Spring 2022

Indel Mapping

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(This abstract is a placeholder for a project to be submitted for publication elsewhere.)

Abstract

Insertion and deletion mutations (InDels) are an understudied dynamic of protein structure. Little real world data exists for these types of mutations. Computational modeling can help fill in these gaps and support researchers in obtaining and analyzing data. In this paper, we present a unique approach to gathering exhaustive data on InDel mutations to create heat maps and other visualizations useful in analysis. Every possible InDel in a set of proteins is modelled in silico, rigidity data is obtained for all of those computational InDels, and the rigidity data of each is then compared to that of the wildtype, providing a complete computational map for what happens for any given InDel mutation in a protein. We provide visualizations of this data, in particular a heat map that will showcase the structural impact of every possible insertion mutation in a given protein.