

Poster C-28

Modeling the evolution of gene and protein interactions



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Short Abstract: Current protein network analyses either use abstract evolutionary models lacking gene context, or model current-day protein interactions without a dynamic evolutionary component. We present a generalizable method for evolving an organism's putative ancestral protein interaction network to its current-day interactions. We compare evolutionary parameters and topology of distinct protein families.

Long Abstract:

Graph-theoretic models ("networks") which use nodes to represent genes and links between the nodes to represent interactions provide valuable insight to our understanding of genetic network evolution [4,1]. However, such evolutionary models are decontextualized, theoretical constructs. Gene networks can be contextualized by mapping them to experimentally-derived protein interactions of model organisms. Although comparative analyses between organisms' gene and protein networks enables evolutionary inferences [3], they don't capture the dynamics of evolution present in their theoretical counterparts. We present a model which evolves the genetic network of an organism from a set of putative ancestral protein interactions to its current-day protein interaction network.

Our evolutionary model incorporates both gene and genome duplication events for gene birth, and loss of gene duplicates for gene death. Recently derived rates for the birth and death of paralogous *Arabidopsis thaliana* genes (the "paranome") [2] inform our model. Subfunctionalization and neofunctionalization are modeled as the gain and loss of interactions between genes. We use a duplication and divergence evolutionary model [4], modified to account for homodimers and genome duplication events is used.

This evolving genetic network model of *Arabidopsis thaliana* permits views of the entire evolving paranome as well as comparative topological analyses between functional subnetworks of genes. The evolving protein interaction networks and subnetworks can also be visualized as an animation of gene births and deaths accompanied by the gain and loss of interactions. The method is applied to *Arabidopsis thaliana* but is generalizable to other model organisms.

Bibliography

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