GATERSLEBEN LECTURE

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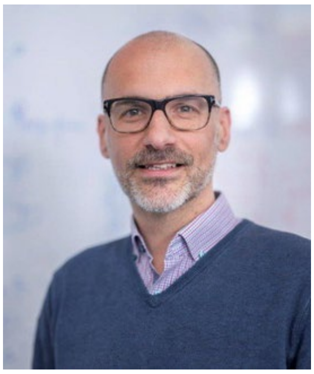

Speaker: **Prof. Dr. Zoran Nikoloski**
Bioinformatics Department, Institute of Biochemistry and Biology, University of Potsdam, Germany

Title: **Predicting dynamic plant responses using genetic markers**

Time: **Tuesday, September 16, 2025, 2 pm**
https://ipk-gatersleben-de.zoom-x.de/j/64783767811?pwd=hndGuIynz0tMsTZ3oKnPjTsgHfQDL8.1
ID: 647 8376 7811
Kenncode: 184928

Place: **IPK Lecture Hall and via Zoom,**
Correnstr. 3, 06466 Seeland OT Gatersleben

Abstract:

Molecular and physiological changes across crop developmental stages shape the plant phenome and render its prediction from genetic markers challenging. Despite advances in technologies for time-resolved phenotyping, we continue to lack approaches for dissecting the genetic architecture and predicting time-resolved traits. I will first present a recent categorization of computational approaches for analyzing time-resolved phenotypes of multiple traits. I will then focus on dynamicGP, an efficient computational approach that combines genomic prediction with dynamic mode decomposition to characterize the temporal changes and to predict genotype-specific dynamics for multiple morphometric, geometric and colourimetric traits scored by high-throughput phenotyping. Using genetic markers and data from high-throughput phenotyping of a maize multiparent advanced generation inter-cross population and an Arabidopsis thaliana diversity panel, I will show that dynamicGP outperforms a baseline genomic prediction approach for the multiple traits. Finally, I will also highlight recent refinements of dynamicGP that facilitates the usage of time-resolved enviromics data to further boost prediction performance. The discussed approaches pave the way for interrogating and integrating the dynamical interactions between genotype and environment over plant development to improve the prediction accuracy of agronomically relevant traits.

Short CV

Since 2017, Prof. Dr. Zoran Nikoloski serves as the Chair of Bioinformatics at the Institute of Biochemistry and Biology, University of Potsdam and is a Cooperative Research Group Leader at the Max Planck Institute of Molecular Plant Physiology, Potsdam, Germany. Trained as a computer scientist in network science research at the University of Central Florida, Orlando, USA, where he received the Hillman Fellowship for excellence in research in 2025, Prof. Dr. Nikoloski moved to plant computational systems biology research after a computer science postdoc at Charles University, Prague, Czechia. In his 15 years of interdisciplinary plant research as a group leader at the Max Plank Institute of Molecular Plant Physiology, Prof. Dr. Nikoloski has developed constraint-based models of plant metabolism and computational approaches for integration of omics data from different technologies to improve the design of metabolic engineering strategies and identify genetic architecture of traits. Prof. Dr. Nikoloski has pioneered the hybrid modeling framework that integrate constraint-based models of metabolism, machine learning, and data from natural variability of different plant species and crops to predict and modify agronomically relevant traits. This framework is currently used to gain understanding of the genetic and molecular basis for plasticity and robustness of metabolic traits to different environmental cues, crucial for the development of climate-resilient crops.

Prof. Dr. N. Stein (organizer) *Prof. Dr. T. Altmann and Dr. J. J. Szymanski (hosts)*