lab1

Kacper Domzal

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Downloading and preparing data for visualizaion

```
dat <- getGEO('GDS39', destdir=".")
```

```
## Using locally cached version of GDS39 found here:
## ./GDS39.soft.gz
```

```
##
## -- Column specification ---------------------------------------------------
## cols(
##   ID_REF = col_double(),
##   IDENTIFIER = col_character(),
##   GSM940 = col_double(),
##   GSM942 = col_double(),
##   GSM910 = col_double(),
##   GSM969 = col_double(),
##   GSM970 = col_double(),
##   GSM973 = col_double(),
##   GSM974 = col_double(),
##   GSM975 = col_double(),
##   GSM976 = col_double(),
##   GSM984 = col_double(),
##   GSM977 = col_double(),
##   GSM903 = col_double(),
##   GSM906 = col_double(),
##   GSM985 = col_double()
## )
```

```
geneexp <- Table(dat)
geneexp.tidy <- gather(geneexp, key="Samples", value="GeneExp", -c(1,2))
rows_missing <- apply(geneexp.tidy, 1, function(x) any(is.na(x)))
geneexp.tidy.complete <- geneexp.tidy[!rows_missing,]
```

Drawing a heapmap using ggplot2

```
ggplot(geneexp.tidy.complete, aes(x=Samples, y=IDENTIFIER, fill=GeneExp)) +
  geom_tile() +
  scale_fill_gradient2(low = "blue", mid = "white", high = "yellow", midpoint = 0, limits=c(-3,3)) +
  theme(axis.text.y=element_blank()) +
  theme(axis.text.x = element_text(angle = 90))
```