Approximate Bayesian inference for identifying sub-populations of cells in large scale single cell RNA-Seq data

A Data Management Plan created using DMPonline

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Project abstract:

This project will provide solutions to identifying sub-populations of cells in large scale single-cell RNA-Seq (scRNA-Seq) data sets, by deriving variational inference schemes for single cell RNA-seq clustering models that we have developed.

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Copyright information:

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Data Collection

Data generated will consist of open source software and notebooks documenting analyses.

The data will be generated by the PI and PDRA working on the project through implementation of the methods developed in the project, and through the analysis of data. In analysing data we will produce quantitative measures of gene expression within sub-populations identified in a dataset. The process of analysis itself will also be recorded in an electronic notebook format.

Documentation and Metadata

The software implementation will include documentation explaining how data can be processed with the software. We will also provide a vignette walking through an analysis of publicly available data. Analyses will be created as Jupyter notebooks with the code to reproduce the analysis alongside text explaining the analysis being performed.

Ethics and Legal Compliance

We do not envision any ethical issues in the generation of software and analysis of data over the course of the project.

All software and data we propose to work with is publicly available. We do not plan to re-distribute existing software. Our software will be licensed through an appropriate open source license.

Storage and Backup

We will ensure that all data, including manuscript drafts, software, and analysis, is backed up using the University of Surrey provided OneDrive service as it is being worked on.

Access to data and security will be managed by the University of Surrey core IT services.

Selection and Preservation

Data that should be preserved in the long term consists of the open source software we produce and the data analyses (Jupyter notebooks) we conduct, to ensure the work is reproducible.

To ensure that project outputs are made available for at least 10 years following UKRI policy, all outputs (Jupyter notebooks, software packages) will be archived on Zenodo, which will also provide a DOI for each output that can be cited. We will also make use of container platforms such as Singularity and nf-core to build reproducible data analysis pipelines, where appropriate.

Data Sharing

Software we produce will be shared on the open source platform Github where it is freely available, and also on the Zenodo platform which will archive software for at least 10 years.

No restrictions are required.

Responsibilities and Resources

The PI will be responsible for data management during the course of the project. This includes:

- Data Acquisition and Data Capture
- Data Backup
- Data Management
- Data Retention

We require services provided by the University of Surrey for backup (OneDrive), and open platforms for data sharing and long term storage (Github, Zenodo).

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