
Python

unknown

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A package for finding projections onto known cell phenotypes, given matrices of raw RNA count data. The theoretical background for this project can be found in [Epigenetic Landscapes Explain Partially Reprogrammed Cells and Identify Key Reprogramming Genes](#) by Alex H. Lang, Hu Li, James J. Collins, and Pankaj Mehta.

A manuscript containing the technical details of applying our method to single-cell RNA-seq is in progress, hopefully to be completed Summer 2022.

SOURCES FOR REFERENCE DATABASES

- Mouse Cell Atlas
- Atlas of Mouse Lung Development

DEPENDENCIES

- NumPy
- Pandas
- SciPy