

POSTER PRESENTATION

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The evolutionary dynamics of protein networks

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From Beyond the Genome: The true gene count, human evolution and disease genomics
Boston, MA, USA. 11-13 October 2010

Background

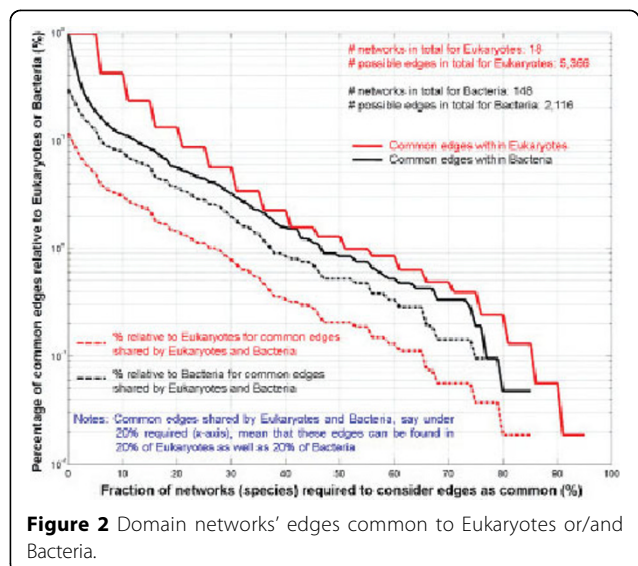
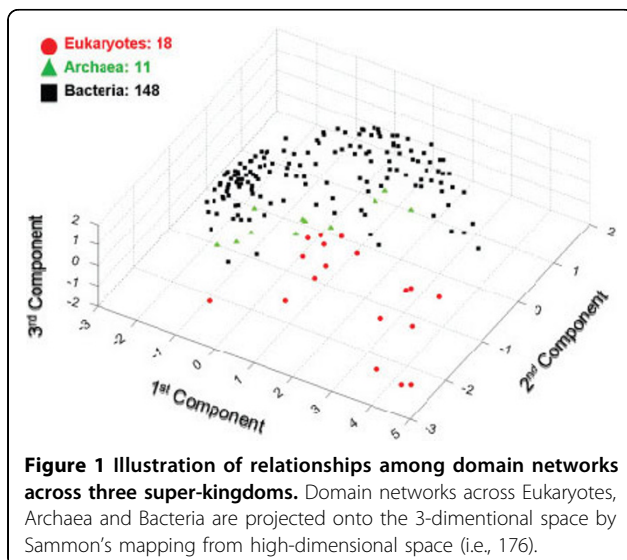
Although the accumulation of protein network data in a wide range of species provides a rich resource for understanding network evolution, exploiting such resources remains challenging. Difficulty in defining orthologous relationships and the noisy and incomplete nature of protein network data [1] are both major obstacles. To overcome the first, we took a domain-based view of the proteome, with domains of known (3D) structure as nodes in the network. This not only provides a structural basis for the interactions, but simplifies the question of orthology. The second is mitigated by an FDR-based statistical inference of the underlying protein domain network from multiple domain interactions between all proteins in the genome. Thus the negative influence of noisy interactions is reduced. The comparisons of these domain networks are also less susceptible to low coverage of networks, especially in less-studied species.

Materials and methods

Accordingly, here we present a statistical inference of domain networks from multiple sources of protein interaction data taken from STRING [2], combined with domain compositions of proteins from SUPERFAMILY [3] across hundreds of species. This is followed by an intersection analysis for comparing domain networks between any two species using a third as reference (thus accounting for differences in coverage).

Results

We have established the first comprehensive database of species-specific domain networks, which we use for exploring evolutionary dynamics at the network level. Figure 1 shows the power of our approach in extracting novel independent and unbiased evolutionary relationships between organisms from three super-kingdoms. We have shown that surprisingly there is little core to the network, revealed by examining common edges shared by Eukaryotes or/and Bacteria (Figure 2). This



implies that network evolution, unlike protein evolution, is largely the result of species-specific specialisation.

Conclusions

Exploring the dynamics of domain interactions across many organisms is leading us to an understanding of the evolution of molecular networks: how they have changed over history, how changes correlate with functional categories and how the fundamental nature of network evolution varies between different parts of the tree of life.

Acknowledgements

This work was supported by BBSRC grant BB/G022771/1.

Published: 11 October 2010

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doi:10.1186/gb-2010-11-S1-P12

Cite this article as: Fang and Gough: The evolutionary dynamics of protein networks. *Genome Biology* 2010 **11**(Suppl 1):P12.

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