## LitPathExplorer: A visual tool for exploring literature-enriched pathway models

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Pathway model curation is a time-consuming, knowledge-intensive task that is often guided by evidence from literature. In order to accelerate curation, a number of text mining-based efforts have sought to provide evidence from scientific literature by extracting information pertaining to biomedical relationships, e.g., protein-protein, drug-target interactions, automatically. Currently, most tools for visualising pathway model reconstructions neither make such literature-based evidence easily accessible to their users, nor do they provide a means for confidence-driven filtering of textmined interactions. Thus, they often require users to cross-reference external literature sources, consolidate evidence passages, and subsequently assess on their own, the reliability of automatically mined interactions. To address these issues, we developed LitPathExplorer, a tool that provides richer visualisation and exploration of reconstructions by integrating literature-based evidence, thus allowing curators to easily frame a pathway interaction in the context of the source statements they were based on. The tool builds upon the JavaScript-based D3 library and accepts any BioPAX-formatted pathway model. Interactions contained in the model are enriched with literature-derived information, based on the output of our text mining workflows which also provide a consolidated confidence value. The enriched model is displayed as a graph where nodes that correspond to biomolecular events, e.g., phosphorylation, are connected to other nodes representing entities participating in such events, e.g., proteins and small molecules. A key feature of LitPathExplorer is its support for visual exploration and flexible querying. This allows users to filter pathway interactions by specifying event attributes that are of interest to them, or by setting a threshold for literature-based confidence values. By enabling users to focus on interactions with more compelling evidence, the tool aids biologists in identifying interactions to prioritise in their experiments. To facilitate interoperability with other modelling standards, e.g., SBML, we are currently wrapping LitPathExplorer as a Garuda gadget.