

Cellular Programs

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Saarland University

Chair of Computational Biology

Assignment 5

Due: 22.1.2018 14:15

Submit your solutions

(a) on paper (printed text) at the beginning of the lecture or in building E21, room 3.14, or

(b) 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: Recent studies on blood development are often based on single-cell data instead of bulk measurements (see [1] and [2], for example).

a) What do "single-cell" and "bulk" mean in this context? Shortly discuss **general** advantages and disadvantages of single-cell vs bulk experiments.

b) In the developmental context single-cell techniques have become very relevant because individual stem or progenitor cells may already be primed towards certain lineages. What does "being primed" mean here and why does it matter? Explain why single-cell studies are better suited to answer **this specific question**.

c) Let us assume that you work on similar research questions as mentioned in b) and that well-understood subpopulations exist, and that you collaborate with an experimental lab that does not have access to single-cell technologies. What sort of additional experimental steps could be employed that would enable you to compare well-characterized subpopulations within your sample? (1,5 pages in total for (a), (b) and (c))

[1] Farlik et al., Cell Stem Cell (2016). DNA Methylation Dynamics of Human Hematopoietic Stem Cell Differentiation.

[2] Moignard et al., Nat. Biotech. (2015). Decoding the regulatory network of early blood development from single-cell gene expression measurements.

Problem 2: CHIP-seq, DNase-seq and ATAC-seq are popular experimental protocols in modern biology.

a) What do these three methods measure?

b) Put all three methods into a **simple flowchart** which starts with the usable cell samples and ends with the determined reads as output.

c) Draw another diagram that shows what steps the three methods share and in which steps the individual methods differ (alternative routes).

(1 page in total = short answer for a) and 2 diagrams for b) and c))