CLACELL: Robust cell type classifier for immune cells

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Single-cell RNA sequencing allows researchers to profile the RNA of individual cells to understand their behavior in health and disease. Cell type annotation is a vital task and a rate limiting step in single-cell RNA sequencing analysis. Existing deep-learning based classifiers suffer from unstable behaviour and manual annotation is a tedious process

In this project, the goal is to create a robust classifier for immune cells, via subsampling or ensemble learning. The project has the following steps and can be extended to a master's thesis.

- Reimplement a marker based annotation strategy from an R package in python using
- Compare maker genes based/non-DL annotation tools.
- Compare existing DL based celltype classifiers on annotated data (literature research, find benchmarks)
- Take the best-performing classifier/tool and make it robust and/or make a meta-classifier that conducts a majority vote.
- Implement a nextflow pipeline module or pip package to perform quick cell type annotation.

Project requirements:

- R and/or python
- Interest in molecular biology
- Independent working style