

Basel Computational Biology Seminar

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Dynamics of transcriptional regulation

Despite gene expression programs being notoriously complex, RNA abundance is usually assumed as a proxy for transcriptional activity. Recently developed approaches, able to disentangle transcriptional and post-transcriptional regulatory processes, have revealed a more complex scenario. It is now possible to work out how synthesis, processing and degradation kinetic rates collectively determine the abundance of each gene's RNA. It has become clear that the same transcriptional output can correspond to different combinations of the kinetic rates.

This underscores the fact that markedly different modes of gene expression regulation exist, each with profound effects on a gene's ability to modulate its own expression. Within this presentation, I will present a suite of computational tools that we developed to quantify the dynamics of RNA metabolism, and how we applied it to study transcriptional and post-transcriptional programs driven by the MYC transcription factor and oncogene.

Date: Monday, March 21, 2022

Time: 16:15 h – 17:30h

Location: Online via Zoom

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