

Department Biozentrum





Basel Computational Biology Seminar: 22830-01 Current Research in Bioinformatics I

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## An RNA perspective of functional genomics

Only 2% of the human genome consists of protein-coding genes. The remaining 98% is non-coding and thought to encode the regulatory information for gene expression. Interpreting this non-coding region is thus key to understanding the functional genome and its implications for complex diseases. To tackle this, we take advantage of biological data generated from breakthroughs in chemical biology and bioengineering such as short- and longread sequencing, oligosynthesis, chemical probing, and click chemistry. In this talk, I'd be sharing some of our research directions in developing technology-specific computational tools for this RNA perspective of functional genomics. Our ultimate goal is to achieve this single-nucleotide resolution at across transcription, processing, modification, translation, decay, and other stages of the RNA life cycle.

Date:	Monday, November 4, 2024
Time:	16:15 h – 17:30h
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