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Chemical and Synthetic Systems Biology

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Born in 1981 in Stuttgart, Germany

Studied Biochemistry at the Eberhard Karls Universität Tübingen and Biophysics at Harvard University

FELLOWSHIP
College for Life Sciences

PROJECT

Modeling Chromatin Dynamics and Cellular Memory

Animal genomes contain the blueprint for developing an extremely complex organism. The genome can be described as an entire library of books, in which the letters of DNA form genes or "chapters". In any given cell and at any given time, only a specific set of relevant volumes and chapters are read and interpreted. Just like errors in the genetic language itself, reading from the wrong pages of the book can be the cause of human disease, such as developmental disorders or cancer. This is why cells use so-called epigenetic information, encoded "on top" of the genetic language to keep track of which chapters are relevant to every given cell at every given point in development. How the cell manages to organize the vast genetic information present in every cell in a way that allows it to translate transient signals from the outside world into long-lasting cellular memory is an unresolved issue.

A family of proteins termed histones dynamically package the genome into the so-called chromatin structure. Chromatin integrates a multitude of signals to control gene expression, some of which have the propensity to be maintained through replication and cell division. In my laboratory, we are developing quantitative methods to study the molecular circuits that underlie epigenetic gene regulation and inheritance. For example, we have established a method to capture genome-wide dynamic changes in chromatin resolved over a period of time ranging from minutes to days. We are particularly interested in Polycomb group proteins, which are evolutionarily conserved master regulators of cell identity and differentiation and have long been a paradigm for epigenetic gene regulation.

Building on my experience with experimental and computational epigenomics, I will focus my stay at the Wissenschaftskolleg on developing mathematical models that integrate our multidimensional quantitative data into accurate mechanistic descriptions of epigenetic processes. To this end, I am looking forward to interacting with Wiko Fellows and experts at the Max Planck Institute for Molecular Genetics and the Berlin Institute for Medical Systems Biology.

Recommended Reading

Elsässer, S. J., R. J. Ernst, O. S. Walker, and J. W. Chin (2016). "Genetic code expansion in stable cell lines enables encoded chromatin modification." Nature Methods 13, 2: 158-164.

Elsässer S. J., K. M. Noh, N. Diaz, C. D. Allis, and L. A. Banaszynski (2015). "Histone H3.3 is required for endogenous retroviral element silencing in embryonic stem cells." Nature 522, 7555: 240-244.

PUBLICATIONS FROM THE FELLOW LIBRARY

Elsässer, Simon (2019)

Quantitative multiplexed ChIP reveals global alterations that shape promoter bivalency in ground state embryonic stem cells

https://kxp.k10plus.de/DB=9.663/PPNSET?PPN=1665457090