Tools and techniques for single-cell RNA-seq data

Luke Zappia

Table of Contents

Abstract

The preface pretty much says it all.

Second paragraph of abstract starts here.

Declaration

This is to certify that:

1. the thesis comprises only their original work towards the [name of the award] except where indicated in the preface;
2. due acknowledgement has been made in the text to all other material used; and
3. the thesis is fewer than the maximum word limit in length, exclusive of tables, maps, bibliographies and appendices or that the thesis is [number of words] as approved by the Research Higher Degrees Committee.

Preface

This is an example of a thesis setup to use the reed thesis document class (for LaTeX) and the R bookdown package, in general.

Acknowledgements

This template is based on thesisdown (<https://github.com/ismayc/thesisdown>) and makes use of RMarkdown (<https://rmarkdown.rstudio.com/>) and bookdown <https://bookdown.org/yihui/bookdown/>. The LaTeX template is based on John Papandriopoulos’ University of Melbourne thesis template (<https://github.com/jpap/phd-thesis-template>). Inspriation also comes from similar projects including beaverdown (<https://github.com/zkamvar/beaverdown>), aggidown (<https://github.com/ryanpeek/aggiedown>), huskydown (<https://github.com/benmarwick/huskydown>) and jayhawkdown (<https://github.com/wjakethompson/jayhawkdown>).

# Introduction

## RNA sequencing

* Central dogma
* Why RNA-seq?

### Capture and reverse transcription

* PolyA capture
* Ribosomal depletion

### High-throughput sequencing

* Illumina sequencing
  + Sequence by synthesis

### Analysis of RNA-seq data

* Experimental design
* Negative binomial
* Normalisation
* Differential expression testing

## Single-cell capture technologies

* First protocol
* Fluidigm

### Droplet based cell capture

* Drop-seq
* Indrop
* 10x Chromium

### Unique Molecular Identifiers

* Why?
* How they work

### Recent advances

* New capture methods
* CITE-seq
* Cell hashing

## Features of single-cell RNA-seq data

* Why use single-cell?
* Low counts
  + Dropout
  + Bursting
  + Biology

## Analysing scRNA-seq data

### Pre-processing and quality control

* Alignment
* Droplet selection
* UMIs
* Doublet detection
* Bad cells
* Gene filtering
* Cell ranger
* scater

### Integrating multiple datasets

* Why?
* Seurat CCA
* New methods

### Grouping cells

* Clustering
* Seurat
* Other approaches

### Ordering cells

* Pseudotime
* Monocle
* Other approaches

### Gene detection and interpretation

* DE
* Marker genes
  + Alternatives - Gini, classifiers
* Reviews
* Classification

## Kidney development

### Structure and function

* Kidney structure
* Nephron structure
* Important cell types

### Stages of development

* Lineage
* Important genes

### Growing kidney organoids

* Why?
  + Disease modelling
* Protocol
* Growth factors
* Characterisation
* Reproducibility

# The scRNA-seq tools landscape

# Simulating scRNA-seq data

## Introduction

## Splatter publication

You can read the Splatter paper [here](https://genomebiology.biomedcentral.com/articles/10.1186/s13059-017-1305-0).

# Visualising clustering across resolutions

# Analysis of kidney organoid scRNA-seq data

# Conclusion

# References