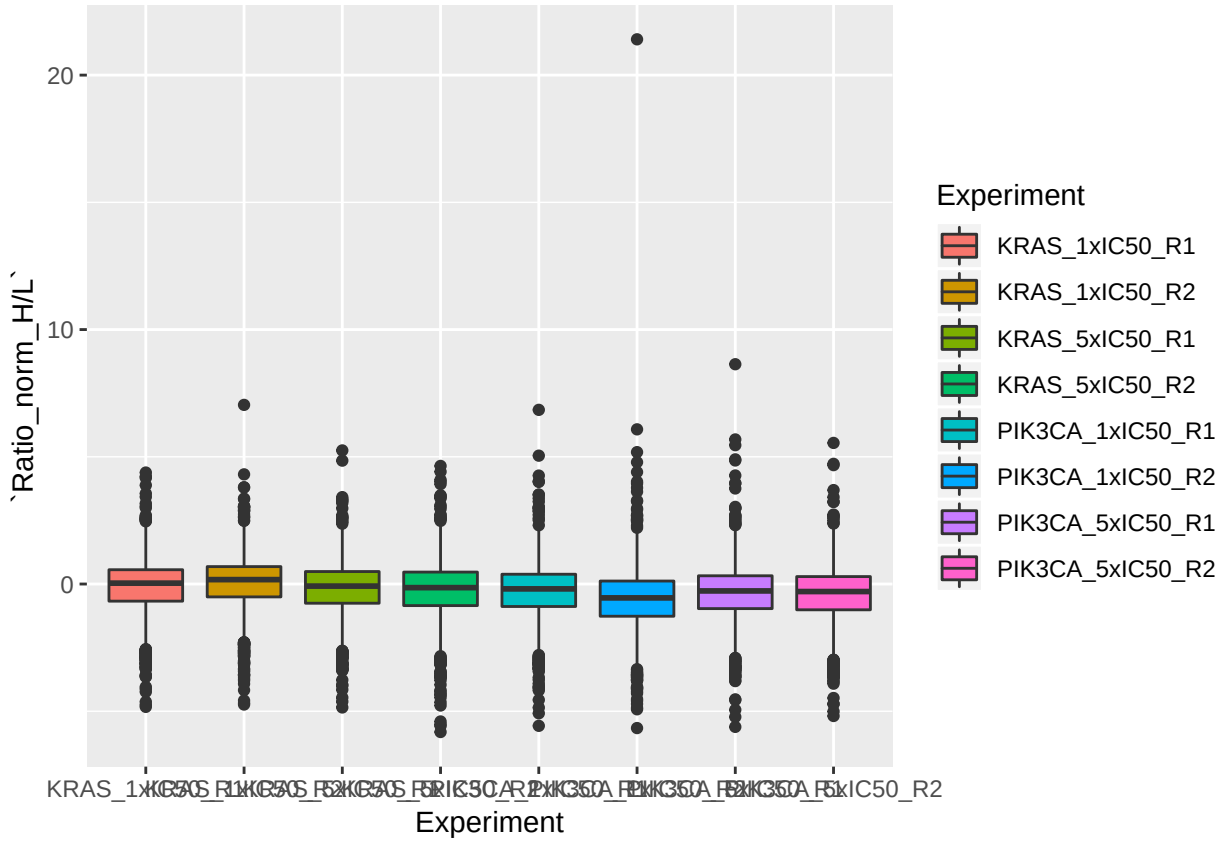
```
is.na(table_merg_f) <- sapply(table_merg_f,is.infinite)
```

More Visualization

Boxplots

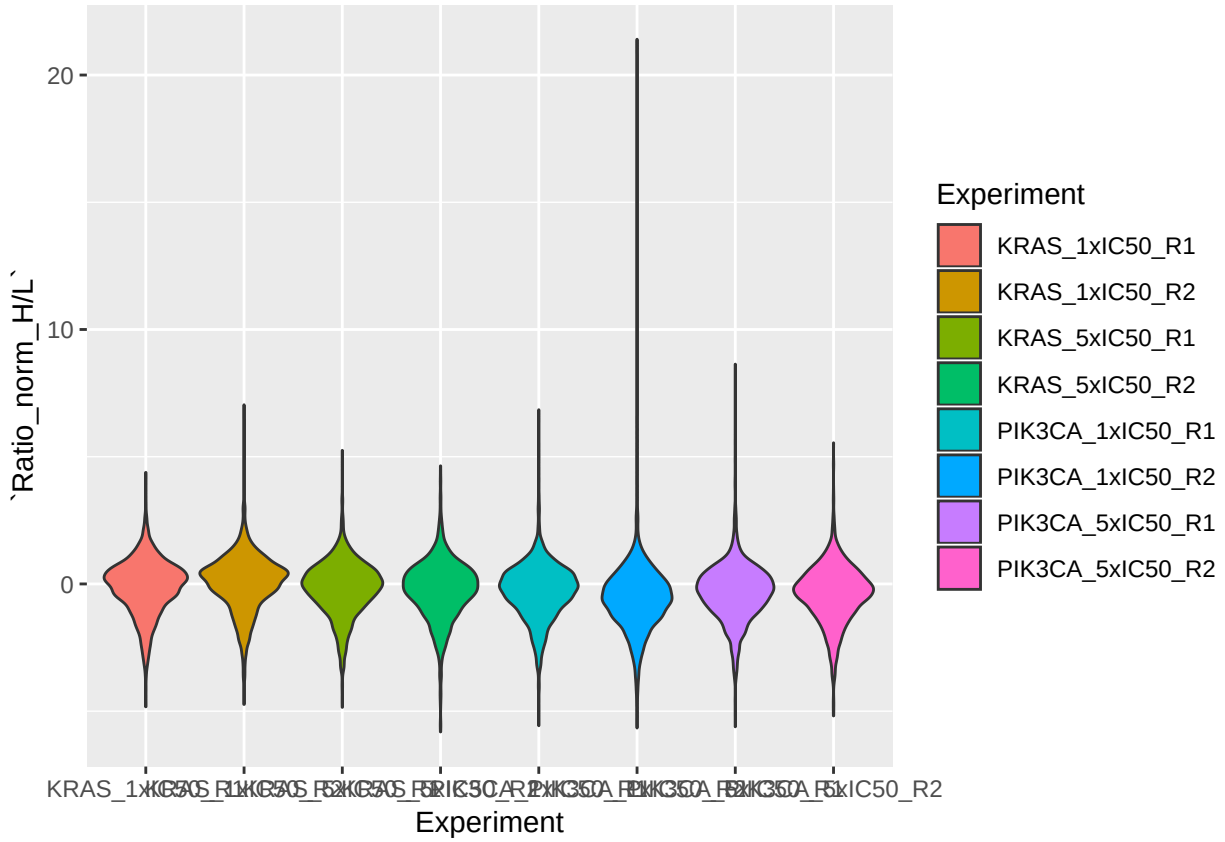
```
ggplot(data = table_merg_f, aes(x =  Experiment ,y = `Ratio_norm_H/L`,fill = Experiment))+
  geom_boxplot()
```

```
## Warning: Removed 14938 rows containing non-finite values (stat_boxplot).
```

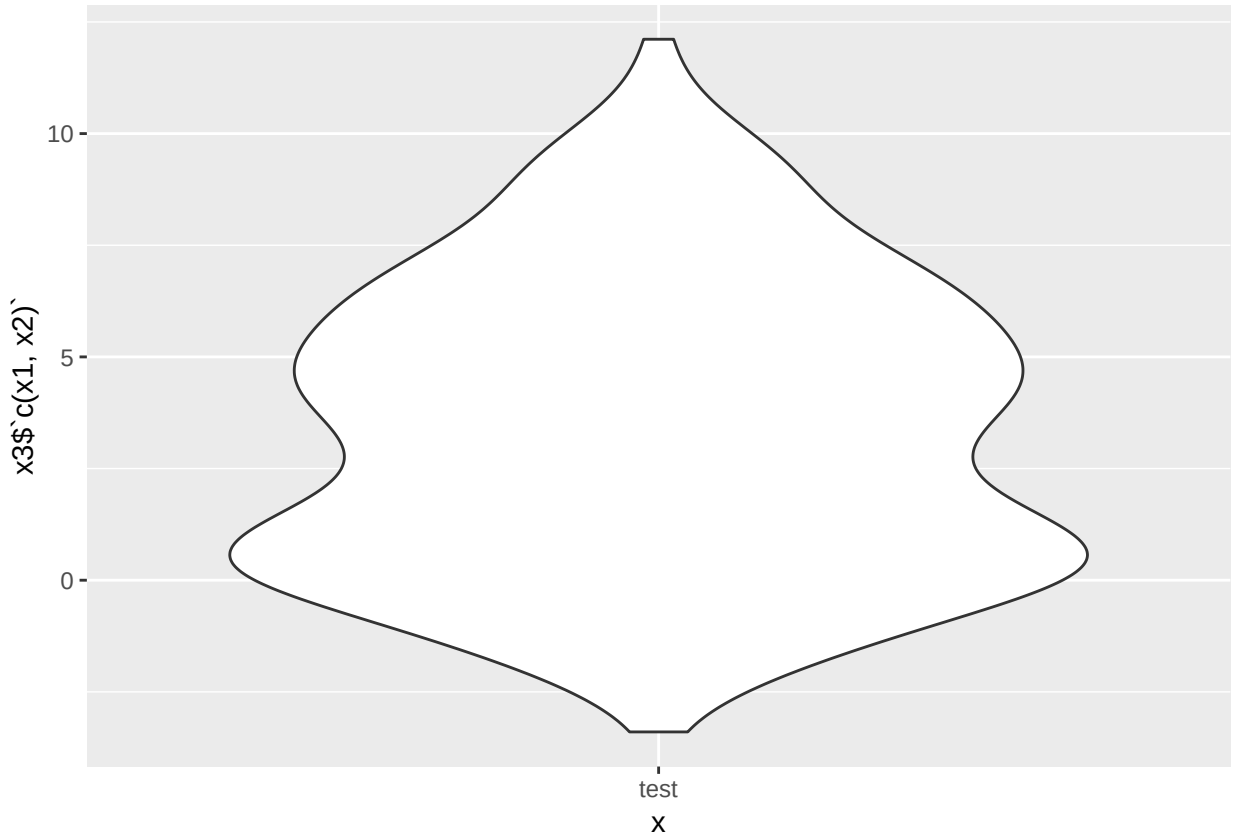



```
ggplot(data = table_merg_f, aes(x =  Experiment ,y = `Ratio_norm_H/L`,fill = Experiment))+
  geom_violin()
```

```
## Warning: Removed 14938 rows containing non-finite values (stat_ydensity).
```

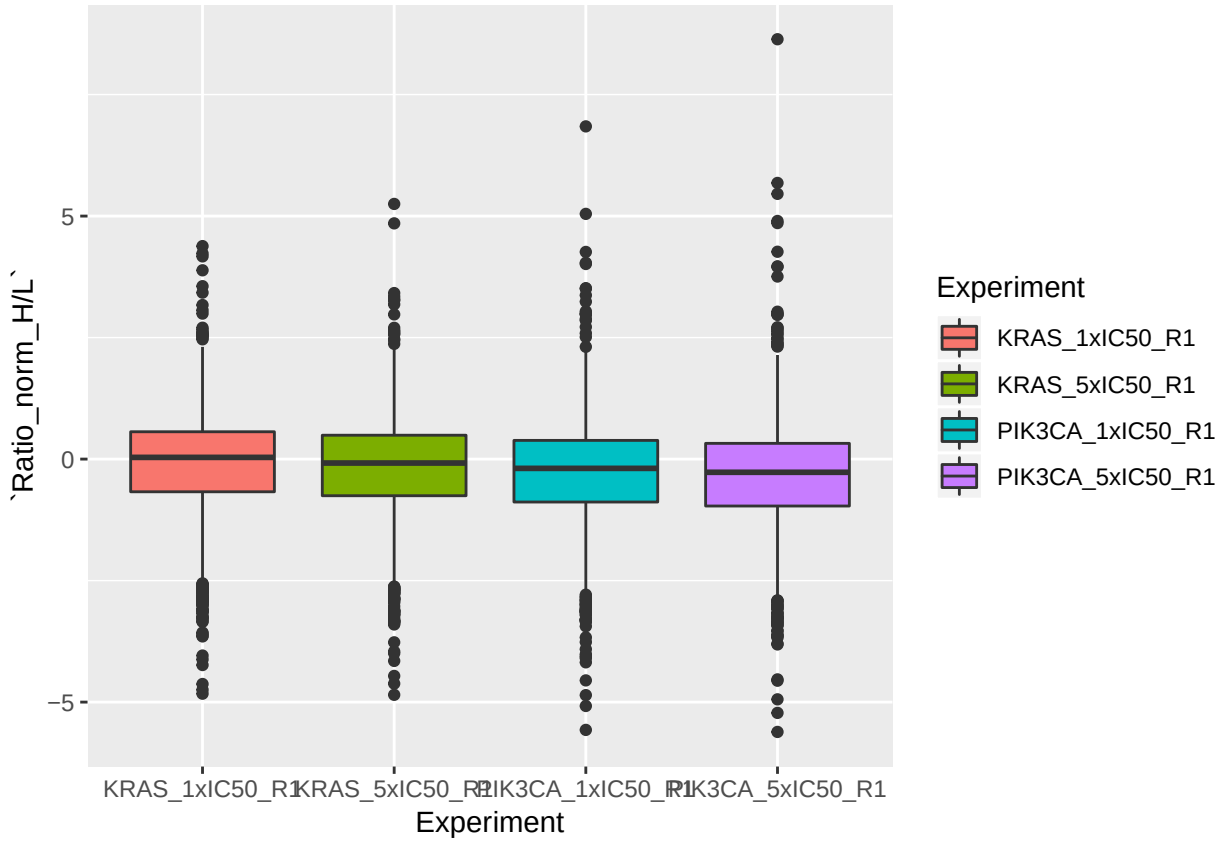



```
###Bimodal distribution

x1 <-  rnorm(100,mean=0 ,sd=1)
x2 <-  rnorm (200, mean=5, sd = 3)
x3 <- data_frame(c(x1,x2))

ggplot(data = x3, aes(x= "test",y = x3$`c(x1, x2)`))+
  geom_violin()
```




```
ggplot(data = table_merg_f %>% filter(str_detect(Experiment,"R1")),aes(x =  Experiment ,y = `Ratio_norm
 geom_boxplot()
```

```
## Warning: Removed 7198 rows containing non-finite values (stat_boxplot).
```

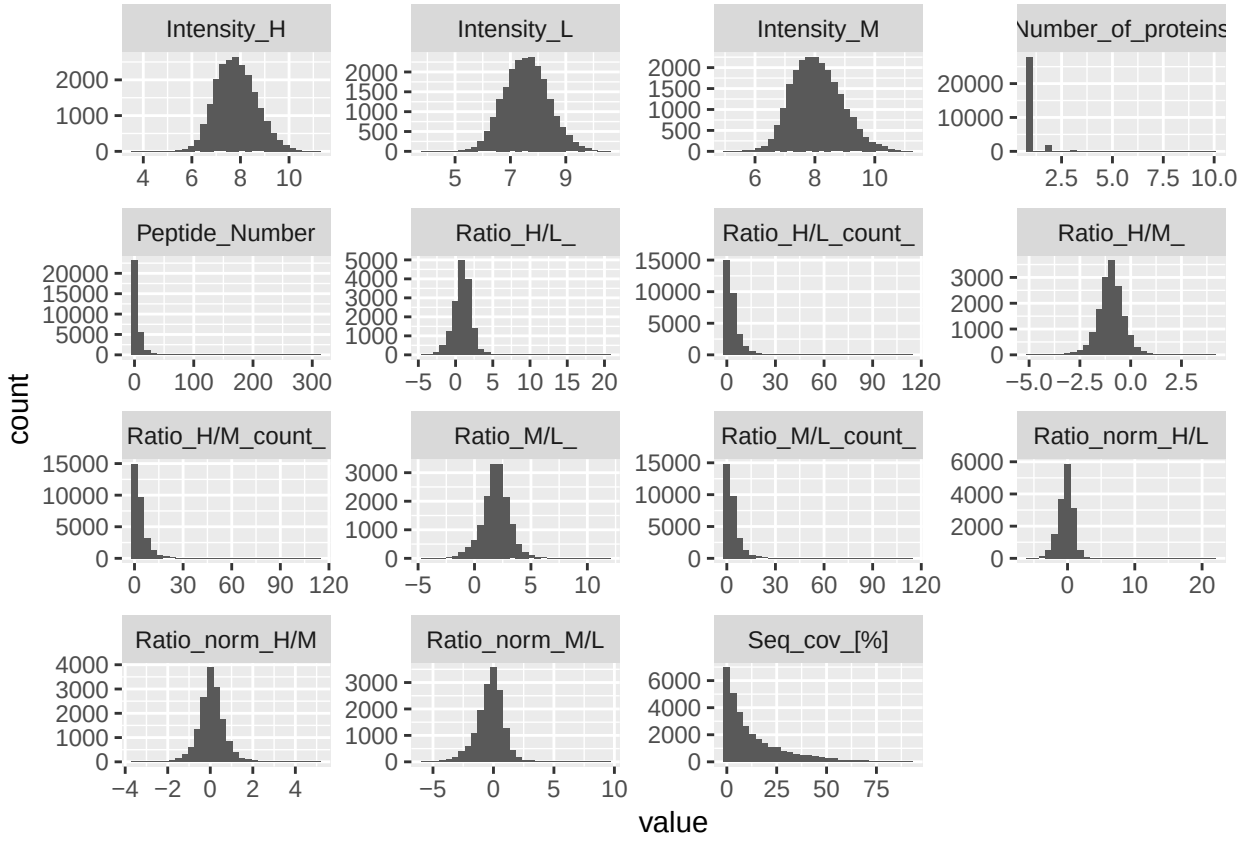


Quick visualization

```
table_merg_f %>%
  keep(is.numeric) %>%
  gather() %>%
  ggplot(aes(value)) +
    facet_wrap(~ key, scales = "free") +
    geom_histogram()
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

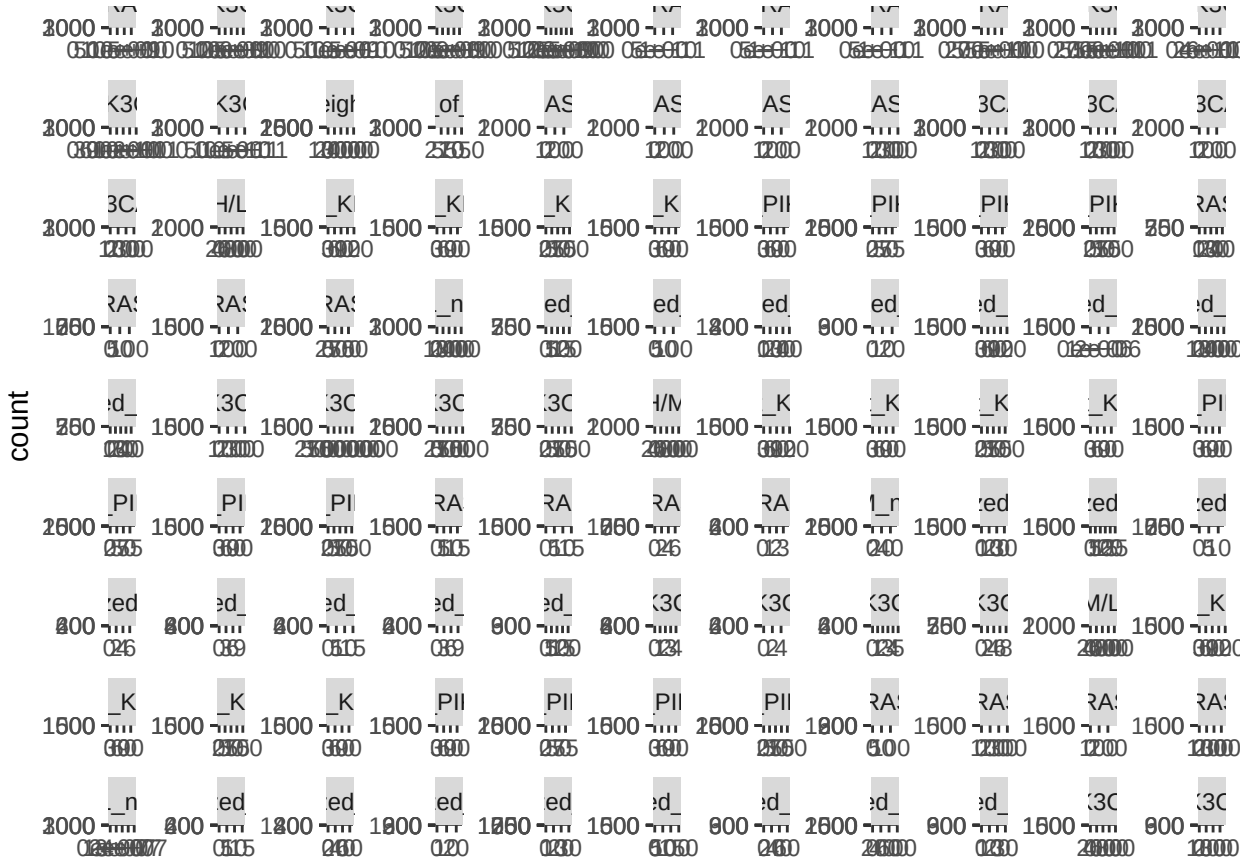
```
## Warning: Removed 114645 rows containing non-finite values (stat_bin).
```




```
prot_f1 %>% keep(is.numeric) %>%
  gather() %>% ggplot(aes(value))+
  facet_wrap(~ key, scales = "free") +
    geom_histogram()
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

```
## Warning: Removed 90735 rows containing non-finite values (stat_bin).
```




```
### R scatter plots

table_merg_f <-  table_merg_f %>% mutate (Replicate = ifelse(str_detect(Experiment,"R1"),paste("R1"),"R

library("GGally")
```

```
##
## Attaching package: 'GGally'
```

```
## The following object is masked from 'package:dplyr':
##
##     nasa
```

```
table_merg_f %>% select(Protein_IDs, Experiment,`Ratio_norm_H/L`) %>% spread(key = "Experiment",value =
```

```
## Warning: Removed 1715 rows containing non-finite values (stat_density).
```

```
## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 1969 rows containing missing values
```

```
## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2005 rows containing missing values
```

```
## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2077 rows containing missing values
```

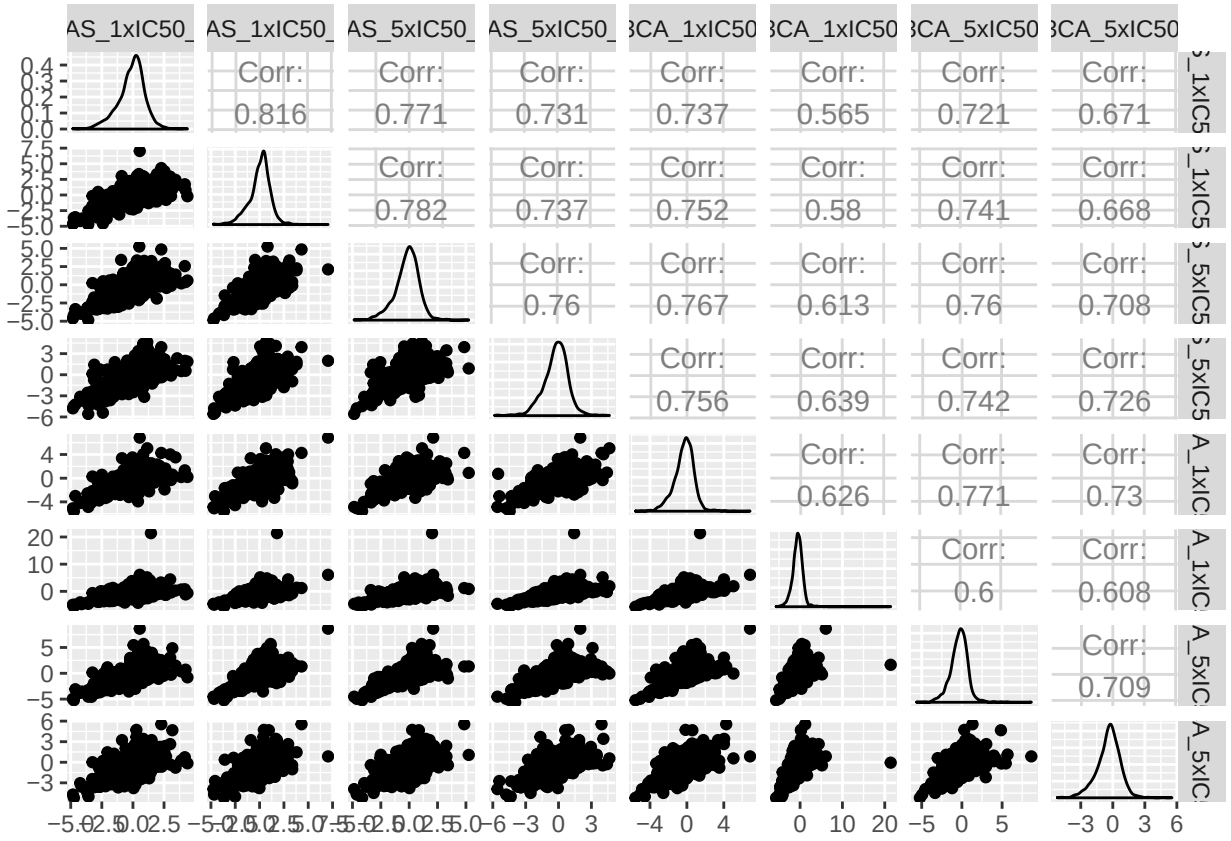
```
## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2116 rows containing missing values
```

```
## Warning in (function (data, mapping, alignPercent = 0.6, method =
```

```
## "pearson", : Removed 2405 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2120 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2207 rows containing missing values

## Warning: Removed 1969 rows containing missing values (geom_point).

## Warning: Removed 1727 rows containing non-finite values (stat_density).

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2024 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2085 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2124 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2405 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2118 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2218 rows containing missing values

## Warning: Removed 2005 rows containing missing values (geom_point).

## Warning: Removed 2024 rows containing missing values (geom_point).

## Warning: Removed 1755 rows containing non-finite values (stat_density).

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2079 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2133 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2400 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2112 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2207 rows containing missing values

## Warning: Removed 2077 rows containing missing values (geom_point).

## Warning: Removed 2085 rows containing missing values (geom_point).

## Warning: Removed 2079 rows containing missing values (geom_point).

## Warning: Removed 1841 rows containing non-finite values (stat_density).

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2128 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2393 rows containing missing values
```

```
## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2119 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2204 rows containing missing values

## Warning: Removed 2116 rows containing missing values (geom_point).

## Warning: Removed 2124 rows containing missing values (geom_point).

## Warning: Removed 2133 rows containing missing values (geom_point).

## Warning: Removed 2128 rows containing missing values (geom_point).

## Warning: Removed 1867 rows containing non-finite values (stat_density).

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2392 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2100 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2190 rows containing missing values

## Warning: Removed 2405 rows containing missing values (geom_point).

## Warning: Removed 2405 rows containing missing values (geom_point).

## Warning: Removed 2400 rows containing missing values (geom_point).

## Warning: Removed 2393 rows containing missing values (geom_point).

## Warning: Removed 2392 rows containing missing values (geom_point).

## Warning: Removed 2228 rows containing non-finite values (stat_density).

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2393 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2391 rows containing missing values

## Warning: Removed 2120 rows containing missing values (geom_point).

## Warning: Removed 2118 rows containing missing values (geom_point).

## Warning: Removed 2112 rows containing missing values (geom_point).

## Warning: Removed 2119 rows containing missing values (geom_point).

## Warning: Removed 2100 rows containing missing values (geom_point).

## Warning: Removed 2393 rows containing missing values (geom_point).

## Warning: Removed 1861 rows containing non-finite values (stat_density).

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2190 rows containing missing values

## Warning: Removed 2207 rows containing missing values (geom_point).

## Warning: Removed 2218 rows containing missing values (geom_point).

## Warning: Removed 2207 rows containing missing values (geom_point).

## Warning: Removed 2204 rows containing missing values (geom_point).
```

```
## Warning: Removed 2190 rows containing missing values (geom_point).
## Warning: Removed 2391 rows containing missing values (geom_point).
## Warning: Removed 2190 rows containing missing values (geom_point).
## Warning: Removed 1944 rows containing non-finite values (stat_density).
```

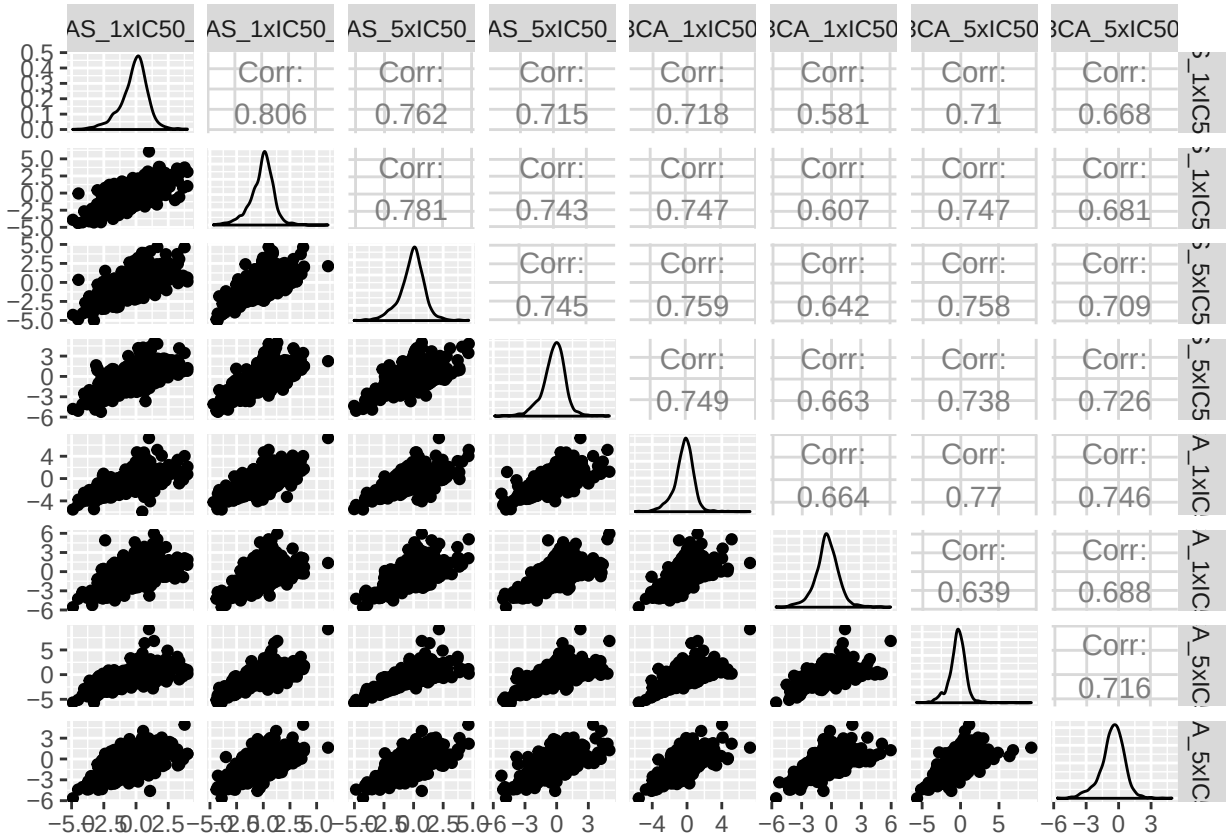



```
table_merg_f %>% select(Protein_IDs, Experiment,`Ratio_norm_M/L`) %>% spread(key = "Experiment",value =
```

```
## Warning: Removed 1708 rows containing non-finite values (stat_density).
## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 1963 rows containing missing values
## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 1996 rows containing missing values
## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2072 rows containing missing values
## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2103 rows containing missing values
## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2395 rows containing missing values
## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2108 rows containing missing values
## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2186 rows containing missing values
```

```
## Warning: Removed 1963 rows containing missing values (geom_point).

## Warning: Removed 1720 rows containing non-finite values (stat_density).

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2013 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2078 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2109 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2392 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2104 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2200 rows containing missing values

## Warning: Removed 1996 rows containing missing values (geom_point).

## Warning: Removed 2013 rows containing missing values (geom_point).

## Warning: Removed 1739 rows containing non-finite values (stat_density).

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2069 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2118 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2388 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2099 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2186 rows containing missing values

## Warning: Removed 2072 rows containing missing values (geom_point).

## Warning: Removed 2078 rows containing missing values (geom_point).

## Warning: Removed 2069 rows containing missing values (geom_point).

## Warning: Removed 1831 rows containing non-finite values (stat_density).

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2113 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2381 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2106 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2184 rows containing missing values

## Warning: Removed 2103 rows containing missing values (geom_point).

## Warning: Removed 2109 rows containing missing values (geom_point).
```

```
## Warning: Removed 2118 rows containing missing values (geom_point).

## Warning: Removed 2113 rows containing missing values (geom_point).

## Warning: Removed 1848 rows containing non-finite values (stat_density).

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2376 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2082 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2168 rows containing missing values

## Warning: Removed 2395 rows containing missing values (geom_point).

## Warning: Removed 2392 rows containing missing values (geom_point).

## Warning: Removed 2388 rows containing missing values (geom_point).

## Warning: Removed 2381 rows containing missing values (geom_point).

## Warning: Removed 2376 rows containing missing values (geom_point).

## Warning: Removed 2213 rows containing non-finite values (stat_density).

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2376 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2378 rows containing missing values

## Warning: Removed 2108 rows containing missing values (geom_point).

## Warning: Removed 2104 rows containing missing values (geom_point).

## Warning: Removed 2099 rows containing missing values (geom_point).

## Warning: Removed 2106 rows containing missing values (geom_point).

## Warning: Removed 2082 rows containing missing values (geom_point).

## Warning: Removed 2376 rows containing missing values (geom_point).

## Warning: Removed 1842 rows containing non-finite values (stat_density).

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2168 rows containing missing values

## Warning: Removed 2186 rows containing missing values (geom_point).

## Warning: Removed 2200 rows containing missing values (geom_point).

## Warning: Removed 2186 rows containing missing values (geom_point).

## Warning: Removed 2184 rows containing missing values (geom_point).

## Warning: Removed 2168 rows containing missing values (geom_point).

## Warning: Removed 2378 rows containing missing values (geom_point).

## Warning: Removed 2168 rows containing missing values (geom_point).

## Warning: Removed 1917 rows containing non-finite values (stat_density).
```




```
table_merg_f %>% select(Protein_IDs, Experiment,`Ratio_norm_H/M`) %>% spread(key = "Experiment",value =
```

```
## Warning: Removed 1715 rows containing non-finite values (stat_density).
```

```
## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 1969 rows containing missing values
```

```
## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2005 rows containing missing values
```

```
## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2077 rows containing missing values
```

```
## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2116 rows containing missing values
```

```
## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2405 rows containing missing values
```

```
## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2120 rows containing missing values
```

```
## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2208 rows containing missing values
```

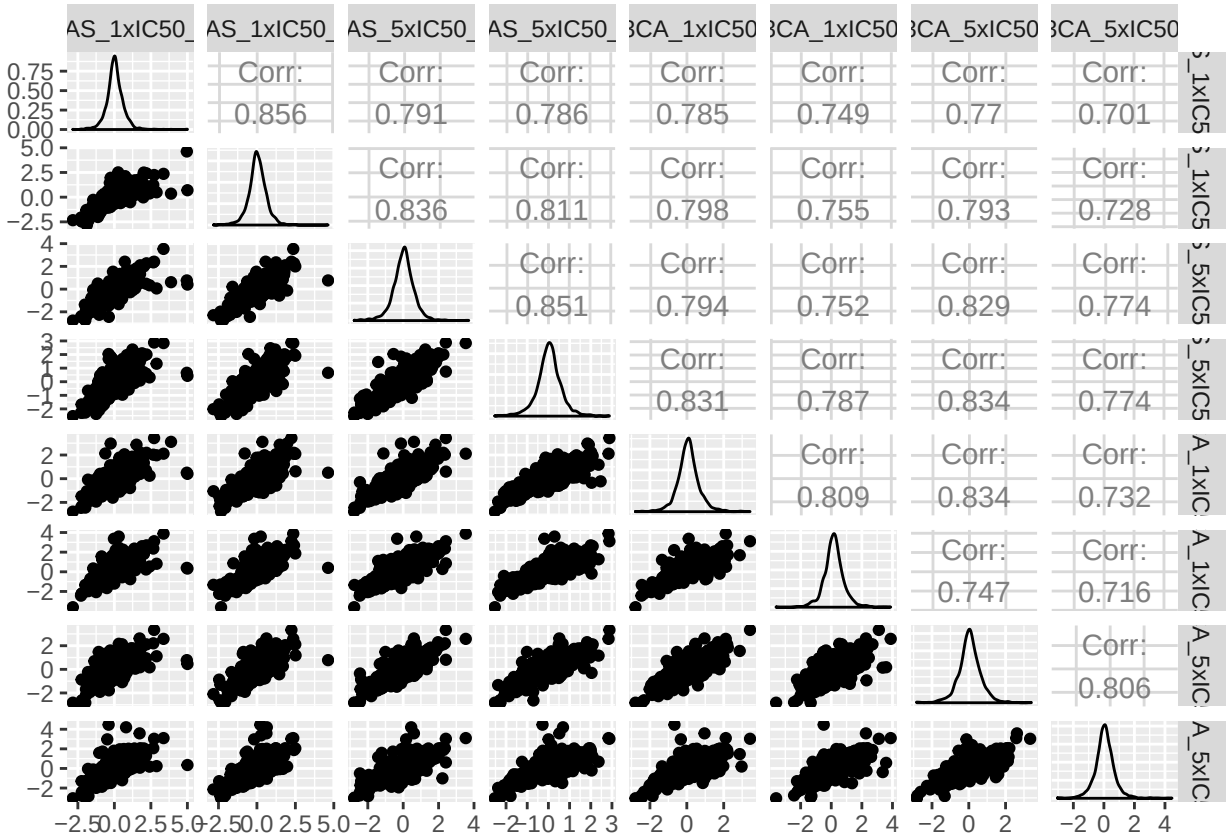
```
## Warning: Removed 1969 rows containing missing values (geom_point).
```

```
## Warning: Removed 1727 rows containing non-finite values (stat_density).
```

```
## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2024 rows containing missing values
```

```
## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2085 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2124 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2405 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2118 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2219 rows containing missing values

## Warning: Removed 2005 rows containing missing values (geom_point).

## Warning: Removed 2024 rows containing missing values (geom_point).

## Warning: Removed 1755 rows containing non-finite values (stat_density).

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2079 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2133 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2400 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2112 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2208 rows containing missing values

## Warning: Removed 2077 rows containing missing values (geom_point).

## Warning: Removed 2085 rows containing missing values (geom_point).

## Warning: Removed 2079 rows containing missing values (geom_point).

## Warning: Removed 1841 rows containing non-finite values (stat_density).

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2128 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2393 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2119 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2205 rows containing missing values

## Warning: Removed 2116 rows containing missing values (geom_point).

## Warning: Removed 2124 rows containing missing values (geom_point).

## Warning: Removed 2133 rows containing missing values (geom_point).

## Warning: Removed 2128 rows containing missing values (geom_point).

## Warning: Removed 1867 rows containing non-finite values (stat_density).
```

```
## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2392 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2100 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2191 rows containing missing values

## Warning: Removed 2405 rows containing missing values (geom_point).

## Warning: Removed 2405 rows containing missing values (geom_point).

## Warning: Removed 2400 rows containing missing values (geom_point).

## Warning: Removed 2393 rows containing missing values (geom_point).

## Warning: Removed 2392 rows containing missing values (geom_point).

## Warning: Removed 2228 rows containing non-finite values (stat_density).

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2393 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2392 rows containing missing values

## Warning: Removed 2120 rows containing missing values (geom_point).

## Warning: Removed 2118 rows containing missing values (geom_point).

## Warning: Removed 2112 rows containing missing values (geom_point).

## Warning: Removed 2119 rows containing missing values (geom_point).

## Warning: Removed 2100 rows containing missing values (geom_point).

## Warning: Removed 2393 rows containing missing values (geom_point).

## Warning: Removed 1861 rows containing non-finite values (stat_density).

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 2190 rows containing missing values

## Warning: Removed 2208 rows containing missing values (geom_point).

## Warning: Removed 2219 rows containing missing values (geom_point).

## Warning: Removed 2208 rows containing missing values (geom_point).

## Warning: Removed 2205 rows containing missing values (geom_point).

## Warning: Removed 2191 rows containing missing values (geom_point).

## Warning: Removed 2392 rows containing missing values (geom_point).

## Warning: Removed 2190 rows containing missing values (geom_point).

## Warning: Removed 1945 rows containing non-finite values (stat_density).
```




```
funs <- list(mean, median ,sd) # In R you can store everything in a list

  funs %>% map(~table_merg_f%>% map_dbl(.x ),.funs)
```

```
## Warning in mean.default(.x[[i]], ...): argument is not numeric or logical:
## returning NA

## Warning in mean.default(.x[[i]], ...): argument is not numeric or logical:
## returning NA

## Warning in mean.default(.x[[i]], ...): argument is not numeric or logical:
## returning NA

## Warning in mean.default(.x[[i]], ...): argument is not numeric or logical:
## returning NA

## Warning in mean.default(.x[[i]], ...): argument is not numeric or logical:
## returning NA

## Warning in mean.default(.x[[i]], ...): argument is not numeric or logical:
## returning NA

## Warning in mean.default(.x[[i]], ...): argument is not numeric or logical:
## returning NA

## Warning in mean.default(.x[[i]], ...): argument is not numeric or logical:
```

```
## returning NA
## Warning in mean.default(sort(x, partial = half + 0L:1L)[half + 0L:1L]):
## argument is not numeric or logical: returning NA

## Warning in mean.default(sort(x, partial = half + 0L:1L)[half + 0L:1L]):
## argument is not numeric or logical: returning NA

## Warning in mean.default(sort(x, partial = half + 0L:1L)[half + 0L:1L]):
## argument is not numeric or logical: returning NA

## Warning in mean.default(sort(x, partial = half + 0L:1L)[half + 0L:1L]):
## argument is not numeric or logical: returning NA

## Warning in mean.default(sort(x, partial = half + 0L:1L)[half + 0L:1L]):
## argument is not numeric or logical: returning NA

## Warning in mean.default(sort(x, partial = half + 0L:1L)[half + 0L:1L]):
## argument is not numeric or logical: returning NA

## Warning in mean.default(sort(x, partial = half + 0L:1L)[half + 0L:1L]):
## argument is not numeric or logical: returning NA

## Warning in mean.default(sort(x, partial = half + 0L:1L)[half + 0L:1L]):
## argument is not numeric or logical: returning NA
## Warning in var(if (is.vector(x) || is.factor(x)) x else as.double(x), na.rm
## = na.rm): NAs introduced by coercion

## Warning in var(if (is.vector(x) || is.factor(x)) x else as.double(x), na.rm
## = na.rm): NAs introduced by coercion

## Warning in var(if (is.vector(x) || is.factor(x)) x else as.double(x), na.rm
## = na.rm): NAs introduced by coercion

## Warning in var(if (is.vector(x) || is.factor(x)) x else as.double(x), na.rm
## = na.rm): NAs introduced by coercion

## Warning in var(if (is.vector(x) || is.factor(x)) x else as.double(x), na.rm
## = na.rm): NAs introduced by coercion

## Warning in var(if (is.vector(x) || is.factor(x)) x else as.double(x), na.rm
## = na.rm): NAs introduced by coercion

## Warning in var(if (is.vector(x) || is.factor(x)) x else as.double(x), na.rm
## = na.rm): NAs introduced by coercion

## Warning in var(if (is.vector(x) || is.factor(x)) x else as.double(x), na.rm
## = na.rm): NAs introduced by coercion
## [[1]]
##          Protein_IDs Majority_protein_IDs        Protein_names
##                   NA                   NA                   NA
##   Number_of_proteins           Gene_names        Fasta_headers
##             1.128549                   NA                   NA
```

```
##           Experiment       Ratio_norm_H/L       Ratio_norm_M/L
##                   NA                   NA                   NA
##       Ratio_norm_H/M     Ratio_H/L_count_     Ratio_H/M_count_
##                   NA             3.377760             3.378187
##     Ratio_M/L_count_           Ratio_H/L_           Ratio_H/M_
##             3.409273                   NA                   NA
##           Ratio_M/L_          Intensity_L          Intensity_M
##                   NA                   NA                   NA
##          Intensity_H       Peptide_Number           Ident_type
##                   NA             4.676065                   NA
##          Seq_cov_[%]            Replicate
##            13.222010                   NA
##
## [[2]]
##          Protein_IDs Majority_protein_IDs        Protein_names
##                   NA                   NA                   NA
##   Number_of_proteins           Gene_names        Fasta_headers
##                  1.0                   NA                   NA
##           Experiment       Ratio_norm_H/L       Ratio_norm_M/L
##                   NA                   NA                   NA
##       Ratio_norm_H/M     Ratio_H/L_count_     Ratio_H/M_count_
##                   NA                  2.0                  2.0
##     Ratio_M/L_count_           Ratio_H/L_           Ratio_H/M_
##                  2.0                   NA                   NA
##           Ratio_M/L_          Intensity_L          Intensity_M
##                   NA                   NA                   NA
##          Intensity_H       Peptide_Number           Ident_type
##                   NA                  2.0                   NA
##          Seq_cov_[%]            Replicate
##                  7.5                   NA
##
## [[3]]
##          Protein_IDs Majority_protein_IDs        Protein_names
##                   NA                   NA                   NA
##   Number_of_proteins           Gene_names        Fasta_headers
##            0.5469966                   NA                   NA
##           Experiment       Ratio_norm_H/L       Ratio_norm_M/L
##                   NA                   NA                   NA
##       Ratio_norm_H/M     Ratio_H/L_count_     Ratio_H/M_count_
##                   NA             5.5348762            5.5350163
##     Ratio_M/L_count_           Ratio_H/L_           Ratio_H/M_
##             5.5553991                   NA                   NA
##           Ratio_M/L_          Intensity_L          Intensity_M
##                   NA                   NA                   NA
##          Intensity_H       Peptide_Number           Ident_type
##                   NA            9.5402629                   NA
##          Seq_cov_[%]            Replicate
##           15.4108825                   NA
```

If we end up having more time we will continue with more exploratory data analysis and ploting stuff