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Generative Modeling for Single Cell Genomics: Tools and an Application for Studying How T Cells Develop in the Thymus

Nir Yosef received his Ph.D. in Computer Science from Tel Aviv University and then completed a postdoctoral training at the Broad Institute, where he worked on transcriptional regulation of T cell differentiation. Nir joined the faculty at UC Berkeley in 2014, where he is now an Associate Professor of Computer Science, a core member at the Center of Computational Biology, and a Chan Zuckerberg Biohub investigator. The Yosef lab is developing data- centric methods for studying how changes in transcription are associated with various phenotypes in the immune system. In that capacity, the lab is developing and applying computational tools that leverage single cell genomics, with the goal of better understanding the factors that contribute to variability between cells, (e.g, metabolism, chromatin structure) and their broader implications (e.g., in autoimmunity). A second area of research is method development for studying regulatory regions in the genome, based on chromatin profiles and massively parallel reporter assays.