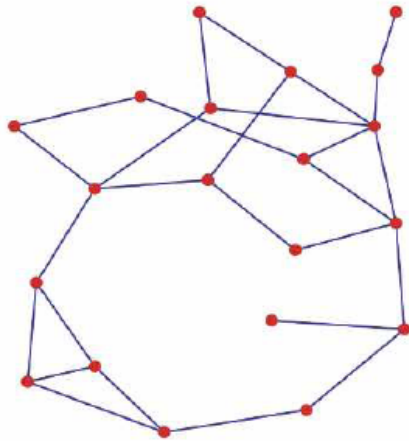


Evolutionary analysis of protein interactions provides insights into the origins of network topology

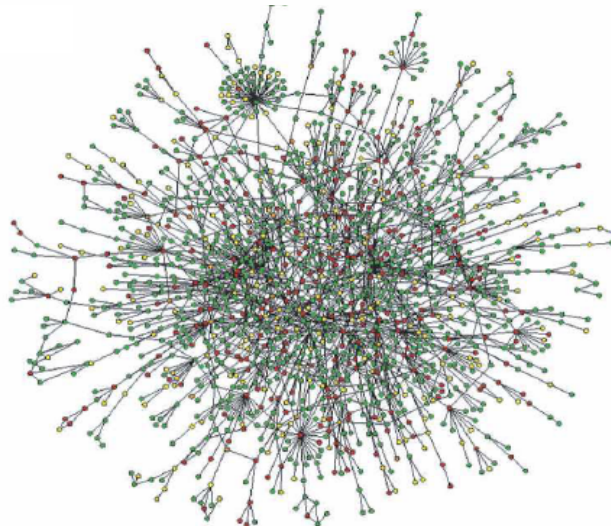
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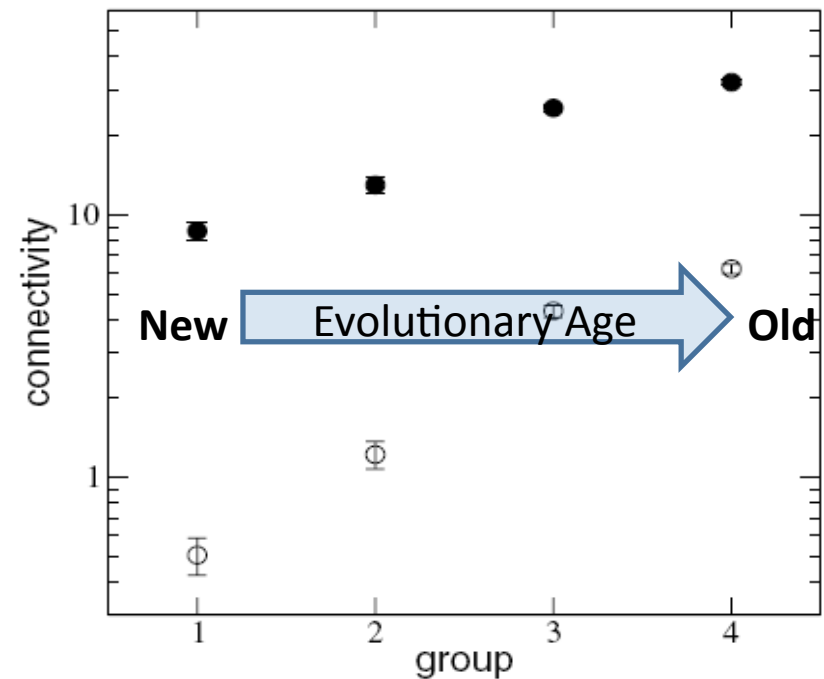
A random network



A scale free network consists of small numbers of 'HUBS' highly connected proteins

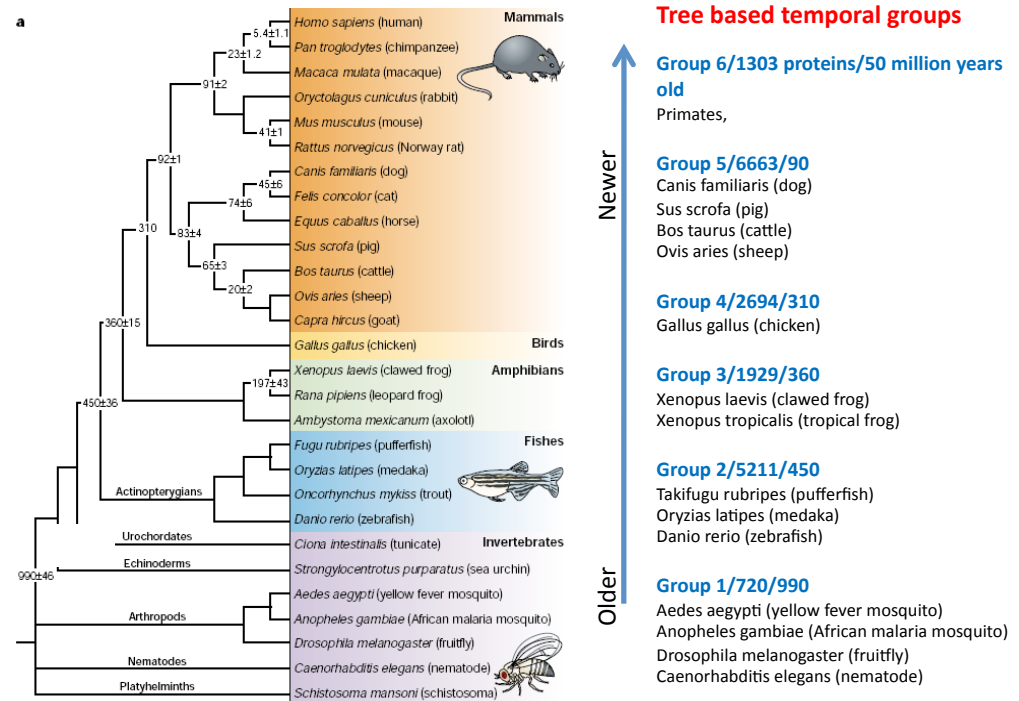


The so-called preferential attachment model suggests that newly evolved proteins evolve to bind more ancient hub proteins



- Human protein interaction data was aggregated from BioGrid, HPRD and Reactome
- Human genes and proteins were grouped into six ‘temporal groups’ based on the similarity to nucleotide sequence in several clades in the evolutionary tree
- In this study, the relationship between gene age and protein interaction network topology was elucidated

When multiple species are included per cluster, do we find that ancient human proteins are more likely to be hubs and does the network support a preferential attachment model?



As expected, more ancient proteins tend to be more highly connected

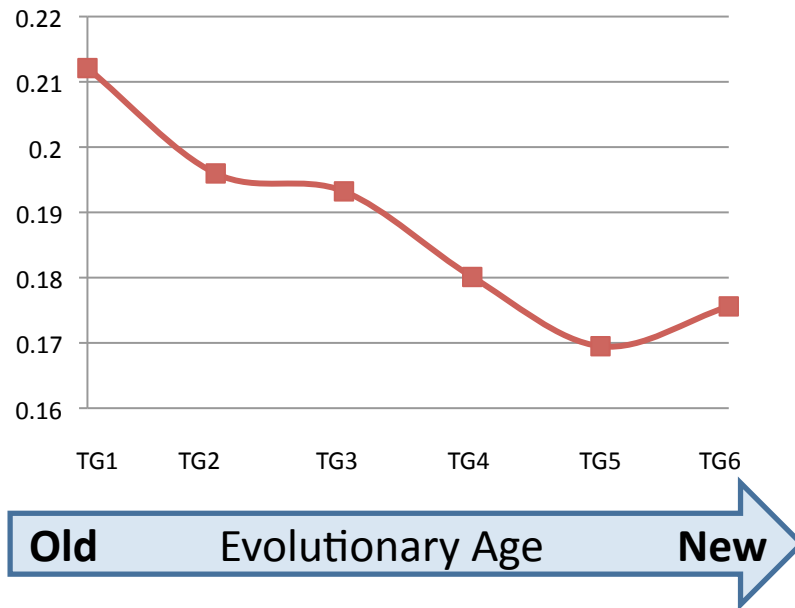
Temporal Group (TG)	Degree
1 (Oldest)	29.509
2	17.399
3	13.100
4	10.061
5	8.623
6 (Newest)	3.434

However, pairwise interactions between proteins tend to be between proteins who are more close in age than would be expected by chance

	Average Temporal Distance Between Partners	Average Temporal Distance Between Ancient Partners (TG≤4)
Actual	1.204	0.811
Permutation	1.594	0.935

Proteins are more likely to interact with partners of closer temporal groups. In a sense, we find that new proteins interact with new proteins.

The clustering coefficient of the network suggests more ancient proteins are more centralized



Interestingly, newer interacted proteins tend to be more tissue specific, when compared to gene expression data

Temporal Group	N	Expression Mean	Expression Coefficient of Variation
1 (Older)	506	9.123	11.761
2	3165	8.648	11.256
3	966	8.461	11.791
4	1149	8.303	12.325
5	2256	8.257	12.988
6 (Newer)	139	7.443	13.802
		P<0.001	P<0.001

Ancient proteins are more centralized (hubs) and new proteins are marginalized (leaves) and tend to be more tissue-specific.

- This work is highly preliminary
- We suggest that the preferential attachment model does not fully explain our findings of both tissue specificity and the finding that proteins tend to interact with proteins of a similar age
- On our poster more details are provided and we suggest a model to explain our observation

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