

Using_Single_Cell_Python_tools_as_an_r_programmer.Rmd

Kevin Stachelek

Hey Martin,

Long time since we talked. Hope you're doing alright. What are you up to? Any new climbing photos I can share with the lab?

I'm writing because we're attempting to use some tools written in python for these single cell sequencing projects and I wanted to 1) get your opinion about reliability and advisability. 2) get a few specific details straightened out.

Are you still able to help out a bit? If so, I'll send you a detailed follow up email. (I didn't want to scare you off with a wall of text)

Thanks!

A few of us went to the Keystone single cell symposium conference where we heard talks from lots of computational biologists and programmers.

A few of the python-based tools

truncated normalization test

biorniv paper

scanpy

Suite of software for exploring and describing single cell datasets similar to Seurat, Bioconductor methods but written in python

scvelo

RNA Velocity determination. 'RNA velocity' is a recently discovered measure of the ratio of unspliced to spliced RNA species. It acts as a measure of active transcription. It is used to aid sorting of scRNAseq data on the basis of developmental state. scvelo is an improved implementation of velocity

DCA - Deep count autoencoder for denoising scRNA-seq data

scGen

biorniv

An application of neural networks to scRNAseq data. Theis likened it to facial simulation approaches (like putting glasses on cells)

termed 'style transfer'. Typical application described was simulation of excitation state/perturbation? across datasets lacking experimental perturbation.