

Event metadata

Event title	Getting started with RNAseq: Transforming raw reads into biological insights
Event type	Webinar
Date of event	06/09/2023
Time of event	1pm AEST
Topic description	<p>RNA sequencing (RNAseq) is a powerful technique for investigating gene expression in biological samples. Processing and analysing RNAseq data involves multiple steps to align raw sequence reads to a reference genome, count the number of reads mapped to each gene, and perform statistical analyses to identify differentially expressed genes and functionally annotate them. RNAseq experiments have many different applications as we apply them to a variety of research questions and organisms. This diversity of applications can make it challenging to appreciate all the design considerations, processing requirements, and limitations of RNAseq experiments as they apply to you.</p> <p>In this webinar, you will gain an understanding of the key considerations for designing and performing your own successful experiments with bulk RNA. We'll start at the lab bench with RNA extraction, quality control, and library preparation, then move to the sequencing machine where you will make essential decisions about sequencing platforms, optimal sequencing depth, and the importance of replicates. We'll talk about bioinformatics workflows for RNAseq data processing and the computational requirements of transforming raw sequencing reads to analysis-ready count data. Finally, we'll discuss how to apply differential expression and functional enrichment analyses to gain biological insights from differentially expressed genes.</p> <p>This webinar was developed by the Sydney Informatics Hub in collaboration with the Australian BioCommons.</p>
Format description	Webinar presentation followed by a brief question and answer session

Identifier(s)/URL	https://www.biocommons.org.au/events/rnaseqwebinar
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 Transcriptomics http://edamontology.org/topic_3308 Gene expression http://edamontology.org/topic_0203 RNA-Seq http://edamontology.org/topic_3170
Contact	training@biocommons.org.au
Audience	This webinar is targeted towards those interested in applying RNAseq datasets to their research questions and who wish to gain a deeper understanding of the design considerations, processing requirements and limitations of RNAseq experiments.
Prerequisites	None
Technical requirements	None
Learning outcomes	By the end of this webinar you should be able to: <ul style="list-style-type: none"> • Outline the steps involved in an RNAseq experiment • List key considerations for designing an RNAseq experiment • Outline the steps involved in analysing RNAseq data • Identify resources for data processing
Speakers	Dr Nandan Deshpande, Senior Research Bioinformatician, Sydney Informatics Hub
Related material	None