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| Author Samuel Lampa | | |
| Title (English) SWI-Prolog as a Semantic Web Tool for semantic querying in Bioclipse: Integration and performance benchmarking | | |
| Abstract <p>The huge amounts of data produced in high-throughput techniques in the life sciences and the need for integration of heterogeneous data from disparate sources in new fields such as Systems Biology and translational drug development, require better approaches to data integration. The semantic web is anticipated to provide solutions through new formats for knowledge representation and management. Software libraries for semantic web formats are becoming mature, but there exist multiple tools based on foundationally different technologies. SWI-Prolog, a tool with semantic web support, was integrated into the Bioclipse bio- and cheminformatics workbench software and evaluated in terms of performance against non-Prolog-based semantic web tools in Bioclipse, Jena and Pellet, for querying a data set consisting of mostly numerical, NMR shift values, in the semantic web format RDF. The integration has given access to the convenience of the Prolog language for working with semantic data and defining data management workflows in Bioclipse. The performance comparison shows that SWI-Prolog is superior in terms of performance over Jena and Pellet for this specific dataset and suggests Prolog-based tools as interesting for further evaluations.</p> | | |
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