Reviewer's report

Title: Mimoza: Web-Based Semantic Zooming and Navigation in Metabolic Networks

Version:1**Date:**4 September 2014

Reviewer number:1

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Major Compulsory Revisions

The work of Zhukova et al. covers the visualisation of large-scale metabolic networks. It is clear that this is very necessary for both the development of such models and for the interpretation of their simulations. The manuscript is clear, the software appears to be well implemented, and the approach of zooming down into the network (a la Google Maps) is a good idea. However, there are issues with the work highlighted below, specifically questions regarding the real-world use of the system.

The examples given on both the website and in the paper are of very small sub-networks of larger models, focussing on the peroxisome, containing ~100 reactions. When attempting to view a larger sub-network, such as the cytoplasm of a typical genome-scale metabolic reconstruction (Yeast 5 - see http://mimoza.bordeaux.inria.fr/yeast4/comp.html?id=C_1), the system hung and then crashed. Could the Authors please comment on the system's suitability for genuinely sized models?

Could the Authors please comment on the performance of the system for unannotated models? These are, unfortunately, far more commonly encountered in practice. How well does the system perform in the absence of molecular annotations that typically require manual addition / editing?

The example given on the website and in the manuscript is of beta-oxidation, which is a special case, given that it involves the breaking down of a specific class of molecule (fatty acids) that undergo several, repeated steps. It is therefore a good exemplar for this work. However, how would the system work for other classes of molecules? The ChEBI ontology would suggest that sugars form a single class of molecules, but their metabolic reactions can be very different; similarly amino acids. How does Mimoza deal with these classes of molecules that, while sharing an ancestor in the ChEBI ontology, undergo different metabolic reactions?

In general, it is hard to determine a use case for the software, and also to determine whom the target user base for the software is. The manuscript is very short and focuses heavily in technical issues (such as JSON formats), which will be of little interest for much of the readership. What is missing from the paper is a concrete example of how Mimoza can be used to perform a necessary task in the

construction or curation of large-scale models, or in the interpretation of their results, that cannot currently be easily performed. In summary, what real-world problem is Mimoza attempting to solve?

Level of interest: An article of limited interest

Quality of written English: Acceptable

Statistical review: No, the manuscript does not need to be seen by a statistician.