

## **Community curation on WikiPathways; how we assist knowledge collection**

Chris Evelo

Biologists typically use knowledge represented as pathways to better understand the results of genomics experiments. Through integration of data from different omics techniques with what we already know, statistical evaluation and subsequent data visualization the results often start to make sense. An important problem is that we often do not have the relevant pathways, or they may be incomplete or not suitable for usage by analytical tools. WikiPathways is meant to be an answer to the problems described above. It uses Mediawiki technology and dedicated open source Java code to allow biologists to edit pathway content on the web. We assist this process through the development of helpful software like a Diff tool, Go and KEGG converters, portal mechanism, webservice and pathway extension through automated suggestions.