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“Computational methods for multiscale analysis of nuclear organization”

The main focus of our ongoing research is the development of machine learning algorithms to reveal fundamental connections between human genome structure and function and their implications in human diseases. We also work on machine learning methods for cohesive integration of multimodal biomedical data and for enhancing model interpretability and generalizability. Recent interests include nuclear genome organization, single-cell epigenomics, spatial omics, comparative genomics, and complex molecular interactions.

https://www.cs.cmu.edu/~jianma/index.html