Title:	Large-scale analysis of single residue mutations on features of protein structure network
Authors:	Kalam, Irfan
Keywords:	protein structure protein structure Large-scale
Issue Date:	Apr-2022
Publisher:	IISER Mohali
Abstract:	Single residue mutations in proteins can cause a wide range of functional and structural affects that varies from no change to a complete loss of protein function/structure. Consequently, many experimental studies of single residue mutations have contributed immensely in deciphering function(s) of proteins. Insights into the pleiotropic affects of amino acid mutations can assist in protein engineering as well as could shed light on protein evolution. In the past, several large-scale systematic studies have been performed to decipher consequences of single residue mutations on proteins structure and/or function. Most of these have largely been focused on predicting or exploring thermostability of proteins or on determining the extent of conformational changes between wild type (WT) and mutant (MT) structures. Interestingly, most previous studies have ignored the subtle changes in the residue interactions in mutant proteins. The residue interactions can be quantified using networks, which can be compared for WT-MT pairs to analyse the local and global affect of single residue mutations. In such comparisons, it is essential to distinguish network perturbation caused by mutation to that arising from experimental conditions of crystallization. In the present work, we have carefully constructed two datasets, viz. WT-WT and WT-MT protein structure pairs primarily to distinguish effect on protein networks due to experimental condition of crystallization from mutations, respectively. We constructed protein structure networks (PSNs) for WT/MT proteins where residue interactions are represented as edges in PSNs. The edge has been drawn between nodes (residues) based on distance, energy or atomic-contact (Ohm). Using these types of PSNs, we have analysed the impact of single residue mutation on protein global/local network properties. The comparison of WT-MT pair of proteins showed that global features of mutant proteins do not change significantly from wild-type proteins except average Eigenvalue centrality showed correlation to conformational changes. Importantly, local network property of Eigenvalue centrality showed changes in Ohm based network. These changes were observed in both WT-WT and WT-MT pairs, suggesting it is difficult to distinguish local network changes arising from mutation to that from crystallization conditions.
URI:	http://hdl.handle.net/123456789/4180
Appears in Collections:	MS-17

Files in This Item:

File	Description	Size	Format	
Yet to obtain consent.pdf		144.56 kB	Adobe PDF	View/Open

Show full item record