

## Basel Computational Biology Seminar

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## Systems epigenetics view of cellular processes during ageing and infection

Phenotypic variation (including disease) across individuals has two main sources: genetic variation, and variation in environmental exposures. In the past decades the field made tremendous advances in mapping common genetic variants to complex traits and diseases. Yet, the majority of these disease-associated variants lie in the non-coding part of the genome, which makes it very difficult to understand the underlying molecular mechanisms. For the environmental impact on complex phenotypes, we still know very little, yet epigenetics may play a significant role. Our vision is to mechanistically understand how non-coding genetic variants affect gene regulation, how they interplay with epigenetic processes, and how these interplay impacts cellular signaling and cell-cell interactions. In this seminar I will present our most recent work on enhancer-mediated regulatory network models that integrate environmental signaling with genetic and epigenetic variation to understand complex phenotypes. I will show two applications of our predictive models: (i) aging of the bone marrow niche and its implication in acute myeloid leukemia (ii) complex interplay of transcription factors in macrophages during bacterial infections. Overall, our integrative approach with a focus on gene regulation provides a powerful to gain mechanistic insights into complex biological processes.

Date: **Monday, March 28<sup>th</sup>, 2022**  
Time: **16:15 h – 17:15 h**  
Room: **U1.197**  
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