

Zadanie 4 - Heatmapa

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1. Dane z etapu końca zadania 3

```
# Zadanie 1 -- start
raw_data <- read.csv("../source_files\\counts.txt", sep = "\t", skip = 1)
geneLengths <- raw_data[, c(1, 6:9)]
TPM_step1 <- geneLengths
TPM_step1$bam.flower.bam <- TPM_step1$bam.flower.bam / TPM_step1$Length
TPM_step1$bam.stem.bam <- TPM_step1$bam.stem.bam / TPM_step1$Length
TPM_step1$bam.leaf.bam <- TPM_step1$bam.leaf.bam / TPM_step1$Length
TPM_step2 <- TPM_step1
TPM_step2$bam.flower.bam <- TPM_step2$bam.flower.bam / (sum(TPM_step2$bam.flower.bam) / 1000000)
TPM_step2$bam.stem.bam <- TPM_step2$bam.stem.bam / (sum(TPM_step2$bam.stem.bam) / 1000000)
TPM_step2$bam.leaf.bam <- TPM_step2$bam.leaf.bam / (sum(TPM_step2$bam.leaf.bam) / 1000000)
dane_TPM <- TPM_step2[,c(1,3:5)]
colnames(dane_TPM)[2:4] <- c("liść_TPM", "pęd_TPM", "kwiat_TPM")
# Zadanie 1 -- koniec

# Zadanie 2 -- start
MYB <- read.csv("../source_files\\MYB.txt", sep = "\t")
library(dplyr)
dane_myb <- dane_TPM %>% filter(Geneid %in% MYB$Locus)
# Zadanie 2 -- koniec

# Zadanie 3 -- start
MYB_Zad3 <- read.csv("../source_files\\MYB_Zad3.txt", sep = "\t")
CEN <- read.csv("../source_files\\CEN.txt", sep = "\t")
dane_myb <- dane_TPM %>% filter(Geneid %in% MYB_Zad3$Locus)
dane_cen <- dane_TPM %>% filter(Geneid %in% CEN$Locus)
dane_myb_OR_cen <- rbind(dane_myb, dane_cen)
dane_myb <- dane_myb_OR_cen
# Zadanie 3 -- koniec
```

2. Instalacja niezbędnych bibliotek

```
# Instalacja ComplexHeatmap - potrzebny Bioconductor
# https://www.bioconductor.org/install/
```

```

if (!requireNamespace("BiocManager", quietly = TRUE))
  install.packages("BiocManager")
BiocManager::install(version = "3.10")

BiocManager::install(c("GenomicFeatures", "AnnotationDbi"))
BiocManager::install(c("ComplexHeatmap"))

```

```
library(ComplexHeatmap)
```

3. Rozwiązanie zadania

Przygotowanie danych

Wykorzystując skalowanie danych za pomocą funkcji `log2()`

```
dim(dane_myb)
```

```
## [1] 114  4
```

```

dane_myb_s <- log2(t(as.matrix(dane_myb[,c(2:4)])))
dane_myb_s <- log2(t(as.matrix(dane_myb[,c(2:4)] + 1))) # zaktualizowano po komentarzu do zadania
dane_myb_s <- t(dane_myb_s)
row.names(dane_myb_s) <- dane_myb$GenID
dane_myb_s1 <- na.omit(dane_myb_s)

```

Utworzenie heatmapy

```

Heatmap(dane_myb_s1, cluster_columns=FALSE,
        row_names_side = "left",
        row_dend_sid = "left",
        row_names_gp=gpar(cex=0.6))

```

