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BIOZENTRUM
The Center for Molecular Life Sciences

Basel Computational Biology Seminar

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Genome-wide study of transcription complexity and ribosome dynamics

One of the biggest challenges in biology is to understand how apparently identical cells respond differently to the same stimulus. During the last decade, thanks to the development of genomic tools, research has uncovered extensive variability in the RNA molecules present within the cells.

By simultaneously sequencing both the 5' and 3' ends of each RNA molecule, we have previously showed that the complexity of overlapping transcript isoforms had been greatly underestimated. We have now developed an optimized version of this approach (TIFSeq2) to interrogate the transcriptional complexity of chronic myeloid leukemia cells (K562) after treatment with tyrosine kinase inhibitors. We will present our study of the transcriptional landscape focusing on the interaction between transcriptional start and polyadenylation sites in humans.

To further expand our understanding of transcriptome complexity, I will present novel work regarding the functional consequences of cryptic transcription in budding yeast. We have analyzed the transcription start site usage, chromatin organization and post-transcriptional mRNA life. Our data suggest that a significant fraction of chromatin-dependent internal cryptic promoters are in fact alternative truncated mRNA isoforms. The expression of these chromatin-dependent isoforms is conserved from yeast to human expanding the functional consequences of cryptic transcription and proteome complexity.

Date:	**Monday, February 25th, 2019**
Time:	**16:00 h**
Room:	**Biozentrum, room 103**
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