# README

This is the landing page for COMP683 Course Project.

### Getting setup

```
# unless you are starting an R session
# from within this directory, source
# the `.Rprofile` from the project root.
source(".Rprofile")

# setup SLICER by installing dependencies
box::use(SLICER[...])
```

## Project Proposal

### DE with SLICER

> **Note**
>
> This is a work in progress

### Group Members

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## Abstract

SLICER is a method to select features (genes) to build a trajectory of cells. In Single Cell RNAseq (scRNAseq), this method may be helpful in the context of cell differentiation analyses. The goal of our project is to investigate Differential Expression (DE) approaches to the features selected by SLICER.

## Formal Statement of the Problem

While SLICER automatically selects genes that are important for defining a trajectory among the data, it does not associate which features are most important to defined cell types.

## Related Work

TBD

## Contributions

## Datasets

We will be using data sets from Single-cell dattasets for temporal gene expression integration, specifically utilizing a few Hematopoiesis differentiation dataset (as there are 2).

## Intended Experiments

TBD

## Expected Challenges

Immediate challenges will be the disparity between softwares. Data is stored in a `h5ad` format that can be read into memory via `scanpy.read_h5ad(...)`. However `SLICER` is implemented in R and will need to be locally installed as it was removed from CRAN in `2022`.

## Implementation

Since `SLICER` is implemented in R, we will be implementing our DE in R as well. Our code will be posted on GitHub

## Preliminary Results

TBD