Expectation-Maximization

Course policies

출석: I0주 이상 참석 (2/3) (학칙)

모든 수업은 zoom사용 예정

수업자료: 포털/과목 메인 페이지

모든 공지는 포털/공지시항에 포스팅 함

수업: video on, audio off

중간, 기말: 반드시 참석 (하나라도 치르지 않으면 F)

학칙이 허용하는 예외 사유만 허용

기말 시험은 offline (14-16주 사이)

중간 시험은 offline이 가능하면 실시 (7-9주 사이).

불가능하면 기말에 같이 실시

질문: 수업 중 마이크 사용하여 직접, 채팅창에서

수업 후 메일로 (타이틀에 [지능형생물정보학] 포함)

Review: Expectation-Maximization (EM) vs. MLE

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? HTTTHHTHTH? HHHHHHHHHHHH? HTHHHHHHHHTH? THHHHTHHHTH
```

$$\hat{\theta}_{A} = ?$$

$$\hat{\theta}_{B} = ?$$

?HHHHTTHTHT

Review: Expectation-Maximization (EM)

EM is a procedure for learning hidden variables from partially observed data

X: observed variable

Z: hidden variable

 θ : parameters for model

assign arbitrary values for parameters θ

iterate until convergence

E step: estimate the values of hidden variable Z by using θ and X

$$Z = \operatorname{argmax} P(Z \mid X, \theta)$$

M step: obtain more accurate parameters θ using observed variable X and estimated Z

(use MLE for parameters)

$$\theta = \operatorname{argmax} P(D \mid \theta_k)$$

$$\Theta_{A}^{(1)} = 0.8, \quad \Theta_{B}^{(1)} = 0.45$$

$$Z = \operatorname{argmax} P(Z \mid X, \theta)$$

| | X | А | В | Z |
|---|---|------|------|---|
| 1 | 5 | 0.1 | 0.9 | В |
| 2 | 9 | 0.98 | 0.02 | Α |
| 3 | 8 | | | Α |
| 4 | 4 | | | А |
| 5 | 7 | | | А |

| | А | В |
|---|------|------|
| 1 | | 5H5T |
| 2 | 9H1T | |
| 3 | 8H2T | |
| 4 | 4H6T | |
| 5 | 7H3T | |

$$P(d_1 \mid \theta_A^{(1)}) = 10C_5 \quad 0.8^5 \quad 0.2^5 = 0.026$$

$$P(d_1 \mid \theta_B^{(1)}) = 10C_5 \quad 0.45^5 \quad 0.55^5 = 0.234$$

$$P(z^{I} = A \mid d_{I}) = \frac{P(d_{I} \mid \theta_{A}^{(I)})}{P(d_{I} \mid \theta_{A}^{(I)}) + P(d_{I} \mid \theta_{B}^{(I)})} = 0.1$$

$$\theta A^{(2)} = 28 / (28 + 12) = 0.7$$

 $\Theta_B^{(2)} = 5 / (5+5) = 0.5$

E-step: assign the expected values to the hidden variable

M-step: update the parameters that maximize the probability

Review: EM: coin example for soft assignment

randomly assigned for the first iteration

$$\theta_{A}^{(0)} = 0.6, \quad \theta_{B}^{(0)} = 0.5$$

$$Z = P(Z \mid X, \theta)$$

| | | * | | |
|---|---|------|------|---|
| | X | Pa | Рв | Z |
| 1 | 5 | 0.45 | 0.55 | |
| 2 | 9 | 0.80 | 0.20 | |
| 3 | 8 | 0.73 | 0.27 | |
| 4 | 4 | 0.35 | 0.65 | |
| | | | | |

0.35

| X | is the number of heads |
|------|------------------------|
| z is | s the type of coin |

0.65

5

E-step: assign the expected values to the hidden variable based on the given model

| Z | |
|---|--|
| В | |
| Α | |
| А | |
| В | |
| А | |

| | А | В |
|---|------|------|
| 1 | | 5H5T |
| 2 | 9H1T | |
| 3 | 8H2T | |
| 4 | | 4H6T |
| 5 | 7H3T | |

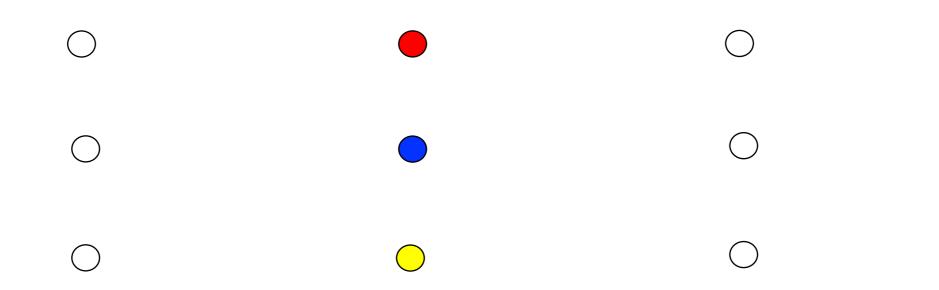
| | Α | В | |
|---|-----------|-----------|------------------|
| 1 | 2.2H 2.2T | 2.8H 2.8H | 5H5 ⁻ |
| 2 | 7.2H 0.8T | 1.8H 0.2T | 9H1 ⁻ |
| 3 | 5.9H 1.5T | 2.1H 0.5T | 8H2 ⁻ |
| 4 | 1.4H 2.1H | 2.6H 3.9T | 4H6 ⁻ |
| 5 | 4.5H 1.9T | 2.5H 1.1T | 7H3 ⁻ |

$$\Theta_A^{(1)} = 21.3 / (21.3 + 8.6) = 0.71$$

$$\Theta_B^{(1)} = 11.7 / (11.7 + 8.4) = 0.58$$

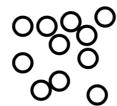
M-step: update the parameters that maximize the probability

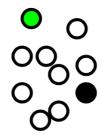
K-means clustering

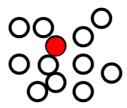


Local optimum: every point is assigned to its nearest center and every center is the mean value of its points

K-means clustering



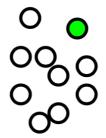


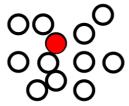


Local optimum: every point is assigned to its nearest center and every center is the mean value of its points

K-means clustering



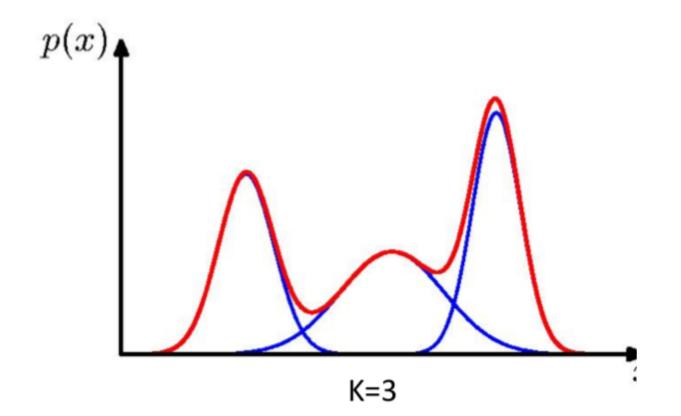




One approach is to pick furthest points (farthest point cluster, k-means ++)

- → Pick the initial point at random
- → Each subsequent point is picked from the remaining points with probability proportional to its squared distance to the points's closest cluster center
- → might be sensitive to outliers

Mixture models



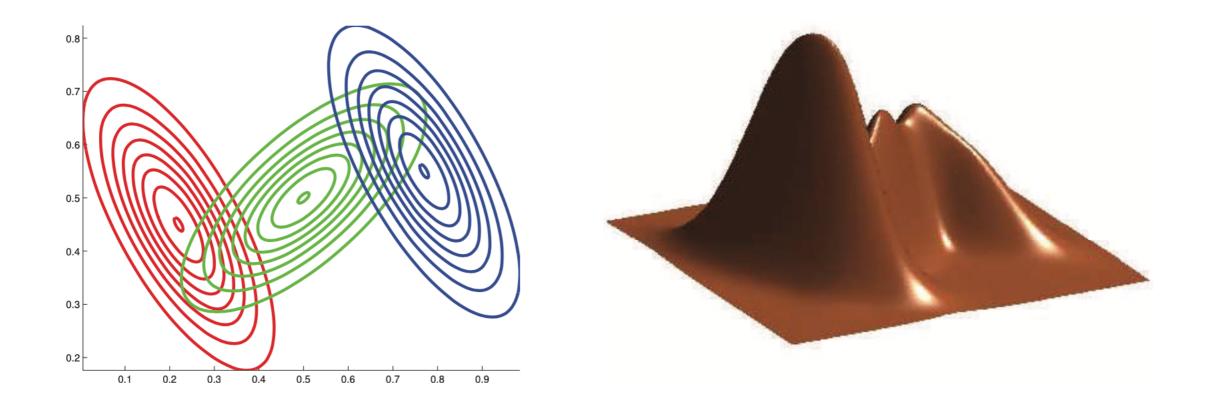
$$p(\mathbf{x}) = \sum_{k=1}^K \pi_k \mathcal{N}(\mathbf{x}|oldsymbol{\mu}_k, oldsymbol{\Sigma}_k)$$
 Component Mixing coefficient (weight)

$$\forall k : \pi_k \geqslant 0 \qquad \sum_{k=1}^K \pi_k = 1$$

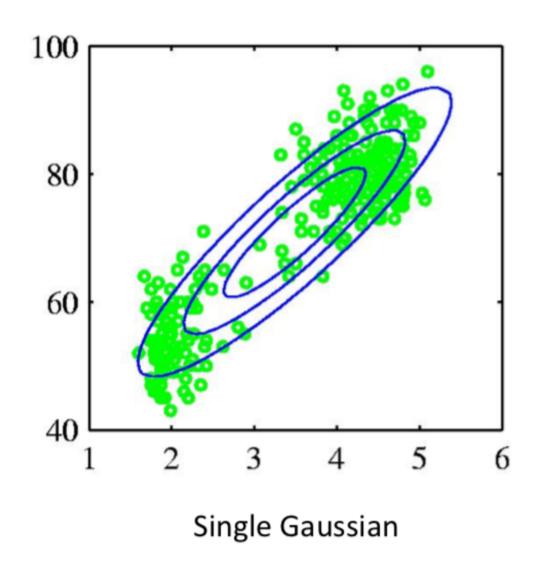
- A probabilistic model for representing the presence of subpopulations within an overall population
- way of doing soft clustering
- each cluster has a generative model such as Gaussian

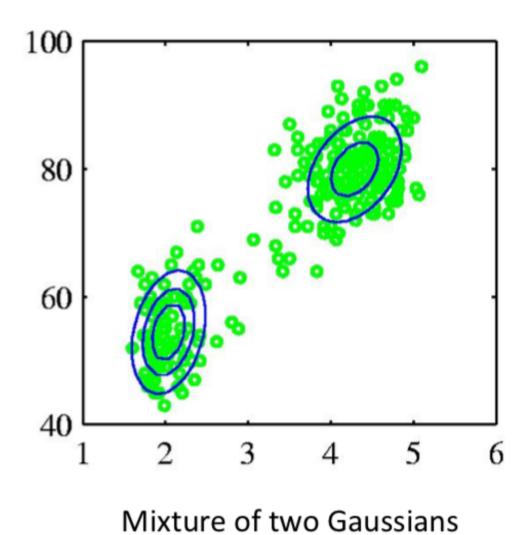
(Gaussian mixture model; GMM)

Mixture models with Multivariate Gaussian

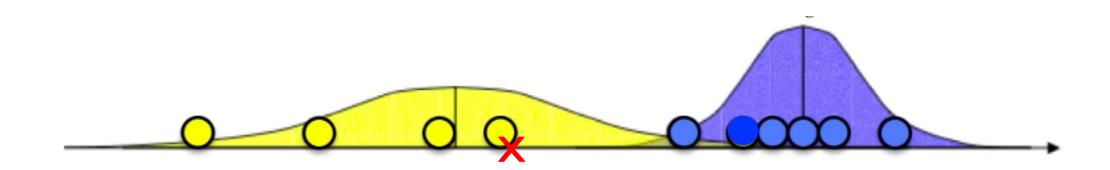


Mixture models with Multivariate Gaussian





Supervised learning



Univariate Gaussian

$$\mu_{MLE} = \frac{1}{N} \sum_{i=1}^{N} x_i \qquad \sigma_{MLE}^2 = \frac{1}{N} \sum_{i=1}^{N} (x_i - \hat{\mu})^2$$

Review: K-means clustering

- K-means clustering uses EM approach
 - choose an initial values for μk
 - repeat two steps
 - E-step: assign each example to the nearest prototype by minimizing J;
 - → determine r_{nk}

$$o$$
 determine r_{nk} $z_i^* = rg \min_j \|\mathbf{x}_n - \boldsymbol{\mu}_j\|^2$ $z_i^* = rg \min_k ||\mathbf{x}_i - \boldsymbol{\mu}_k||_2^2$ $r_{nk} = egin{cases} 1 & ext{if } k = rg \min_j \|\mathbf{x}_n - \boldsymbol{\mu}_j\|^2 \\ 0 & ext{otherwise.} \end{cases}$

$$z_i^* = rg \min_k ||\mathbf{x}_i - \boldsymbol{\mu}_k||_2^2$$

- M-step: update the prototypes with the data points assigned;
 - \rightarrow determine μk with the new $r_n k$

$$J = \sum_{n=1}^{N} \sum_{k=1}^{K} r_{nk} \|\mathbf{x}_n - \boldsymbol{\mu}_k\|^2$$

$$2\sum_{n=1}^N r_{nk}(\mathbf{x}_n - \boldsymbol{\mu}_k) = 0$$
 For each k, set the derivative of J to 0 with respect to μ_k

$$oldsymbol{\mu}_k = rac{\sum_n r_{nk} \mathbf{x}_n}{\sum_n r_{nk}}$$

EM for Gaussian mixture

$$r_{ik} \triangleq p(z_i = k | \mathbf{x}_i, \boldsymbol{\theta}) = \frac{p(z_i = k | \boldsymbol{\theta}) p(\mathbf{x}_i | z_i = k, \boldsymbol{\theta})}{\sum_{k'=1}^{K} p(z_i = k' | \boldsymbol{\theta}) p(\mathbf{x}_i | z_i = k', \boldsymbol{\theta})}$$

→ Responsibility of cluster k for data i

soft assignment vs hard assignment in E step

$$z_i^* = \arg\max_k r_{ik}$$

EM for Gaussian mixture

E-step: evaluate the responsibilities (assignments)

$$r_{ik} = \frac{\pi_k p(\mathbf{x}_i | \boldsymbol{\theta}_k^{(t-1)})}{\sum_{k'} \pi_{k'} p(\mathbf{x}_i | \boldsymbol{\theta}_{k'}^{(t-1)})}$$

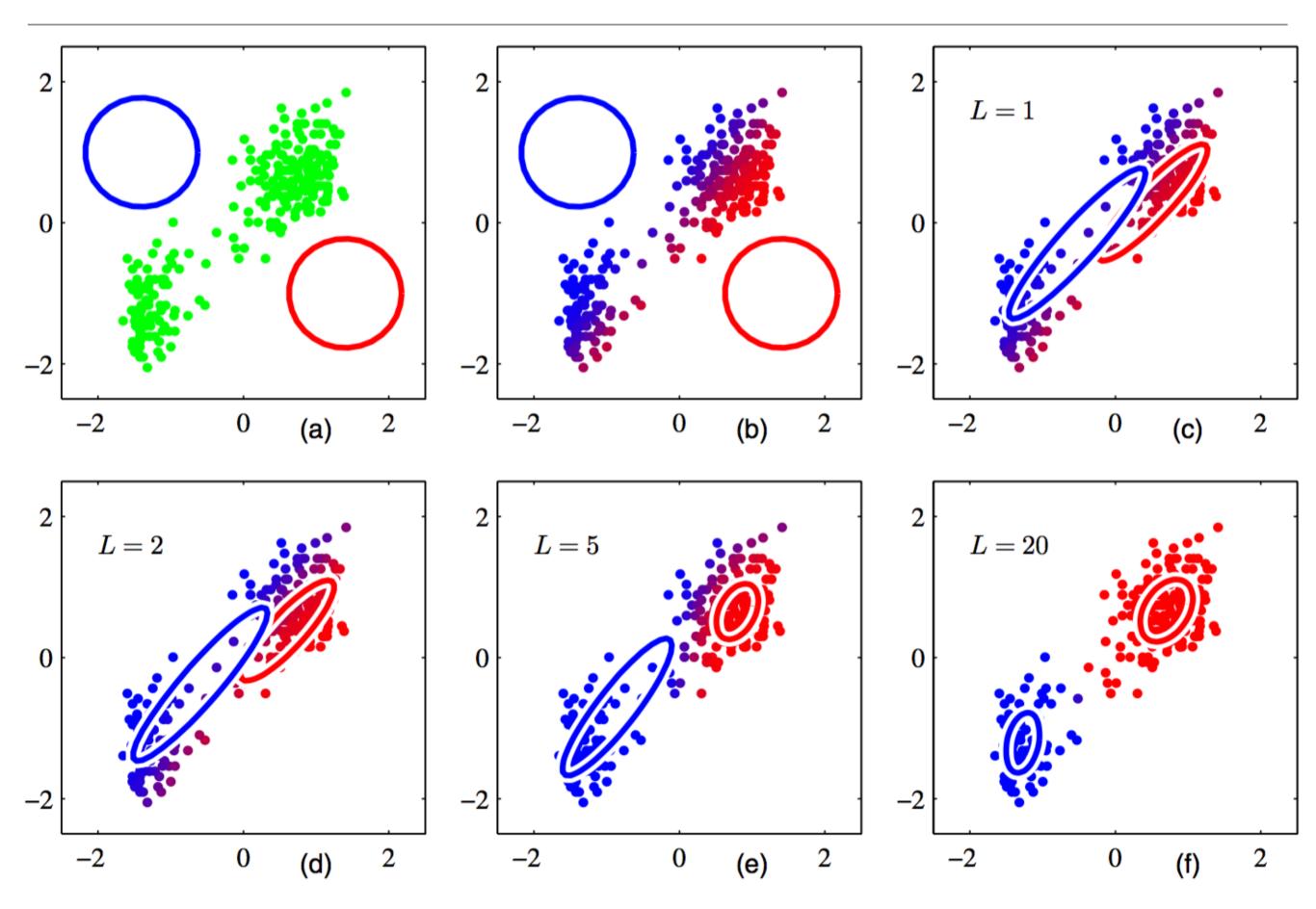
M-step: re-estimate the means, covariances, and mixing coefficients

$$\pi_k = \frac{1}{N} \sum_i r_{ik} = \frac{r_k}{N}$$
 — Weighted number of data assigned to cluster k

$$egin{array}{lcl} oldsymbol{\mu}_k & = & rac{\sum_i r_{ik} \mathbf{x}_i}{r_k} \ oldsymbol{\Sigma}_k & = & rac{\sum_i r_{ik} (\mathbf{x}_i - oldsymbol{\mu}_k) (\mathbf{x}_i - oldsymbol{\mu}_k)^T}{r_k} \end{array}$$

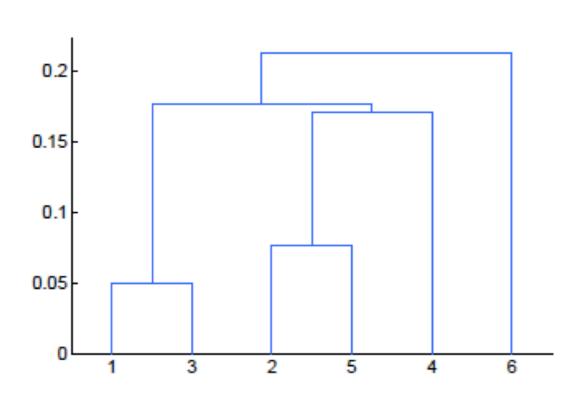
$$oldsymbol{\Sigma}_k = rac{\sum_i r_{ik} (\mathbf{x}_i - oldsymbol{\mu}_k) (\mathbf{x}_i - oldsymbol{\mu}_k)^T}{r_k}$$

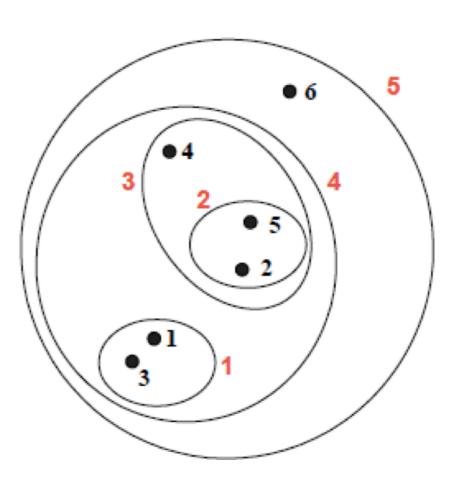
- The mean of cluster k is the weighted average of all data points assigned to cluster k
- The covariance is proportional to the weighted empirical scatter matrix



Hierarchical clustering

- use distance matrix
- do not need the number of clusters (=k) as input
- need to decide when to stop
- bottom-up(agglomerative) and top-down(divisive) approaches

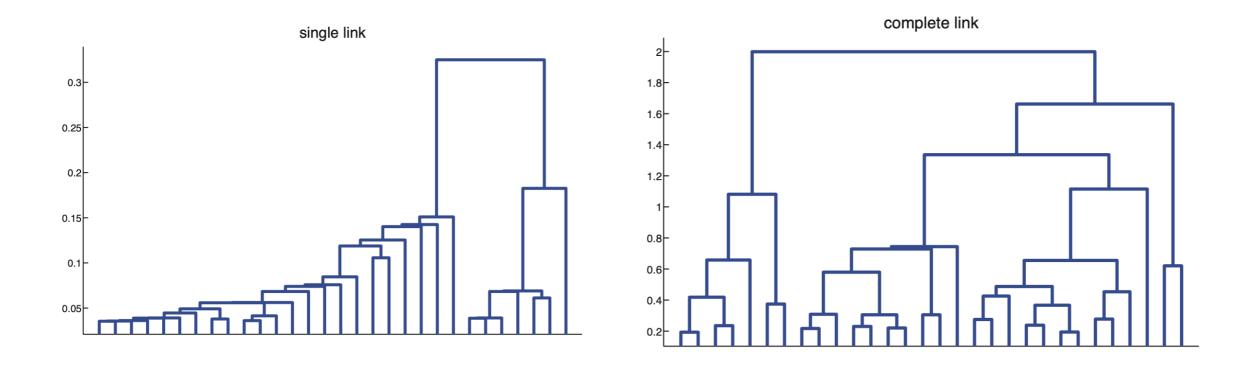


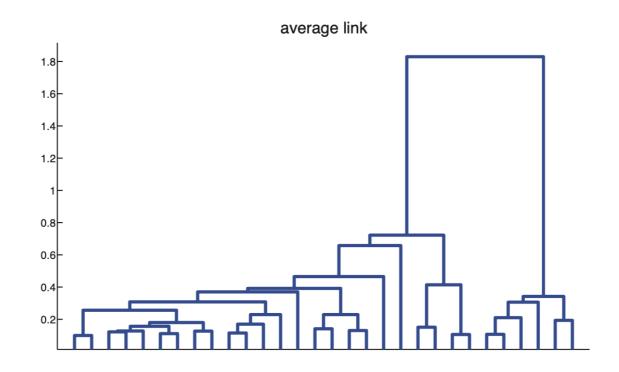


Algorithm

```
1 initialize clusters as singletons: for i \leftarrow 1 to n do C_i \leftarrow \{i\};
   initialize set of clusters available for merging: S \leftarrow \{1, \ldots, n\};
 3 repeat
        Pick 2 most similar clusters to merge: (j,k) \leftarrow \arg\min_{j,k \in S} d_{j,k};
 4
        Create new cluster C_{\ell} \leftarrow C_{i} \cup C_{k};
 5
        Mark j and k as unavailable: S \leftarrow S \setminus \{j, k\};
 6
        if C_{\ell} \neq \{1, \ldots, n\} then
 7
             Mark \ell as available, S \leftarrow S \cup \{\ell\};
 8
        foreach i \in S do
 9
             Update dissimilarity matrix d(i, \ell);
10
11 until no more clusters are available for merging;
```

Agglomerative clustering

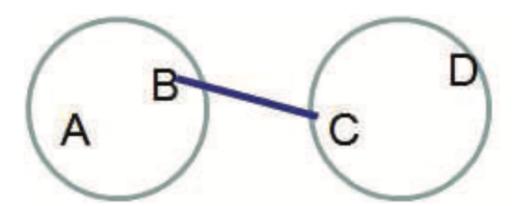




Single link clustering

- Nearest neighbor clustering
- The distance between two groups G and H is defined as the distance between the two closest members of each group

$$d_{SL}(G,H) = \min_{i \in G, i' \in H} d_{i,i'}$$



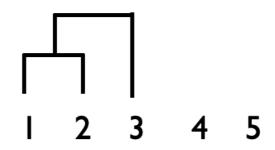
Bottom-up approach

$$\begin{aligned} d_{(1,2),3} &= \min\{d_{1,3},d_{2,3}\} = \min\left\{6,3\right\} = 3\\ d_{(1,2),4} &= \min\{d_{1,4},d_{2,4}\} = \min\left\{10,9\right\} = 9\\ d_{(1,2),5} &= \min\{d_{1,5},d_{2,5}\} = \min\left\{9,8\right\} = 8 \end{aligned}$$

Bottom-up approach

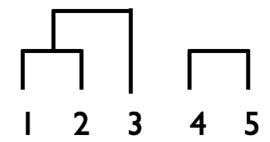
$$d_{(1,2,3),4} = \min\{d_{(1,2),4}, d_{3,4}\} = \min\{9, 7\} = 7$$

$$d_{(1,2,3),5} = \min\{d_{(1,2),4}, d_{3,4}\} = \min\{8, 5\} = 5$$



Bottom-up approach

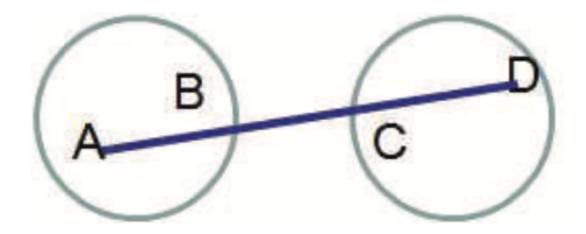
$$d_{(1,2,3),(4,5)} = \min\{d_{(1,2,3),4}, d_{(1,2,3),5}\} = \min\{7,5\} = 5$$



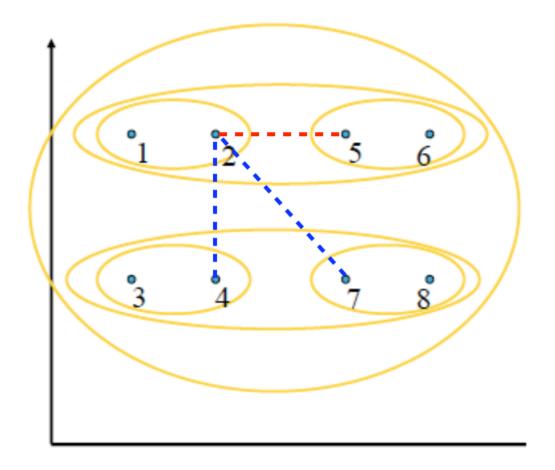
Complete link clustering

- Furthest neighbor clustering
- The distance between two groups G and H is defined as the distance between the two closest members of each group

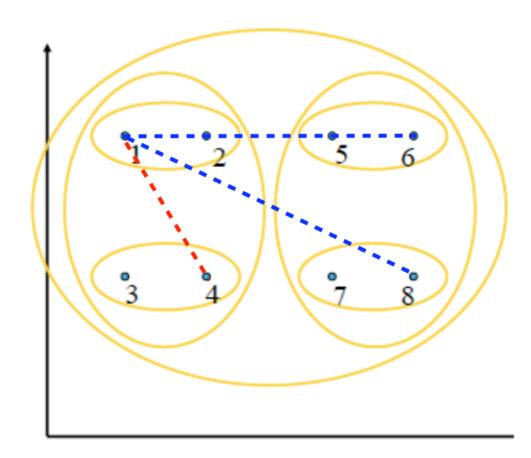
$$d_{CL}(G,H) = \max_{i \in G, i' \in H} d_{i,i'}$$



single linkage



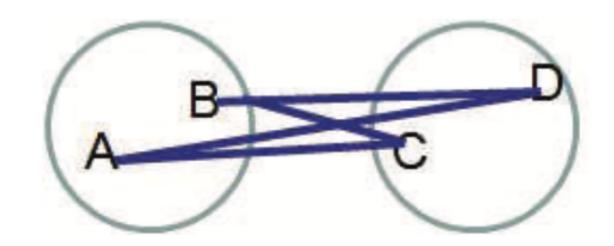
complete linkage



Average link clustering

- Measures the average distance between all pairs

$$d_{avg}(G, H) = \frac{1}{n_G n_H} \sum_{i \in G} \sum_{i' \in H} d_{i,i'}$$



Ward's method

- The distance between two clusters is how much the sum of squares will increase when the clusters are merged
- Keep the growth of this merging cost as small as possible

$$\Delta(A,B) = \sum_{i \in A \cup B} \|\vec{x}_i - \vec{m}_{A \cup B}\|^2 - \sum_{i \in A} \|\vec{x}_i - \vec{m}_A\|^2 - \sum_{i \in B} \|\vec{x}_i - \vec{m}_B\|^2$$

Divisive clustering

Bisecting k-means

- Pick the cluster with the largest diameter and split it using the k-means algorithm with K=2