



RNAseq reads to differential genes and pathways

27 & 28 September 2022

Additional resources curated by the Sydney Informatics Hub

Training materials

<https://sydney-informatics-hub.github.io/training.RNAseq.series-quarto/>

Additional information about Pawsey Nimbus:

- Portable, reproducible, scalable bioinformatics with Nextflow and Pawsey Nimbus cloud webinar <https://youtu.be/VnLX63yXbJU>
- Nimbus user documentation <https://support.pawsey.org.au/documentation/display/US/Cloud+Documentation>
- Nimbus for Bioinformatics <https://support.pawsey.org.au/documentation/display/US/Nimbus+for+Bioinformatics>

Additional information about day 1 content: raw sequence to gene counts

- Nextflow workflow manager <https://www.nextflow.io/>
- nf-core (repository of open source, supported Nextflow workflows) <https://nf-co.re/>
 - nf-core/rnaseq parameters <https://nf-co.re/rnaseq/3.8.1/parameters>
 - nf-core/rnaseq introductory lecture https://www.youtube.com/watch?v=qMuUt8oVhHw&feature=emb_logo

Additional information about day 2 content: counts to functional enrichments

Cheat-sheets

- RStudio <https://www.rstudio.com/resources/cheatsheets/>
- Base R <https://iqss.github.io/dss-workshops/R/Rintro/base-r-cheat-sheet.pdf>
- Rmarkdown <https://github.com/rstudio/cheatsheets/blob/main/rmarkdown-2.0.pdf>
- Data-visualization <https://github.com/rstudio/cheatsheets/blob/main/data-visualization-2.1.pdf>

DESeq2 user documentation

<https://bioconductor.org/packages/release/bioc/vignettes/DESeq2/inst/doc/DESeq2.html>

Bioinformatics forums where you can get and provide support to the bioinformatics community:

- Biostars <https://www.biostars.org/>
- Bioconductor <https://www.bioconductor.org/>
- SEQanswers (RNA-Seq)
<https://www.seqanswers.com/forum/applications-forums/rna-sequencing>
- Bad dispersion plot example <https://support.bioconductor.org/p/107937/>

Functional enrichment analysis

- Pantherdb <http://pantherdb.org/>
- Enrichr <https://maayanlab.cloud/Enrichr/>
- David <https://david.ncifcrf.gov/>
- gprofiler <https://biit.cs.ut.ee/gprofiler/>
- Ingenuity Pathway Analysis (IPA) <https://www.qiagen.com/us/>
- Metacore <https://portal.genego.com/>

Interesting read

Urgent need for consistent standards in functional enrichment analysis

<https://journals.plos.org/ploscompbiol/article?id=10.1371/journal.pcbi.1009935#sec007>