CSCE 478/878 Lecture 8: Clustering

Stephen Scott

sscott@cse.unl.edu

←□ → ←団 → ← 분 → ← 분 → りへ(~)

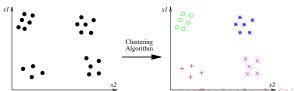
4 D > 4 D > 4 E > 4 E > E +990

Nebraska

Introduction

 If no label information is available, can still perform unsupervised learning

- Looking for structural information about instance space instead of label prediction function
- Approaches: density estimation, clustering, dimensionality reduction
- Clustering algorithms group similar instances together based on a similarity measure



Nebraska

Outline

Outline

- Clustering background
 - Similarity/dissimilarity measures
- k-means clustering
- Hierarchical clustering

Nebraska

Clustering Background

 Goal: Place patterns into "sensible" clusters that reveal similarities and differences

Definition of "sensible" depends on application

seagull



cat lizard viper cat seagull zard frog



- gold fish lizard sheep dog cat red-mulle blue shark
- (a) How they bear young
- (c) Environment
- (b) Existence of lungs

(d) Both (a), & (b)

Nebraska

Clustering Background

Types of clustering problems:

- Hard (crisp): partition data into non-overlapping clusters; each instance belongs in exactly one cluster
- Fuzzy: Each instance could be a member of multiple clusters, with a real-valued function indicating the degree of membership
- Hierarchical: partition instances into numerous small clusters, then group the clusters into larger ones, and so on (applicable to phylogeny)
 - End up with a tree with instances at leaves

Nebraska

Clustering Background (Dis-)similarity Measures: Between Instances

Dissimilarity measure: Weighted L_p norm:

$$L_p(\mathbf{x}, \mathbf{y}) = \left(\sum_{i=1}^n w_i |x_i - y_i|^p\right)^{1/p}$$

Special cases include weighted *Euclidian distance* (p = 2), weighted Manhattan distance

$$L_1(\mathbf{x},\mathbf{y}) = \sum_{i=1}^n w_i |x_i - y_i|,$$

and weighted L_{∞} norm

$$L_{\infty}(\mathbf{x}, \mathbf{y}) = \max_{1 \le i \le n} \{ w_i | x_i - y_i | \}$$

Similarity measure: Dot product between two vectors (kernel) 4 D > 4 B > 4 E > 4 E > 9 Q C

4 D > 4 B > 4 B > 4 B > 8 9 9 9

Clustering Background

(Dis-)similarity Measures: Between Instances (cont'd)

If attributes come from $\{0,\ldots,k-1\}$, can use measures for real-valued attributes, plus:

- Hamming distance: DM measuring number of places where x and y differ
- Tanimoto measure: SM measuring number of places where x and y are same, divided by total number of
 - Ignore places i where $x_i = y_i = 0$
 - Useful for ordinal features where x_i is degree to which \mathbf{x} possesses ith feature



Nebraska

Clustering Background

(Dis-)similarity Measures: Between Instance and Set

Might want to measure proximity of point x to existing

- Can measure proximity α by using all points of C or by using a representative of C
- If all points of C used, common choices:

$$\begin{split} &\alpha_{max}^{ps}(\mathbf{x},C) = \max_{\mathbf{y} \in C} \left\{ \alpha(\mathbf{x},\mathbf{y}) \right\} \\ &\alpha_{min}^{ps}(\mathbf{x},C) = \min_{\mathbf{y} \in C} \left\{ \alpha(\mathbf{x},\mathbf{y}) \right\} \\ &\alpha_{avg}^{ps}(\mathbf{x},C) = \frac{1}{|C|} \sum_{\mathbf{y} \in C} \alpha(\mathbf{x},\mathbf{y}) \;, \end{split}$$

where $\alpha(\mathbf{x}, \mathbf{y})$ is any measure between \mathbf{x} and \mathbf{y}



Nebraska

Clustering Background

(Dis-)similarity Measures: Between Instance and Set (cont'd)

Alternative: Measure distance between point x and a representative of the cluster C

- Mean vector $\mathbf{m}_p = \frac{1}{|C|} \sum_{\mathbf{y} \in C} \mathbf{y}$
- Mean center $\mathbf{m}_c \in C$:

$$\sum_{\mathbf{y}\in C} d(\mathbf{m}_c, \mathbf{y}) \leq \sum_{\mathbf{y}\in C} d(\mathbf{z}, \mathbf{y}) \quad \forall \mathbf{z}\in C,$$

where $d(\cdot, \cdot)$ is DM (if SM used, reverse ineq.)

• Median center. For each point $y \in C$, find median dissimilarity from y to all other points of C, then take min; so $\mathbf{m}_{med} \in C$ is defined as

$$\mathsf{med}_{\mathbf{y} \in C} \left\{ d(\mathbf{m}_{med}, \mathbf{y}) \right\} \leq \mathsf{med}_{\mathbf{y} \in C} \left\{ d(\mathbf{z}, \mathbf{y}) \right\} \quad \forall \mathbf{z} \in C$$

Now can measure proximity between C's representative and x with standard measures 10148131313131000

Nebraska

Clustering Background (Dis-)similarity Measures: Between Sets

• Max: $\alpha_{max}^{ss}(C_i, C_j) = \max_{\mathbf{x} \in C_i, \mathbf{y} \in C_j} \{\alpha(\mathbf{x}, \mathbf{y})\}$

- Min: $\alpha_{min}^{ss}(C_i, C_j) = \min_{\mathbf{x} \in C_i, \mathbf{y} \in C_j} \{\alpha(\mathbf{x}, \mathbf{y})\}$
- $\bullet \ \textit{Average} : \alpha_{avg}^{ss}(C_i, C_j) = \frac{1}{|C_i| \ |C_j|} \sum_{\mathbf{x} \in C_i} \sum_{\mathbf{y} \in C_j} \alpha(\mathbf{x}, \mathbf{y})$
- Representative (mean): $\alpha_{mean}^{ss}(C_i, C_j) = \alpha(\mathbf{m}_{C_i}, \mathbf{m}_{C_j}),$

Given sets of instances C_i and C_i and proximity measure



Nebraska

k-Means Clustering

- Very popular clustering algorithm
- Represents cluster i (out of k total) by specifying its representative \mathbf{m}_i (not necessarily part of the original set of instances \mathcal{X})
- Each instance $x \in \mathcal{X}$ is assigned to the cluster with nearest representative
- Goal is to find a set of k representatives such that sum of distances between instances and their representatives is minimized
 - NP-hard in general
- Will use an algorithm that alternates between determining representatives and assigning clusters until convergence (in the style of the EM algorithm)

Nebraska

k-Means Clustering Algorithm

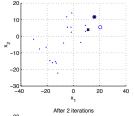
Clustering

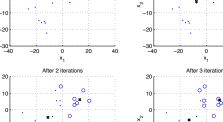
- Choose value for parameter k
- Initialize k arbitrary representatives $\mathbf{m}_1, \dots, \mathbf{m}_k$
 - E.g., k randomly selected instances from X
- Repeat until representatives $\mathbf{m}_1, \dots, \mathbf{m}_k$ don't change
 - - Assign x to cluster C_j such that ||x − m_j|| (or other measure) is minimized
 - I.e., nearest representative

$$\mathbf{m}_j = \frac{1}{C_j} \sum_{\mathbf{y} \in C_j} \mathbf{y}$$

k-Means Clustering







Nebraska

Hierarchical Clustering

- Useful in capturing hierarchical relationships, e.g., evolutionary tree of biological sequences
- End result is a sequence (hierarchy) of clusterings
- Two types of algorithms:
 - Agglomerative: Repeatedly merge two clusters into one
 - Divisive: Repeatedly divide one cluster into two





Hierarchical Clustering Definitions

-20

• Let $C_t = \{C_1, \dots, C_{m_t}\}$ be a *level-t clustering* of $X = \{\mathbf{x}_1, \dots, \mathbf{x}_N\}$, where \mathcal{C}_t meets definition of hard clustering

• C_t is *nested* in $C_{t'}$ (written $C_t \sqsubseteq C_{t'}$) if each cluster in C_t is a subset of a cluster in $C_{t'}$ and at least one cluster in C_t is a proper subset of some cluster in $C_{t'}$

$$\mathcal{C}_{1} = \left\{ \left\{ x_{1}, x_{3} \right\}, \left\{ x_{4} \right\}, \left\{ x_{2}, x_{5} \right\} \right\} \sqsubseteq \left\{ \left\{ x_{1}, x_{3}, x_{4} \right\}, \left\{ x_{2}, x_{5} \right\} \right\}$$

$$\mathcal{C}_{1} \not\sqsubseteq \left\{ \left\{ x_{1}, x_{4} \right\}, \left\{ x_{3} \right\}, \left\{ x_{2}, x_{5} \right\} \right\}$$





Hierarchical Clustering Definitions (cont'd)

- Agglomerative algorithms start with $C_0 = \{\{\mathbf{x}_1\}, \dots, \{\mathbf{x}_N\}\}\$ and at each step t merge two clusters into one, yielding $|\mathcal{C}_{t+1}| = |\mathcal{C}_t| - 1$ and $\mathcal{C}_t \sqsubset \mathcal{C}_{t+1}$
- At final step (step N-1) have hierarchy:

$$C_0 = \{\{\mathbf{x}_1\}, \dots, \{\mathbf{x}_N\}\} \sqsubseteq C_1 \sqsubseteq \dots \sqsubseteq C_{N-1} = \{\{\mathbf{x}_1, \dots, \mathbf{x}_N\}\}\$$

- ullet Divisive algorithms start with $\mathcal{C}_0 = \{\{\mathbf{x}_1, \dots, \mathbf{x}_N\}\}$ and at each step t split one cluster into two, yielding $|\mathcal{C}_{t+1}| = |\mathcal{C}_t| + 1$ and $\mathcal{C}_{t+1} \sqsubseteq \mathcal{C}_t$
- At step N-1 have hierarchy:

$$C_{N-1} = \{\{\mathbf{x}_1\}, \dots, \{\mathbf{x}_N\}\} \sqsubset \dots \sqsubset C_0 = \{\{\mathbf{x}_1, \dots, \mathbf{x}_N\}\}\$$



Nebraska

Hierarchical Clustering Pseudocode

1 Initialize $C_0 = \{\{\mathbf{x}_1\}, \dots, \{\mathbf{x}_N\}\}, t = 0$ **2** For t = 1 to N - 1

• Find closest pair of clusters:

$$\begin{split} &(C_i,C_j) = \mathop{\mathrm{argmin}}_{C_s,C_r \in C_{t-1},r \neq s} \left\{ d\left(C_s,C_r\right) \right\} \\ &\bullet \ \ \mathcal{C}_t = \left(\mathcal{C}_{t-1} - \left\{C_i,C_j\right\}\right) \cup \left\{\left\{C_i \cup C_j\right\}\right\} \text{ and update} \end{split}$$
representatives if necessary

If SM used, replace argmin with argmax

Number of calls to $d(C_k, C_r)$ is $\Theta(N^3)$

Nebraska

Hierarchical Clustering

Outline

 $\mathbf{x}_1 = [1, 1]^T$, $\mathbf{x}_2 = [2, 1]^T$, $\mathbf{x}_3 = [5, 4]^T$, $\mathbf{x}_4 = [6, 5]^T$, $\mathbf{x}_5 = [6.5, 6]^T$, DM = Euclidian/ α_{min}^{ss}

An $(N-t) \times (N-t)$ proximity matrix P_t gives the proximity between all pairs of clusters at level (iteration) t

$$P_0 = \begin{bmatrix} 0 & 1 & 5 & 6.4 & 7.4 \\ 1 & 0 & 4.2 & 5.7 & 6.7 \\ 5 & 4.2 & 0 & 1.4 & 2.5 \\ 6.4 & 5.7 & 1.4 & 0 & 1.1 \\ 7.4 & 6.7 & 2.5 & 1.1 & 0 \end{bmatrix}$$

Each iteration, find minimum off-diagonal element (i, j) in P_{t-1} , merge clusters i and j, remove rows/columns i and j from P_{t-1} , and add new row/column for new cluster to get P_t

Hierarchical Clustering Pseudocode (cont'd)

CSCE 478/878 Lecture 8: Clustering

Stephen Sco

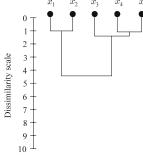
Outline

k-Means Clustering

Hierarchica Clustering

Example

A *proximity dendogram* is a tree that indicates hierarchy of clusterings, including the proximity between two clusters when they are merged



Cutting the dendogram at any level yields a single clustering