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Describing and quantifying the binding pathway of histone H1

Histones H1 or linker histones are highly dynamic proteins that diffuse throughout the cell nucleus and interact with the chromatin structure (DNA and associated proteins), regulating its organization and DNA accessibility to transcription factors. The binding mechanism of histone H1 has been proven to involve a kinetic process characterized by rapid and slow binding interactions with the chromatin structure. When considering these two types of binding interactions explicitly in a mathematical model for the purpose of describing and quantifying the dynamics of histone H1 it becomes apparent that there could be several binding pathways to the chromatin structure. In this work, we model all these different pathways using systems of reaction-diffusion equations and carry out a model comparison analysis using FRAP (Fluorescence Recovery After Photobleaching) experimental data from different histone H1 variants to determine the most feasible binding pathway of histone H1. The analysis favors two different types of binding pathways which share common features that provide new meaningful biological information on histone H1 dynamics. To illustrate the applicability of the results, we use the mathematical model describing one of the favored pathways to assess the kinetic changes of histone H1 after core histone acetylation.