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Fractal networks model the conformational transition dynamics in native proteins

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Most if not all enzymatic proteins display a purely stochastic dynamics of transitions between a variety of conformational substates composing their native state. The slow character of this dynamics makes a possibility of chemical transformations to proceed before the conformational equilibrium has been reached in the actual chemical state. In the closed reactor, this results in the presence of a transient, non-exponential stage of the enzymatic reaction and in an essential dynamical correction to the reaction rate constant describing the final, exponential stage. In the open reactor remaining in the steady state, a consequence is the necessity of determining the reaction fluxes by the mean first passage times between some distinguished conformational substates rather than by conventional reaction rate constants. Often, the time course of transient reaction stages and the time correlation functions of steady-state fluxes display a characteristic power-law behavior. Both theory and Monte Carlo simulations indicate that this is a result of the conformational transition dynamics represented by diffusion on fractal networks.