



Online
seminar

Monday **November 23, 2020** at 16:30

Hosted on: **Meet**

Jan Mikelson

Senior scientist at MSD - Zurich

Bayesian modeling and inference in Systems Biology: Investigating ERK signaling with Nested Sampling

Prof. Cappelletti introduces the seminar.

Abstract

Over the last two decades, the field of Systems Biology has emerged as a distinct approach of investigating and understanding biological systems.

Rather than focusing on single interactions between proteins, genes, and metabolites, Systems Biology aims at understanding biological processes on a systems-level. The advancement of experimental techniques and the subsequent availability of high-throughput single-cell data has driven the demand for increasingly quantitative analysis and modeling methods.

The development of mechanistic models of biological systems has thus become a central part of Systems Biology. The role of these models is to reproduce previously observed biological behaviors faithfully and to predict responses to previously unobserved stimulations accurately. This need for accurate modeling has stirred an interest in the development of efficient model inference techniques as well as in ways to apply sophisticated mathematical models for the investigation of biological questions. In this talk, I will focus on the problem of Bayesian parameter inference and introduce a novel likelihood-free nested sampling method for the inference of the model parameters of stochastic kinetic models from single-cell data. In the second part of the talk, I will show how such inference techniques are applied to ERK signaling in order to discover novel bio-molecular mechanisms.

Biography

Jan Mikelson currently works as a senior scientist in biostatistics at MSD in Zurich. After receiving his B.Sc in Mathematics from the TU Munich, and his M.Sc in Mathematics from ETH Zurich, he finished his PhD Studies in Computational Systems Biology at the Systems Biology Department (D-BSSE) of the ETH Zurich in 2019.

His research was focused on Bayesian inference methods for stochastic kinetic models and their application to questions of bio-molecular mechanisms of cell signaling.