Deciphering the gene regulatory code: from modelling to applications to genetic diseases

My lab is interested in understanding how gene expression is encoded in genomes, and how to leverage this knowledge for medical applications. To this end, we employ statistical modelling of ‘omics data and work in close collaboration with experimentalists. I will provide an overview of published and unpublished results on genetic determinants of RNA metabolism and protein expression. I will also report on a recent study with which we established RNA-sequencing as a powerful companion tool to genome sequencing for pinpointing molecular causes of genetic disorders. The talk will end with a discussion of the model zoo kipoi.org, an international project we just launched enabling the sharing and integration of predictive models for genomics.

References:
Schwalb et al. TT-seq maps the human transient transcriptome. Science (2016)

Date: Monday, April 23rd, 2018
Time: 16:00 h
Room: Lounge (level 13), Klingelbergstrasse 61 (vis-à-vis Pharmazentrum)
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