Title: Integrating Pathway knowledge using Semantic Web technologies

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Abstract:

Pathway knowledge bases have proliferated to the point where it is essential to stop thinking about them in isolation. There is a need to develop methodologies that allow rigorous evaluation of the quality of knowledge bases, enable the evaluation of their relative strengths and that offer the most effective way to combine them in order to gain insights about how biological processes work. In our previous work, we have developed methods to proofread a single knowledge base in isolation in order to determine its suitability to support computer-aided information integration and inference[1][2]. We believe that additional proofreading power and effective computer-aided reasoning can be gained from combining multiple knowledge bases.

The emergence and adoption of Biological Pathways Exchange (BioPAX), an OWL based format for exchanging pathway information, provides a unique opportunity to integrate knowledge from multiple pathway databases using Semantic Web technologies. We describe a case study integrating multiple pathway databases using BioPAX[3]. We then report on our current work aimed at evaluating the ability of BioPAX in conjunction with SPARQL and SWRL: 1) to enable integrated querying of multiple knowledge bases, 2) to enable proofreading of multiple knowledge bases, and 3) to enable estimation of the degree of complementarity between knowledge bases.

[1] www.biomedcentral.com/1471-2105/7/196
[2] www.hybrow.org
[3] http://pkb.stanford.edu