Class 3 In-Class Exercises: Solutions

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Load the data

```
setwd("~/Documents/rclass")
data <- read.csv("yeastmutants.csv", header = TRUE)
```

1. Plot the average pheromone response for all three cell types. Plot them as lines, not points (remember: the argument `type` for `plot` and the function `lines` which is similar to `points`). Make each cell type a different color and create a legend to match.

```
plot(x = data$Time, y = data$sst2.avg, type = "l", main = "Yeast Response to Pheromone",
     xlab = "Time (minutes)", ylab = "Mean pheromone response", col = "green")
lines(x = data$Time, y = data$gpa1.avg, col = "red")
lines(x = data$Time, y = data$wt.avg, col = "black")
legend("bottomright", c("sst2 mutant","gpa1 mutant","wild type"), lty = 1,
       col = c("green","red","black"))
```
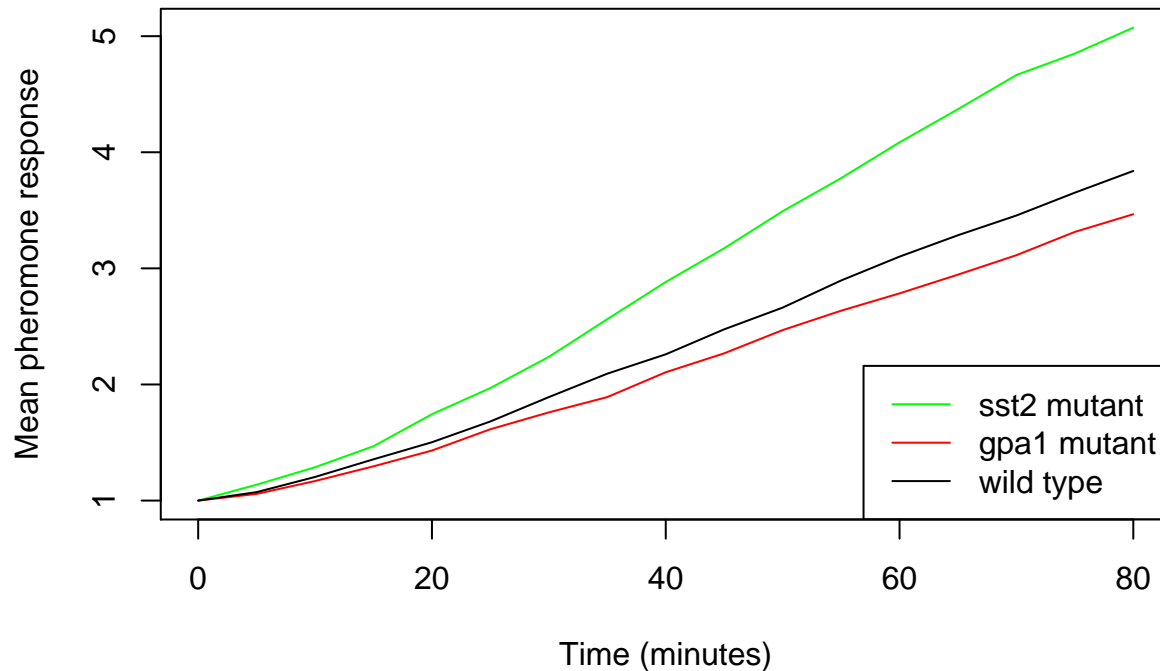
2. Plot the standard deviation of the pheromone response for all three cell types. Plot them as points making each cell type a different color. Create a legend to match.

```r
plot(x = data$Time, y = data$sst2.stdev, type = "l", main = "Yeast Response to Pheromone",
     xlab = "Time (minutes)", ylab = "Standard deviation of pheromone response", col = "green")
lines(x = data$Time, y = data$gpa1.stdev, col = "red")
lines(x = data$Time, y = data$wt.stdev, col = "black")
legend("bottomright", c("sst2 mutant","gpa1 mutant","wild type"), lty = 1,
       col = c("green","red","black"))
```
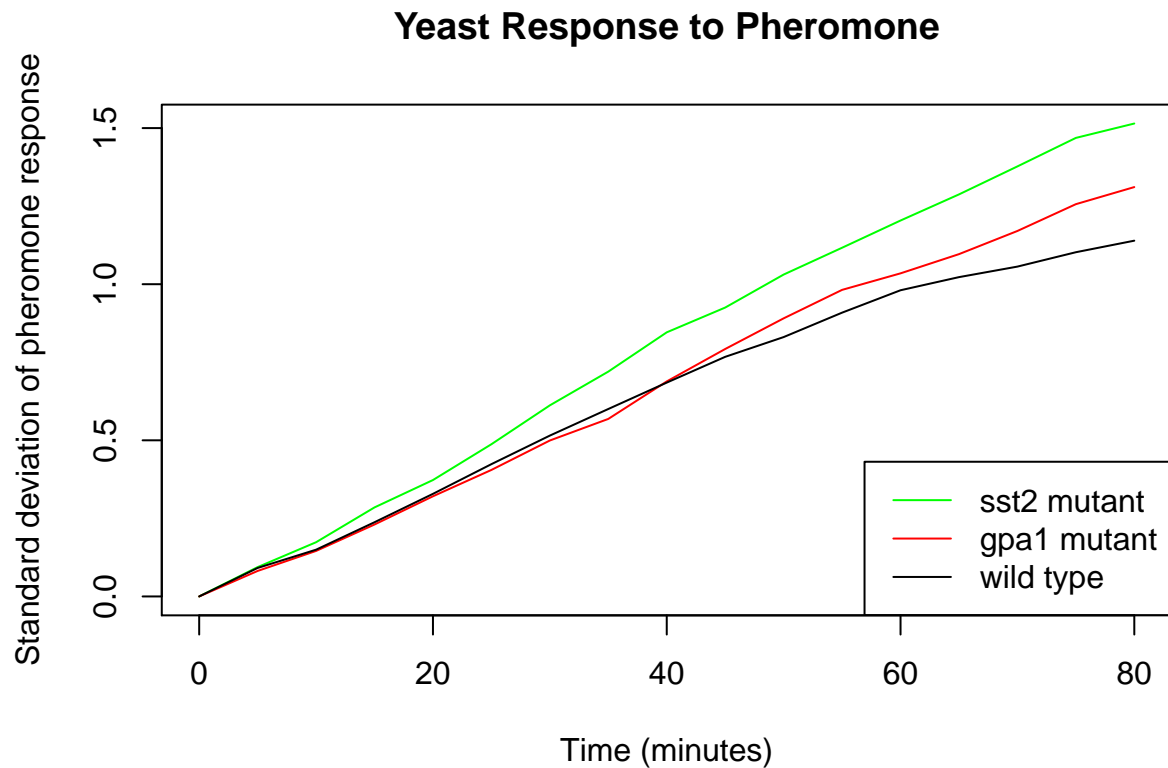
3. Noise in cells is often quantified by the coefficient of variation (CV) because it normalizes the standard deviation for differences in the mean. CV is defined as $CV = \sigma/\mu$ where σ is the standard deviation and μ is mean. Create new variables in the data frame for the CV for each cell type. (Rememeber: you can use subsetting to assign new variables). Then create a plot of the CV for all cell types following the same guidelines as in questions 1 and 2.

```r
data$wt.cv <- data$wt.stdev/data$wt.avg
data$gpa1.cv <- data$gpa1.stdev/data$gpa1.avg
data$sst2.cv <- data$sst2.stdev/data$sst2.avg
plot(x = data$Time, y = data$gpa1.cv, type = "l", main = "Yeast Response to Pheromone",
     xlab = "Time (minutes)", ylab = "Standard deviation of pheromone response", col = "red")
lines(x = data$Time, y = data$sst2.cv, col = "green")
lines(x = data$Time, y = data$wt.cv, col = "black")
legend("bottomright", c("sst2 mutant","gpa1 mutant","wild type"), lty = 1,
       col = c("green","red","black"))
```