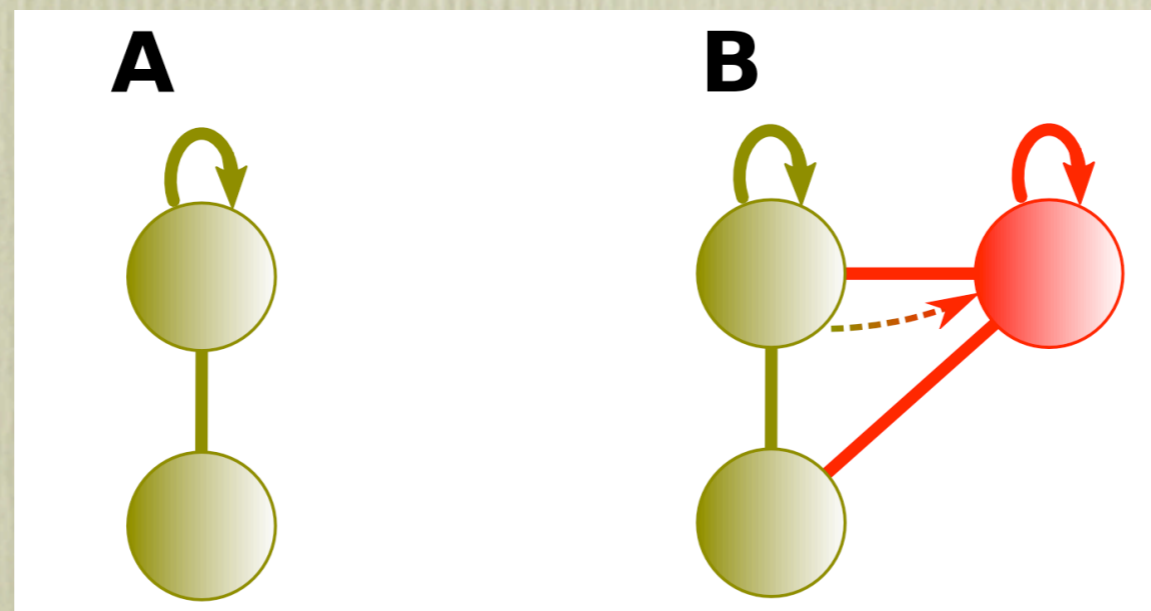
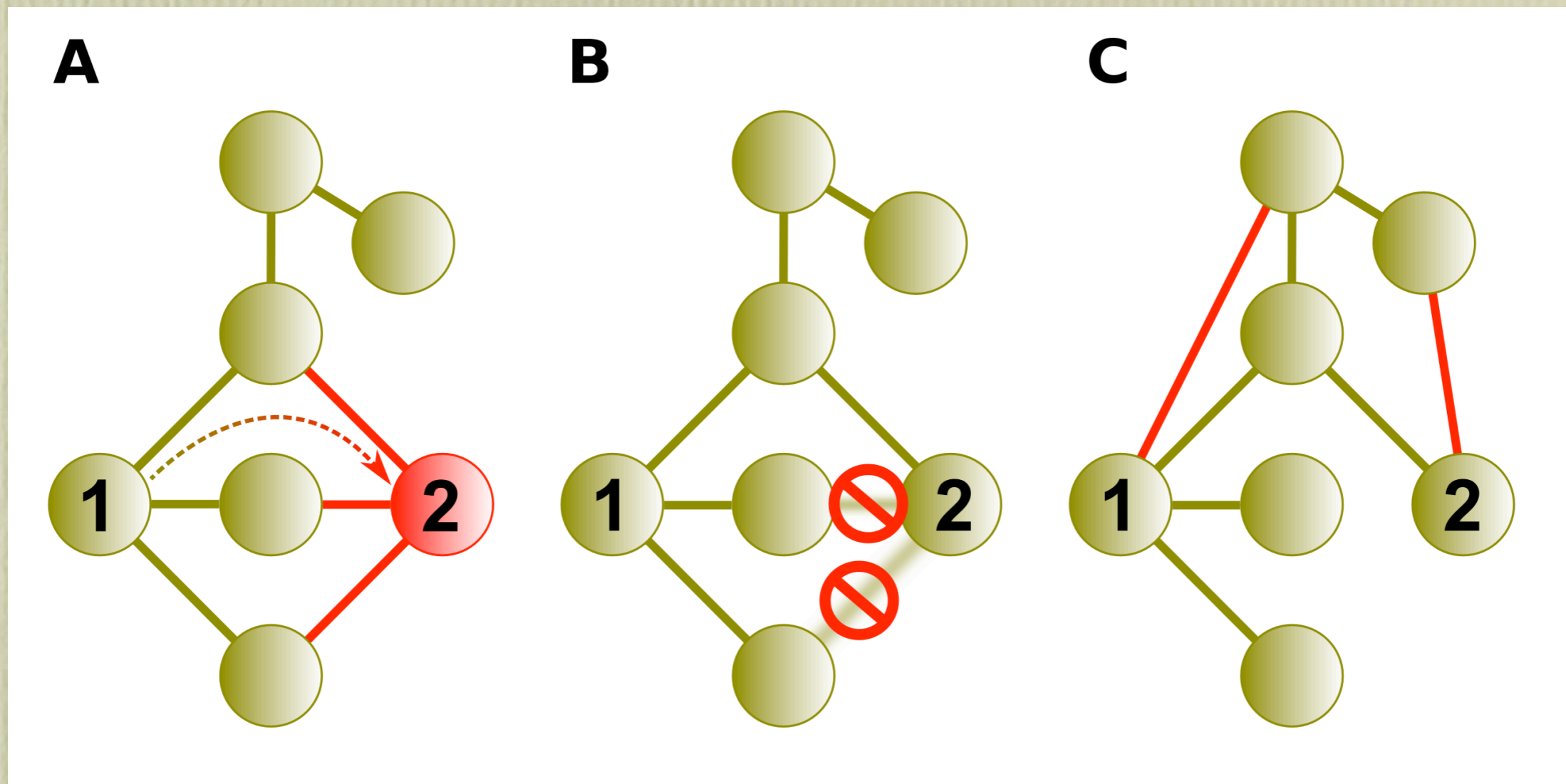


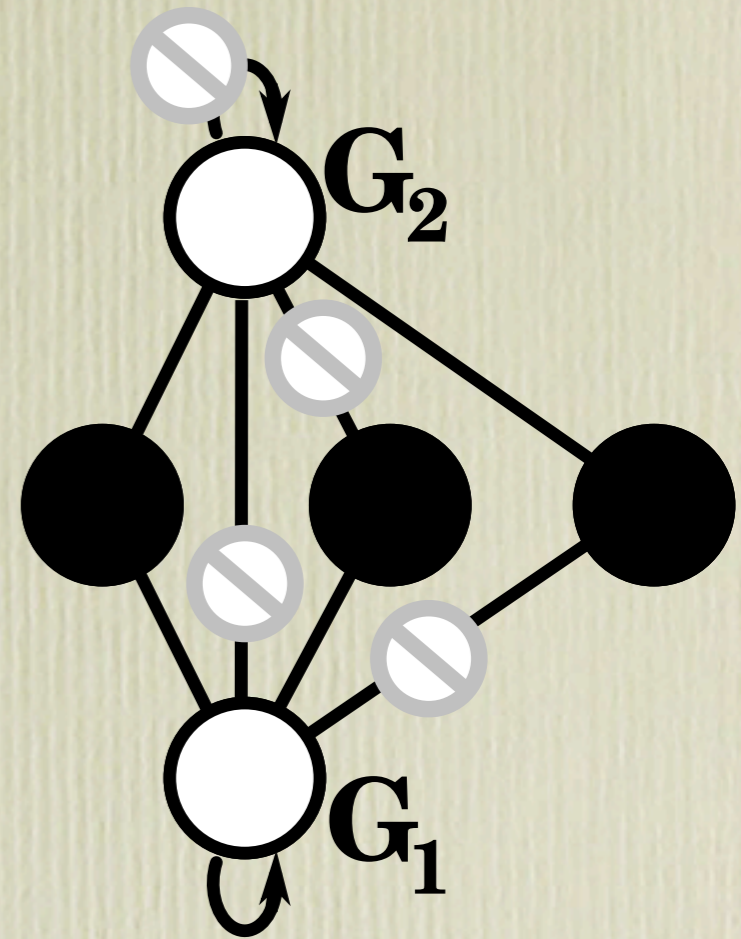
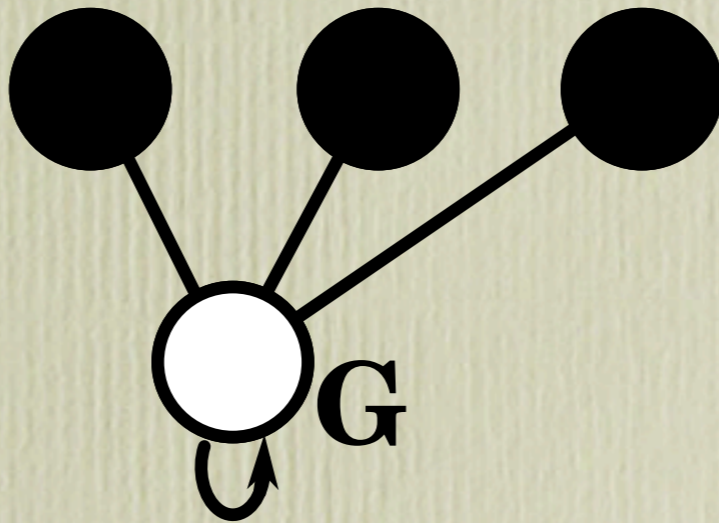
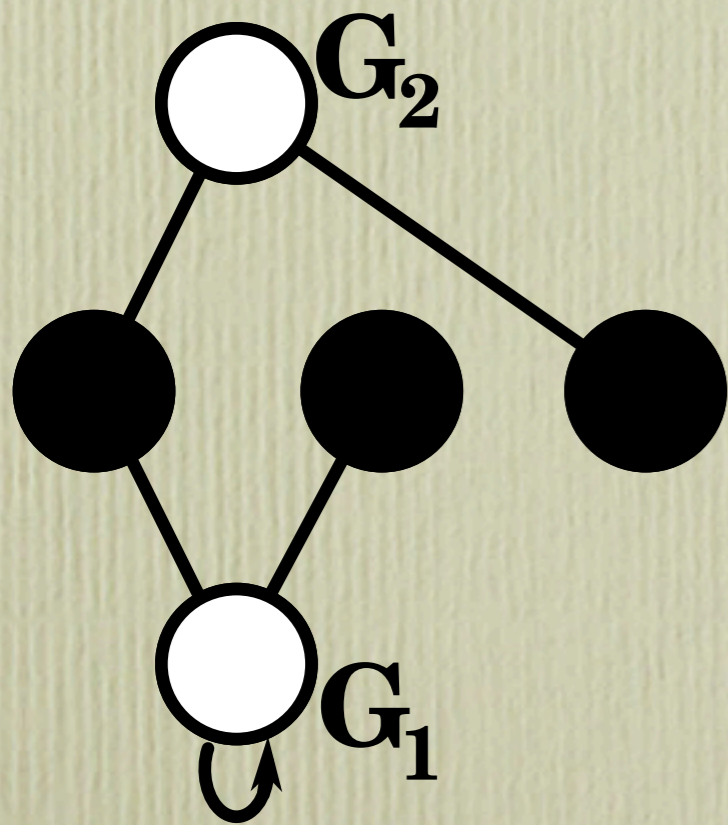
Reverse-engineering protein interaction network evolution

Todd A. Gibson
Debra S. Goldberg

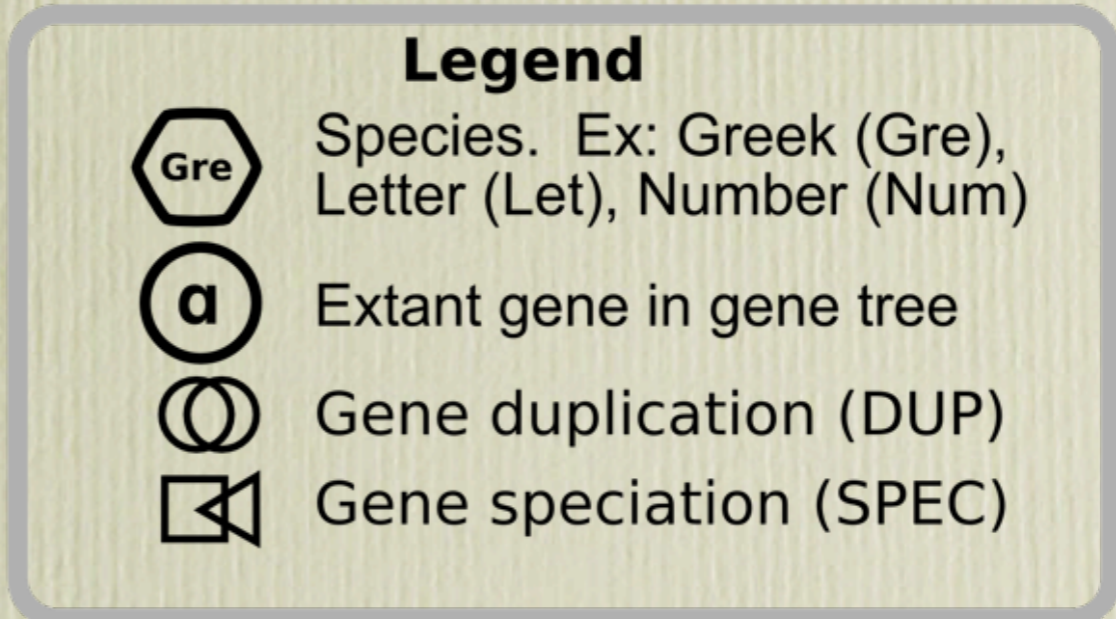
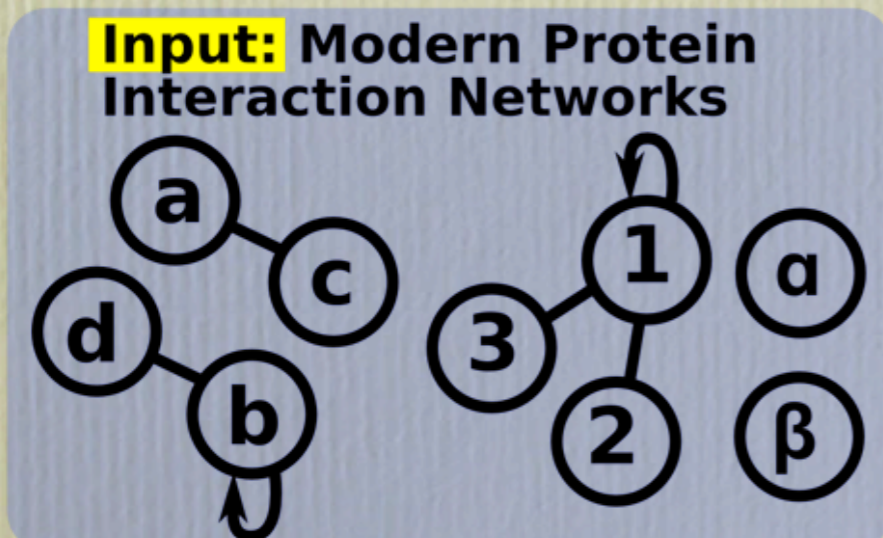
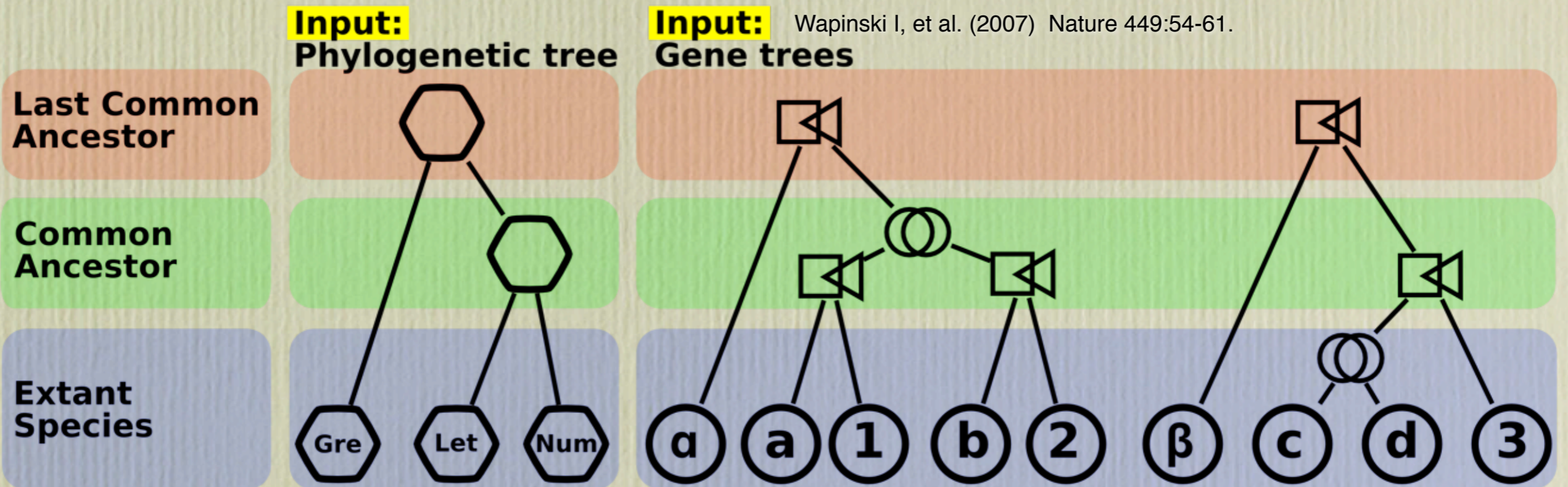
Gene duplication & link dynamics



Evolution: reverse and forward



Framework inputs



Tarassov K, et al. (2008) Science 320:1465-1470.

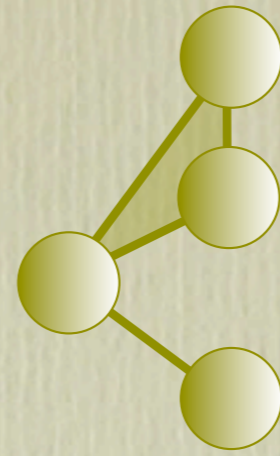
Batada N N, et al. (2007) PLoS Biol 5:e154.

Framework characteristics

- Network may be comprised of protein interactions from multiple organisms.
 - Increased coverage of ancestral network
- Protein interaction networks may be calculated for species without interaction data.
 - Novel derivation: Last Common Ancestor rather than sequence homology exclusively

$$C = \frac{3T}{\Gamma}$$

C Clustering Coefficient
 T Number of triangles
 Γ Number of connected triples



$$\frac{3(1)}{5} = 0.6$$

