Mutation mining–A prospector's tale

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Abstract

Protein structure visualization tools render images that allow the user to explore structural features of a protein. Context specific information relating to a particular protein or protein family is, however, not easily integrated and must be uploaded from databases or provided through manual curation of input files. Protein Engineers spend considerable time iteratively reviewing both literature and protein structure visualizations manually annotated with mutated residues. Meanwhile, text mining tools are increasingly used to extract specific units of raw text from scientific literature and have demonstrated the potential to support the activities of Protein Engineers.

The transfer of mutation specific raw-text annotations to protein structures requires integrated data processing pipelines that can co-ordinate information retrieval, information extraction, protein sequence retrieval, sequence alignment and mutant residue mapping. We describe the Mutation Miner pipeline designed for this purpose and present case study evaluations of the key steps in the process. Starting with literature about mutations made to protein families; haloalkane dehalogenase, bi-phenyl dioxygenase, and xylanase we enumerate relevant documents available for text mining analysis, the available electronic formats, and the number of mutations made to a given protein family. We review the efficiency of NLP driven protein sequence

retrieval from databases and report on the effectiveness of Mutation Miner in mapping annotations to protein structure visualizations. We highlight the feasibility and practicability of the approach.

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