





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

## **Alex Popinga**

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## Model, Fit, and Predict the Dynamics of Life with the SSIT: The Stochastic System Identification Toolkit

Stochastic modelling is important for systems whose states may experience significant fluctuations through time from the mean behaviour and dynamics of a large system, thus affecting the inference of the underlying model and rate parameters which drive the system, and subsequently the accuracy of predictions. Noisy behaviour is particularly prevalent in small effective populations or low count data, as is the case in chemical reaction networks that drive biological processes such as gene expression, epidemiological and ecological models. The Stochastic System Identification Toolkit (SSIT) enables end-to-end probabilistic modelling for data-rich biology, from single-cell counts to RNA-seq. I will demonstrate how the SSIT captures the stochasticity prevalent in biological systems, incorporating and accounting for both intrinsic noise and experimental, extrinsic noise through probabilistic distortion operators (PDOs); offers a variety of model reduction methods for high-dimensional systems to improve computational efficiency; provides a suite of methods for full statistical inference; performs parameter sensitivity analysis and Fisher Information computation; and produces calibrated, testable predictions that can guide experiment design and model discrimination.

Date: Monday, September 22, 2025

**Time:** 16:15 h – 17:30h

Location: Biozentrum, 02.073

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