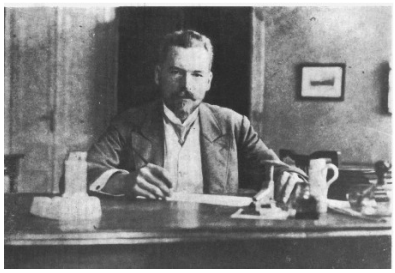

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Information processing in biological molecular machines

Biological molecular machines are enzymes that simultaneously catalyze two processes, one donating free energy and second accepting it. Recent studies show that most native protein enzymes have a rich stochastic dynamics that often manifests in fluctuating rates of the calatyzed processes and the presence of short-term memory resulting from transient non-ergodicity. For such dynamics, we prove the generalized fluctuation theorem predicting a possible reduction of energy dissipation at the expence of creating some information stored in memory. The theoretical relationships are verified in computer simulations of random walk on a model critical complex network. The transient utilization of memory turns out to be crucial for the movement of protein motors and the reason for most protein machines to operate as dimers or higher organized assemblies. Our conclusions are based on analysis of the simulated time course of the catalyzed processes expressed by the strings of discrete jumps at random moments of time. Since similar signals can be registered in the experiments, all the theses of our studies are open for experimental verification.

Summary

No summary

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