Mutation Miner

Submitted by witte [1] on Sat, 2011-01-01 09:07

- Open Mutation Miner [2]
- Bioinformatics [3]
- Text Mining [4]

Title	Mutation Miner
Publication Type	Conference Paper
Year of Publication	2005
Refereed Designation	Refereed
Authors	Baker, C. J. O. [5], and R. Witte [6]
Conference Name	13th Annual International conference on Intelligent Systems for Molecular Biology (ISMB 2005)
Date Published	June 25–29
Conference Location	Detroit, Michigan, USA
Type of Work	Poster
Abstract	Biological researchers today have access to vast amounts of exponentially growing research data in a structured form within several publicly accessible databases. A large proportion of salient information is however still hidden within individual research papers, since costly manual database curation efforts are overwhelmed by the scale of new information being generated. In the domain of protein engineering, critical units of information required from the literature include: the identity of the mutated protein, the identity and position of wild type residues that are mutated, the identity of the resulting mutant residues and the impacts of the mutations on functional properties of the proteins. Mutation Miner is a system designed to automate the extraction of mutations and textual annotations describing the impacts of mutations on protein properties (mutation annotations) from full text scientific literature. Furthermore, the system retrieves and carries out bioinformatic analyses on mutated sequences providing the mapped coordinates of mutants on a selected structure. Integration of multiple formatted mutation annotations with associated residue coordinates facilitates their rendering with structure visualization tools. We describe the architecture and tools that support Mutation Miner (Text mining-NLP, Sequence Analysis, Structure Visualization) and present performance evaluations that demonstrate the feasibility of this approach.

Attachment	Size
ISMB2005-poster.png [7]	411.18 KB

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[4] https://www.semanticsoftware.info/category/topic/text-mining
[5] https://www.semanticsoftware.info/biblio/author/16
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