Aligning Biological Networks

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Abstract

Molecular biologists are gradually assembling the structures and constituents of numerous biological networks. These networks represent interactions that take place within a living organism between proteins, basic compounds, and other important biological molecules. Biologists increasingly rely on software tools for analysing such biological data. In this poster, we present a new algorithm for aligning two given biological networks (Fig. 1).

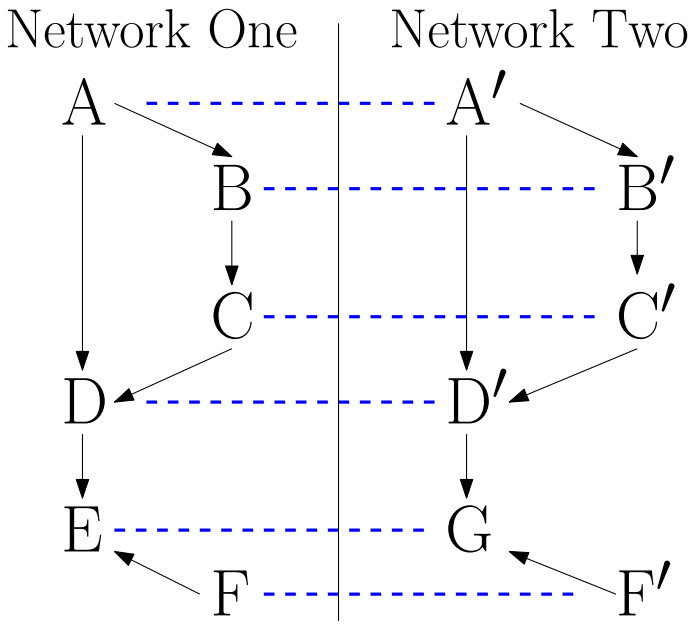

Figure 1: An alignment of two networks. Biological molecules at primed nodes are very similar to the corresponding unprimed node. Nodes E and G are aligned because of neighbourhood similarity.

Alignments of networks expose conserved subnetworks, which in turn can reveal how the networks evolved, as well as provide insight into the evolutionary relationships between their source organisms. Many algorithms exist for aligning biological sequences and molecular structures, but there are relatively few alignment algorithms available for biological networks. This algorithm has been specialised to align two metabolic, signaling, or regulatory networks.

The alignment is produced through a matching of the most similar nodes from the two networks, with the similarity measure based on comparison of the biological molecules at the nodes being compared, as well as the local network around those nodes, referred to as their neighbourhoods. The project explored many different definitions of a node's neighbourhood, as well as ways of combining information about a neighbourhood to form a similarity value. The preliminary results of this exploration show that the complete algorithm performs much better than matching based on node sequence similarity alone for aligning both metabolic and signaling networks.