

Setup

```
library(rWSBIM1322)
library(rWSBIM1207)
library("SummarizedExperiment")
library(tidyverse)
library(ggplot2)
library(dplyr)

a <- as_tibble(assay(cptac_se))
c <- as_tibble(colData(cptac_se))
r <- as_tibble(rowData(cptac_se))
```

Exercise 2

4

Extract the quantitative information for the peptides AIGVLPQLIHDR, NLDAAPTLR and YGLNHVVS-LIENKK for samples 6A_7 and 6B_8.

```
a <- a %>% mutate(Sequence = r$Sequence)

fj <- full_join(r,a) %>% select(-Proteins, -nNA)
```

```
## Joining, by = "Sequence"
```

```
x <- fj[c("AIGVLPQLIHDR", "NLDAAPTLR",
         "YGLNHVVS-LIENKK"), c(1, 2, 6)]
x
```

```
## # A tibble: 3 x 3
##   Sequence `6A_7` `6B_8`
##   <chr>      <dbl> <dbl>
## 1 <NA>        NA      NA
## 2 <NA>        NA      NA
## 3 <NA>        NA      NA
```

```
# ??????????????????????
```

6

What is the average expression of LSAAQAELAYAETGAHDK in the groups 6A and 6B?

```
longer <- pivot_longer(fj, cols = -Sequence,  
  names_to = "groups",  
  values_to = "expression")  
  
LSA <- longer %>% filter(Sequence == "LSAAQAELAYAETGAHDK")
```

Exercise 3

2

Import the data from two tab-separated files into R.