University of Basel
Department Biozentrum

SIB Swiss Institute of Bioinformatics

BIOZENTRUM
The Center for Molecular Life Sciences

Basel Computational Biology Seminar

21563 Current research in Bioinformatics II

Prof. Niko Beerenwinkel

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Computational analysis of tumor single-cell sequencing data

Cancer progression is an evolutionary process characterized by the accumulation of genetic alterations and responsible for tumor growth, clinical progression, and drug resistance development. We discuss how to reconstruct the evolutionary history of a tumor from single-cell sequencing data and present probabilistic models and efficient inference algorithms for mutation calling and learning tumor phylogenies from mutation and copy number data. We present methods for integrating singlecell DNA and RNA data obtained from tumor biopsies, for detecting signatures of selection pressure in single-cell samples, and for finding common patterns of tumor evolution among patients, including re-occurring evolutionary trajectories and clonally exclusive mutations.

Date: Monday, April 22, 2024

Time: 16:15 h – 17:15h

Location: Biozentrum, U1.191

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