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Studying nuclear actin and histone H1 dynamics using FRAP experiments

Fluorescence recovery after photobleaching (FRAP) has become a common fluorescence microscopy technique for measuring the mobility of proteins within the cell nucleus. By photobleaching a region of a cell nucleus populated with a specific fluorescent fusion protein, recording the fluorescence recovery of the region over time, and interpreting this recovery with a mathematical model it is possible to extract in vivo kinetic properties of the protein under investigation.

Experimental FRAP recovery curves of two nuclear proteins, namely actin and histone H1, exhibit two distinct types of behaviour. To characterize these types of behaviour mathematically and to obtain information on the dynamics of the proteins, FRAP data are interpreted with a linear reaction-diffusion system of equations. The kinetic analysis of the model and the data

(i) enables us to understand that the two distinct types of behaviour correspond to two asymptotic cases of the reaction-diffusion model,

(ii) supports the relevant biological fact that actin exists in the nucleus in both monomeric and polymeric forms, and

(iii) allows us to conclude that histone H1 can have both high and low binding affinities to the chromatin structure.