Cellular Programs

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Winter Semester 2020/21 — Chair of Computational Biology

Assignment 4 (about paper #7)

Handed out: 15.12.20

Due: 5.1.2021 10:15

Submit your solutions by e-mail with a single PDF attachment to

kerstin.gronow-p@bioinformatik.uni-saarland.de

Every student should submit his/her own solution. Plagiarism of solutions will be penalized. Don't forget to label your assignment sheet with your name and Matrikelnummer.

Don't exceed specified page lengths by more than 0.25 pages.

Problem 1:

What are the advantages of performing scRNA-seq analysis over bulk RNA-seq for eQLT identification? (0.25 page)

Problem 2:

Is scRNA-seq analysis or bulk RNA-seq analysis more favorable while studying:
(a) Pathological phenotypes loci
(b) Alternative splicing
(c) Development of early embryos in high resolution
Please briefly explain your answer for each scenario. (0.5 page)

Problem 3:

In the legend of Fig. 1c, the authors write that "cells are ordered by pseudotime, defined as the first principal component (PC1)."
Explain based on the top graphics of Fig. 1c, why the authors define the developmental "pseudotime" in this fashion (0.25 page)

Paper #7 Cuomo et al. (2020) Nature Commun. 11, 810, Single-cell RNA-sequencing of differentiating iPS cells reveals dynamic genetic effects on gene expression**.**