Tools and techniques for single-cell RNA-seq data

Luke Zappia

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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

# 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