Cellular Programs

Prof. Dr. Volkhard Helms — Saarland University

Winter Semester 2020/21 — Chair of Computational Biology

Assignment 2 (about paper #4)

Handed out: 24.11.20

Due: 1.12.2020 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:

The authors compared data from GRO-seq and RNA-seq. They found that the results differ somehow. What is measured by GRO-seq and what is measured by RNA-seq? (0.25 page).

Problem 2:

In most current studies, RNA-seq is used to sample the transcriptomic profile of cells or tissues. But here, the authors noticed clear differences between GRO-seq and RNA-seq. When is it okay to apply RNA-seq and when not? (0.25 page)

Problem 3:

On p.3477, bottom of left column, the authors cite two studies that measured half-lives of mammalian genes (1 min to more than 3 hours).
On p. 3474, middle of right column, the authors report that "genes with higher transcription in G1/S than in G0/G1 and M phases were enriched for the GO term "M phase".
(a) Why does one annotate such genes as "M phase" genes?
(b) What do you expect for the half-lives of these genes? (0.25 page)

Problem 4:

The author stated: „Further inspection of the top differentially transcribed genes in cluster 3, such as TNS3 and LDLRAD4, found them to be of larger size." What problem do these unusually-long genes pose to the GRO-seq analysis? Why is there a need for the cells to clear actively engaged Pol II from mitotic chromatin via mitotic transcriptional activation? (0.25 page)

Paper #4 Liu et al. (2017) Proceedings of the National Academy of Sciences USA 114, 3473-3478, Transcriptional landscape of the human cell cycle.