# Enhanced semantic access to the protein engineering literature using ontologies populated by text mining

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- automated reasoning in bioinformatics [2]
- description logics [3]
- Ontological NLP [4]
- Open Mutation Miner [5]
- protein mutations [6]
- querying OWL-DL ontologies [7]
- Semantic Web [8]
- Text Mining [9]
- Bioinformatics [10]
- Ontology [11]
- Text Mining [12]

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automated reasoning in bioinformatics [16], description logics [17], ontological NLP [18], protein mutations [19], querying OWL-DL ontologies [20], Semantic Web [21], text mining [22] The biomedical literature is growing at an ever-increasing rate, which pronounces the need to support scientists with advanced, automated means of accessing knowledge. We investigate a novel approach employing description logics (DL)-based queries made to formal ontologies that have been created using the results of text mining full-text research papers. In this paradigm, an OWL-DL ontology becomes populated with instances detected through natural language processing (NLP). The generated ontology can be queried by biologists using DL reasoners or integrated into bioinformatics workflows for further automated analyses. We demonstrate the feasibility of this approach with a system targeting the protein mutation literature.

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- [14] https://www.semanticsoftware.info/biblio/author/30
- [15] https://www.semanticsoftware.info/biblio/author/16
- [16] https://www.semanticsoftware.info/biblio/keyword/50
- [17] https://www.semanticsoftware.info/biblio/keyword/52
- [18] https://www.semanticsoftware.info/biblio/keyword/48
- [19] https://www.semanticsoftware.info/biblio/keyword/49
- [20] https://www.semanticsoftware.info/biblio/keyword/51
- [21] https://www.semanticsoftware.info/biblio/keyword/2
- [22] https://www.semanticsoftware.info/biblio/keyword/19
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