

**Dr. Tobias Jores, Institute of Synthetic Biology**

**»Massively parallel characterization and deep learning of regulatory DNA«**

Precise control of gene expression is essential for growth, development, and environmental adaptation. This control is encoded in *cis*-regulatory elements—including core promoters, enhancers, silencers, and insulators—that can interact in context-dependent ways. However, the rules by which these elements integrate signals to determine when, where, and how strongly genes are transcribed remain largely unknown. Defining this *cis*-regulatory code is a central challenge in modern biology and is key to understanding genome function, interpreting non-coding variation, and enabling predictive control of gene expression.

My lab addresses this challenge using massively parallel reporter assays to characterize the species- and condition-specific regulatory activity of hundreds of thousands of candidate regulatory elements. The massive scale and complexity of the data generated by these assays is ideally suited to train computational deep learning models that predict regulatory activity directly from DNA sequence and reveal the underlying functional motifs. Although our work focuses on plant gene regulation, these assays are broadly adaptable to any organism that can be transformed efficiently.

In this talk, I will present how I developed Plant STARR-seq, a massively parallel report assay for plants, and how this work laid the foundation for establishing my own research group, including the funding sources that supported me along the way. I will then highlight current projects that use Plant STARR-seq and deep learning to study different layers of plant gene regulation. Finally, I will introduce a new web-based tool we are developing to make our computational models easily accessible to the broader scientific community.