Array Expression Data Analysis report

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```
d <- read.table("~/Desktop/temp/1kb.ld", header = T)

## Warning:  cannot open file '/Users/vgupta/Desktop/temp/1kb.ld':  No such file or directory
## Error:  cannot open the connection

head(d)

## Error:  object 'd' not found

plot(d$L1, d$L2)

## Error:  object 'd' not found
```

1. Introduction

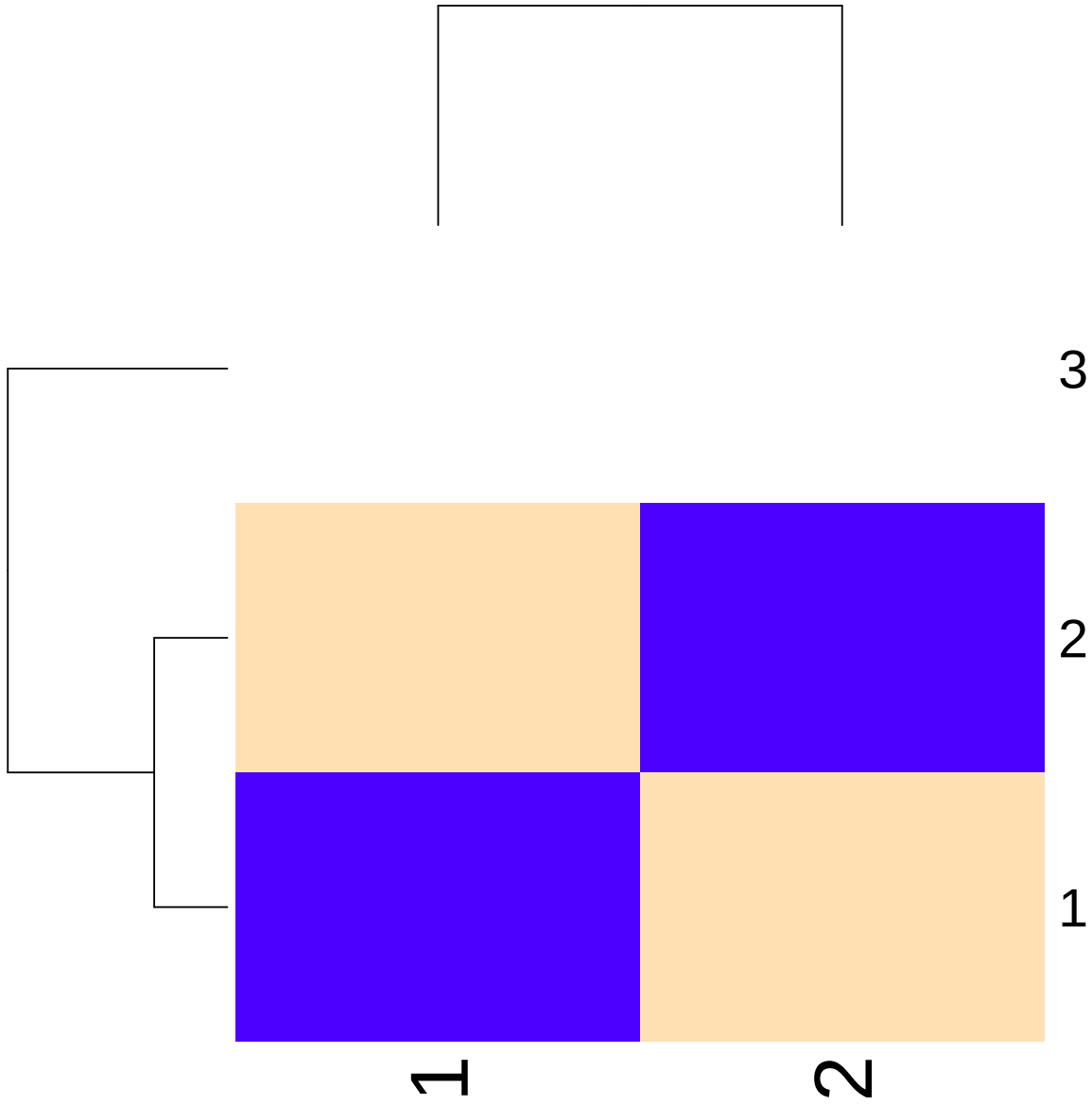
2. WorkFlow

```
source("http://www.bioconductor.org/biocLite.R")

## A new version of Bioconductor is available after installing the most recent
##  version of R; see http://bioconductor.org/install
## BiocInstaller version 1.4.9, ?biocLite for help
## A newer version of Bioconductor is available for this version of R, ?BiocUpgrade for help

biocLite("ALL")

## BioC_mirror:  http://bioconductor.org
## Using R version 2.15, BiocInstaller version 1.4.9.
## Installing package(s) 'ALL'
## Error:  cannot remove prior installation of package 'ALL'
```

```
library("ALL")

## Error:  there is no package called 'ALL'

data("ALL")

## Warning:  data set 'ALL' not found
```

```
ALL

## Error:  object 'ALL' not found

ALL$mol.biol

## Error:  object 'ALL' not found

eset <- ALL[, ALL$mol.biol %in% c("BCR/ABL", "ALL1/AF4")]

## Error:  object 'ALL' not found

heatmap(exprs(eset[1:100, ]))

## Error:  could not find function "exprs"
```

```
mat <- matrix(c(1, 2, NA, 2, 1, 4), nrow = 3, ncol = 2)
heatmap(mat, col = topo.colors(100), Colv = NULL, na.rm = T)
```




```
jpeg("~/Desktop/03_Lotus_annotation/2013_week44/04_genelist.txt.arrayData.jpg", width = 2600,
    height = 1800, quality = 90, units = "px")
d <- read.table("~/Desktop/03_Lotus_annotation/2013_week44/04_genelist.txt.arrayData", header = T)
# d_all <-
# read.table('~/Desktop/03_Lotus_annotation/2013_week44/export_2013-11-04-02-43-41_5411.txt.means',
# header=T) head(d) names(d) plot(d$Mean_WT_control1, d$Std_WT_control1)
# plot(d_all$Mean_WT_control1, d_all$Std_WT_control1, col='red')
# length(which(d_all$Std_WT_control1/d_all$Mean_WT_control1 >0.2))
par(mfcol = c(1, 1), mar = c(2.5, 2.5, 2.5, 2.5), oma = c(25, 1, 1, 80))
d2 <- as.matrix(d[, ])
```

```
# seed - lightblue pod - blue flower - yellow shoot - green petiole - pink leaf - violet
# stem - white root - gray nodules - red nodules+root - orange

colors <- c(rep("lightblue", length = 5), rep("blue", length = 1), rep("yellow", length = 2),
    rep("green", length = 30), rep("pink", length = 1), rep("violet", length = 2), rep("white",
        length = 2), rep("gray", length = 28), rep("red", length = 5), rep("orange", length = 2))
heatmap(d2, labRow = rownames(d), labCol = c(colnames(d)), col = topo.colors(100), keep.dendro = FALSE,
    Colv = NA, cex.axis = 0.1, pch = 10, cex.lab = 1.1, cexRow = 2.5, cexCol = 1.5, ColSideColors = colo
dev.off()

## pdf
##   2
```

3. Plotting