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| **Title** | **scRNA-seq Differential Expression Approaches** |
| Summary (140 char max) | In this workshop we’ll be walking through various differential expression and integration techniques to analyse real experimental scRNA-seq data from a treatment and control group. |
| Training material | [github repo link] |
| Trainer(s) | [x] |
| Duration | 3-4 hours |
| Venue / delivery requirements | Melbourne Bioinformatics |
| Advertising tags | Bioinformatics, single-cell, RNA-seq, scRNA-seq, transcriptomics, RNA, differential expression |
| **Description** |  |
| Overview | This workshop aims to equip participants with the necessary knowledge and skills to analyse scRNA-seq data from two experimental groups effectively, enabling them to integrate multiple datasets, extract differentially expressed genes with different approaches.  This workshop is designed to build on top of what was covered in the intro to scRNA-seq workshop. Students should have a basic understanding and prior experience using standard Seurat processing workflow steps.  Topics covered and tools used will include:   * How to approach quality control in scRNA-seq data analyses * How to use Seurat’s in built FindMarker() functions to identify differentially expressed genes * An in-depth look at various integration and batch correction methods within Seurat to combine data from two experimental groups * How to aggregate scRNA-seq expression data into pseudo-bulk representations * How to use DESeq2 (and other bulk DE methods) on pseudo-bulked scRNA-seq data * How to visualise differentially expressed genes using in-built Seurat functions and extract data from Seurat objects to create custom heatmaps/visualisations * How to export visualisations/graphs into pdf or png files   During this training, participants will:   * Learn the fundamental concepts and principles of working with scRNA-seq data from multiple experimental groups. * Gain hands-on experience in running scRNA-seq differential expression analysis using both in-built Seurat functions and popular bulk RNA-seq tools like DESeq2 * Follow step-by-step instructions and complete practical exercises to reinforce the concepts learned. |
| Learning objectives | At the end of this training, you will be able to:   * Understand when and how to use various data integration strategies to correct for batch-effects and enable comparative analyses between multiple single-cell datasets from different experimental groups. * Understand the differences between Seurat’s in build differential expression functions and when to use them: FindMarkers(), FindConservedMarkers(), and FindAllMarkers() * Learn how to use DE tools meant for bulk data (e.g. DESeq2 and limma) for single cell ‘pseudobulk’ data, and understand why you might choose this approach * Take advantage of the Seurat R package to perform the analysis, generate plots and interpret the results. |
| Target audience | The target audience for this training includes:   * Researchers and scientists in the fields of biology, genetics, bioinformatics, and related disciplines who are interested in or working with scRNA-seq data. * Students and early-career researchers or graduate students who are new to scRNA-seq data analysis. * Experienced bioinformaticians or computational biologists who want to expand their knowledge and skills in scRNA-seq data analysis techniques. * Wet-lab researchers who aim to gain a better understanding of the computational methods used to analyse and interpret scRNA-seq data. |
| Delivery interface(s) or environment | R-Studio |
| Tools used | R, R-Studio and Seurat |
| Prerequisite skills or experience | Participants are expected to have familiarity with the R programming language and basic familiarity with Seurat scRNA-seq workflow steps.  This R training workshop provides the necessary skills: <https://www.melbournebioinformatics.org.au/tutorials/tutorials/intro_R_biologists/intro_R_biologists/>  The following workshop training material provides a basic introduction to standard Seurat Workflow steps:  <https://melbintgen.github.io/Intro-to-scRNA-seq-analysis/scRNAseq_workshop.html> |
| Required equipment or software | This is a hands-on workshop and attendees must supply their own charged laptop (chargers also recommended) with access to the internet/wifi and the following software preinstalled:   * Participants must install R, and R-Studio prior to the workshop session. * Additionally, please install and test Seurat, SeuratData, DESeq2, and pheatmap. Instructions for this are included at the beginning of the workshop material. |
|  | If you require any further information, or have any access requirements in order to participate in this workshop, please contact the workshop organiser [Melbourne Bioinformatics](https://www.melbournebioinformatics.org.au/) as soon as possible to discuss your requirements:  bioinformatics-training@unimelb.edu.au |
| Questions to include in Eventbrite registration |  |
| Any notes and useful info to assist in workshop delivery, not covered above. |  |
| Version history | This workshop description was:  created by: Manveer Chauhan  on : October 3, 2024 |
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