

PlantTissueCultureAnalysis.R

r1559235

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```
library(gplots)

##
## Attaching package: 'gplots'
## The following object is masked from 'package:stats':
##
##      lowess

library(tidyverse)

## -- Attaching packages ----- tidyverse 1.3.2 --
## v ggplot2 3.3.6      v purrr   0.3.4
## v tibble  3.1.8      v dplyr   1.0.9
## v tidyr   1.2.0      v stringr 1.4.0
## v readr   2.1.2      v forcats 0.5.1
## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()

df <- data.frame(Bacteria = c(9,0,0,0,0,1,7,1,2,15,5,18,4,2,7,17,3),
                  Fungi = c(19,15,3,4,5,35,36,45,53,72,47,107,69,40,39,69,65),
                  Mites = c(0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0),
                  Other = c(1,0,2,0,0,0,2,2,0,3,1,2,0,7,2,1,0))

rownames(df) <- c("O002", "T128", "T126", "T127", "D216.1", "D216.2", "D217", "D218", "D219", "D220", "D221", "D222")

mymatrix <- data.matrix(df)

yp <- colorRampPalette(c("White", "Red"))
heatmap.2(mymatrix, col = yp, main = "Plant Tissue Culture",
          margins = c(10,12))
```

