

## **Bachelor project: MicroRNA target patterns in signaling pathways and the link to human diseases**

MicroRNAs are small non-protein coding RNA molecules that have recently emerged as post-transcriptional regulators, known to influence diverse cellular processes ranging from stem cell differentiation to apoptosis. They mostly target the 3' UTR of a target mRNA, thereby destabilizing the transcript and inhibiting its translation. We recently studied the enrichment of microRNAs in signaling pathways, their preferred target protein location and function, and localization of targets within the signaling network.

In this bachelor project, we want to answer the question whether miRNA target proteins share common biological functions and topological properties within signaling networks.

Furthermore, we want to link signaling pathways sharing interesting network features with human diseases. To that end, we will use the PhenomiR database (<http://mips.helmholtz-muenchen.de/phenomir/>), a manually curated database containing disease-associated microRNAs in human disorders at our Institute.

If you are interested, have in look in these papers and call us or write us a mail:

W. P. Kloosterman, R. H. A. Plasterk. The diverse functions of micrnas in animal development and disease. *Dev Cell*, 11(4):441–450, 2006.

J. Xu, C. Wong. A computational screen for mouse signaling pathways targeted by microrna clusters. *RNA*, 14(7):1276–1283, 2008.

A. Ruepp, A. Kowarsch, D. Schmidl, F. Bruggenthin, B. Brauner, I. Dunger, G. Fobo, G. Frishman, C. Montrone, F. J. Theis. Phenomir: a knowledgebase for microrna expression in diseases and biological processes. *Genome Biol*, 11(1):R6, Jan 2010.

### **Required:**

- Programming skills (Java, Python, Perl)
- Basic biological background
- Basic statistical background (R, Matlab, Mathematica)

### **Contact:**

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Computational Modeling in Biology

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