



AMOS TANAY

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CHALLENGES, OPPORTUNITIES AND CANCER

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The Tanay lab is developing probabilistic algorithms for modeling epigenetic and chromosomal organization and for the inference of such models from experimental data. The group is combining the derived models with genomic sequences, constructing sequence-based predictions for epigenomic features while taking into account the multiple correlations among different genomic activity patterns. In particular, the group is collaborating with network members to study chromosomal organization in flies and DNA methylation in normal cells and cancer. As an interdisciplinary team that combines within the same group theoretical and computational work with the development of new experimental approaches to epigenetics, the Tanay lab also co-coordinates the construction of a computational toolbox that aims to promote the integration of the computational biology and epigenetics communities.

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