

## Master thesis project

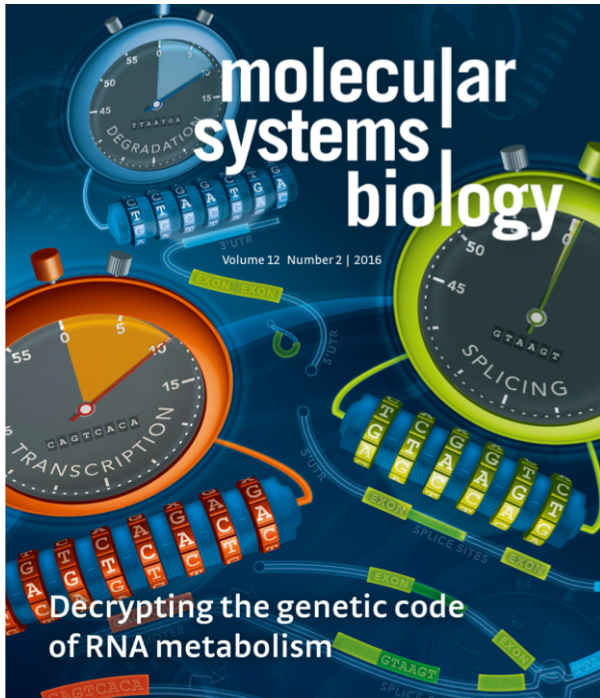
### Modeling of gene expression from DNA sequence by convolutional network

Gagneur lab

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The lab of Julien Gagneur is looking for a student to perform his/her Master thesis. Our goal is an improved understanding of the genetic basis of gene regulation and its implication in diseases. To this end, we employ statistical modeling of 'omic data and work in close collaboration with experimentalists.

Gene expression is the fundamental process that dictates when, where, and how much cells read out genes and expresses their encoded proteins. We want to predict gene



expression from genome sequence and understand which proteins regulate this process and their preferred sequences (regulatory code). The goal of this master thesis is to develop a robust statistical model that jointly models the regulatory code (Fig.1) and the activity of the regulatory proteins. The student will extend CONCISE (CONvolutional neural Network for CIS-regulatory Elements), a Tensorflow framework we recently developed [1]. The initial dataset will be the expression profile of 6,000 yeast genes across 1,484 gene knockouts strains [2]. Work will be done in collaboration with a PhD student, Žiga Avsec, author of CONCISE, and should lead to publication of the software. **Figure 1. Cover MSB, Feb. 2016 [3]**

The project is open to bioinformatics, statistics, physics, and computer science

students. A taste for mathematical modeling and interest in biological questions is expected. Fluency in English is essential. Our group is a young, international and multidisciplinary group. We are located at the Informatics faculty of the Technical university of Munich in Garching. There is a perspective to afterward join as a PhD student either as part of the TUM Informatics Graduate School or the Graduate School of Quantitative Biosciences Munich. More information on our website.

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### References

1. <https://github.com/Avsecz/concise>
2. Kemmeren P., et al. (2014) Large-Scale Genetic Perturbations Reveal Regulatory Networks and an Abundance of Gene-Specific Repressors, *Cell* 157, 740–752
3. Eser P. and Wachutka L., et. al. (2016) Determinants of RNA metabolism in the Schizosaccharomyces pombe genome, *Mol Syst Biol.* (2016) 12: 857