

Spatial Transcriptomics Data Analysis using R

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February 3, 2024

Overview: The workshop will cover methods for analyzing spatial transcriptomics data. Broadly, we will cover the following topics:

1. Review of spatial transcriptomics technologies.
2. Spatial transcriptomics data structure and storage in R.
3. Finding spatially variable genes.
4. Dimension reduction, clustering, and identification of marker genes.

The topics will be motivated by an in-depth analysis of a real spatial transcriptomics dataset from the human brain.

Software prerequisites: R (≥ 4.0) and a relatively new version of R Studio will be required to follow along on your computer. To install R and R Studio, please [follow this guide](#). If you are unsure about your version of R/R Studio, please download the workshop materials and see if the files can be opened.

Ability to run Unix commands is preferable but not required.

Workshop materials: The workshop materials are available on GitHub:

https://github.com/phillipnicol/UPR_ST_workshop

The files can be downloaded to your computer as a ZIP file using the website, or from the terminal using:

git clone https://github.com/phillipnicol/UPR_ST_workshop.git

Before the workshop, it would be helpful to install the necessary R packages by running the `install_packages.R` script. It is okay if the SPARK package cannot be installed.