Event metadata

Event title	WORKSHOP: RNASeq: reads to differential genes and pathways
Event type	Workshop
Date of event	11 and 12 October 2023
Time of event	1:30 - 4:30pm AEDT
Topic description	RNA sequencing (RNAseq) is a popular and powerful technique used to understand the activity of genes. Using differential gene profiling methods, we can use RNAseq data to gain valuable insights into gene activity and identify variability in gene expression between samples to understand the molecular pathways underpinning many different traits. In this hands-on workshop, you will learn RNAseq fundamentals as you process, analyse, and interpret the results from a real RNAseq experiment on the command-line. In session one, you will convert raw sequence reads to analysis-ready count data with the nf-core/rnaseq workflow. In session two, you'll work interactively in RStudio to identify differentially expressed genes,perform functional enrichment analysis, and visualise and interpret your results using popular and best practice R packages. This workshop was delivered as a part of the Australian BioCommons Bring Your Own Data Platforms Project and will provide you with an opportunity to explore services and infrastructure built specifically for life scientists working at the command line. By the end of the workshop, you will be familiar with Pawsey's Nimbus cloud platform and be able to process your own RNAseq datasets and perform differential expression analysis on the command-line.
Format description	Workshop, online via Zoom over two three hour sessions. Georgina Samaha and Nandan Deshpande lead the training by introducing key concepts and demonstrating the steps involved in the analysis. Participants then moved into breakout rooms where they had the chance to apply these skills with support from facilitators. The workshop followed the tutorial linked in the 'Related work' section. A breakdown of timings and topics is provided in the schedule included in the materials. Participation was free but subject to application with selection. Applications were reviewed by the organising committee. Number of participants = 41

	Breakout room size approximately 10 participants: 1 trainer
Identifier(s)/URL	https://www.biocommons.org.au/events/rnaseq2023
Licence	Materials are shared under a Creative Commons Attribution 4.0 International agreement unless otherwise stated on the materials
Keywords	Bioinformatics http://edamontology.org/topic_0091 Analysis http://edamontology.org/operation_2945 Transcriptomics http://edamontology.org/topic_3308 RNA- seq http://edamontology.org/topic_3170 Workflows http://edamontology.org/topic_0769 Nextflow nf-co.re
Contact	training@biocommons.org.au
Audience	This workshop is for Australian researchers or bioinformaticians who are new to working with RNAseq datasets on the command-line interface and have or will be using bulk RNAseq datasets to identify differentially expressed genes as part of their projects. You must be associated with an Australian organisation for your application to be considered.
Prerequisites	The workshop was conducted in a Unix environment and used R/RStudio. Basic command line knowledge was required. Participants must know how to navigate the directory structure and copy files between the computers. Basic knowledge of R/RStudio was required. Participants must know how to set up directories, run commands, reading in and outputting files. It's recommended that participants watch the following webinars before joining the workshop: ● Getting started with RNAseq: Transforming raw reads into biological insights ● Portable, reproducible and scalable bioinformatics workflows using Nextflow and Pawsey Nimbus Cloud.
Technical requirements	● Slack was used to facilitate discussions. ● Access to the internet, speakers, a webcam, microphone and Zoom. ● Participants were provided with access to virtual machines running on Pawsey Nimbus infrastructure. Packages, workflows and data were preinstalled as described here: https://sydney-informatics-hub.github.io/rnaseq-workshop-2023/setup.html
Learning outcomes	By the end of the workshop participants should be able to:

	• List the steps involved in RNAseq data processing and differential expression analysis
	• Understand key concepts and considerations for RNAseq experiments
	• Describe the benefits of using nf-core workflows
	• Run the nf-core/rnaseq workflow to perform:
	  ○ Quality control
	  ○ Read alignment
	  ○ Read quantification to generate raw counts
	• Use R/RStudio on to perform:
	  ○ Quality control
	  ○ Identify differentially expressed genes
	  ○ Perform functional enrichment/pathway analysis

Lead Trainers	Dr Nandan Deshpande, Senior Research Bioinformatician, Sydney Informatics Hub Dr Georgina Samaha, Bioinformatics Group Lead, Sydney Informatics Hub
Facilitators	Ching-Yu Lu, Bioinformatics Officer, Sydney Informatics Hub Jessica Chung, Bioinformatician (Research Assistant), Melbourne Bioinformatics
Related work	This workshop follows the tutorial 'Introduction to RNAseq workshop: reads to differential gene expression' developed by the Sydney Informatics Hub. https://sydney-informatics-hub.github.io/rnaseq-workshop-2023/