

Zadanie 8 - Heatmapa z clastrowaniem genów i próbek dla genów

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9 05 2020

1. Importowanie danych wygenerowanych przez program feature-Counts na serwerze

```
data22 <- read.csv('../source_files/counts_22.txt', sep = '\t', skip = 1)
dataERCC92 <- read.csv('../source_files/counts_ERCC92.txt', sep = '\t', skip = 1)
```

2. Normalizacja danych

```
#BiocManager::install(c("DESeq2"))
library(DESeq2)

normalize <- function(data) {
  countData <- data[, 7:12]
  rownames(countData) = data$Geneid
  samples <- names(countData)
  cond_1 <- rep("cond1", 3)
  cond_2 <- rep("cond2", 3)
  condition <- factor(c(cond_1, cond_2))
  colData <- data.frame(samples = samples, condition = condition)
  dds <- DESeqDataSetFromMatrix(countData = countData, colData = colData, design = ~condition)

  log_data <- rlog(dds)
  normalized_data <- assay(log_data)
  normalized_data <- as.data.frame(normalized_data)

  return(normalized_data)
}

normalized_data22 <- normalize(data22)
normalized_ERCC92 <- normalize(dataERCC92)
```

3. Rozwiązanie zadania

Przygotowanie heatmap

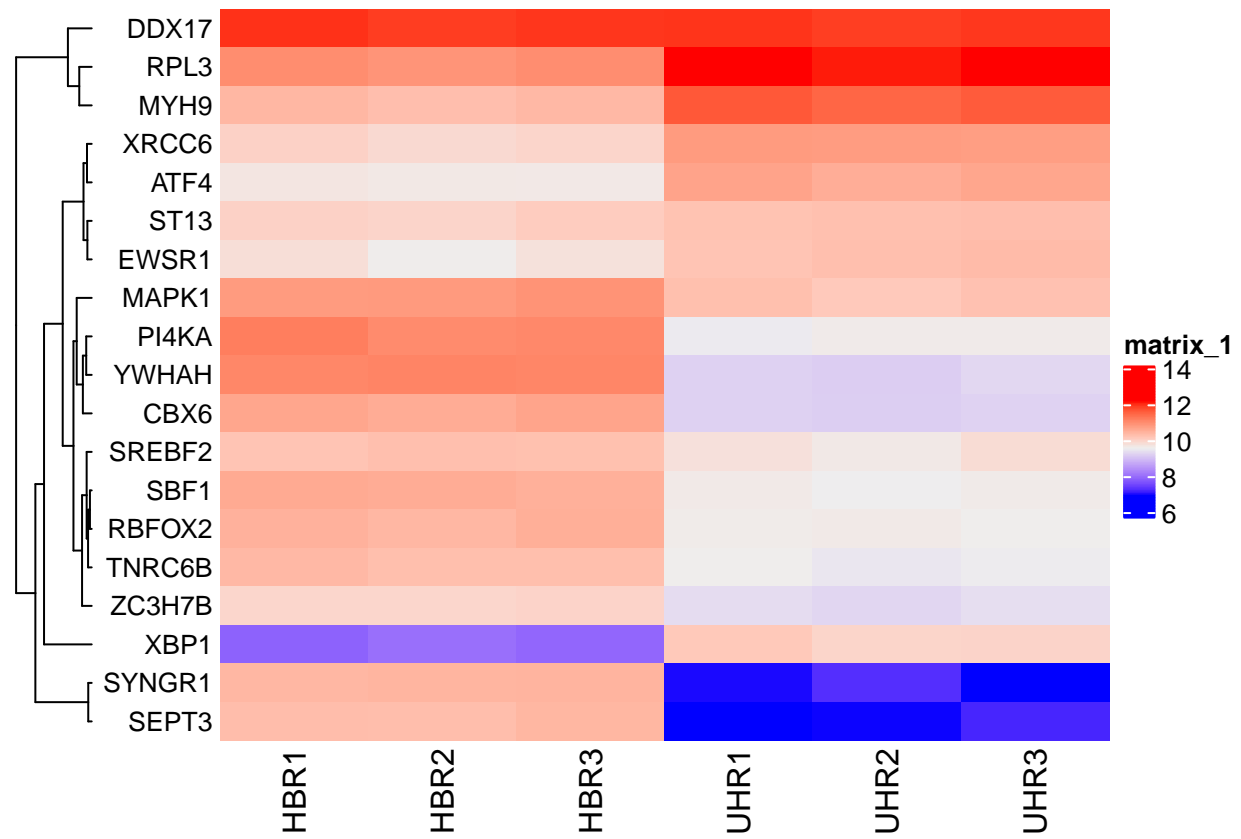
```
#BiocManager::install(c("ComplexHeatmap"))
library(ComplexHeatmap)

drawHeatmap <- function(data) {
  threshold <- 10
  data <- data[
    data$X.home.bioinformatyka.s119494.BAM_indeks.BAM_FILES.HBR_1.bam > threshold |
    data$X.home.bioinformatyka.s119494.BAM_indeks.BAM_FILES.HBR_2.bam > threshold |
    data$X.home.bioinformatyka.s119494.BAM_indeks.BAM_FILES.HBR_3.bam > threshold |
    data$X.home.bioinformatyka.s119494.BAM_indeks.BAM_FILES.UHR_1.bam > threshold |
    data$X.home.bioinformatyka.s119494.BAM_indeks.BAM_FILES.UHR_2.bam > threshold |
    data$X.home.bioinformatyka.s119494.BAM_indeks.BAM_FILES.UHR_3.bam > threshold
  ,
  ]
  renamed_data <- data
  colnames(renamed_data) <- c("HBR1","HBR2","HBR3", "UHR1", "UHR2", "UHR3")

  Heatmap(renamed_data , cluster_columns = FALSE,
    row_names_side = "left",
    row_dend_side = "left",
    row_names_gp=gpar(cex = 0.8))
}
```

Utworzenie heatmap

```
drawHeatmap(normalized_data22)
```



```
drawHeatmap(normalized_ERCC99)
```

