Event title	WORKSHOP: RNA-Seq: reads to differential genes and pathways
Event type	Workshop
Date of event	27 & 28 September 2022
Time of event	1:30-5pm AEST
Topic description	RNA sequencing (RNA-seq) is a common method used to understand the differences in gene expression and molecular pathways between two or more groups. This workshop introduces the fundamental concepts of RNA sequencing experiments and will allow you to try out the analysis using data from a study of Williams-Beuren Syndrome, a rare disease. In the first part of the workshop you will learn how to convert sequence reads into analysis ready count data. To do this we will use nf-core/rnaseq - a portable, scalable, reproducible and publicly available workflow on Pawsey Nimbus Cloud. In the second part of the workshop you will use the count data you created to identify differential genes and pathways using R/Rstudio. By the end of the workshop, you should be able to perform your own RNA-seq analysis for differential gene expression and pathway analysis! This workshop is presented by the Australian BioCommons and Sydney Informatics Hub with the assistance of a network of facilitators from the national Bioinformatics Training Cooperative.
Format description	Workshop, online via Zoom over two three and a half hour sessions. Nandan Deshpande led 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. 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/rnaseq-2022
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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 who have or will work on RNAseq data as part of their projects.
Prerequisites	The workshop was conducted in a Unix environment and used R/RStudio. Basic command line knowledge is required. You must know how to navigate the directory structure and copy files between the computers. If you need a refresher on Unix/Linux try this online tutorial. Basic knowledge of R/RStudio is required. You must know how to set up directories, run commands, reading in and outputting files. If you need a refresher on R/RStudio try the Introduction to R and RStudio section of this online tutorial. It's recommended that you watch the webinar Portable, reproducible and scalable bioinformatics workflows using Nextflow and Pawsey Nimbus Cloud in advance. You may join this webinar live on 20 September 2022. A recording will be posted on the Australian BioCommons YouTube Channel.
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/training.RNAseq.series-quarto/setup.html

Learning outcomes	By the end of the workshop you should be able to:
	• List the steps involved in analysis of RNA-seq data
	• Describe key concepts and considerations for RNA-seq experiments
	• Describe the benefits of using nf-core workflows
	• Deploy an RNA-seq nf-core workflow on Pawsey's Nimbus Cloud to perform:
	  ○ Quality control
	  ○ Alignment

	○ Quantification to generate raw counts ● Use R/RStudio on Pawsey's Nimbus Cloud to perform ○ Quality control ○ Identify differentially expressed genes using DESeq2 ○ Perform functional enrichment/pathway analysis
Lead Trainers	Nandan Deshpande, Sydney Informatics Hub
Facilitators	Georgina Samaha, Sydney Informatics Hub Tracy Chew, Sydney Informatics Hub Steven Morgan, Melbourne Bioinformatics Sarah Beecroft, Pawsey Supercomputing Research Centre
Related work	This workshop follows the tutorial 'RNA-seq: reads to differential gene expression workshop series' developed by the Sydney Informatics Hub. https://sydney-informatics-hub.github.io/training.RNAseq.series-quarto/