

Abstract Submitted
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Modeling the Dynamics of Bivalent Histone Modifications in Embryonic Stem Cells WAI LIM KU, Department of Physics, University of Maryland, College Park, GUO CHENG YUAN, Assistant Professor, Department of Biostatistics and Computational Biology, Dana-Farber Cancer Institute, FRANCESCO SORRENTINO, Department of Mechanical Engineering, the University of New Mexico, MICHELLE GIRVAN, EDWARD OTT, Department of Physics, University of Maryland, College Park — Epigenetic modifications to histones may either promote the activation or repression of the transcription of nearby genes. Recent experiments have discovered bivalent domains of nucleosomes in which the domain as a whole contains both active and repressive marks. These domains occur in the promoters of most lineage-control genes in embryonic stem cells. It is generally agreed that bivalent domains play an important role in stem cell differentiation, but the mechanisms remain unclear. Here we propose and study a dynamical model of histone modification which, unlike previous models, captures the general features of the bivalent domains observed in experiments. A key feature of our model is the existence of “A/R states,” by which we mean states in which there are a significant number of nucleosomes *each* of which *individually* has both active and repressive marks. We use our model to investigate the formation and decay of A/R states, the localization of A/R nucleosomes, and the effect of DNA replication on the stability of A/R states. The goals of our model are to help understand the underlying principles and mechanisms of bivalent domain dynamics and to suggest directions for future experiments.

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