

Theoriekolloquium

Am **30. Mai 2024** um **14.15 Uhr** in **W15 0-23** hält

Herr Prof. Dr. Marc-Thorsten Hütt (Bremen)

einen Vortrag mit dem Titel

How patterns in data help us understand biological complexity

For a long time, it has been hypothesized that bacterial gene regulation involves an intricate interplay of the transcriptional regulatory network (TRN) and the spatial organization of genes along the circular chromosome.

Here we illustrate, how gene expression ('transcriptomics') patterns are shaped by this interplay. Our analysis employs concepts from network science, machine learning and mathematical modeling. In this way, it illuminates the full complexity of this biological system.

As an outlook, we will provide a stylized perspective on this intricate biological system by approximating the TRN as a random Boolean network and the impact of chromosomal organization as the local update rules of a cellular automaton running on the circular chromosome.

By studying the complexity of the spatiotemporal dynamics as a function of network architecture and spatial computation, we can delineate, which systemic features enhance or reduce stability.

Interessierte sind herzlich eingeladen.

gez. Prof. Dr. Bernd Blasius