



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



Chase Broedersz

Learning the dynamic organization of a replicating bacterial chromosome from time-course Hi-C data

Bacterial chromosomes are in continual motion as they undergo concurrent transcription, replication, and segregation. Time-course Hi-C experiments hold promise for studying chromosome organization across the cell cycle, but interpreting Hi-C data from dynamic systems remains challenging. Here, we develop a rigorous and fully data-driven 4D Maximum Entropy approach to extract a model for the dynamic organization of a replicating bacterial chromosome directly from time-course Hi-C and microscopy data. After validating our 4D data-driven model for *Caulobacter crescentus* against independent microscopy data, we infer quantitative information about changes in chromosome organization across the bacterial replication cycle, such as global positioning of chromosomal loci and replication-induced local changes in chromosome compaction. We discuss how these data-driven inferences can be used to develop mechanistic insights into the contributions of various chromosome segregation mechanisms, including ParABS and loop-extruding SMC complexes. Together, our results illustrate how changes in the geometry and topology of the polymer, induced by DNA-replication and loop-extrusion, impact the organization and segregation of bacterial chromosomes.



Event Details

Date: Monday, April 20, 2026

Time: 16:15 – 17:15 h

Location: Biozentrum, U1.197

Host: Ludovico Calabrese

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