



University
of Basel

Department
Biozentrum



Swiss Institute of
Bioinformatics

BIOZENTRUM

The Center for
Molecular Life Sciences

Basel Computational Biology Seminar

21563 Current research in Bioinformatics II



Florian Erhard

Dissecting the Dynamic Transcriptome: From Computational Methods to Applications in Single Cells

Single-cell RNA-seq captures static snapshots of transcriptional signatures of individual cells without direct information on dynamic changes in gene expression. Purely computational inference of dynamics often fails during acute perturbations (e.g., drug treatment, infection) occurring within hours. Metabolic RNA labeling coupled with nucleotide conversion resolves this by directly capturing rapid transcriptional dynamics in both bulk and single cells. We develop computational methods to overcome challenges in the analysis of such data, including (i) the estimation of biophysical parameters (synthesis rates, RNA half-lives, transcriptional bursting), (ii) single-cell trajectory reconstruction post-perturbation, and (iii) "Heterogeneity-sequencing," a novel framework to identify causal drivers of heterogeneous responses to a perturbation. I will present our recent methodological advances and their application in mapping the complex, early host-pathogen interplay during human cytomegalovirus infection.

Speaker Information

Name: Prof. Florian Erhard

Institute: Universität Regensburg
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Event Details

Date: Monday, May 18, 2026

Time: 16:15 – 17:15 h

Location: Biozentrum, U1.197

Host: Aleksei Mironov

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