AUSHANG

FREIE UNIVERSITÄT BERLIN
Fachbereich Mathematik und Informatik

Promotionsbüro, Arnimallee 14, 14195 Berlin

DISPUTATION

Montag, 12. Februar 2018, 10.00 Uhr

Ort: Takustr. 9, Raum 053, 14195 Berlin

Disputation über die Doktorarbeit von

Frau Khadija El Amrani

Thema der Dissertation:

Computational methods for the identification and characterization of tissues and cells

Thema der Disputation:

Computational methods for cellular transdifferentiation

Die Arbeit wurde unter der Betreuung von **Prof. Dr. P. N. Robinson** durchgeführt.

Abstract: Direct lineage reprogramming by overexpression of defined transcription factors (TFs) is a promising approach for research and regenerative medicine. However, the experimental identification of key TFs that control cell identity is expensive and time-consuming. Thus, fast computational methods are needed to accelerate the discovery of sets of factors that drive the transdifferentiation of a cell type into another.

In this talk I will present Mogrify [1], a computational approach that combines gene expression data with regulatory network information, in order to predict the reprogramming factors necessary to induce cell conversion.

Further, I will compare this method to two other methods for predicting TFs for cell conversion, namely CellNet [2], and the method developed by D’Allessio et al. [3]. Finally, I will consider the similarities and differences of the three methods [4].

References:

[1] Rackham, O.J.L., Firas, J., Fang, H., Oates, M.E., Holmes, M.L., Knaupp, A.S., Suzuki, H., Nefzger, C.M., Daub, C.O., Shin, J.W., Petretto, E., Forrest, A.R.R., Hayashizaki, Y., Polo, J.M., Gough, J., Gough, J.: A predictive computational framework for direct reprogramming between human cell types. Nature Genetics 48(3), 331–335 (2016). doi:10.1038/ng.3487

[2] Cahan, P., Li, H., Morris, S.A., Lummertz, E., Rocha, D., Daley, G.Q., Collins, J.J.: CellNet: Network Biology Applied to Stem Cell Engineering. Cell 158, 903–915 (2014). doi:10.1016/j.cell.2014.07.020

[3] D’Alessio, A., Fan, Z., Wert, K., Baranov, P., Cohen, M., Saini, J., Cohick, E., Charniga, C., Dadon, D., Hannett, N., Young, M., Temple, S., Jaenisch, R., Lee, T., Young, R.: A Systematic approach to identify candidate transcription factors that control cell identity. Stem Cell Reports 5(5), 763–775 (2015). doi:10.1016/j.stemcr.2015.09.016

[4] Kamaraj, U.S., Gough, J., Polo, J.M., Petretto, E., Rackham, O.J.L

Die Disputation besteht aus dem o. g. Vortrag, danach der Vorstellung der Dissertation einschließlich jeweils anschließenden Aussprachen.

Interessierte werden hiermit herzlich eingeladen

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