BioKC: a platform for quality controlled curation and annotation of systems biology models

Carlos Vega

Luxembourg Centre for Systems Biomedicine, Esch-sur-Alzette, Luxembourg

Standardisation of biomedical knowledge into systems biology models is essential for the study of the biological function. However, biomedical knowledge curation is a laborious manual process aggravated by the ever increasing growth of biomedical literature. High quality curation currently relies on pathway databases where outsider participation is minimal.

The increasing demand of systems biology knowledge presents new challenges regarding curation, calling for new collaborative functionalities to improve quality control of the review process. These features are missing in the current systems biology environment, whose tools are not well suited for an open community-based model curation workflow. On one hand, diagram editors such as CellDesigner or Newt provide limited annotation features. On the other hand, most popular text annotations tools are not aimed to biomedical text annotation or model curation. Detaching the model curation and annotation tasks from diagram editing improves model iteration and centralizes the annotation of such models with supporting evidence.

In this vain, we present BioKC, a web-based platform for systematic quality-controlled collaborative curation and annotation of biomedical knowledge following the standard data model from Systems Biology Markup Language.

References and useful links
http://biokb.lcsb.uni.lu/