Clustering Lecture 1: Basics

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Outline

• Basics

- Motivation, definition, evaluation

Methods

- Partitional
- Hierarchical
- Density-based
- Mixture model
- Spectral methods

Advanced topics

- Clustering in MapReduce
- Clustering ensemble
- Semi-supervised clustering, subspace clustering, co-clustering, etc.

Readings

- Tan, Steinbach, Kumar, Chapters 8 and 9.
- Han, Kamber, Pei. Data Mining: Concepts and Techniques. Chapters 10 and 11.
- Additional readings posted on website

Clustering Basics

- Definition and Motivation
- Data Preprocessing and Similarity Computation
- Objective of Clustering
- Clustering Evaluation

Clustering

 Finding groups of objects such that the objects in a group will be similar (or related) to one another and different from (or unrelated to) the objects in other groups



Application Examples

- A stand-alone tool: explore data distribution
- A preprocessing step for other algorithms
- Pattern recognition, spatial data analysis, image processing, market research, WWW, ...
 - Cluster documents
 - Cluster web log data to discover groups of similar access patterns

Clustering Co-expressed Genes

Gene Expression Data Matrix

	Α	В	C	D	E	F	G	H
1	-0.26958	-1.11968	-1.61092	-0.01726	-0.91858	-0.39625	-0.59544	0.223919
2	-1.22081	-0.61064	-1.4015	0.408471	-0.32483	-0.40845	0.667481	-0.99353
3	0.65037	-0.93969	-1.87056	-1.75382	-0.985	-0.28842	-0.37445	1.216714
4	-0.31764	-1.90086	-1.68162	-1.07273	-0.54844	0.243838	0.064647	-0.22084
5	0.039959	-1.07316	-2.0859	0.312404	-0.82065	-0.6364	-0.74902	-0.32929
6	-1.42209	0.214419	-1.30109	-0.20728	-0.42058	-0.95167	-0.85251	-1.84193
7	-0.5303	1.209095	-1.23959	0.355066	-0.5467	-0.60259	-0.31395	-0.57044
8	-0.75512	-0.71537	-1.0849	-0.00374	-0.68283	-0.37029	-0.42753	0.593289
9	-0.47879	-1.02277	-1.01239	-0.33202	0.33603	0.862159	0.979181	-0.2768
10	-0.72888	-0.64282	-1.04118	0.13236	-0.18425	-0.17339	0.524335	-0.97261
11	-1.54334	-0.90966	-1.23333	0.801135	-0.35393	-0.0496	0.422014	-1.39041
12	0.734163	0.336594	-1.74861	0.177696	-0.36607	-1.01617	-0.91572	0.285304
13	-0.08299	-1.03087	-1.56255	-0.3983	0.028534	-0.00045	-0.63836	-0.70778
14	-0.75259	-0.88778	-1.20852	0.703398	-0.79132	-1.07037	0.257377	-0.10077
15	0.811	0.130058	-1.16391	-0.16098	-1.10368	-1.23961	-0.92942	0.503864
16	-1.50545	-0.22578	0.446751	-1.05506	-1.52191	-1.15962	-1.14207	-1.33865
17	-1.88456	-0.19605	0.822872	1.34748	-1.09371	-0.4543	-0.54614	-1.05905
18	-0.71679	-0.97829	-0.95782	0.964454	0.420057	0.314381	0.7907	-0.43544
19	-0.15942	-0.59816	-1.86775	1.819711	0.429999	0.167825	0.447172	-0.46287
20	-0.65254	0.467307	-0.11772	1.380863	0.0606	0.214798	0.317073	-0.63938
21	0.125219	-0.87144	-1.40036	0.776659	-1.84147	-0.20126	-0.79696	0.58284
22	-1.03492	0.206928	-1.18701	0.951558	-0.84569	-0.94715	-0.57483	-0.83308
23	-0.88779	-0.8295	-1.18472	0.889415	-0.42327	-0.39738	-0.26231	-1.38634
24	-0.61967	-0.727	-1.27885	0.265871	-0.05476	-0.2753	-0.30522	-0.82088
25	-1.26181	0.630099	-0.16568	0.127351	0.021887	0.022302	0.12727	-0.75273
26	-0.9317	-0.59289	-0.70058	-0.64865	-0.244	-0.03328	0.003402	-0.96184
27	-1.00066	-0.79028	-1.00607	-0.04573	-0.24725	-0.12933	-0.0095	-0.70748
28	-0.09631	-1.48009	-1.5084	-0.07404	-0.02446	0.068175	0.217438	0.411357
29	0.328346	-0.62071	-1.81974	-0.20051	-0.72874	-0.74451	-0.28102	0.400385
30	-0.89746	0.069834	-0.47114	0.831606	0.208512	-0.16735	0.506605	-0.18187
31	-0.61731	-0.35206	-0.65678	0.919952	0.129398	-0.07423	0.645191	-0.11715
32	-1.11754	1.056664	0.351571	-0.1779	-0.66105	-0.89209	-0.28012	-0.80815
33	-0.46696	-1.18017	-1.16218	0.215408	0.104611	0.42643	0.768182	-0.60385
34	-1.68415	-0.46408	-0.38539	0.286911	-0.03672	0.021101	0.691408	-1.03612
35	-0.44974	-1.17955	-1.25839	-0.23573	0.168901	0.036602	0.788574	-0.2853
36	0.63699	0.993603	-0.44663	-0.20089	-1.1892	-1.19508	-1.35657	0.3804
37	0.180332	0.193894	-0.14022	-0.39459	-0.86483	-0.71266	-0.54127	0.056965
38	0.031928	-0.21662	-1.08205	0.13115	-0.72443	-0.82681	-0.84647	0.709053
39	1.346822	0.313961	-1.21197	-0.62689	-1.07646	-1.06614	-1.34569	0.736034
40	0.360505	-1.2221	-1.43524	0.394193	-0.08287	-0.24353	0.203362	0.534584
41	-1.62892	0.158886	-0.28768	1.263494	0.627216	0.777965	1.095598	-1.36229
42	-1.28297	-1.01468	-0.49856	2.444438	-0.25267	-0.63069	0.04216	-0.10562
43	-1.0645	-0.10843	0.376248	0.125929	-0.44348	-0.03026	0.263266	-0.4077

Gene Expression Patterns







Why looking for co-expressed genes? *¾* Co-expression indicates co-function; *¾* Co-expression also indicates co-regulation.

Gene-based Clustering

	A	в	C	D	E	E E	G	н
1	-0.26958	-1.11968	-1.61092	-0.01726	-0.91858	-0.39625	-0.59544	0.223919
2	-1.22081	-0.61064	-1.4015	0.408471	-0.32483	-0.40845	0.667481	-0.99353
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4	-0.31764	-1.90086	-1.68162	-1.07273	-0.54844	0.243838	0.064647	-0.22084
5	0.039959	-1.07316	-2.0859	0.312404	-0.82065	-0.6364	-0.74902	-0.32929
6	-1.42209	0.214419	-1.30109	-0.20728	-0.42058	-0.95167	-0.85251	-1.84193
7	-0.5303	1.209095	-1.23959	0.355066	-0.5467	-0.60259	-0.31395	-0.57044
8	-0.75512	-0.71537	-1.0849	-0.00374	-0.68283	-0.37029	-0.42753	0.593289
9	-0.47879	-1.02277	-1.01239	-0.33202	0.33603	0.882159	0.979181	-0.2768
10	-0.72888	-0.64282	-1.04118	0.13236	-0.18425	-0.17339	0.524335	-0.97261
11	-1.54334	-0.90966	-1.23333	0.801135	-0.35393	-0.0496	0.422014	-1.39041
12	0.734163	0.336594	-1.74851	0.177696	-0.36607	-1.01617	-0.91572	0.285304
13	-0.08299	-1.03087	-1.56255	-0.3983	0.028534	-0.00045	-0.63836	-0.70778
14	-0.75259	-0.88778	-1.20852	0.703398	-0.79132	-1.07037	0.257377	-0.10077
15	0.811	0.130058	-1.16391	-0.16098	-1.10368	-1.23961	-0.92942	0.503864
16	-1.50545	-0.22578	0.446751	-1.05506	-1.52191	-1.15962	-1.14207	-1.33865
17	-1.88456	-0.19605	0.822872	1.34748	-1.09371	-0.4543	-0.54614	-1.05905
18	-0.71679	-0.97829	-0.95782	0.964454	0.420057	0.314381	0.7907	-0.43544
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20	-0.65254	0.467307	-0.11772	1.380863	0.0606	0.214798	0.317073	-0.63938
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23	-0.88779	-0.8295	-1.18472	0.869415	-0.42327	-0.39738	-0.26231	-1.38634
24	-0.61967	-0.727	-1.27885	0.265871	-0.05476	-0.2753	-0.30522	-0.82088
25	-1.26181	0.630099	-0.16568	0.127351	0.021887	0.022302	0.12727	-0.75273
26	-0.9317	-0.59289	-0.70058	-0.64865	-0.244	-0.03328	0.003402	-0.96184
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28	-0.09831	-1.48009	-1.5084	-0.07404	-0.02446	0.068175	0.217438	0.411357
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33	-0.46696	-1.18017	-1.16218	0.215408	0.104611	0.42643	0.768182	-0.60385
34	-1.68415	-0.46408	-0.38539	0.286911	-0.03672	0.021101	0.691408	-1.03612
35	-0.44974	-1.17955	-1.25839	-0.23573	0.168901	0.036602	0.788574	-0.2853
36	0.63699	0.993603	-0.44663	-0.20089	-1.1892	-1.19508	-1.35657	0.3804
37	0.180332	0.193894	-0.14022	-0.39459	-0.86483	-0.71266	-0.54127	0.056965
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43	-1.0645	-0.10843	0.376248	0.125929	-0.44348	-0.03026	0.263266	-0.4077



Examples of co-expressed genes and coherent patterns in gene expression data

Iyer's data ^[2]

 € [2] Iyer, V.R. et al. The transcriptional program in the response of human fibroblasts to serum. *Science*, 283:83–87, 1999.

Other Applications

- Marketing: Help marketers discover distinct groups in their customer bases, and then use this knowledge to develop targeted marketing programs
- City-planning: Identifying groups of houses according to their house type, value, and geographical location
- Climate: understanding earth climate, find patterns of atmosphere and ocean

Two Important Aspects

- Properties of input data
 - Define the similarity or dissimilarity between points
- Requirement of clustering
 - Define the objective and methodology

Clustering Basics

- Definition and Motivation
- Data Preprocessing and Distance computation
- Objective of Clustering
- Clustering Evaluation

Data Representation

Objects

- Data: Collection of data objects and their attributes
- An attribute is a property or characteristic of an object
 - Examples: eye color of a person, temperature, etc.
 - Attribute is also known as dimension, variable, field, characteristic, or feature
- A collection of attributes describe an object
 - Object is also known as record, point, case, sample, entity, or instance



Data Matrix

• Represents *n* objects with *p* attributes

– An *n* by *p* matrix



Gene Expression Data

	condition 1	condition 2	condition 3	condition 4	condition
gene 1	0.13	0.72	0.1	0.57	
gene 2	0.34	1.58	1.05	1.15	
gene 3	0.43	1.1	0.97	1	
gene 4	1.22	0.97	1	0.85	
gene 5	-0.89	1.21	1.29	1.08	and the second
gene 6	1.1	1.45	1.44	1.12	
gene 7	0.83	1.15	1.1	1	13 10 12
gene 8	0.87	1.32	1.35	1.13	
gene 9	-0.33	1.01	1.38	1.21	San Charles
gene 10	0.10	0.85	1.03	1	and the second
gene		Barlan			N. Bandan
			1.1.1		the United

Clustering genes

- •Genes are objects
- •Experiment conditions are attributes
- Find genes with similar behavior

Similarity and Dissimilarity

• Similarity

- Numerical measure of how alike two data objects are
- Is higher when objects are more alike
- Often falls in the range [0,1]

• Dissimilarity

- Numerical measure of how different are two data objects
- Lower when objects are more alike
- Minimum dissimilarity is often 0
- Upper limit varies

Types of Attributes

• Discrete

- Has only a finite or countably infinite set of values
- Examples: zip codes, counts, or the set of words in a collection of documents
- Note: binary attributes are a special case of discrete attributes

• Ordinal

- Has only a finite or countably infinite set of values
- Order of values is important
- Examples: rankings (e.g., pain level 1-10), grades (A, B, C, D)

Continuous

- Has real numbers as attribute values
- Examples: temperature, height, or weight
- Continuous attributes are typically represented as floating-point variables

Similarity/Dissimilarity for Simple Attributes

p and *q* are the attribute values for two data objects.

Attribute	Dissimilarity	Similarity
Type		
Discrete	$d = \left\{egin{array}{cc} 0 & ext{if} \ p = q \ 1 & ext{if} \ p eq q \end{array} ight.$	$s = \left\{egin{array}{ccc} 1 & ext{if} \; p = q \ 0 & ext{if} \; p eq q \end{array} ight.$
Ordinal	$d = \frac{ p-q }{n-1}$ (values mapped to integers 0 to $n-1$, where n is the number of values)	$s = 1 - \frac{ p-q }{n-1}$
Continuous	d = p-q	$s = -d, s = \frac{1}{1+d}$ or
		$s = 1 - \frac{d - min_d}{max_d - min_d}$

Dissimilarity and similarity between *p* and *q*

Distance Matrix

• Represents pairwise distance in *n* objects

- An *n* by *n* matrix
- d(i,j): distance or dissimilarity between objects i and j
- Nonnegative
- Close to 0: similar

Data Matrix -> Distance Matrix

	s 1	s 2	s 3	s 4	
g 1	0.13	0.72	0.1	0.57	
g 2	0.34	1.58	1.05	1.15	in the U
g 3	0.43	1.1	0.97	1	1910
g 4	1.22	0.97	1	0.85	
g 5	-0.89	1.21	1.29	1.08	
g 6	1.1	1.45	1.44	1.12	
g 7	0.83	1.15	1.1	1	13.0
g 8	0.87	1.32	1.35	1.13	- 10 M
g 9	-0.33	1.01	1.38	1.21	
g 10	0.10	0.85	1.03	1	

Original Data Matrix

	g 1	g 2	g 3	g 4	
g 1	0	<i>d</i> (1,2)	<i>d</i> (1,3)	<i>d</i> (1,4)	
g 2		0	<i>d</i> (2,3)	<i>d</i> (2,4)	
g 3			0	<i>d</i> (3,4)	
g 4				0	

Distance Matrix

Minkowski Distance—Continuous Attribute

• Minkowski distance: a generalization

$$d(i,j) = \sqrt{\frac{q}{1} |x_{i_1} - x_{j_1}|^q + |x_{i_2} - x_{j_2}|^q + \dots + |x_{i_p} - x_{j_p}|^q} \quad (q > 0)$$

- If q = 2, d is Euclidean distance
- If q = 1, d is Manhattan distance





Standardization

Calculate the mean absolute deviation

$$m_f = \frac{1}{n}(x_{1f} + x_{2f} + \dots + x_{nf})$$

$$s_f = \frac{1}{n} (|x_{1f} - m_f| + |x_{2f} - m_f| + \dots + |x_{nf} - m_f|)$$

• Calculate the standardized measurement (z-score)

$$z_{if} = \frac{x_{if} - m_f}{s_f}$$

Mahalanobis Distance

$$d(p,q) = (p - q) \mathbf{a}^{-1} (p - q)^{T}$$



S is the covariance matrix of the input data *X*

$$\mathbf{S}_{j,k} = \frac{1}{n-1} \mathop{\mathbf{a}}\limits_{i=1}^{n} (X_{ij} - \overline{X}_j)(X_{ik} - \overline{X}_k)$$

For red points, the Euclidean distance is 14.7, Mahalanobis distance is 6.

Mahalanobis Distance



Common Properties of a Distance

- Distances, such as the Euclidean distance, have some well known properties
 - 1. $d(p, q) \stackrel{3}{=} 0$ for all p and q and d(p, q) = 0 only if p = q. (Positive definiteness)
 - 2. d(p, q) = d(q, p) for all p and q. (Symmetry)
 - 3. $d(p, r) \pounds d(p, q) + d(q, r)$ for all points p, q, and r. (Triangle Inequality)

where d(p, q) is the distance (dissimilarity) between points (data objects), p and q.

 A distance that satisfies these properties is a metric

Similarity for Binary Attributes

- Common situation is that objects, *p* and *q*, have only binary attributes
- Compute similarities using the following quantities
 M₀₁ = the number of attributes where p was 0 and q was 1
 M₁₀ = the number of attributes where p was 1 and q was 0
 M₀₀ = the number of attributes where p was 0 and q was 0
 M₁₁ = the number of attributes where p was 1 and q was 1
- Simple Matching and Jaccard Coefficients

SMC = number of matches / total number of attributes = $(M_{11} + M_{00}) / (M_{01} + M_{10} + M_{11} + M_{00})$

J = number of matches / number of not-both-zero attributes values = $(M_{11}) / (M_{01} + M_{10} + M_{11})$

SMC versus Jaccard: Example

p = 1000000000q = 00000001001

 $M_{01} = 2$ (the number of attributes where p was 0 and q was 1) $M_{10} = 1$ (the number of attributes where p was 1 and q was 0) $M_{00} = 7$ (the number of attributes where p was 0 and q was 0) $M_{11} = 0$ (the number of attributes where p was 1 and q was 1)

$$SMC = (M_{11} + M_{00})/(M_{01} + M_{10} + M_{11} + M_{00}) = (0+7)/(2+1+0+7) = 0.7$$

$$J = (M_{11}) / (M_{01} + M_{10} + M_{11}) = 0 / (2 + 1 + 0) = 0$$

Document Data

- Each document becomes a `term' vector,
 - each term is a component (attribute) of the vector,
 - the value of each component is the number of times the corresponding term occurs in the document.

	team	coach	pla y	ball	score	game	wi n	lost	timeout	season
Document 1	3	0	5	0	2	6	0	2	0	2
Document 2	0	7	0	2	1	0	0	3	0	0
Document 3	0	1	0	0	1	2	2	0	3	0

Cosine Similarity

 If d₁ and d₂ are two document vectors, then cos(d₁, d₂) = (d₁ · d₂) / ||d₁|| ||d₂||, where · indicates vector dot product and ||d|| is the length of vector d.

• Example:

 $d_1 = 3205000200$ $d_2 = 100000102$

 $\begin{aligned} d_1 \cdot d_2 &= 3^*1 + 2^*0 + 0^*0 + 5^*0 + 0^*0 + 0^*0 + 0^*0 + 2^*1 + 0^*0 + 0^*2 = 5 \\ &||d_1|| = (3^*3 + 2^*2 + 0^*0 + 5^*5 + 0^*0 + 0^*0 + 0^*0 + 2^*2 + 0^*0 + 0^*0)^{0.5} = (42)^{0.5} = 6.481 \\ &||d_2|| = (1^*1 + 0^*0 + 0^*0 + 0^*0 + 0^*0 + 0^*0 + 1^*1 + 0^*0 + 2^*2)^{0.5} = (6)^{0.5} = 2.245 \end{aligned}$

 $\cos(d_1, d_2) = .3150$

Correlation

- Correlation measures the linear relationship between objects
- To compute correlation, we standardize data objects, p and q, and then take their dot product (continuous attributes)

$$p \not c = (p_k - mean(p)) / std(p)$$
$$q \not c = (q_k - mean(q)) / std(q)$$
$$s(p,q) = p \not c q \not c$$

Common Properties of a Similarity

- Similarities, also have some well known properties.
 - 1. s(p, q) = 1 (or maximum similarity) only if p = q.
 - 2. s(p, q) = s(q, p) for all p and q. (Symmetry)

where s(p, q) is the similarity between points (data objects), p and q.

Characteristics of the Input Data Are Important

- Sparseness
- Attribute type
- Type of Data
- Dimensionality
- Noise and Outliers
- Type of Distribution
- => Conduct preprocessing and select the appropriate dissimilarity or similarity measure
- => Determine the objective of clustering and choose the appropriate method

Clustering Basics

- Definition and Motivation
- Data Preprocessing and Distance computation
- Objective of Clustering
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Considerations for Cluster Analysis

• Partitioning criteria

Single level vs. hierarchical partitioning (often, multi-level hierarchical partitioning is desirable)

• Separation of clusters

 Exclusive (e.g., one customer belongs to only one region) vs. overlapping (e.g., one document may belong to more than one topic)

Hard versus fuzzy

- In fuzzy clustering, a point belongs to every cluster with some weight between 0 and 1
- Weights must sum to 1
- Probabilistic clustering has similar characteristics
- Similarity measure and data types
- Heterogeneous versus homogeneous
 - Cluster of widely different sizes, shapes, and densities

Requirements of Clustering

- Scalability
- Ability to deal with different types of attributes
- Minimal requirements for domain knowledge to determine input parameters
- Able to deal with noise and outliers
- Discovery of clusters with arbitrary shape
- Insensitive to order of input records
- High dimensionality
- Incorporation of user-specified constraints
- Interpretability and usability
- What clustering results we want to get?

Notion of a Cluster can be Ambiguous



Two Clusters

Four Clusters

Partitional Clustering



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Hierarchical Clustering



Clustering Solution 2

Types of Clusters: Center-Based

Center-based

- A cluster is a set of objects such that an object in a cluster is closer (more similar) to the "center" of a cluster, than to the center of any other cluster
- The center of a cluster is often a centroid, the average of all the points in the cluster, or a medoid, the most "representative" point of a cluster



4 center-based clusters

Types of Clusters: Density-Based

• Density-based

- A cluster is a dense region of points, which is separated by lowdensity regions, from other regions of high density.
- Used when the clusters are irregular or intertwined, and when noise and outliers are present.

6 density-based clusters

Clustering Basics

- Definition and Motivation
- Data Preprocessing and Distance computation
- Objective of Clustering
- Clustering Evaluation

Cluster Validation

Cluster validation

- Quality: "goodness" of clusters
- Assess the quality and reliability of clustering results

• Why validation?

- To avoid finding clusters formed by chance
- To compare clustering algorithms
- To choose clustering parameters
 - e.g., the number of clusters

Aspects of Cluster Validation

- Comparing the clustering results to *ground truth* (externally known results)
 - External Index
- Evaluating the quality of clusters *without* reference to external information
 - Use only the data
 - Internal Index
- Determining the *reliability* of clusters
 - To what confidence level, the clusters are not formed by chance
 - Statistical framework

Comparing to Ground Truth

Notation

- N: number of objects in the data set
- $P=\{P_1,...,P_s\}$: the set of "ground truth" clusters
- $C = \{C_1, ..., C_t\}$: the set of clusters reported by a clustering algorithm
- The "incidence matrix"
 - N´ N (both rows and columns correspond to objects)
 - P_{ij} = 1 if O_i and O_j belong to the same "ground truth" cluster in P; P_{ij} =0 otherwise
 - $C_{ij} = 1$ if O_i and O_j belong to the same cluster in C; $C_{ij}=0$ otherwise

Rand Index and Jaccard Coefficient

- A pair of data object (O_{i}, O_{j}) falls into one of the following categories
 - SS: $C_{ij}=1$ and $P_{ij}=1$; (agree) - DD: $C_{ij}=0$ and $P_{ij}=0$; (agree)
 - SD: C_{ij} =1 and P_{ij} =0; (disagree)
 - DS: $C_{ij}=0$ and $P_{ij}=1$; (disagree)
- **Rand index** $Rand = \frac{|Agree|}{|Agree| + |Disagree|} = \frac{|SS| + |DD|}{|SS| + |SD| + |DS| + |DD|}$

may be dominated by DD

Jaccard Coefficient

Jaccard coefficient = $\frac{|SS|}{|SS| + |SD| + |DS|}$

Clustering

		g 1	g 2	g 3	g 4	g 5	
	g 1	1	1	1	0	0	
	g 2	1	1	1	0	0	
	g 3	1	1	1	0	0	
Î	g 4	0	0	0	1	1	Ground
	g 5	0	0	0	1	1	

Clustering

		Same	Different
		Cluster	Cluster
th	Same Cluster	9	4
\rightarrow	Different Cluster	4	8

Groundtruth

	g 1	g 2	g 3	g 4	g 5
g 1	1	1	0	0	0
g 2	1	1	0	0	0
g 3	0	0	1	1	1
g 4	0	0	1	1	1
g 5	0	0	1	1	1

$$Rand = \frac{|SS| + |DD|}{|SS| + |SD| + |DS| + |DD|} = \frac{17}{25}$$

$$Jaccard = \frac{|SS|}{|SS| + |SD| + |DS|} = \frac{9}{17}$$

Entropy and Purity

• Notation

- $|C_k \mathbf{\hat{C}} P_j|$ the number of objects in both the *k*-th cluster of the clustering solution and *j*-th cluster of the groundtruth
- $|C_k|$ the number of objects in the *k*-th cluster of the clustering solution
- $|P_j|$ the number of objects in the *j*-th cluster of the groundtruth

• **Purity**
$$Purity = \frac{1}{N} \overset{\circ}{a}_{k} \max_{j} |C_{k} \not C P_{j}|$$

Normalized Mutual Information

$$NMI = \frac{I(C,P)}{\sqrt{H(C)H(P)}} \qquad I(C,P) = \mathop{\texttt{a}}_{k} \mathop{\texttt{a}}_{j} \frac{|C_{k} \operatorname{\texttt{C}} P_{j}|}{N} \log \frac{N \rtimes |C_{k} \operatorname{\texttt{C}} P_{j}|}{|C_{k} || P_{j}|}$$
$$H(C) = \mathop{\texttt{a}}_{k} \frac{|C_{k}|}{N} \log \frac{|C_{k}|}{N} \qquad H(P) = \mathop{\texttt{a}}_{j} \frac{|P_{j}|}{N} \log \frac{|P_{j}|}{N} \log \frac{|P_{j}|}{N} \log \frac{|P_{j}|}{N}$$

Example

	P 1	P 2	Р3	P 4	P5	P6	Total
C1	3	5	40	506	96	27	677
C 2	4	7	280	29	39	2	361
C 3	1	1	1	7	4	671	685
C 4	10	162	3	119	73	2	369
C 5	331	22	5	70	13	23	464
C 6	5	358	12	212	48	13	648
total	354	555	341	943	273	738	3204

$$Purity = \frac{1}{N} \mathop{\text{a}}_{k} \max_{j} |C_{k} \bigvee P_{j}|$$

$$Purity = \frac{506 + 280 + 671 + 162 + 331 + 358}{3204}$$
$$= 0.7203$$

$$NMI = \frac{I(C, P)}{\sqrt{H(C)H(P)}} \qquad I(C, P) = \mathop{\texttt{a}}_{k} \mathop{\texttt{a}}_{j} \frac{|C_{k} \bigvee P_{j}|}{N} \log \frac{N \rtimes |C_{k} \bigvee P_{j}|}{|C_{k} ||P_{j}|}$$
$$H(C) = \mathop{\texttt{a}}_{k} \frac{|C_{k}|}{N} \log \frac{|C_{k}|}{N} \qquad H(P) = \mathop{\texttt{a}}_{j} \frac{|P_{j}|}{N} \log \frac{|P_{j}|}{N} \qquad 47$$

Internal Index

- "Ground truth" may be unavailable
- Use only the data to measure cluster quality
 - Measure the "cohesion" and "separation" of clusters
 - Calculate the *correlation* between clustering results and distance matrix

Cohesion and Separation

• **Cohesion** is measured by the within cluster sum of squares

$$WSS = \mathop{\text{a}}_{i} \mathop{\text{a}}_{xi}^{\circ} (x - m_i)^2$$

• **Separation** is measured by the between cluster sum of squares

$$BSS = \mathop{\mathbf{a}}_{i} |C_{i}| (m - m_{i})^{2}$$

where |*Ci*| is the size of cluster *i*, m is the centroid of the whole data set

- BSS + WSS = constant
- WSS (Cohesion) measure is called Sum of Squared Error (SSE)—a commonly used measure
- A larger number of clusters tend to result in smaller SSE

Example

Silhouette Coefficient

- Silhouette Coefficient combines ideas of both cohesion and separation
- For an individual point, *i*
 - Calculate a = average distance of i to the points in its cluster
 - Calculate b = min (average distance of i to points in another cluster)
 - The silhouette coefficient for a point is then given by

s = 1 - a/b if a < b, (s = b/a - 1 if a ³ b, not the usual case)

- Typically between 0 and 1
- The closer to 1 the better

• Can calculate the Average Silhouette width for a cluster or a clustering

Correlation with Distance Matrix

- Distance Matrix
 - D_{ij} is the similarity between object O_i and O_j
- Incidence Matrix
 - $C_{ij}=1$ if O_i and O_j belong to the same cluster, $C_{ij}=0$ otherwise
- Compute the correlation between the two matrices
 - Only *n*(*n*-1)/2 entries needs to be calculated
- High correlation indicates good clustering

Correlation with Distance Matrix

- Given Distance Matrix D = $\{d_{11}, d_{12}, ..., d_{nn}\}$ and Incidence Matrix $C = \{c_{11}, c_{12}, ..., c_{nn}\}$.
- Correlation *r* between *D* and *C* is given by

$$r = \frac{\overset{n}{\mathbf{a}} (d_{ij} - \bar{d})(c_{ij} - \bar{c})}{\sqrt{\overset{n}{\overset{n}{\mathbf{a}}} (d_{ij} - \bar{d})^2} \sqrt{\overset{n}{\overset{n}{\mathbf{a}}} (c_{ij} - \bar{c})^2}}$$

Are There Clusters in the Data?

Measuring Cluster Validity Via Correlation

• Correlation of incidence and distance matrices for the Kmeans clusterings of the following two data sets

Corr = -0.9235

Corr = -0.5810

Using Similarity Matrix for Cluster Validation

• Order the similarity matrix with respect to cluster labels and inspect visually.

Using Similarity Matrix for Cluster Validation

• Clusters in random data are not so crisp

Reliability of Clusters

- Need a framework to interpret any measure
 - For example, if our measure of evaluation has the value, 10, is that good, fair, or poor?
- Statistics provide a framework for cluster validity
 - The more "atypical" a clustering result is, the more likely it represents valid structure in the data

Statistical Framework for SSE

• Example

- Compare SSE of 0.005 against three clusters in random data
- SSE Histogram of 500 sets of random data points of size 100 lowest SSE is 0.0173

Determine the Number of Clusters Using SSE

• SSE curve

Clustering of Input Data

SSE wrt K

Take-away Message

- What's clustering?
- Why clustering is important?
- How to preprocess data and compute dissimilarity/similarity from data?
- What's a good clustering solution?
- How to evaluate the clustering results?