

Cellular Programs

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Saarland University

Chair of Computational Biology

Assignment 6

Handed out: 29.1.18

Due: 5.2.2018 14:15

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.

Problem 1: Traditionally, hematopoiesis used a tree-like schema to describe the differentiation of blood cells from hematopoietic stem cells over intermediate-stage or progenitor cells into terminally differentiated blood cells. Each stage is characterized by a set of characteristic marker proteins on the cell surface. Cells are assigned to different stages by FACS analysis.

Paper #13 presented an alternative data-driven approach where gene expression data of all genes was used to split single cells into different clusters. Analysis of Gene Ontology terms was used to associate clusters with the traditional cell types. However, paper #13 did not classify intermediate (progenitor) stages. They only had one stage similar to HSCs and 4 stages similar to differentiated cell types.

- (a) List the benefits and downsides of traditional and data-driven approaches. (0.5 page)
- (b) Discuss whether the data-driven approach of paper #13 can be extended to also include intermediate stages. (0.5 page)

Problem 2: As was discussed in the lecture, epigenetic marks (DNA methylation and histone marks) also show characteristic changes during differentiation from stem cells into differentiated cells.

Discuss whether one can perform the same data-driven assignment of cell stages (as was done in paper #13) also based on epigenetic marks instead of gene expression data? Do you expect that both approaches will lead to similar results? (0.5 page)