Reviewer's report

**Title:** Multilevel layout algorithm for biological network visualization

**Version:** 1  **Date:** 21 December 2011

**Reviewer:** Marylyn Ritchie

**Reviewer's report:**

This is a very interesting paper. Biological networks have become a very popular approach to looking at complex datasets. It is often very challenging to create and interpret these network diagrams, and the visualization of the networks is paramount to their utility in the field. So this work is timely and important.

**Minor Essential Revisions**

It is clear that because of the random initialization, this approach is sensitive to initial parameters, and the authors indicate that the resulting network will be different in multiple runs. What is not clear is the degree of difference. Are the resulting networks permutations of the same linkages and hubs; or are the resulting networks dramatically different? It would be helpful to provide some more detail on the degree of difference.

Figure 2 is helpful in seeing a quantitative difference in the different methods, however, the generation of the provided p-values is lacking. What statistics were used to generate these comparisons?

Because there are no space limitations, I think it would be really helpful if the authors could take one of their example datasets and show the resulting networks from each of the methods. That would allow readers to better understand the differences and perhaps take away the increased benefit of the MLL-C approach.

**Level of interest:** An article of importance in its field

**Quality of written English:** Acceptable

**Statistical review:** Yes, and I have assessed the statistics in my report.

**Declaration of competing interests:**

I declare that I have no competing interests.