Researchers from the Faculty of Mathematics and Information Science – Prof. Dariusz Plewczyński and Krzysztof Banecki - have recently co-authored a publication in Nature Methods (5-year Impact Factor: 45.6), one of the world’s leading journals in the field.
The article, available at <https://doi.org/10.1038/s41592-025-02658-7>, is the result of an international collaboration led by the Laboratory of Bioinformatics and Computational Genomics, in partnership with:

* Life Sciences Institute, Zhejiang University, Hangzhou, China
* Institute of Reproduction and Development, Fudan University, Shanghai, China
* Department of Genome Sciences, University of Washington, Seattle, WA, USA

This recognition underscores the Faculty’s growing impact at the intersection of mathematics, informatics, and life sciences.

Exploring the genomic basis of transcriptional programs has been a long-standing research focus. Here we report a single-cell method, ChAIR, to map chromatin accessibility, chromatin interactions and RNA expression simultaneously. After validating in cultured cells, we applied ChAIR to whole mouse brains and delineated the concerted dynamics of epigenome, three-dimensional (3D) genome and transcriptome during maturation and aging. In particular, gene-centric chromatin interactions and open chromatin states provided 3D epigenomic mechanism underlying cell-type-specific transcription and revealed spatially resolved specificity. Importantly, the composition of short-range and ultralong chromatin contacts in individual cells is remarkably correlated with transcriptional activity, open chromatin state and genome folding density. This genomic property, along with associated cellular properties, differs in neurons and non-neuronal cells across different anatomic regions throughout the lifespan, implying divergent nuclear mechano-genomic mechanisms at play in brain cells. Our results demonstrate ChAIR’s robustness in revealing single-cell 3D epigenomic states of cell-type-specific transcription in complex tissues.