UNIVERSITÀ DEGLI STUDI DI MILANO BICOCCA · ReGAInS · FORGENOM II · PANGAIA · Pinc · BIAS Bioinformatica e Algoritmica Sperimentale

OUTREACH Lectures · OPEN TO ALL

The Human Pangenome Project

for an inclusive genomics

DATE	TIME	VENUE
9 July 2026	9:30 – 12:30	Aula Sironi, U4-8

OVERVIEW

The Human Pangenome Project is breaking down several important barriers in genomics: a human DNA reference built from only a handful of individuals, incomplete access to entire chromosomes — including their most complex regions — and ethical challenges of sharing genetic data across diverse populations. By overcoming these obstacles, the project is constructing a **Pangenome Graph**: a highly inclusive, precise, and dynamic reference that empowers scientists and clinicians worldwide. Driven by breakthroughs in large-scale population algorithms and data structures, this initiative paves the way for a new era of biomedical research and truly global precision medicine.

KEY ASPECTS

Equitable Healthcare

Pangenome graphs provide a global reference that reduces diagnostic bias.

Population-wide Variant Detection

Tracking complex variants across whole populations.

Scalable Computing

Computational methods able to manage pangenome graphs in an efficient way.

PROGRAMME

Prof. Paola Bonizzoni

University of Milano-Bicocca, Department of Informatics, Systems and Communication
Project leader of MSCA-RISE for Pangenome Graph Algorithms and Data Integration

“Opening and introduction”

Prof. Benedict Paten (Keynote speaker)

Department of Biomolecular Engineering, University of California, Santa Cruz
Associate Director UC Santa Cruz Genomics Institute, PI of the Human Pangenome Reference Consortium

“The revolution behind the release of the Human Reference Pangenome”

Prof. Mattia Pelizzola

University of Milano-Bicocca, Department of Biotechnology and Biosciences
Group leader of Gene Expression Regulation

“Uncovering the complexity of genomes and transcriptomes through long-read sequencing”

Dr. Luca Denti

University of Comenius Bratislava, Department of Computer Science
MSCA Postdoctoral Fellow, CompBio Research Group

“Breaking computational barriers in Computational Pangenomics”

Dr. Simone Ciccolella

University of Milano-Bicocca, Department of Informatics, Systems and Communication
Postodoctoral researcher at BiasLab

“Learning methodologies for massive genomic data analysis”

FREE ENTRY · NO REGISTRATION REQUIRED

09/07/2026 · Aula L. Sironi U4-8