Lab #2
Data visualization
<u>Solutions</u>

2.)
dat <- read.table("C:\\Users\\higgsb\\Dropbox\\JHU\\Microarrays\\Data\\
spellman.txt",header=T,row.names=1)

3) dim(dat)
[1] 6178   77

4.)
> dat <- dat[,23:46]

> names(dat)
 [1] "cdc15_10" "cdc15_30" "cdc15_50" "cdc15_70" "cdc15_80" "cdc15_90"
 [7] "cdc15_100" "cdc15_110" "cdc15_120" "cdc15_130" "cdc15_140" "cdc15_150"
[13] "cdc15_160" "cdc15_170" "cdc15_180" "cdc15_190" "cdc15_200" "cdc15_210"
[19] "cdc15_220" "cdc15_230" "cdc15_240" "cdc15_250" "cdc15_270" "cdc15_290"

5.)
```
library(gplots)
dat.cor <- cor(dat,use="pairwise.complete.obs")

layout(matrix(c(1,1,1,1,1,1,1,1,2,2), 5, 2, byrow = TRUE))
par(oma=c(5,7,1,1))
cx <- rev(colorpanel(25,"red","white","blue"))
leg <- seq(min(dat.cor,na.rm=T),max(dat.cor,na.rm=T),length=10)
image(dat.cor,main="Pearson's correlation matrix\nCDC15 experiment",axes=F,col=cx)
axis(1,at=seq(0,1,length=ncol(dat.cor)),label=dimnames(dat.cor)[[2]],cex.axis=0.9,las=2)
axis(2,at=seq(0,1,length=ncol(dat.cor)),label=dimnames(dat.cor)[[2]],cex.axis=0.9,las=2)

image(as.matrix(leg),col=cx,axes=F)
tmp <- round(leg,2)
axis(1,at=seq(0,1,length=length(leg)),labels=tmp,cex.axis=1)
```
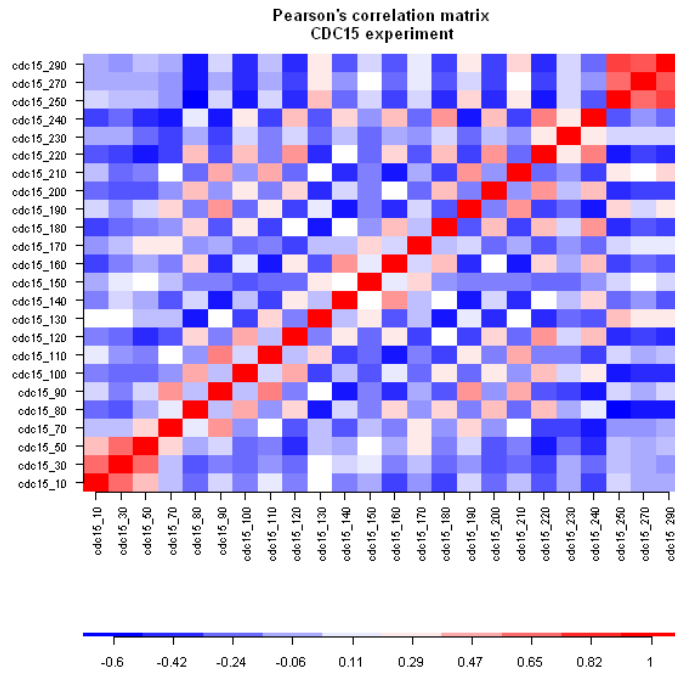
Pearson's correlation matrix
CDC15 experiment

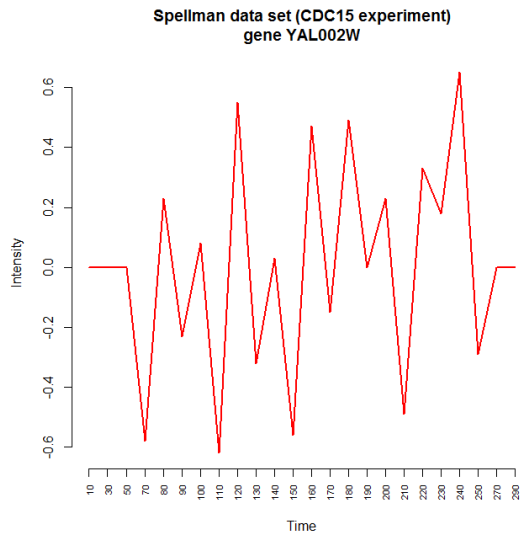6.)
```
> dat.m <- mean(as.numeric(as.matrix(dat["YAL002W",])), na.rm=T)
> dat.m
[1] 3.857953e-18

> dat["YAL002W",is.na(dat["YAL002W",])] <- dat.m
```

7.)
```
plot(as.numeric(dat["YAL002W",]),type='l',lwd=2,col='red', main="Spellman data set
(CDC15 experiment)\ngene YAL002W" ,xlab="Time", ylab="Intensity",axes=F)
axis(1,at=c(1:ncol(dat)),labels=sub("cdc15_","",names(dat)),las=2,cex.axis=0.7)
axis(2)
```

Spellman data set (CDC15 experiment)
gene YAL002W

8.)

```r
library(shiny)
server <- function(input, output) {

    # Combine the selected variables into a new data frame
    selectedData <- reactive({
        dat[, c(input$xcol, input$ycol)]
    })

    output$plot1 <- renderPlot({
        par(mar = c(5.1, 4.1, 0, 1))
        plot(selectedData(), col=1, bg = input$colx, pch = 21, cex = 0.5)
    })
}

ui <-   fluidPage(
            sidebarLayout(
            sidebarPanel(
            selectInput('xcol', 'X Variable', dimnames(dat)[[2]]),
            selectInput('ycol', 'Y Variable', dimnames(dat)[[2]],
                                selected=dimnames(dat)[[2]][1]),
            selectInput('colx', 'Point color', c("red","blue","green","black","orange"))
        ),
        mainPanel(
            plotOutput('plot1')
        )
        )
)
```

shinyApp(ui = ui, server = server)

Appendix
(alternative means to obtain yeast cell cycle dastaset using R built-in datasets)
> library(Biobase)
> library(annotate)
> library(yeastCC)
> data(yeastCC)
> dat <- exprs(yeastCC)   # expression data