```
---
title: "RNASeq Expression Task"
output:
  html_notebook: default
  pdf_document: default
---
```

This is an [R Markdown](http://rmarkdown.rstudio.com) Notebook. When you execute code within the notebook, the results appear beneath the code.

Try executing this chunk by clicking the *Run* button within the chunk or by placing your cursor inside it and pressing *Cmd+Shift+Enter*.

````{r}
GeneExpressionData <-
read.table("https://gist.githubusercontent.com/stephenturner/806e31fce55a8b7175af/raw/1a507c4c3f9f1baaa3a69187223ff3d3050628d4/results
header= TRUE)
head(GeneExpressionData)
str(GeneExpressionData)

install.packages("ggplot2")
library(ggplot2)
GeneExpressionData$significant <- ifelse(GeneExpressionData$padj <0.05 & abs(GeneExpressionData$log2FoldChange) >1, "Significant",
"Not Significant")
View(GeneExpressionData)

ggplot(GeneExpressionData, aes(x = log2FoldChange, y = -log10(pvalue))) +
  geom_point(aes(color = (log2FoldChange > 1 & pvalue < 0.01) | (log2FoldChange < -1 & pvalue < 0.01)), alpha = 0.5) +
  scale_color_manual(values = c("grey", "red")) +
  labs(title = "Volcano Plot", x = "log2 Fold Change", y = "-log10(p-value)") +
  theme_minimal()
````
Upregulated and Downregulated genes in the dataset

Determine upregulated genes (log2FoldChange > 1 and pvalue < 0.01)
Determine downregulated genes (log2FoldChange < -1 and pvalue < 0.01)
````{r}
par(mfrow= c(1,2))
upregulated_genes <- GeneExpressionData[GeneExpressionData$log2FoldChange > 1 & GeneExpressionData$pvalue < 0.01, ]
print(upregulated_genes)

downregulated_genes <- GeneExpressionData[GeneExpressionData$log2FoldChange < -1 & GeneExpressionData$pvalue < 0.01, ]
print(downregulated_genes)
````

Add a new chunk by clicking the *Insert Chunk* button on the toolbar or by pressing *Cmd+Option+I*.

When you save the notebook, an HTML file containing the code and output will be saved alongside it (click the *Preview* button or press *Cmd+Shift+K* to preview the HTML file).

The preview shows you a rendered HTML copy of the contents of the editor. Consequently, unlike *Knit*, *Preview* does not run any R code chunks. Instead, the output of the chunk when it was last run in the editor is displayed.