Sequencing: Bulk RNA-seq homework

Koen Van den Berge

8/6/2021

Contents

1 Default edgeR analysis

Analyze the data using edgeR, by using the code in the RNA-seq analysis intro lecture. Focus on the contrast comparing DPN to control at 48h.

2 Impact of blocking

Assess the difference in number of DE genes when not blocking on patient, i.e., removing the patient effect of the model. Compare the p-value distributions between these two models.

3 Analyze using full-quantile normalization

3.1 Implement and apply full-quantile normalization

```
### implement FQ normalization
FQnorm <- function(counts){
  ...
}

### normalize the data using FQ
```

3.2 `edgeR` analysis using full-quantile normalized data

Don't forgot to remove the `calcNormFactors` step as data have already been normalized!

```
### use FQ-normalized data as input to the edgeR analysis
```

3.3 Compare DE genes at 5% FDR