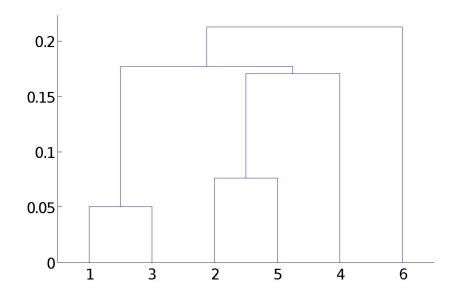
Pattern Recognition

- S. S. Samant

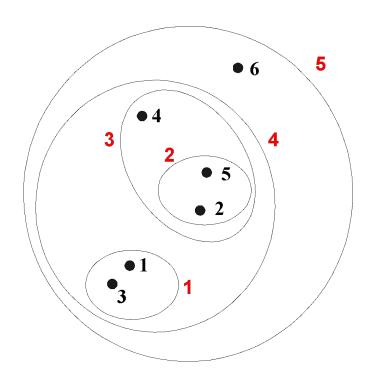
Agglomerative Hierarchical Clustering

- Starts with each point being a cluster, and at each step, merge the closest pair of clusters
- Displayed graphically using a dendrogram a tree like structure (dendro "tree", gramma "drawing")



Agglomerative Hierarchical Clustering

- Starts with each point being a cluster, and at each step, merge the closest pair of clusters
- Can also be displayed graphically using a nested cluster diagram



Agglomerative Hierarchical Clustering

Basic algorithm

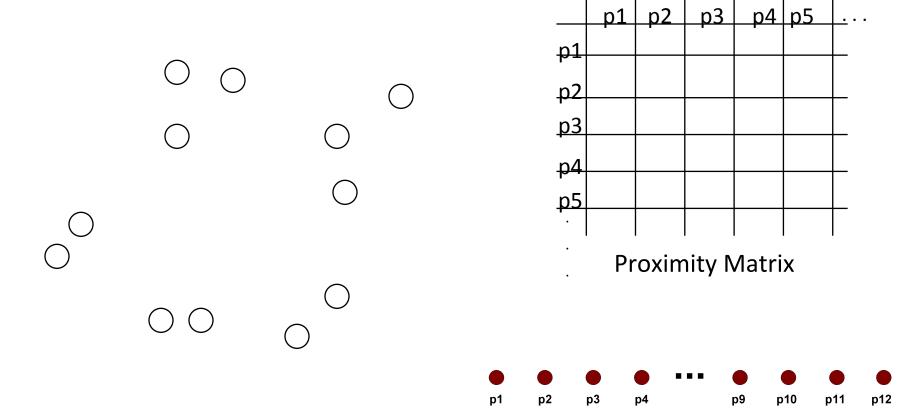
- Compute the proximity matrix
- Let each data point be a cluster
- 3. Repeat
- 4. Merge the two closest clusters
- 5. Update the proximity matrix
- **6. Until** only a single cluster remains

Key operation is the computation of the proximity of two clusters

 Different approaches to defining the distance between clusters distinguish the different algorithms

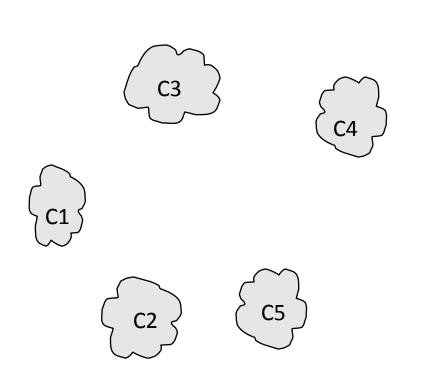
Starting Situation

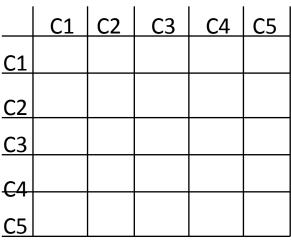
•Start with clusters of individual points and a proximity matrix



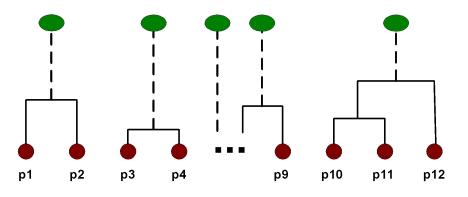
Intermediate Situation

After some merging steps, we have some clusters





Proximity Matrix



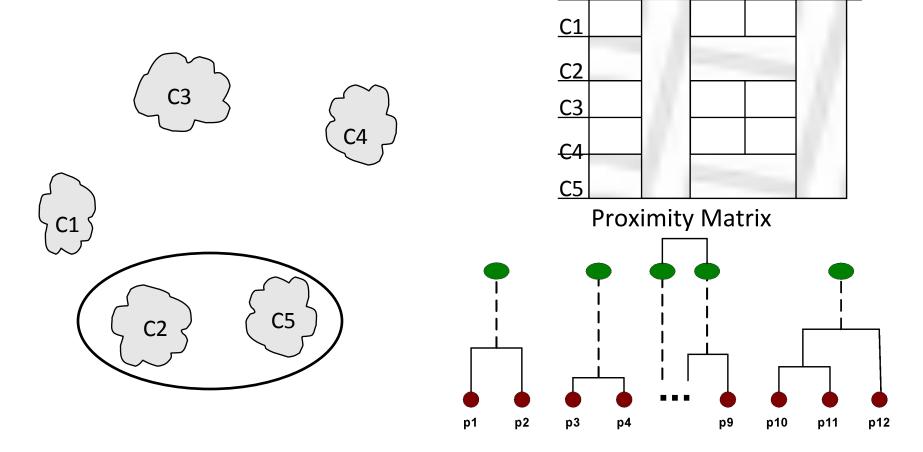
C3

C4 C5

Intermediate Situation

We want to merge the two closest clusters (C2 and C5)

and update the proximity matrix.



p10

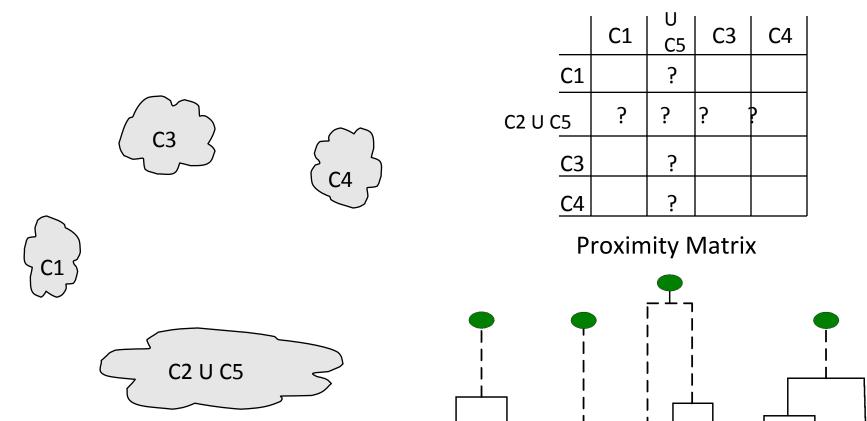
p11

p12

p9

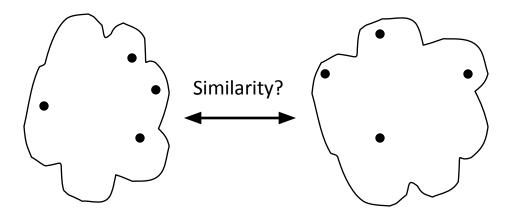
After Merging

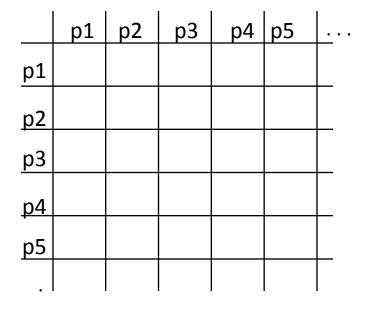
• The question is "How do we update the proximity matrix?"



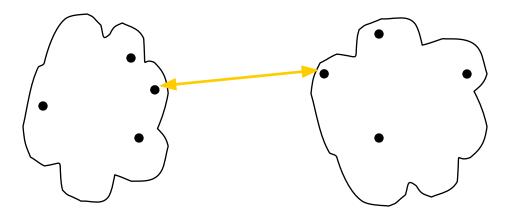
р1

p2



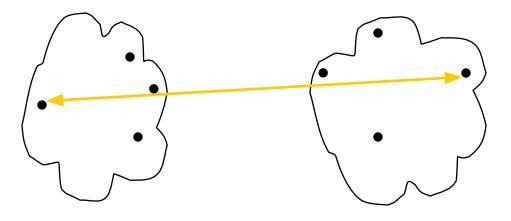


- MIN
- MAX
- Group Average
- Distance Between Centroids



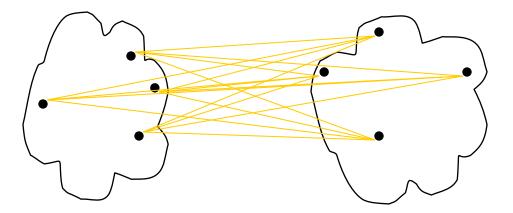
	p1	p2	рЗ	р4	p5	<u> </u>
<u>p1</u>						
<u>p2</u>						
<u>p2</u> <u>p3</u>						_
						_
<u>p4</u> <u>p5</u>						

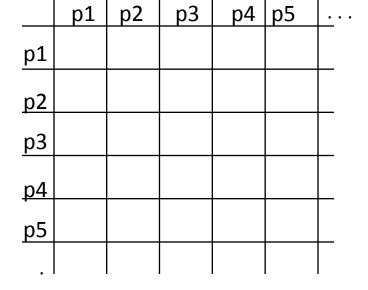
- MIN
- MAX
- Group Average
- Distance Between Centroids



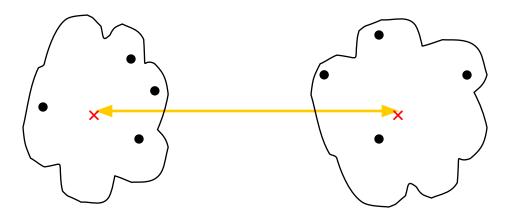
	p1	p2	рЗ	p4	р5	<u>.</u>
p1						
p2						
<u>p2</u> <u>p3</u>						
<u>p4</u> <u>p5</u>						

- MIN
- MAX
- Group Average
- Distance Between Centroids





- MIN
- MAX
- Group Average
- Distance Between Centroids



	p1	p2	р3	p4	p5	<u>.</u>
<u>p1</u>						
<u>p2</u>						
<u>p2</u> <u>p3</u>						
<u>р4</u> р5						

- MIN
- MAX
- Group Average
- Distance Between Centroids

Cluster Similarity: MIN or Single Link

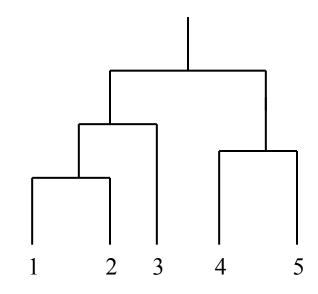
•Similarity of two clusters is based on the two closest points in the different clusters

	<u> 11 </u>	12	13	4	15
11	1.00	0.90 1.00 0.70 0.60 0.50	0.10	0.65	0.20
12	0.90	1.00	0.70	0.60	0.50
13	0.10	0.70	1.00	0.40	0.30
14	0.65	0.60	0.40	1.00	0.80
15	0.20	0.50	0.30	0.80	1.00

Cluster Similarity: MIN or Single Link

•Similarity of two clusters is based on the two closest points in the different clusters

	I 1	12	13	1 4	<u> 15</u>
11	1.00	0.90	0.10	0.65	0.20 0.50 0.30 0.80 1.00
12	0.90	1.00	0.70	0.60	0.50
13	0.10	0.70	1.00	0.40	0.30
14	0.65	0.60	0.40	1.00	0.80
15	0.20	0.50	0.30	0.80	1.00



Cluster Similarity: MAX or Complete Linkage

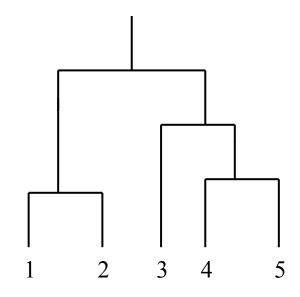
•Similarity of two clusters is based on the two farthest points in the different clusters

	<u> </u> 11	12	I 3	14	15
11	1.00 0.90 0.10 0.65 0.20	0.90	0.10	0.65	0.20
12	0.90	1.00	0.70	0.60	0.50
13	0.10	0.70	1.00	0.40	0.30
14	0.65	0.60	0.40	1.00	0.80
15	0.20	0.50	0.30	0.80	1.00

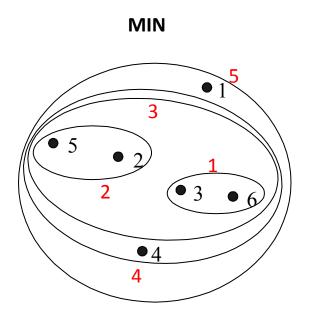
Cluster Similarity: MAX or Complete Linkage

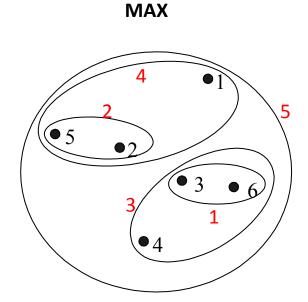
•Similarity of two clusters is based on the two farthest points in the different clusters

	I 1	12	13	14	<u> 15</u>
11	1.00 0.90 0.10 0.65 0.20	0.90	0.10	0.65	0.20
12	0.90	1.00	0.70	0.60	0.50
13	0.10	0.70	1.00	0.40	0.30
14	0.65	0.60	0.40	1.00	0.80
15	0.20	0.50	0.30	0.80	1.00



Hierarchical Clustering: Comparison





Examples

	p1	p2	р3	p4	p5
p1	1.00	0.10	0.41	0.55	0.35
p2	0.10	1.00	0.64	0.47	0.98
p3	0.41	0.64	1.00	0.44	0.85
p4	0.55	0.47	0.44	1.00	0.76
p5	0.35	0.98	0.85	0.76	1.00

Given the data above, perform single link and complete link hierarchical clustering. Draw dendrogram of your results.

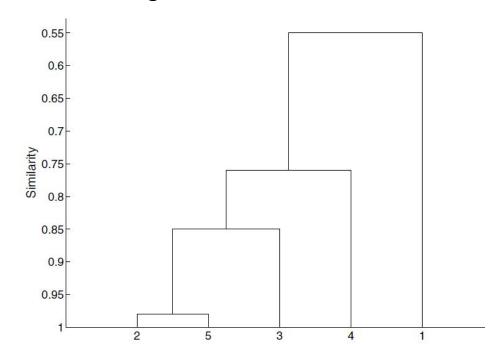
Single Link:

Examples

	p1	p2	р3	p4	p5
p1	1.00	0.10	0.41	0.55	0.35
p2	0.10	1.00	0.64	0.47	0.98
p3	0.41	0.64	1.00	0.44	0.85
p4	0.55	0.47	0.44	1.00	0.76
p5	0.35	0.98	0.85	0.76	1.00

Given the data above, perform single link and complete link hierarchical clustering. Draw dendrogram of your results.

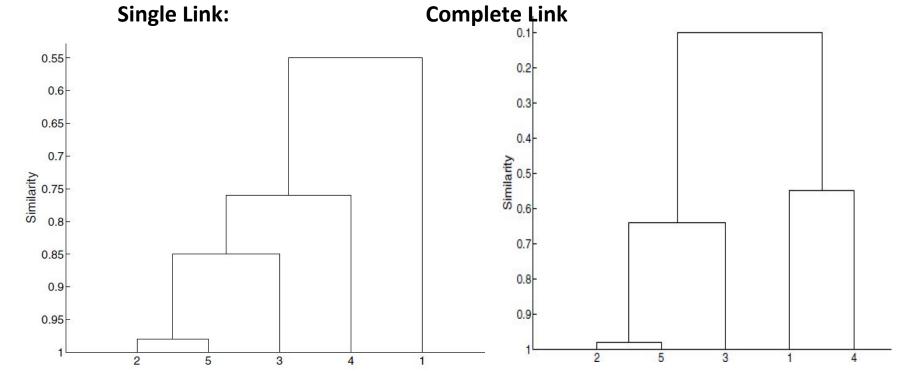
Single Link:



Examples

	p1	p2	р3	p4	p_5
p1	1.00	0.10	0.41	0.55	0.35
p2	0.10	1.00	0.64	0.47	0.98
p3	0.41	0.64	1.00	0.44	0.85
p4	0.55	0.47	0.44	1.00	0.76
p5	0.35	0.98	0.85	0.76	1.00

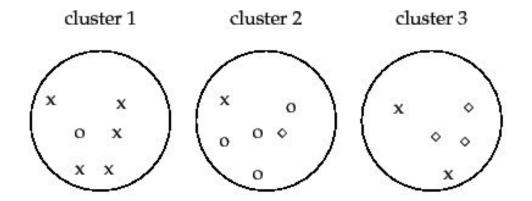
Given the data above, perform single link and complete link hierarchical clustering. Draw dendrogram of your results.



Example - HAC on Iris dataset

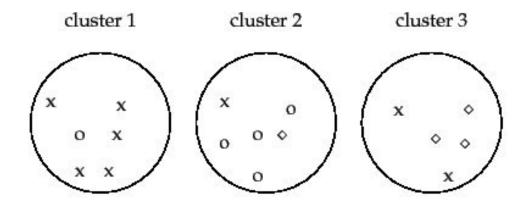
```
from sklearn import datasets
import matplotlib.pyplot as plt
from sklearn.cluster import AgglomerativeClustering
from sklearn import metrics
iris = datasets.load iris()
X = iris.data
y = iris.target
plt.scatter(X[:,0], X[:,1], c=y, cmap='rainbow', s=10)
plt.title('Actual',fontsize=15, fontweight='bold')
plt.xlabel('Sepal Length',fontsize=15)
plt.ylabel('Petal Length',fontsize=15)
plt.figure()
cls = AgglomerativeClustering(n clusters = 3, linkage='average')
cls.fit(X)
hac labels = cls.labels
print (metrics.silhouette score(X, hac labels))
plt.scatter(X[:,0], X[:,1],c=hac labels, cmap='rainbow', s=10)
plt.xlabel('Sepal Length',fontsize=15)
plt.ylabel('Petal Length',fontsize=15)
plt.title('Predicted clusters',fontsize=15, fontweight='bold')
```

External Evaluation - Purity



What is the purity of the clustering?

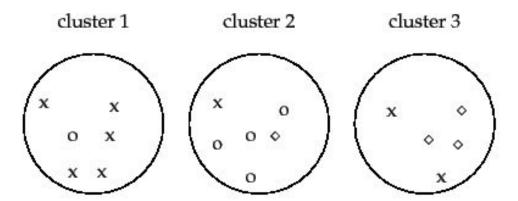
External Evaluation - Purity



What is the purity of the clustering?

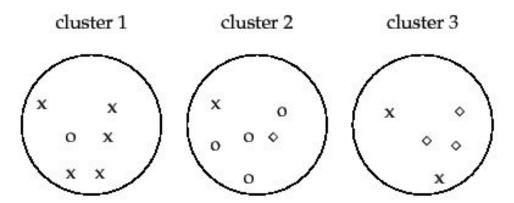
$$= (5+4+3)/17$$

$$= 0.71$$



- Look at the example in pairs
- If there are a N examples, then N(N-1)/2 pairs
- A good clustering assigns two similar examples to same cluster, and two dissimilar examples to different clusters. Everything else is bad!
- Let TP be the number of similar pairs assigned to the same cluster, TN be the number of dissimilar pairs assigned to different clusters, FP be the number of dissimilar pairs to same cluster, and FN be the no. of similar pairs assigned to different clusters

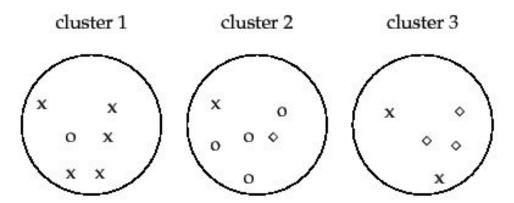
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$$ext{RI} = rac{ ext{TP} + ext{TN}}{ ext{TP} + ext{FP} + ext{FN} + ext{TN}}$$

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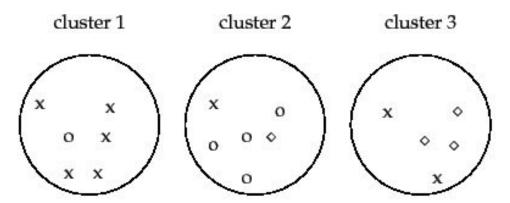


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$$RI = \frac{TP + TN}{TP + FP + FN + TN} \longrightarrow {}^{N}C_{2}$$



External Evaluation – Rand Index

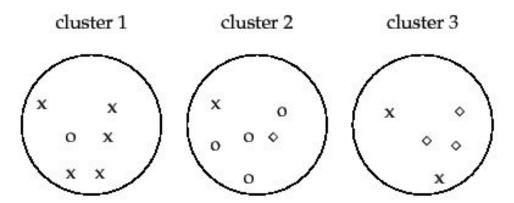


- Look at the example in pairs
- If there are a N examples, then N(N-1)/2 pairs
- A good clustering assigns two similar examples to same cluster, and two dissimilar examples to different clusters. Everything else is bad!
- Let TP be the number of similar pairs assigned to same cluster, TN be the number of dissimilar pairs assigned to different clusters, FP be the number of dissimilar pairs to same cluster, and FN be the no. of similar pairs assigned to different clusters

$$RI = \frac{TP + TN}{TP + FP + FN + TN}$$

Find TP, TN, FP, FN

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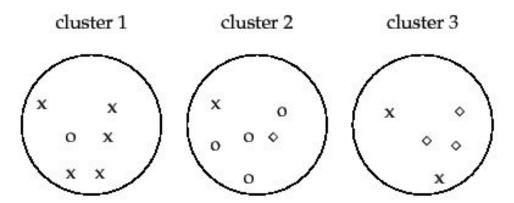
- Look at the example in pairs
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	Same cluster	Diff. clusters
Same class	20	24
Diff. class	20	72

$$RI = \frac{TP + TN}{TP + FP + FN + TN}$$

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External Evaluation – Rand Index



- Look at the example in pairs
- If there are a N examples, then N(N-1)/2 pairs
- A good clustering assigns two similar examples to same cluster, and two dissimilar examples to different clusters. Everything else is bad!
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	Same cluster	Diff. clusters
Same class	20	24
Diff. class	20	72

RI = 0.68

Thank You!