

**Recommendations:****05 Jul 2013****Recommended**[Follow](#)**Technical Advance**

This paper describes a useful tool that implements a message-passing model for refining biological networks using data from many different sources.

Biological networks, in this context, particularly regulatory networks, are difficult to construct accurately from single datasets, but combining data from multiple sources can improve the accuracy of the networks. In this paper, PANDA (Passing Attributes between Networks for Data Assimilation) was developed, which models network communication using message passing. It uses agreement between different data sources to refine and improve networks and, in their evaluation, the tool was able to recover the correct edges in simulated network data. The authors applied PANDA to yeast data, where they found an improvement over other methods and were able to show plausible biological networks for the specific conditions. Tools such as PANDA are needed in the field of biological networks, where models based on individual datasets tend to have inaccuracies.

**Disclosures**

None declared

[Add Comment](#)

No comments yet.

**Comments:****Abstract:**

Regulatory network reconstruction is a fundamental problem in computational biology. There are significant limitations to such reconstruction using individual datasets, and increasingly people attempt to construct networks using multiple, independent datasets obtained from complementary sources, but methods for this integration are lacking. We developed PANDA (Passing Attributes between Networks for Data Assimilation), a message-passing model using multiple sources of information to predict regulatory relationships, and used it to integrate protein-protein interaction, gene expression, and sequence motif data to reconstruct genome-wide, condition-specific regulatory networks in yeast as a model. The resulting networks were not only more accurate than those produced using individual data sets and other existing methods, but they also captured information regarding specific biological mechanisms and pathways that were missed using other methodologies. PANDA is scalable to higher eukaryotes, applicable to specific tissue or cell type data and conceptually generalizable to include a variety of regulatory, interaction, expression, and other genome-scale data. An implementation of the PANDA algorithm is available at [www.sourceforge.net/projects/panda-net](http://www.sourceforge.net/projects/panda-net).

**DOI:** [10.1371/journal.pone.0064832](https://doi.org/10.1371/journal.pone.0064832)**PMID:** [23741402](#)

Abstract courtesy of PubMed: A service of the National Library of Medicine and the National Institutes of Health.