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Distinguishing cell type using epigenotype[1] THOMAS WYTOCK, ADILSON E MOTTER, Dept. Physics and Astronomy, Northwestern University — Recently, researchers have proposed that unique cell types are attractors of their epigenetic dynamics including gene expression and chromatin conformation patterns. Traditionally, cell types have been classified by their function, morphology, cytochemistry, and other macroscopically observable properties. Because these properties are the result of many proteins working together, it should be possible to predict cell types from gene expression or chromatin conformation profiles. In this talk, I present a maximum entropy approach to identify and distinguish cell type attractors on the basis of correlations within these profiles. I will demonstrate the flexibility of this method through its separate application to gene expression and chromatin conformation datasets. I show that our method out-performs other machine-learning techniques and uncorrelated benchmarks. We adapt our method to predict growth rate from gene expression in E. coli and S. cerevisiae and compare our predictions with those from metabolic models. In addition, our method identifies a nearly convex region of state-space associated with each cell type attractor basin. Estimates of the growth rate and attractor basin make it possible to rationally control gene regulatory networks independent of a model.

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