

The background features a dark blue gradient with a subtle pattern of white dots. On the left side, there are several circular diagrams. One prominent diagram is a large circle with a scale from 140 to 260 in increments of 10. Inside this circle, there are smaller concentric circles and arrows indicating a clockwise direction. Other similar but smaller diagrams are scattered across the background, some with dashed lines and arrows.

INFERRING GENE FUNCTIONALITY WITH CLUSTERING

By Juacall Bernard
Advisor: Miao,Heh

OUTLINE

- Introduction
- Goal and Objectives
- Clustering Overview
- Algorithms & Implementation
- Result Evaluation
- Conclusion

INTRODUCTION

- Viewing and analyzing vast amounts of biological data as a whole set can be difficult.
- An easier way to interpret the data is to partition the data set into clusters.

GOAL

- In this project I will attempt to infer gene functions and determine the type of a known or unknown gene by way of clustering.

OBJECTIVES

- Determine the optimal number of clusters.
- Choose a better algorithm.

CLUSTERING REVIEW

What is clustering?

What is clustering useful for?

Are there any problems with clustering?

ALGORITHMS & IMPLEMENTATION

- K-Means Clustering
- Spectral Clustering

K-MEANS CLUSTERING

- How does it work?
- Input
- Disadvantages

K-MEANS CLUSTERING

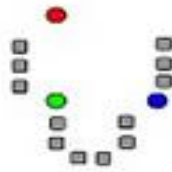
- Description

Given a set of observations $(\mathbf{x}_1, \mathbf{x}_2, \dots, \mathbf{x}_n)$, where each observation is a d -dimensional real vector, k -means clustering aims to partition the n observations into k sets $(k \leq n) \mathbf{S} = \{S_1, S_2, \dots, S_k\}$ so as to minimize the within-cluster sum of squares (WCSS):

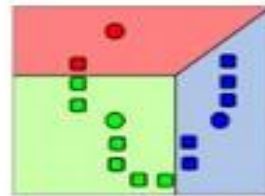
$$\arg \min_{\mathbf{S}} \sum_{i=1}^k \sum_{x_j \in S_i} \|x_j - u_i\|^2$$

where μ_i is the mean of points in S_i .

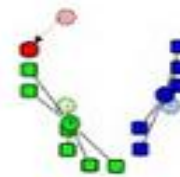
- Standard Algorithm



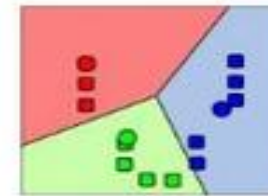
1) k initial "means" (in this case $k=3$) are randomly selected from the data set.



2) k clusters are created by associating every observation with the nearest mean.



3) The centroid of each of the k clusters becomes the new means.



4) Steps 2 and 3 are repeated until convergence has been reached.

SIMILARITY MATRIX

- ϵ -neighborhood graph
- K-nearest graph
- Fully connected graph

DISADVANTAGES

- Sensitive to outliers
- Fixed K values
- Less effective with non globular clusters

SPECTRAL CLUSTERING

- What is Spectral Clustering
- Laplacian Matrix

WHAT IS SPECTRAL CLUSTERING

- A Principal Component Analysis Method
- Principal component analysis is a mathematical procedure that uses orthogonal transformation to convert a set of observations of possibly correlated variables into a set of values of linearly uncorrelated variables called principal components.
- Spectral Clustering can find optimal partition of the data set.

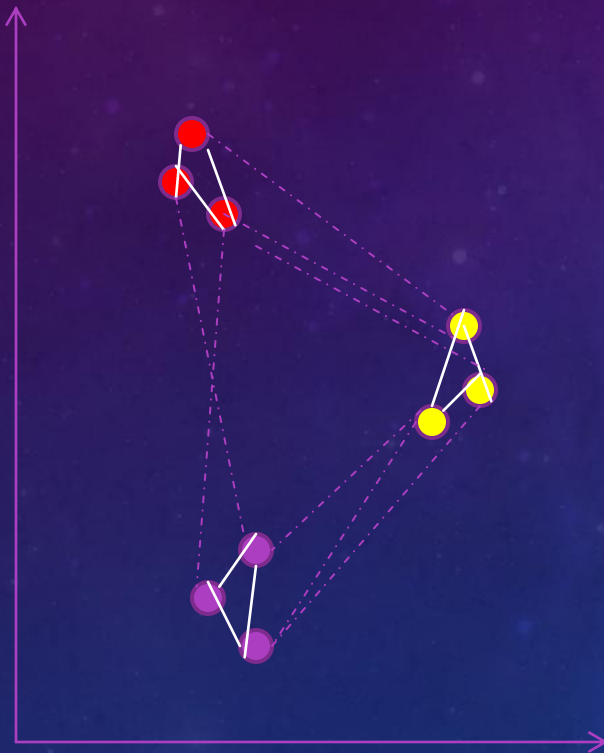
LAPLACIAN MATRIX

- A matrix representation of a graph.
- Main tools for spectral clustering

SPECTRAL CLUSTERING (AFFINITY-BASED CLUSTERING)



Similarity Matrix



X	X	X
X	X	X
X	X	X
...	X	X	X
...	X	X	X
...	X	X	X
...	X	X	X
...	X	X	X
...	X	X	X

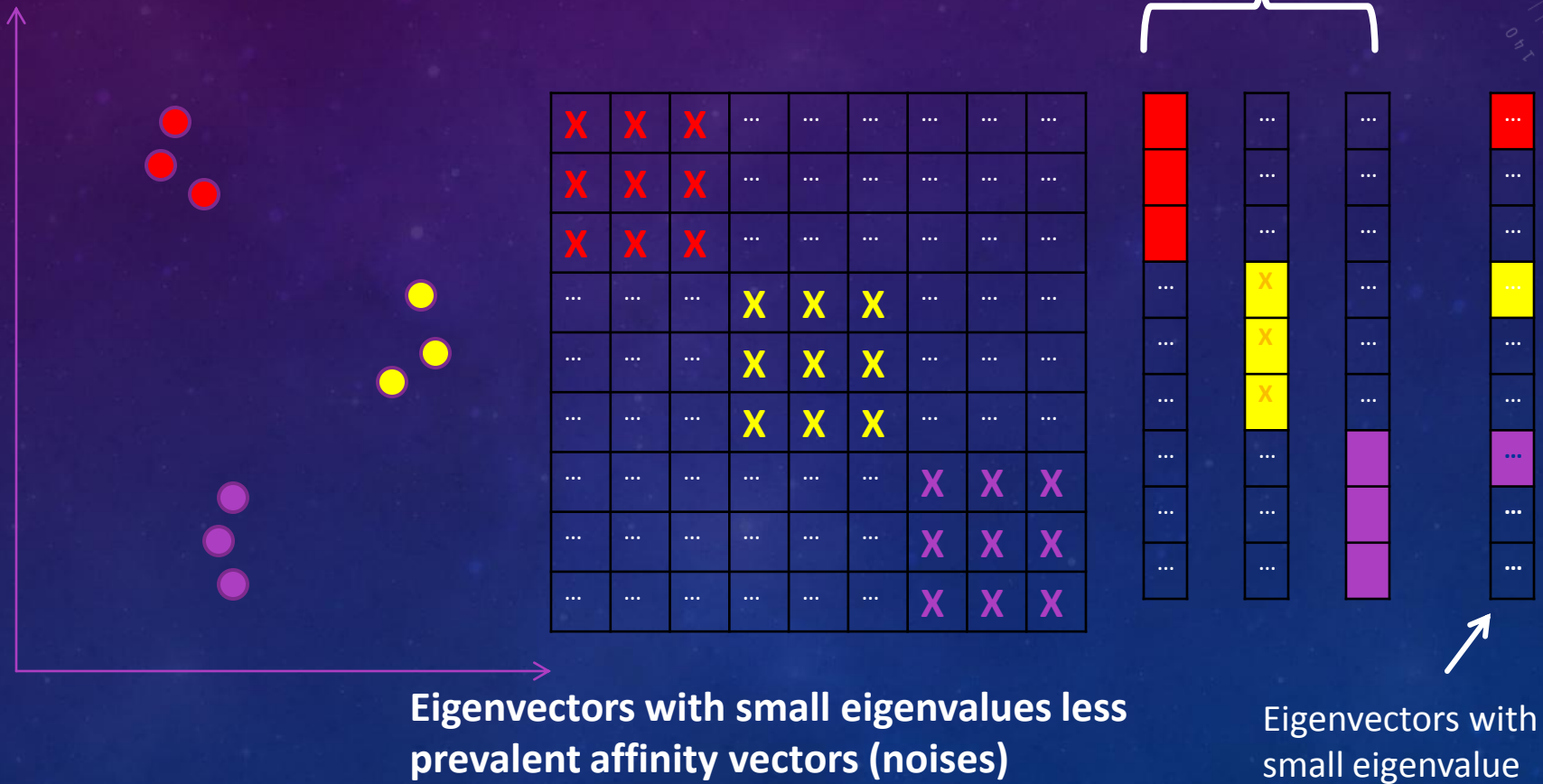
EIGENVECTORS AND EIGENVALUES

- Are used to identify uncorrelated vectors
- Each eigenvector has an eigenvalue that represents how prevalent the eigenvector is in the original data set.
- Eigenvectors of different eigenvalues are orthogonal. They form the dimensionality of a data space, and hence are very useful in clustering data set.

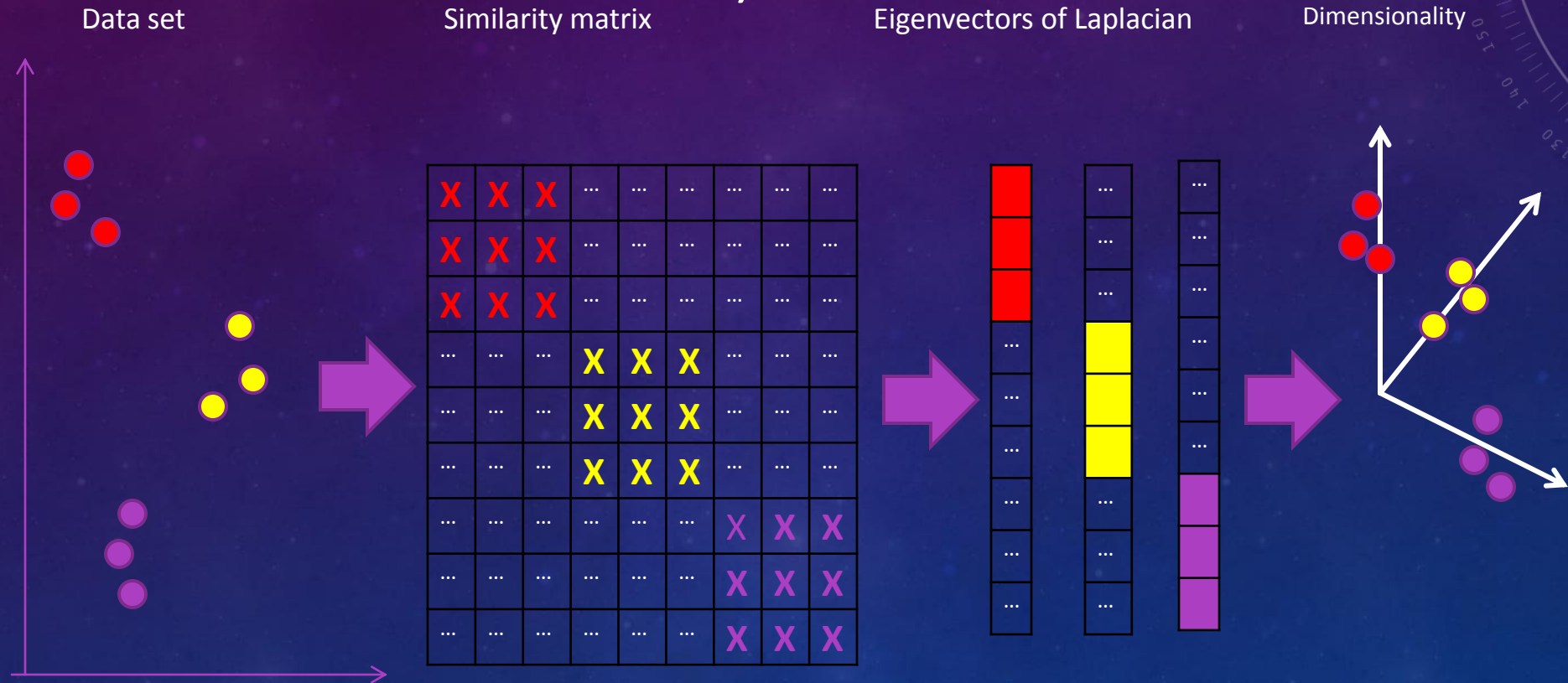
AFFINITY MATRIX AND AFFINITY VECTORS

Eigenvectors with large eigenvalues are most dominant affinity vectors

Eigenvectors with large eigenvalues

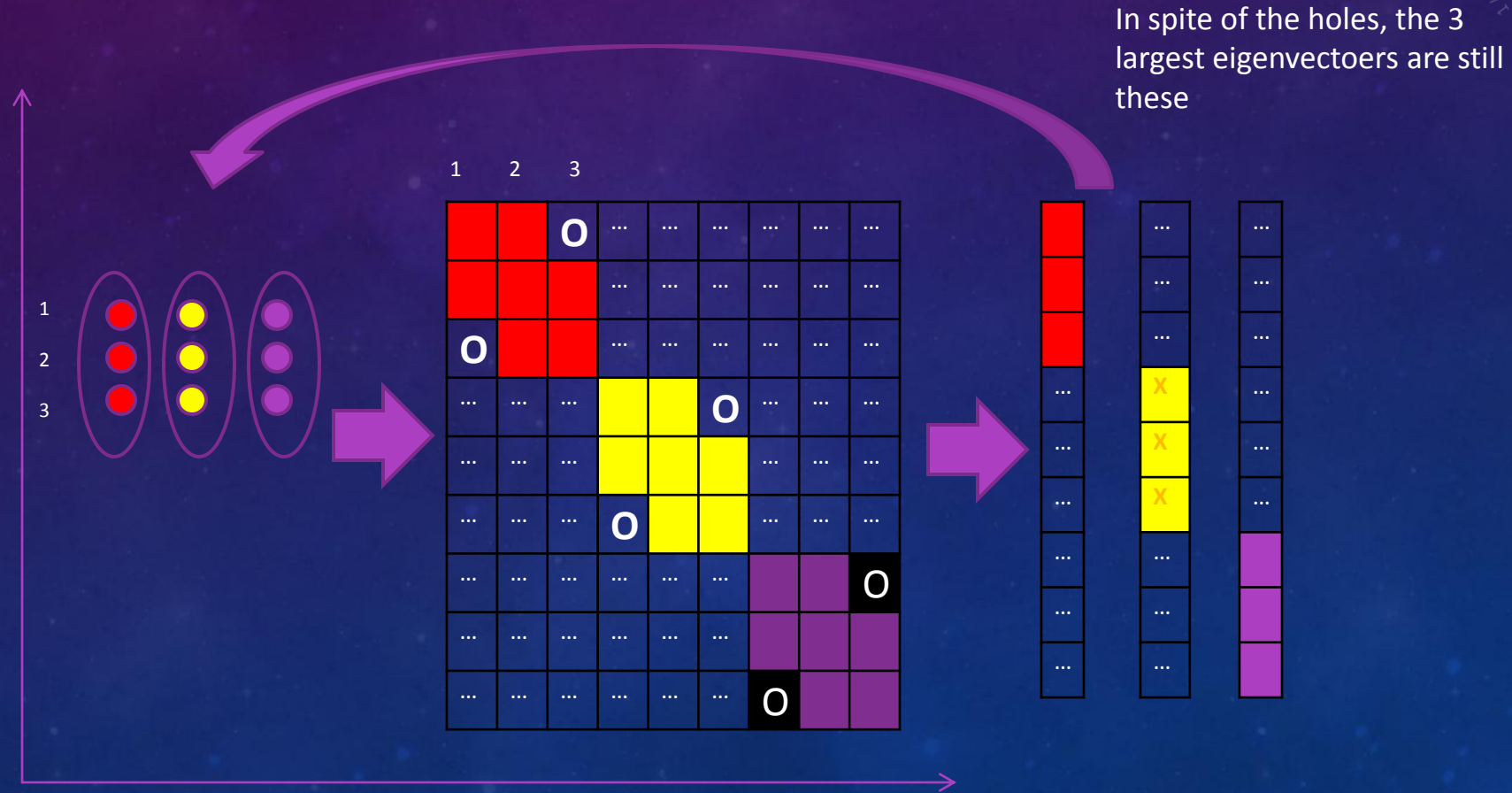


AFFINITY BASED CLUSTERING (SPECTRAL CLUSTERING)



WHAT'S THE DIFFERENCE?

- With Spectral Clustering, the data set can be easily assigned to the shown clusters, which would not be quite the case in traditional clustering techniques.



ID_REF	IDENTIFIER	GSM873553	GSM873560	GSM873556	GSM873554	GSM873561	GSM873557	GSM873555	GSM873562	GSM873558	GSM873559	GSM873563	
1559249_at	ATXN1	5.16315	4.84565	5.0189	5.48071	5.50036	5.16499	5.43235	5.44588	5.08937	5.66378	6.08232	
227253_at	CP	4.41578	4.33503	4.3595	4.50626	4.43327	4.37124	4.43327	4.45255	4.30465	4.47151	4.55466	
AFFX-ThrX-5_at	--Control		6.75607	6.61952	6.63172	6.79804	6.76952	6.66731	6.72926	6.77472	6.66322	6.74018	6.82836
1555259_at	ZAK	4.82752	4.48254	4.5782	4.92335	4.94501	4.71301	4.78801	4.78801	4.62087	4.80276	4.90172	
1560434_x_at	CLTA	5.51325	5.16526	5.50102	5.50036	5.50036	5.50036	5.50036	5.59692	5.32581	5.49819	5.72867	
204183_s_at	ADRBK2	6.71684	6.42238	6.62878	6.67332	6.67332	6.63903	6.74214	6.75695	6.47245	6.73201	6.78983	
235684_s_at	SESN3	3.88256	3.87059	nan	nan	nan	nan	4.52603	4.31859	4.00351	4.22824	4.49628	
236725_at	WWC1	nan	nan	5.64539	5.96895	5.74611	5.71416	nan	nan	nan	nan	5.87998	
216074_x_at	WWC1	nan	8.20288	nan	nan	8.31114	nan	8.36605	8.33877	8.18102	8.28856	8.36082	
237131_at	RIIAD1	nan	5.65672	nan	5.87734	5.80434	nan	nan	nan	nan	nan	nan	
201258_at	RPS16	13.5452	13.5075	13.5353	13.6149	13.5603	13.5727	13.5783	13.5743	13.488	13.5464	13.5815	
1555970_at	FBXO28	7.17163	6.97289	7.08666	7.23711	7.17163	7.14419	7.27538	7.2268	6.85886	7.17577	7.17163	
1554518_at	GSTCD	6.34827	6.27897	6.29245	6.45299	6.36867	6.22971	6.40111	6.37339	6.19733	6.33649	6.33774	
238935_at	RPS27L	7.79837	7.65866	7.87836	8.03873	7.79837	7.51758	7.93888	7.79837	7.4819	7.7907	7.90875	
1555125_at	GCFC1	5.57353	5.58721	5.54289	5.6976	5.51946	5.46784	5.65482	5.59804	nan	5.58721	5.61257	
241900_at	AW195928		3.65341	3.56948	3.58872	3.79631	3.53893	nan	3.75762	3.68988	3.47165	nan	3.69033
222624_s_at	ZNF639	8.65084	8.45147	8.61608	8.61129	8.61129	8.48919	8.66195	8.56387	8.58503	8.61129	8.74657	
218673_s_at	ATG7	7.53643	7.46611	7.56944	7.57859	7.56965	7.44337	7.58226	7.53276	7.56459	7.56965	7.70423	
242943_at	ST8SIA4	4.37632	4.02134	4.31119	4.4709	4.45471	4.09128	4.55887	4.42075	4.16215	4.38922	4.60188	
235554_x_at	PACRGL	6.31877	6.26627	6.55754	6.56299	6.60894	6.064	6.61297	6.43804	6.20181	6.44249	6.50166	
221192_x_at	MFSD11	6.97239	6.89723	6.98734	7.02291	7.07121	6.82075	7.1081	7.01131	6.89949	6.95735	7.03373	
209342_s_at	IKBKB	6.15813	5.99268	6.20537	6.13433	6.19222	5.85913	6.23613	6.11557	5.98742	5.97413	6.2784	
1566990_x_at	ARID1B	7.97378	7.78171	7.99942	nan	nan	nan	8.36219	7.97612	nan	8.09932	8.02209	
206222_at	TNFRSF10C		nan	nan	nan	4.49607	4.47521	nan	nan	nan	4.40536	nan	4.65789
1553494_at	TDH	nan	2.85924	3.47656	3.39581	nan	nan	nan	3.29428	nan	3.48164	nan	
1557380_at	AGAP11	nan	nan	nan	3.56787	3.50901	3.29523	nan	nan	nan	nan	3.87004	
207413_s_at	SCN5A	nan	nan	5.10909	nan	nan	nan	nan	nan	5.07468	5.131	nan	
213006_at	CEBPD	nan	nan	nan	3.71296	3.77298	3.71296	nan	nan	nan	4.70259	5.20294	
1569005_at	BC015604		3.83152	3.82532	4.05226	nan	4.05226	nan	4.27924	4.10024	nan	nan	4.08334
AFFX-PheX-M_at	--Control		7.1696	7.025	7.11488	7.09214	7.13911	7.00224	7.20057	7.07102	7.04831	7.18668	7.21677
208588_at	FKSG2	4.27715	3.84335	4.09374	nan	4.09224	nan	4.27491	3.92944	3.95521	4.30823	nan	
1554558_at	DCAF5	3.76043	3.50746	3.75533	3.74411	4.03766	3.63557	3.74176	3.76043	3.83943	3.88954	4.22129	
222149_x_at	GOLGA8DP		7.04544	6.96323	7.01542	7.01855	7.18134	6.93198	6.9903	7.11109	7.06044	7.14206	7.22517
206141_at	MOCS3	6.83714	6.85872	6.92988	6.90874	7.13217	6.90359	6.96571	6.89338	6.91167	7.08031	7.20353	
206794_at	ERBB4	5.00394	4.89414	5.18472	5.03969	5.50577	5.14558	5.27467	5.14962	5.07829	5.53603	5.5249	
229576_s_at	TBX3	6.44249	6.28323	6.35727	6.44249	6.60571	6.44249	6.44249	6.45001	6.43363	6.51725	6.54205	
233019_at	CNOT7	4.24658	3.67586	4.01075	4.0932	4.50532	3.92567	nan	4.01075	nan	4.08564	4.38723	
211917_s_at	PRLR	3.9991	3.84699	3.94571	4.06127	4.12198	nan	4.08484	nan	3.99012	3.9991	3.9991	

Cluster 1:
(227253_at)
(242943_at)
(1554558_at)
(233303_at)
Cluster 2:
(1555259_at)
(1553148_a_at)
(243051_at)

Cluster 3:

Cluster 4:
(242225_at)

Cluster 5:

Cluster 6:
(208047_s_at)

Cluster 7:
(1559249_at)
(1560434_x_at)
(206794_at)
(236350_at)
(244803_at)
(238315_s_at)
(1566480_x_at)

Cluster 8:
(242928_at)
(243672_at)

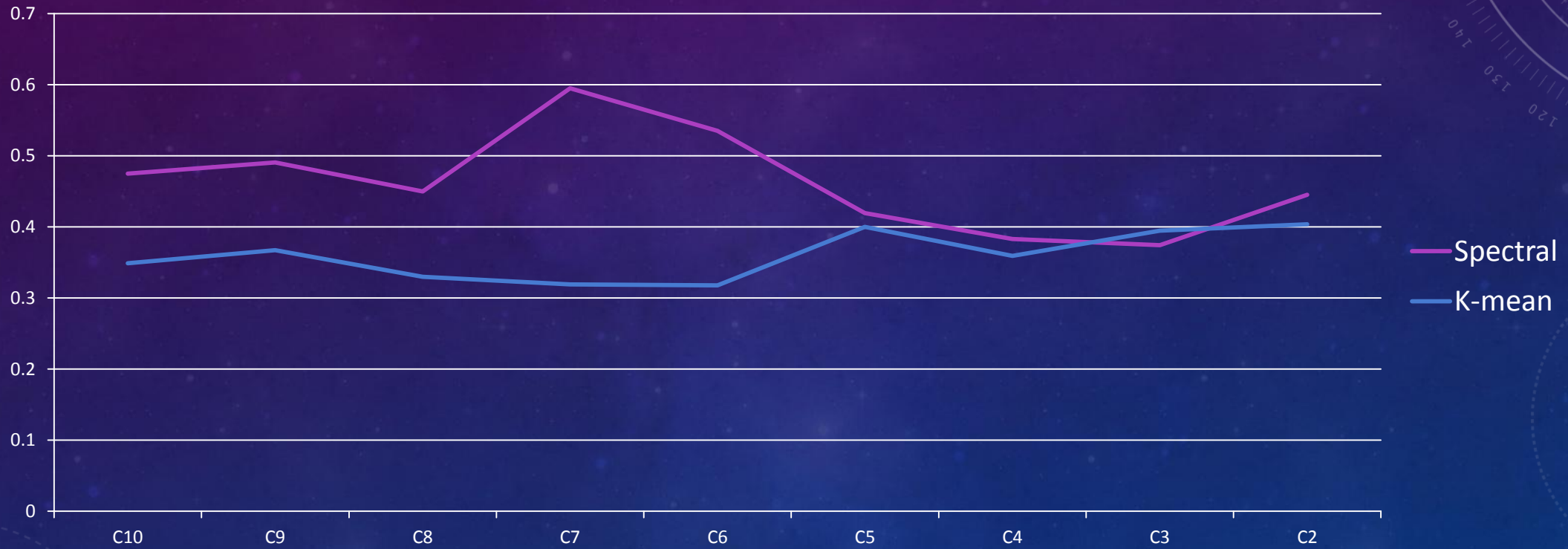
Cluster 9:
(AFFX-ThrX-5_at)
(204183_s_at)
(235684_s_at)
(236725_at)
(216074_x_at)

<

ABOUT SILHOUETTE

- Method of cluster validation.
- The silhouette can validate in cluster genes similarity.
- Can also validate overall clustering output.

RESULTS



CONCLUSION

- Clustering is a faster more efficient way of finding similarities than sequencing.
- Spectral Clustering out performs k-means in most cases.