



University  
of Basel

Department  
Biozentrum



Swiss Institute of  
Bioinformatics

BIOZENTRUM

The Center for  
Molecular Life Sciences

## Basel Computational Biology Seminar 21563 Current research in Bioinformatics II



# Shamil Sunyaev

## Hotspots of human mutation detectable in population genetic data point to positive selection in spermatogonia

Sequencing datasets spanning hundreds of thousands of individuals uncover properties of rare genetic variation in humans. Owing to the size of recent human population, a large fraction of rare variants arise by mutation more than once. Due to such recurrent mutations, sites of higher de novo mutation rate are expected to harbor variants observed at higher counts than sites with low mutation rate. Recent progress in theoretical understanding of sampling properties of rare variants together with estimates of de novo mutation rate helps describing rare variation in humans with high precision. We estimated gene and variant-specific population genetics parameters from 700,000 exomes of the gnomAD v4 dataset. New estimates of strength of selection improved prioritization of pathogenic variants. We developed a method to detect mutational hotspots for protein truncating variants using population data alone. Our analysis identified known and predicted new genes involved in clonal expansion in spermatogonia (CES) and supported the hypothesis that CES is a major mechanism responsible for mutation hotspots.

### Speaker Information

**Name:** Shamil Sunyaev

**Institute:** Harvard Medical  
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### Event Details

**Date:** Monday, March 16, 2026

**Time:** 16:15 – 17:15 h

**Location:** Biozentrum, U1.197

**Host:** Aleksei Mironov

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