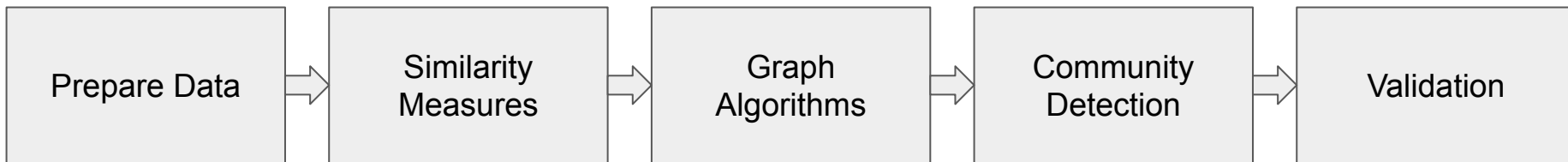


# Identifying Co-regulated Yeast Genes Using Graph-theoretic Methods

Rubin McLuen

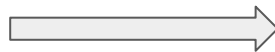
# Research Approach



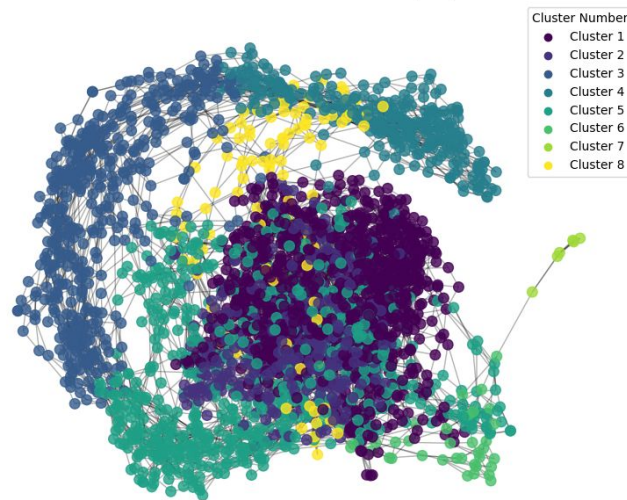
Conditions

	1	2	3
YAL001C	161	110	139
YAL002W	238	139	69
YAL003W	425	429	451

Genes

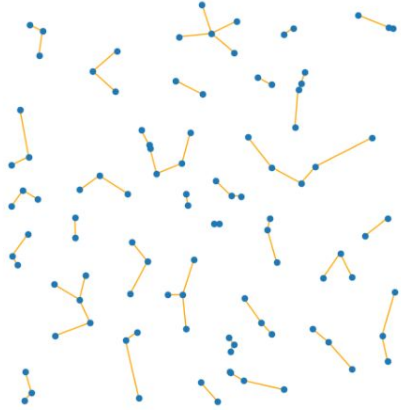


Euclidean Connected kNNG Clusters (k=8)

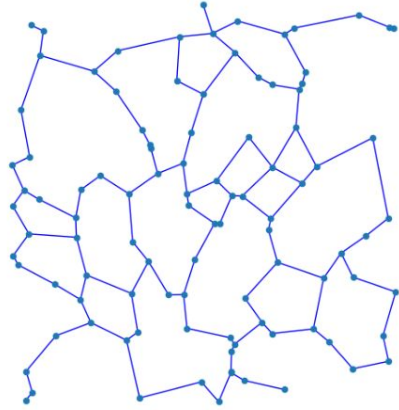


# Graph Algorithms

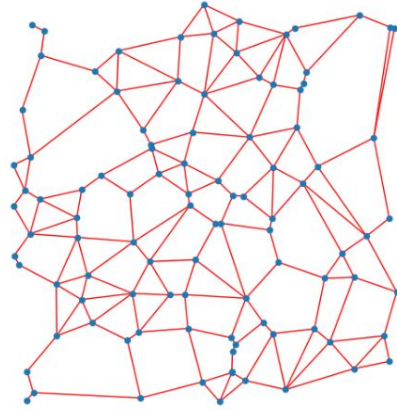
NNG (Nearest Neighbor Graph)



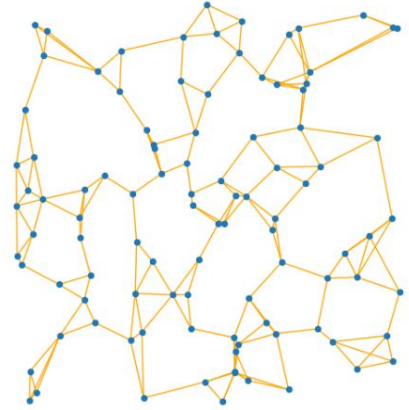
RNG (Relative Neighbor Graph)



GG (Gabriel Graph)

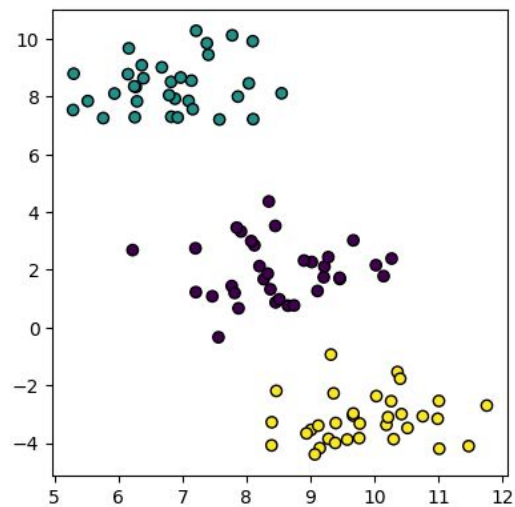


Connected k-NNG

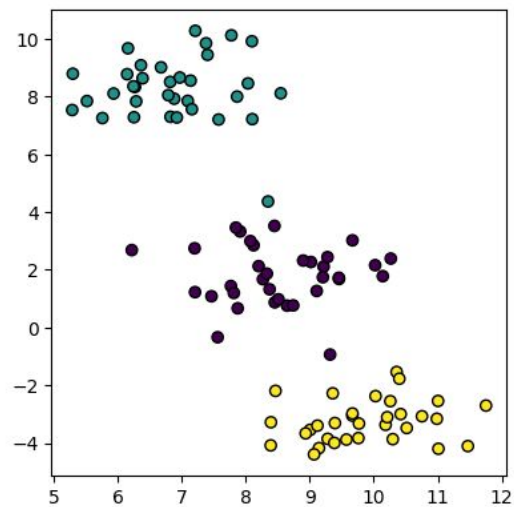


Neighborhood Graphs On 100 Random Points

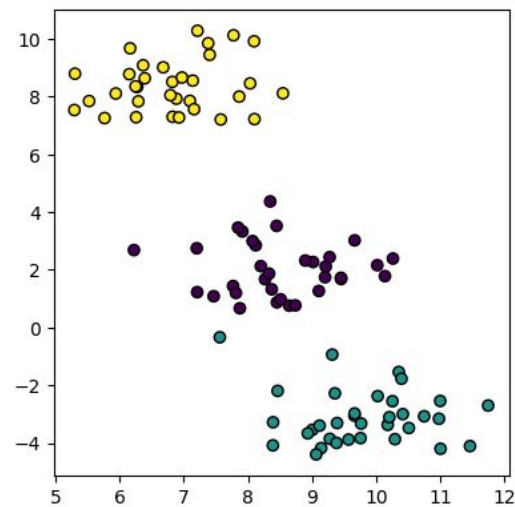
RNG Clusters



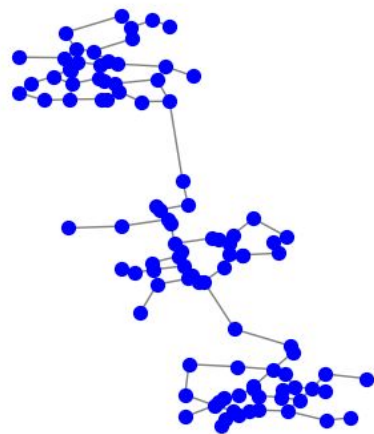
GG Clusters



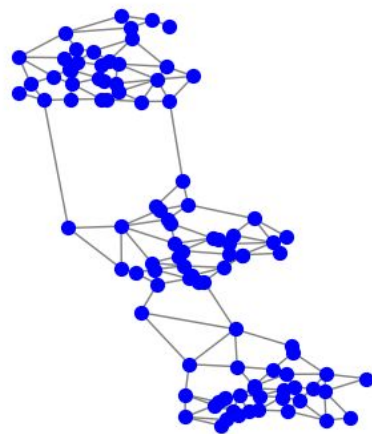
connected kNNG Clusters



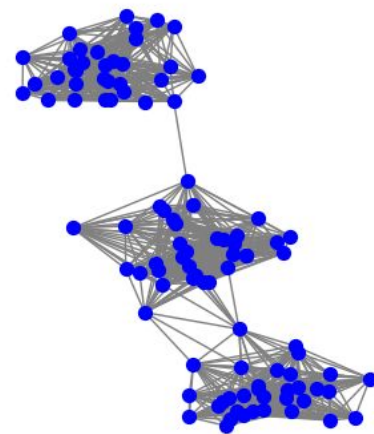
RNG



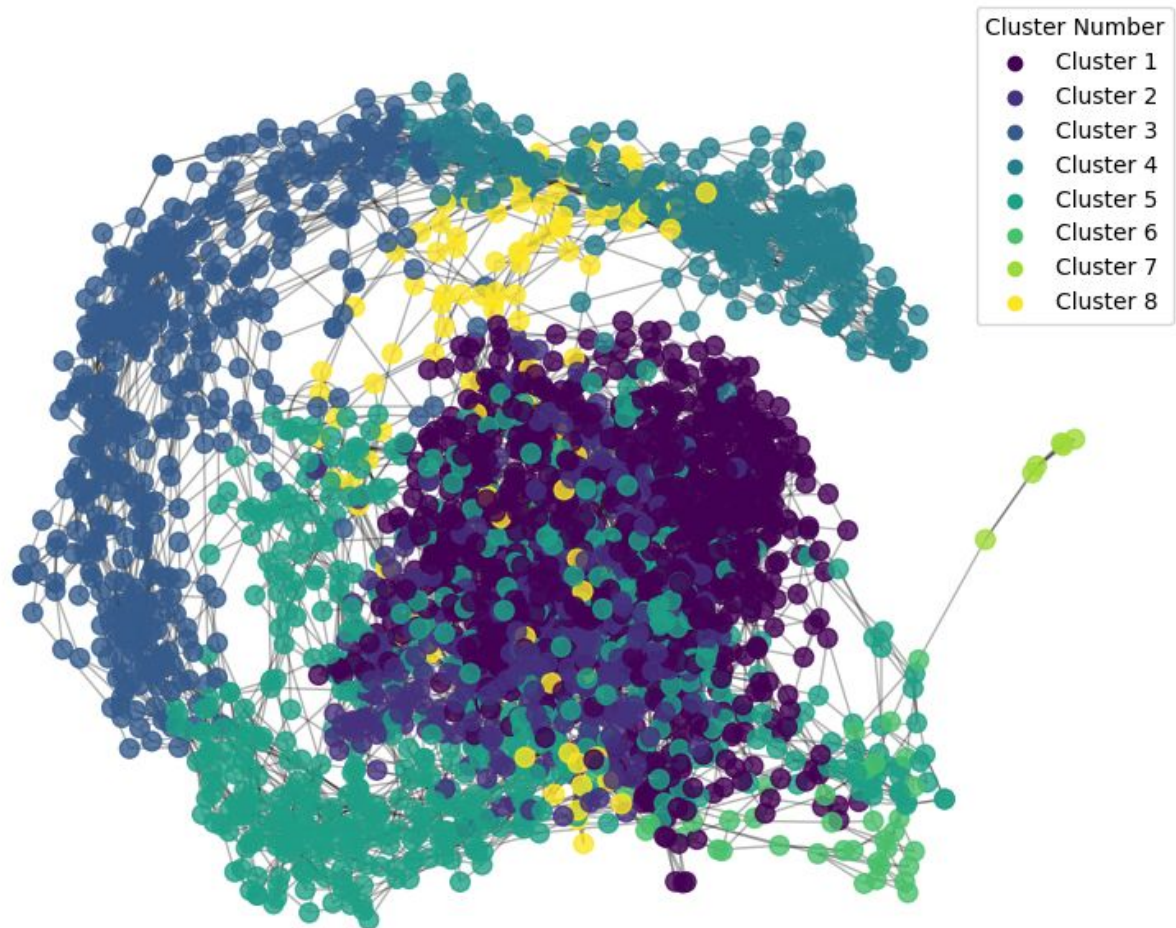
GG



connected kNNG

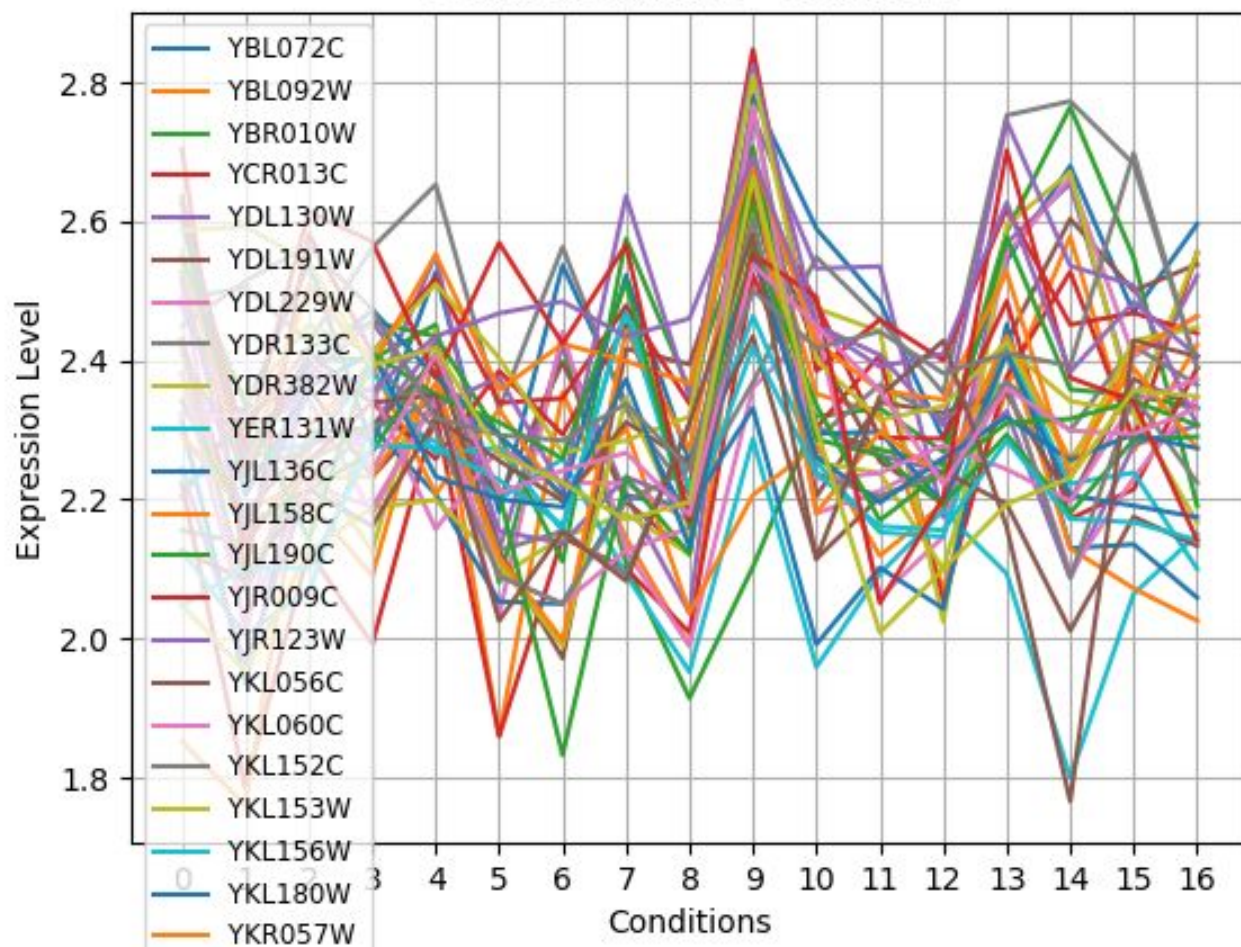


Euclidean Connected kNNG Clusters (k=8)





Connected kNNG - Cluster 5



Euclidean - FOM Across Different Graph Types

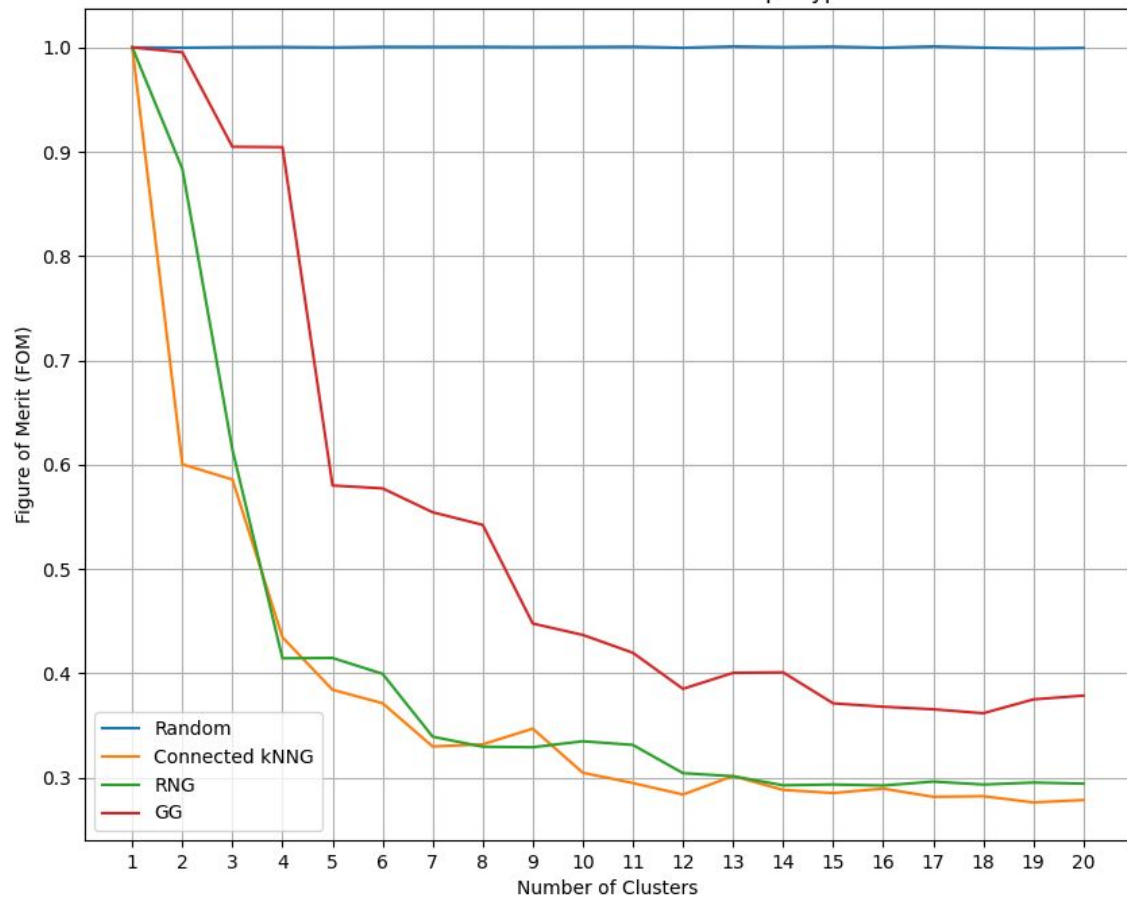
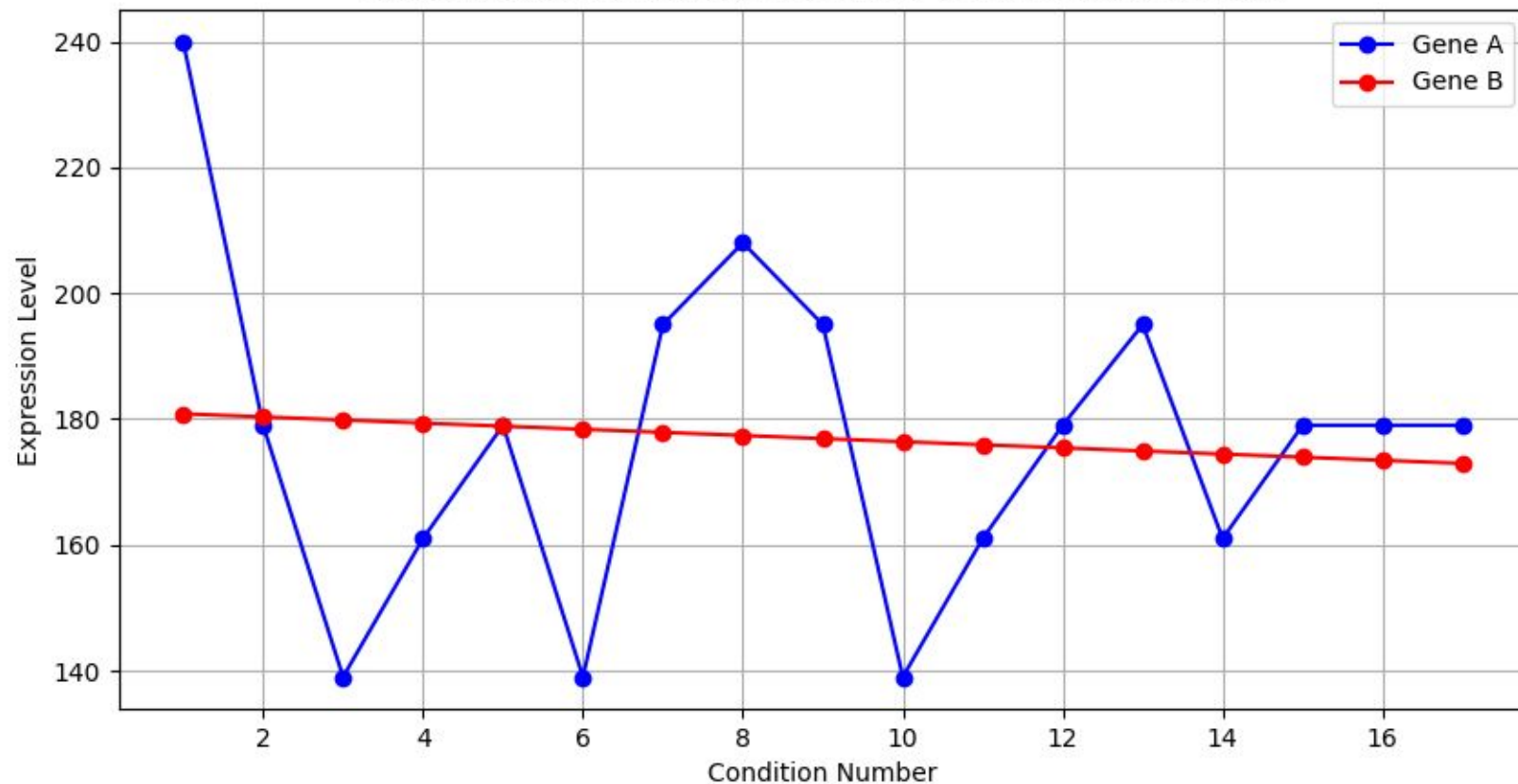


Figure of Merit at 8 Clusters

	Euclidean	Manhattan	Mahalanobis	Pearson	Uncentered	Spearman	Absolute	Squared
kNNG	0.332	0.337	0.881	0.931	0.531	0.993	0.976	0.336
RNG	0.33	0.339	0.964	0.983	0.514	0.996	0.998	0.351
GG	0.542	1.0	1.0	-	-	-	-	-



Demonstration of Euclidean Distance vs. Pearson Correlation



# Conclusion

I quantitatively compared the relative performance of different similarity measures and graph algorithms in their ability to help identify clusters of coregulated yeast genes.