Emerging Technologies meets ThemeNights

Bioinformatics

March 12, 5-7 pm

University Hospital Bonn
Venusberg-Campus 1
Life & Brain Center
Building C76
Ground floor R612-2

Please register for the talk:

After the talk we will provide pizza and drinks.

Please contact Andreas Buness (Core Bioinformatics, Andreas.Buness@uni-bonn.de) if you would like to talk to the speaker before the lecture.

Julien Gagneur
Technische Universität München

Where does it hurt (in your genome)?

Pinpointing genetic variants with strong phenotypic consequences is of high relevance to biology and medicine. Recent and ongoing work spanning genome language models, models of aberrant gene expression, and rare variant association testing.

Refs:
1. Tomaz da Silva et al. Nucleotide dependency analysis of DNA language models reveals genomic functional elements. Nature genetics (in press)
2. Hölzlwimmer et al. Aberrant gene expression prediction across human tissues. Nature Communications, 2025.
3. Clarke et al. Integration of variant annotations using deep set networks boosts rare variant association genetics. Nature Genetics 2024.

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