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A recruitment-reaction model for chromatin-associated regulatory processes

Computational frameworks for gene regulation have focused on the sequence-specific binding of transcription factors and the subsequent recruitment of cofactors to DNA. Combining mathematical modeling and quantitative experimentation, we have developed kinetic models for gene regulation and DNA repair in mammalian cells. The experimental data forced the inclusion of biochemical reaction steps executed by the recruited proteins. I will show how the resulting recruitment-reaction models make testable predictions on rate, fidelity and memory in chromatin-associated regulatory processes.