Mutual information analysis of mutation, nonlinearity and triple interactions in proteins

Burak Erman[1]

[1]Koc Universitesi

May 14, 2022

Abstract

Mutations are the cause of several diseases as well as the underlying force of evolution. A thorough understanding of its biophysical consequences is essential. We present a computational framework for evaluating different levels of mutual information (MI) and its dependence on mutation. We used molecular dynamics trajectories of the third PDZ domain and its different mutations. MI calculated from these trajectories shows that: (i) the multivariate Gaussian distribution of joint probabilities characterizes the MI between residue pairs with sufficient accuracy. Nonlinearities in joint probabilities calculated by tensor Hermite polynomials up to the fifth order contribute insignificantly. (ii) Changes in MI between residue pairs show the characteristic patterns resulting from specific mutations. (iii) Triple correlations are characterized by evaluating MI between triplets of residues, certain triplets are strongly affected by mutation. (iv) Susceptibility of residues to perturbation are obtained by MI and discussed in terms of linear response theory.

Hosted file

`MANUSCRIPT.docx` available at https://authorea.com/users/482583/articles/569095-mutual-information-analysis-of-mutation-nonlinearity-and-triple-interactions-in-proteins