

Event title	WORKSHOP: Single cell RNAseq analysis in R
Event type	Workshop
Date of event	22 & 23 August 2022
Time of event	1:30-5pm AEST
Topic description	<p>Analysis and interpretation of single cell RNAseq (scRNAseq) data requires dedicated workflows. In this hands-on workshop we will show you how to perform single cell analysis using Seurat - an R package for QC, analysis, and exploration of single-cell RNAseq data.</p> <p>We will discuss the 'why' behind each step and cover reading in the count data, quality control, filtering, normalisation, clustering, UMAP layout and identification of cluster markers. We will also explore various ways of visualising single cell expression data.</p> <p>This workshop is presented by the Australian BioCommons and Queensland Cyber Infrastructure Foundation (QCIF) with the assistance of a network of facilitators from the national Bioinformatics Training Cooperative.</p>
Format description	<p>Workshop, online via Zoom over two three and a half hour sessions.</p> <p>Sarah Williams and Ahmed Mehdi 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.</p> <p>The workshop followed the tutorial linked in the 'Related work' section.</p> <p>A breakdown of timings and topics is provided in the schedule.</p> <p>Participation was free but subject to application with selection.</p> <p>Applications were reviewed by the organising committee.</p> <p>Number of participants = 70</p> <p>Breakout room size = 10 participants, 1 trainer</p>
Identifier(s)/URL	https://www.biocommons.org.au/events/scrnaseq
Licence	Materials are shared under a Creative Commons Attribution 4.0 International agreement unless otherwise stated on the materials
Keywords	<p>Bioinformatics http://edamontology.org/topic_0091</p> <p>Analysis http://edamontology.org/operation_2945</p> <p>Transcriptomics http://edamontology.org/topic_3308</p>

	Single cell RNAseq Seurat R statistical software
Contact	training@biocommons.org.au
Audience	<p>This workshop is for Australian researchers who have or will work on scRNAseq data as part of their projects. You must be associated with an Australian organisation for your application to be considered.</p> <p>This workshop will not teach you the basics of R. While you don't need to be an expert, you require some basic familiarity with R. For example you should be able to work with tables of data, know how to load an R package, make basic plots (ideally with ggplot2).</p> <p>You should also have basic knowledge of single cell RNA sequencing technology.</p>
Prerequisites	<p>This workshop will not teach you the basics of R. While you don't need to be an expert, you require some basic familiarity with R. For example you should be able to work with tables of data, know how to load an R package, make basic plots (ideally with ggplot2).</p> <p>You should also have basic knowledge of single cell RNA sequencing technology.</p>
Technical requirements	<ul style="list-style-type: none"> • 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 RStudio via a Nectar Cloud instance (. Packages and data were preinstalled as described here: https://github.com/swbioinf/scRNAseqInR_Doco/blob/main/scripts/lib_intstallation.R •
Learning outcomes	<p>By the end of the workshop you should be able to:</p> <ul style="list-style-type: none"> • Load gene counts into a Seurat format • Perform QC and select cells for further analysis • Filter and normalise scRNAseq data • Cluster cells and identify cluster markers • Visualise scRNAseq expression data • Identify sources of help and support from the R community
Lead Trainers	<p>Dr Sarah Williams, Senior Bioinformatician, QCIF Dr Ahmed Mehdi, Senior Biostatistician, QCIF</p>



Facilitators	Mr Nick Matigan, Biostatistician and Bioinformatician, QCIF Ms Adele Barugahare, Monash Bioinformatics Platform Dr Paul Harrison, Monash Bioinformatics Platform Dr Steven Morgan, Melbourne Bioinformatics Ms Holly Whitfield, University of Melbourne.
Related work	<p>This workshop follows the tutorial 'scRNAseq Analysis in R with Seurat'</p> <p>https://swbioinf.github.io/scRNAseqInR_Doco/index.html</p> <p>This material is based on the introductory Guided Clustering Tutorial tutorial from Seurat.</p> <p>It is also drawing from a similar workshop held by Monash Bioinformatics Platform Single-Cell-Workshop, with material here.</p>