

Data Analysis Meeting

CRC 1310 Predictability in Evolution



Bioinformatics tea with Dr. Till Baar

We would like to invite you to our informal bioinformatic meetings to discuss advanced methods for detecting modified bases in **Oxford Nanopore Technologies** (ONT) sequencing. The first session will begin with a 30-minute lecture by Dr. Till Baar, who will share his insights into current strategies and challenges in base modification detection.

Dr. Baar is a molecular biologist and bioinformatician at the Institute of Medical Statistics and Computational Biology, University of Cologne. He has extensive experience in long-read sequencing technologies and epigenetic signal analysis. His research focuses on the development of computational pipelines for the detection and interpretation of DNA modifications.

Using long-read sequencing, such as ONT, enables direct detection of modified bases without bisulfite conversion or PCR, preserving native DNA structure. Its ability to sequence full-length molecules improves genome assembly, structural variant detection and reveals complex epigenetic patterns that are inaccessible with short reads.

Hosted by: Jan & Viera on behalf of the Z3 project

Wednesday, May 14th, 2025, 14:00
Institute for Biological Physics, Zülpicher Str. 77a
Meeting Room first floor, R1.04