```
> library(tidyverse)
> library(dslabs)
>
> data("tissue_gene_expression")
> dim(as.matrix(tissue_gene_expression))
[1] 2 1
> names(tissue_gene_expression)
[1] "x" "y"
> dim(tissue_gene_expression$x)
[1] 189 500
> dim(as.matrix(tissue_gene_expression$y))
[1] 189    1
>
>
> d <- dist(tissue_gene_expression$x - rowMeans(tissue_gene_expression$x))
> class(d)
[1] "dist"
>
>
> h <- hclust(d)
> h

Call:
hclust(d = d)

Cluster method   : complete
Distance         : euclidean
Number of objects: 189

> plot(h)
>
>
> cl <- kmeans(tissue_gene_expression$x, centers = 7)
> class(cl)
[1] "kmeans"
> names(cl)
[1] "cluster"      "centers"      "totss"        "withinss"     "tot.withinss"
[6] "betweenss"    "size"         "iter"         "ifault"
> table(cl$cluster, tissue_gene_expression$y)

    cerebellum colon endometrium hippocampus kidney liver placenta
  1          0     0           0           0      0    26        0
  2          0     0          14           0     38     0        0
  3          6     0           0           0      0     0        0
  4          0     0           0           0      0     0        6
  5          0    34           1           0      1     0        0
  6         32     0           0           0      0     0        0
  7          0     0           0          31      0     0        0
>
> cl <- kmeans(tissue_gene_expression$x, centers = 7)
> table(cl$cluster, tissue_gene_expression$y)

    cerebellum colon endometrium hippocampus kidney liver placenta
  1          0     0          14           0     37     0        0
  2          5     0           0          31      0     0        0
  3          0    34           1           0      0     0        0
  4         31     0           0           0      0     0        0
  5          2     0           0           0      2     2        0
  6          0     0           0           0      0    24        0
  7          0     0           0           0      0     0        6
>
> cl <- kmeans(tissue_gene_expression$x, centers = 7)
> table(cl$cluster, tissue_gene_expression$y)

    cerebellum colon endometrium hippocampus kidney liver placenta
```

```
1            0     0         0         0     0     0         6
2            0    34         0         0     0     0         0
3            0     0         0         0    33     0         0
4            0     0        15         0     6     0         0
5            5     0         0         0     0     0         0
6           33     0         0        31     0     0         0
7            0     0         0         0     0    26         0
>
> cl <- kmeans(tissue_gene_expression$x, centers = 7)
> table(cl$cluster, tissue_gene_expression$y)

    cerebellum colon endometrium hippocampus kidney liver placenta
1            2     0         0         0     2     2         0
2            0     0         0         0     0    24         0
3           31     0         0         0     0     0         0
4            5     0         0         0     0     0         0
5            0     0         0        31     0     0         0
6            0    34        15         0     1     0         6
7            0     0         0         0    36     0         0
>
> cl <- kmeans(tissue_gene_expression$x, centers = 7)
> table(cl$cluster, tissue_gene_expression$y)

    cerebellum colon endometrium hippocampus kidney liver placenta
1            0     0         0         0    33    24         0
2            2     0         0         0     2     2         0
3            0     0         0        13     0     0         0
4            5     0         0         0     0     0         0
5            0     0         0        18     0     0         0
6            0    34        15         0     4     0         6
7           31     0         0         0     0     0         0
>
>
>
> library(RColorBrewer)
> sds <- matrixStats::colSds(tissue_gene_expression$x)
> ind <- order(sds, decreasing = TRUE)[1:50]
> colors <- brewer.pal(7, "Dark2")[as.numeric(tissue_gene_expression$y)]
> heatmap(t(tissue_gene_expression$x[,ind]), col = brewer.pal(11, "RdBu"), scale = "row", ColSideColors =
colors)
>
```