

# Assessing models of protein interaction network evolution

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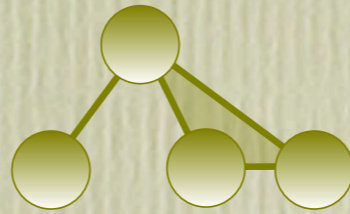
# Constraining Rollback

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

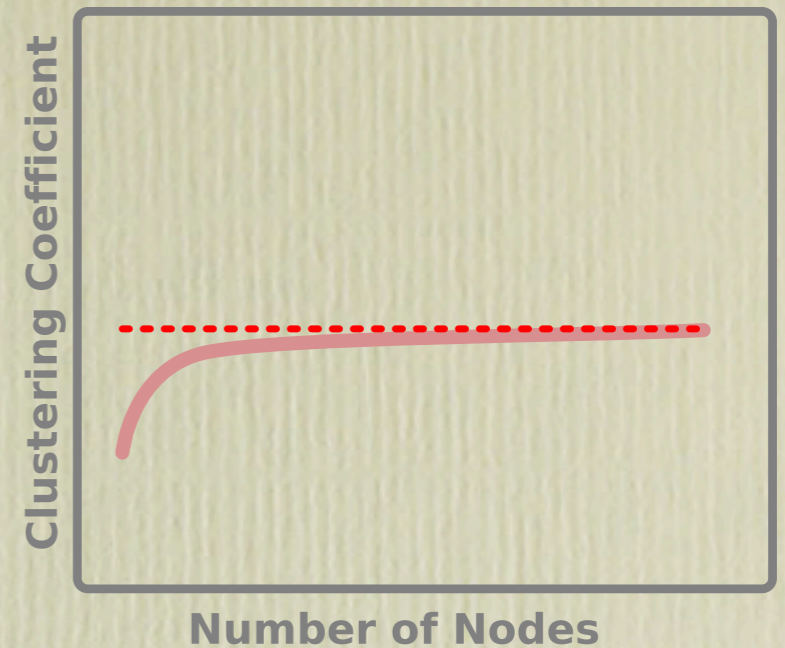
$C$  Clustering Coefficient

$T$  Number of triangles

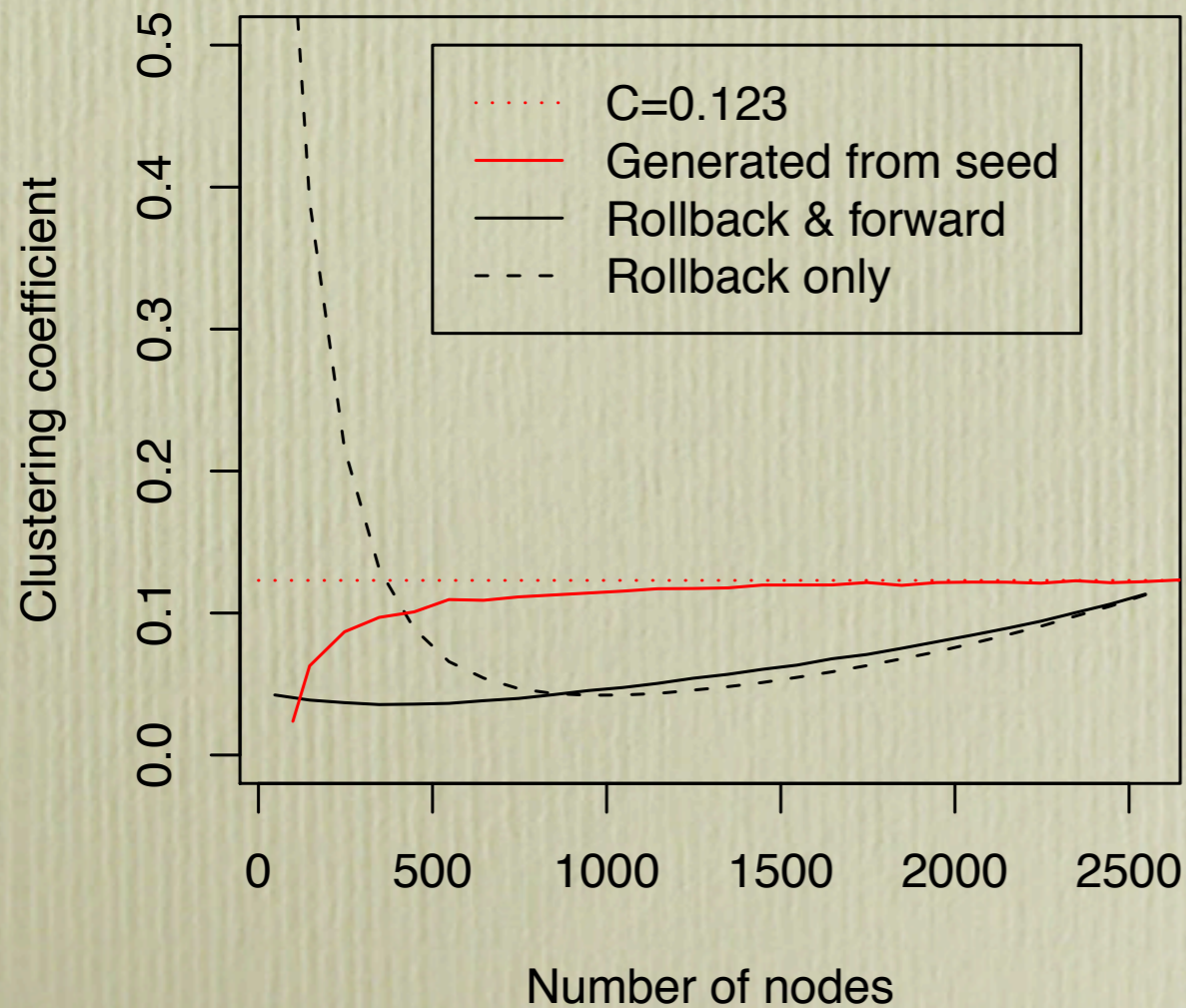
$\Gamma$  Number of connected triples



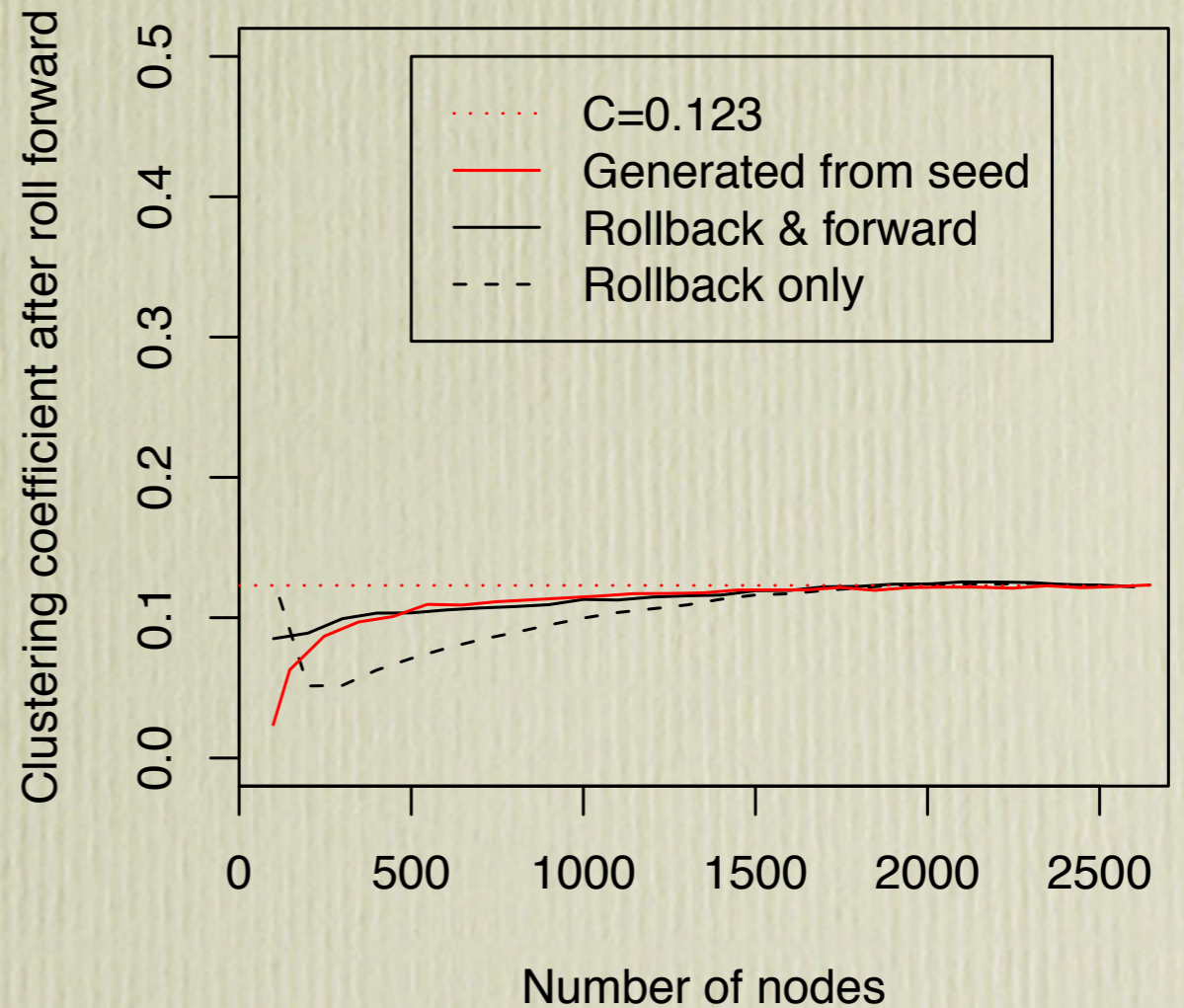
$$\frac{3(1)}{5} = 0.6$$



## Naive Pair Selection Rollback

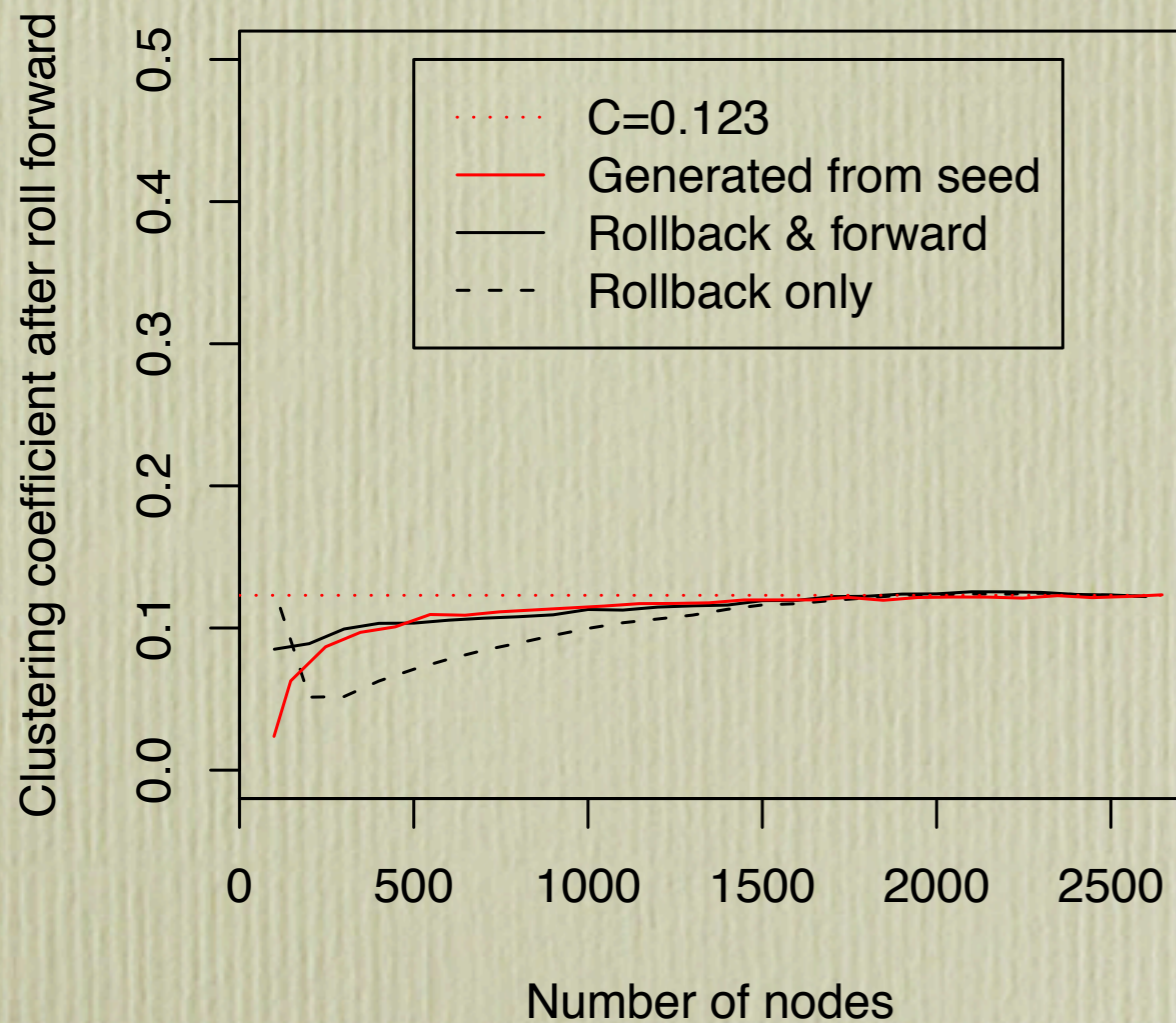


## Constrained using Observed Means

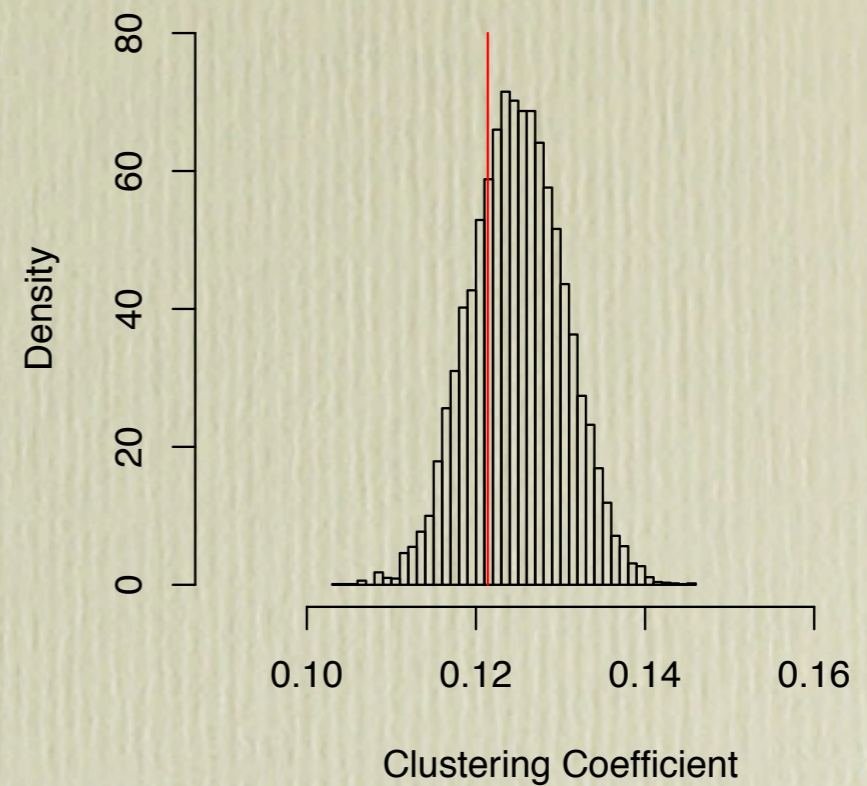


# Constraining Rollback

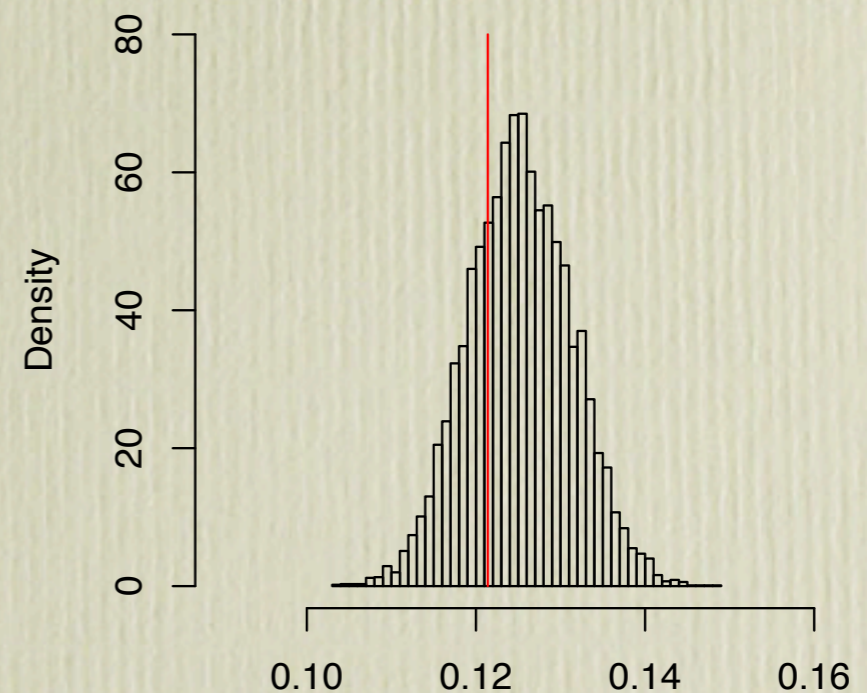
## Constrained using Observed Means



## Wind/Unwind Modified Vazquez, 298 nodes



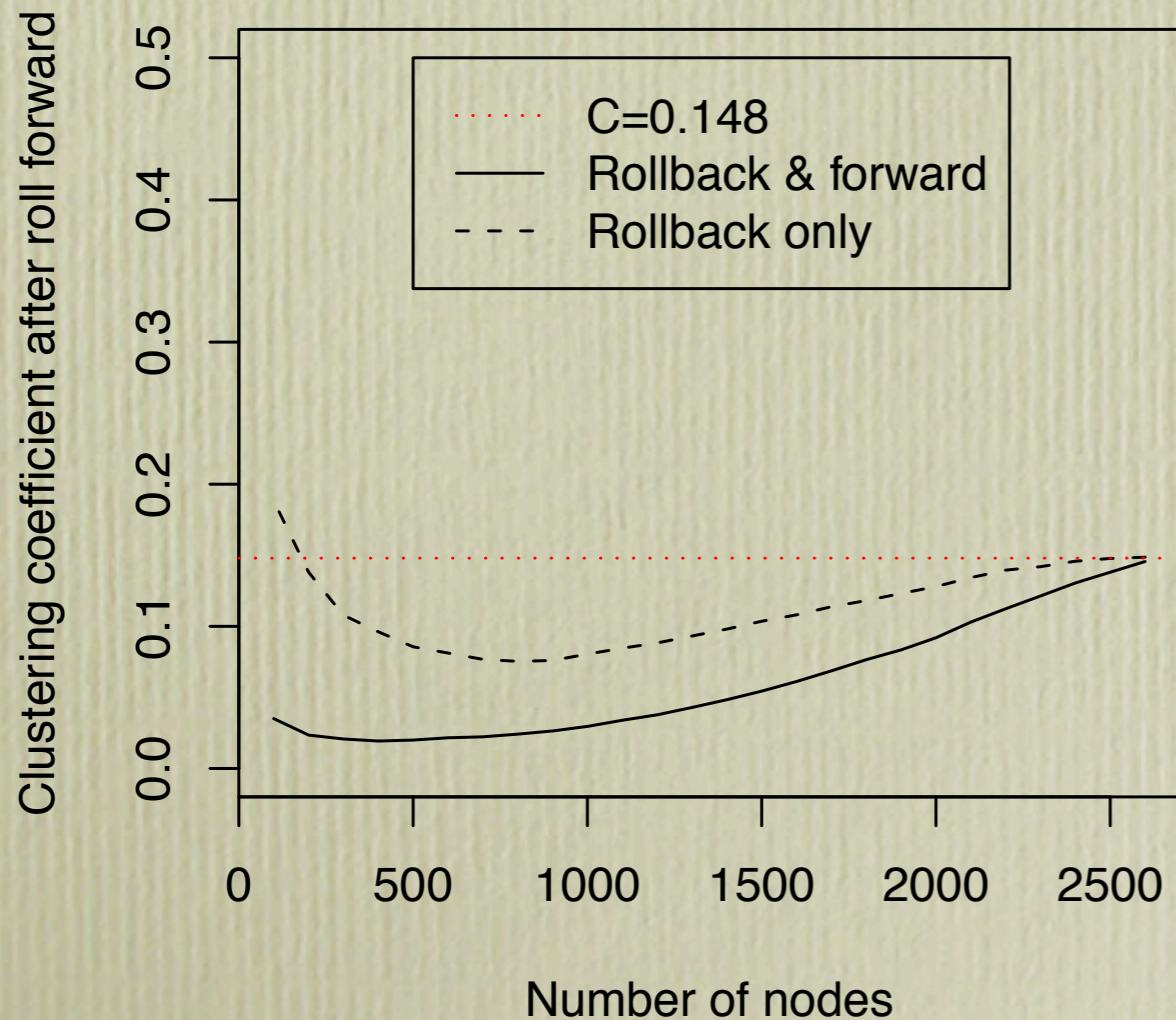
## Wind/Unwind Modified Vazquez, 398 nodes



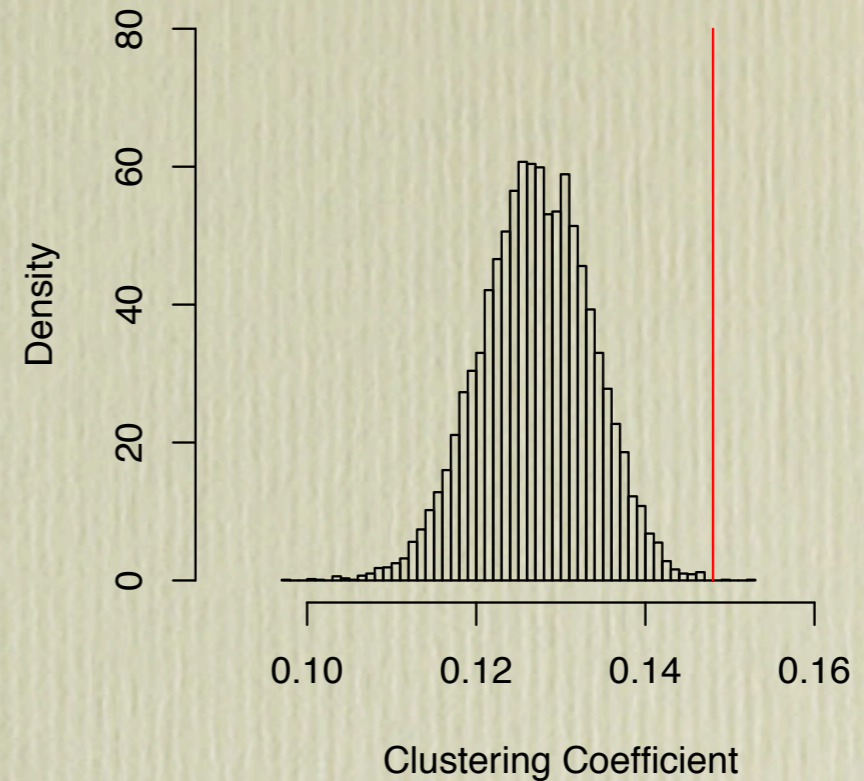
# Testing the null hypothesis

**Null hypothesis:**  
empirical data  
generated by the model

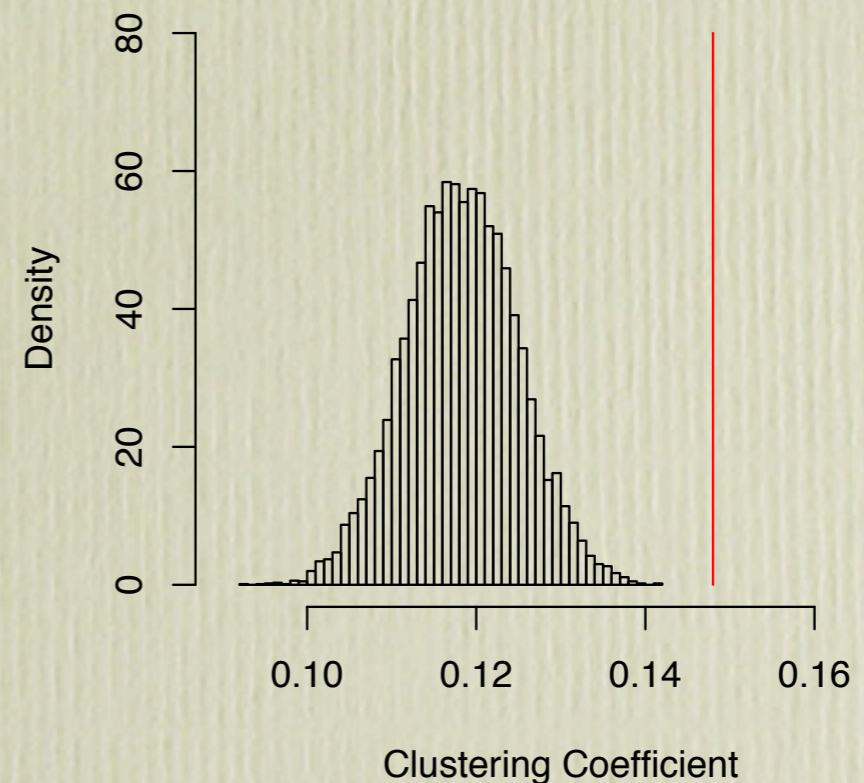
**Constrained using Observed Mean**  
Empirical interaction network



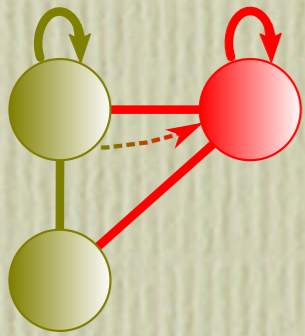
Wind/Unwind S. cer., 298 nodes



Wind/Unwind S. cer., 398 nodes



# Significance of Homomeric Duplications



Phylogenetic Timeperiod	Homo. Dups	Aggregate $\Delta C_{\text{pot}}$	P-value
2	16	0.0260	$1.1 \times 10^{-4}$
6	64	0.0650	$< 10^{-6}$

# Conclusion

- Null hypothesis rejection suggests that modified Vázquez, et al. model does not sufficiently reflect evolutionary mechanics of *Saccharomyces cerevisiae* interaction network.
- Duplication of highly clustered homomeric proteins has contributed to the high clustering in *Saccharomyces cerevisiae*.