



University
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Department
Biozentrum



Swiss Institute of
Bioinformatics

BIOZENTRUM

The Center for
Molecular Life Sciences

Basel Computational Biology Seminar

21563 Current research in Bioinformatics II



Pille Hallast, PhD

From telomere-to-telomere assemblies to Leonardo da Vinci: new views of the Y chromosome

The human Y chromosome is among the most repetitive and structurally dynamic chromosomes in the human genome, yet it also serves as a uniquely informative marker of paternal ancestry. Recent long-read sequencing and telomere-to-telomere assembly approaches are transforming our understanding of Y chromosome biology and diversity. Our recent analysis of 142 near telomere-to-telomere human Y chromosomes spanning 17 major haplogroups and approximately 180,000 years of evolution reveals extensive structural variation across repeat-rich compartments such as AZFc, the centromere, and Yq12, while also showing that this diversity is constrained and repeatedly funneled into a limited set of architectural outcomes. The same chromosome also has powerful applications in genealogy and cultural heritage science. One example comes from our work on Leonardo da Vinci-associated material, where Y-chromosome markers were explored as a means of recovering paternal lineage information from historical artifacts. Together, these studies illustrate the Y chromosome as both a model for repetitive genome biology and a powerful record of human paternal history.

Speaker Information

Name: Pille Hallast, PhD

Institute: The Jackson Laboratory
Farmington CT, USA

Event Details

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Location: Biozentrum, 02.073

Host: David Thaler, david.thaler@unibas.ch