

Introduction to Bulk RNAseq data analysis

Initial exploration of RNA-seq data - solutions

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Contents

Data

```
library(tximport)
library(DESeq2)
library(tidyverse)
```

Challenge 1

1. Use the DESeq2 function `rlog` to transform the count data. This function also normalises for library size.
2. Plot the count distribution boxplots with this data. How has this effected the count distributions?

```
rlogcounts <- rlog(filtCounts)

# Check distributions of samples using boxplots
boxplot(rlogcounts,
        xlab="",
        ylab="Log2(Counts)",
        las=2,
        col=statusCols)

# Let's add a blue horizontal line that corresponds to the median logCPM
abline(h=median(as.matrix(rlogcounts)), col="blue")
```

