

Speaker: **Prof. Dr. Michael Schatz**
Johns Hopkins University,
Department of Computer Science,
Baltimore, USA



Title: ***Pangenome to Phenotype: Trait Mapping in Solanum and Beyond***

Time: **Tuesday, April 21, 2026, 2 pm**

<https://ipk-gatersleben-de.zoom-x.de/j/64783767811?pwd=hndGulynz0tMsTZ3oKnPjTsgHfQDL8.1>

ID: 647 8376 7811

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

Abstract:

The shift from single reference genomes to pangenomes is transforming our ability to link genetic variation to phenotype, particularly in plants where structural variation, gene presence-absence, and paralog diversification shape trait diversity. In this talk, I will present recent work combining telomere-to-telomere (T2T) genome sequencing, cross-species genome editing, and pangenome-enabled association mapping to dissect the genetic basis of fruit size and flowering time across diverse *Solanum* species. These analyses reveal that paralog evolution, including duplication, neofunctionalization, and pseudogenization, creates evolutionary contingencies that can both constrain and channel adaptation, with repeated selection on paralogs of key developmental regulators such as *CLV3* and *SP5G* across domesticated and wild lineages. I will also introduce Panagram, an ultrafast, alignment-free platform for resolving haplotype architecture within pangenomes, enabling scalable identification of conserved and lineage-specific variation and facilitating trait association across hundreds of genomes. Together, these results highlight how exposing paralog-driven contingencies and haplotype structure provides a generalizable pangenome-to-phenotype (P2P) framework for accelerating trait discovery in crops, animals, and human genetics.

Biography:

Dr. Michael Schatz is the Bloomberg Distinguished Professor of Computer Science and Biology at Johns Hopkins University. His research sits at the intersection of computer science, genomics, and biotechnology, where he develops novel algorithms and computational systems for comparative genomics, human genetics, and precision medicine. He is a recipient of the 2015 Alfred P. Sloan Foundation Fellowship, the 2014 NSF CAREER Award, and was named one of the most influential people in the world by TIME magazine in 2022 for his contributions to completing the first telomere-to-telomere (T2T) human genome. Dr. Schatz received his Ph.D. in Computer Science from the University of Maryland and his B.S. in Computer Science from Carnegie Mellon University. More information is available at <http://schatz-lab.org>.

Prof. Dr. Nils Stein (organizer and host)