Data Mining (W4240 Section 001) Clustering (part 1)

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Outline

Context: Supervised vs Unsupervised

K-Means

K-Means in R

Mixture Models

K-Means vs Mixture Models

Choosing K

Key Administrative Notes

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Mixture Models

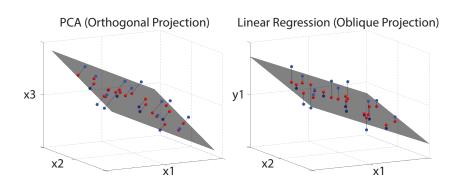
K-Means vs Mixture Models

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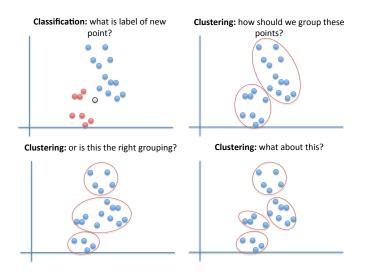
PCA vs Linear Regression

- Unsupervised learning seeks explanatory factors
- Supervised learning asserts explanatory factors



Today: Clustering

The essential difference here is again unsupervised/supervised:



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Sample space
$$=C_1 \cup C_2 \cup \cdots \cup C_K$$
, with $C_k \cap C_j = \emptyset$

K-means is the simplest clustering method available.

Start with a notion of $\underline{\text{distance}}$ between each pair of points (Euclidean, 0-1 loss, some combination thereof)

Each cluster k has a *centroid*, or average value μ_k

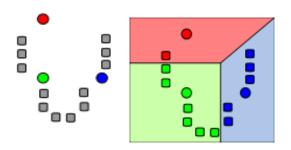
Example: data for cluster k is (0,1), (0.5,0.5), (1,1)

$$\mu_{k1} = \frac{1}{3}(0 + 0.5 + 1) = \frac{1}{2}$$

$$\mu_{k2} = \frac{1}{3}(1 + 0.5 + 1) = \frac{5}{6}$$

质心

Once we have a set of centroids, μ_1, \ldots, μ_K , we can ask which data are closest to the centroids¹



Note: the regions have linear boundaries

¹Photo credit: Wikipedia

K-Means迭代算法 First of all, SCALE THE DATA!!!

Conceptually, we fit K clusters with the following steps:

- 1. pick K initial cluster means
- 2. associate all points closest to mean k with cluster k
- 3. use points in cluster k to <u>update</u> mean for that cluster
- 4. re-associate points closest to new mean for k with cluster k
- 5. use new points in cluster k to update mean for that cluster
- 6. ...
- 7. stop when <u>no change</u> between updates

Within-Clustering Variation (WCV):

$$WCV = \sum_{k=1}^{K} \frac{1}{|C_k|} \sum_{i,\ell \in C_k} \sum_{j=1}^{p} (x_{ij} - x_{\ell j})^2$$

Residual Sum of Squares (RSS):

$$RSS = \sum_{k} \sum_{i:C_i = k} \underline{d(\mathbf{x}_i, \boldsymbol{\mu}_k)}$$
$$= \sum_{k=1}^{K} \sum_{i \in C_k} \sum_{j=1}^{p} (x_{ij} - \underline{\mu}_{kj})^2$$

The K-means algorithm is guaranteed to decrease the WCV since

$$\frac{1}{|C_k|} \sum_{i,\ell \in C_k} \sum_{j=1}^p (x_{ij} - x_{\ell j})^2 = 2 \sum_{i \in C_k} \sum_{j=1}^p (x_{ij} - \overline{x}_{kj})^2,$$

where $\overline{x}_{kj} = \frac{1}{|C_k|} \sum_{i \in C_k} x_{ij}$.

K-means:

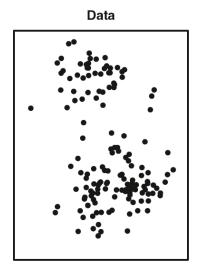
1. Minimize RSS over cluster assignments C_i :

$$\arg\min_{C_i} \sum_{k=1}^K \sum_{i:C_i=k} \sum_{j=1}^p (x_{ij} - \mu_{kj})^2$$

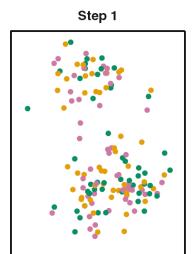
2. Minimize RSS over cluster centroids μ_k :

$$\arg\min_{\mu_k} \sum_{k=1}^K \sum_{i:C_i=k} \sum_{j=1}^p (x_{ij} - \mu_{kj})^2$$

K-Means: Observations

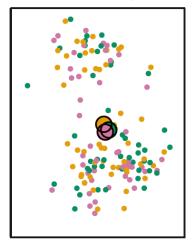


K-Means: observation randomly assigned to a cluster



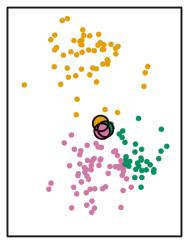
K-Means: cluster centroids

Iteration 1, Step 2a



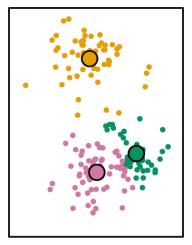
K-Means: each obs is assigned to the nearest centroid

Iteration 1, Step 2b



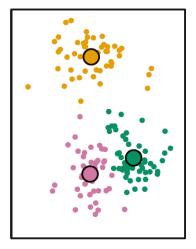
K-Means: new cluster centroids

Iteration 2, Step 2a



K-Means: results after 10 iterations

Final Results



Will K-means converge? Can't it just limit cycle?

- reassignment: each observation moves to closest centroid
- update: new centroid minimizes RSS for this assignment

$$RSS_k(\mu) = \sum_{i:C_i=k} \sum_{j=1}^d (x_{ij} - \mu_{kj})^2$$
$$\frac{\partial}{\partial \mu_j} RSS_k(\mu) = \sum_{i:C_i=k} 2(x_{ij} - \mu_{kj})$$
$$\mu_{kj} = \frac{1}{n_k} \sum_{i:C_i=k} x_{ij}$$

Will the final labels and means always be the same?

Will K-means converge? Can't it just limit cycle?

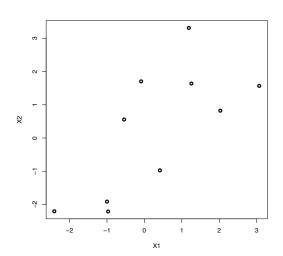
- reassignment: each observation moves to closest centroid
- update: new centroid minimizes RSS for this assignment

$$RSS_k(\mu) = \sum_{i:C_i=k} \sum_{j=1}^d (x_{ij} - \mu_{kj})^2$$
$$\frac{\partial}{\partial \mu_j} RSS_k(\mu) = \sum_{i:C_i=k} 2(x_{ij} - \mu_{kj})$$
$$\mu_{kj} = \frac{1}{n_k} \sum_{i:C_i=k} x_{ij}$$

- Will the final labels and means always be the same?
- No. K-means has (many) local optima.

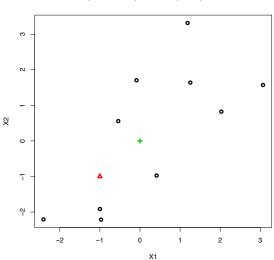
Data:

x_1	x_2
0.4	-1.0
-1.0	-2.2
-2.4	-2.2
-1.0	-1.9
-0.5	0.6
-0.1	1.7
1.2	3.3
3.1	1.6
1.3	1.6
2.0	0.8



Pick K centers (randomly):

$$\left(-1,-1\right)$$
 and $\left(0,0\right)$



Calculate distance between points and those centers:

x_2	(-1, -1)	(0,0)
-1.0	1.4	1.1
-2.2	1.2	2.4
-2.2	1.9	3.3
-1.9	0.9	2.2
0.6	1.6	8.0
1.7	2.9	1.7
3.3	4.8	3.5
1.6	4.8	3.4
1.6	3.5	2.1
0.8	3.5	2.2
	-1.0 -2.2 -2.2 -1.9 0.6 1.7 3.3 1.6 1.6	-1.0

```
> centers <- rbind(c(-1,-1),c(0,0))
> dist1 <- apply(x,1,function(x) sqrt(sum((x-centers[1,])^2)))
> dist2 <- apply(x,1,function(x) sqrt(sum((x-centers[2,])^2)))</pre>
```

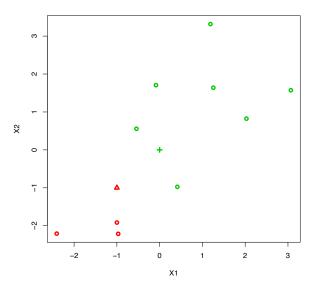
Choose mean with smaller distance:

x_1	x_2	(-1, -1)	(0,0)
0.4	-1.0	1.4	1.1
-1.0	-2.2	1.2	2.4
-2.4	-2.2	1.9	3.3
-1.0	-1.9	0.9	2.2
-0.5	0.6	1.6	0.8
-0.1	1.7	2.9	1.7
1.2	3.3	4.8	3.5
3.1	1.6	4.8	3.4
1.3	1.6	3.5	2.1
2.0	0.8	3.5	2.2

> dists <- cbind(dist1,dist2)</pre>

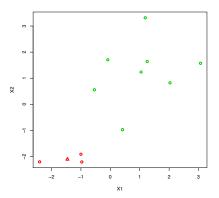
> cluster.ind <- apply(dists,1,which.min)</pre>

New clusters:



Refit means for each cluster:

- ▶ cluster 1: (-1.0, -2.2), (-2.4, -2.2), (-1.0, -1.9)
- new mean: (-1.5, -2.1)
- ▶ cluster 2: (0.4, -1.0), (-0.5, 0.6), (-0.1, 1.7), (1.2, 3.3), (3.1, 1.6), (1.3, 1.6), (2.0, 0.8)
- new mean: (1.0, 1.2)



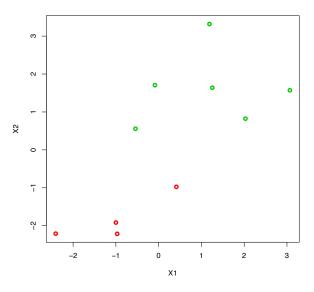
Recalculate distances for each cluster:

		1 /	
x_1	x_2	(-1.5, -2.1)	(1.0, 1.2)
0.4	-1.0	2.2	2.3
-1.0	-2.2	0.5	4.0
-2.4	-2.2	1.0	4.9
-1.0	-1.9	0.5	3.8
-0.5	0.6	2.8	1.7
-0.1	1.7	4.1	1.2
1.2	3.3	6.0	2.1
3.1	1.6	5.8	2.0
1.3	1.6	4.6	0.5
2.0	0.8	4.6	1.1
		·	

Choose mean with smaller distance:

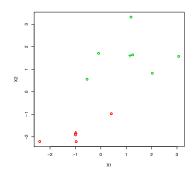
x_1	x_2	(-1.5, -2.1)	(1.0, 1.2)
0.4	-1.0	2.2	2.3
-1.0	-2.2	0.5	4.0
-2.4	-2.2	1.0	4.9
-1.0	-1.9	0.5	3.8
-0.5	0.6	2.8	1.7
-0.1	1.7	4.1	1.2
1.2	3.3	6.0	2.1
3.1	1.6	5.8	2.0
1.3	1.6	4.6	0.5
2.0	8.0	4.6	1.1

New clusters:



Refit means for each cluster:

- ▶ cluster 1: (0.4, -1.0), (-1.0, -2.2), (-2.4, -2.2), (-1.0, -1.9)
- new mean: (-1.0, -1.8)
- ▶ cluster 2: (-0.5, 0.6), (-0.1, 1.7), (1.2, 3.3), (3.1, 1.6), (1.3, 1.6), (2.0, 0.8)
- new mean: (1.2, 1.6)



Recalculate distances for each cluster:

x_1	x_2	(-1.0, -1.8)	(1.2, 1.6)
0.4	-1.0	1.6	2.7
-1.0	-2.2	0.4	4.4
-2.4	-2.2	1.5	5.2
-1.0	-1.9	0.1	4.1
-0.5	0.6	2.4	2.0
-0.1	1.7	3.6	1.2
1.2	3.3	5.6	1.7
3.1	1.6	5.3	1.9
1.3	1.6	4.1	0.1
2.0	8.0	4.0	1.2

Select smallest distance and compare these clusters with previous:

Table: New Clusters

x_1	x_2	(-1.0, -1.8)	(1.2, 1.6)
0.4	-1.0	1.6	2.7
-1.0	-2.2	0.4	4.4
-2.4	-2.2	1.5	5.2
-1.0	-1.9	0.1	4.1
-0.5	0.6	2.4	2.0
-0.1	1.7	3.6	1.2
1.2	3.3	5.6	1.7
3.1	1.6	5.3	1.9
1.3	1.6	4.1	0.1
2.0	0.8	4.0	1.2

Table: Old Clusters

(-1.5, -2.1)	(1.0, 1.2)
2.2	2.3
0.5	4.0
1.0	4.9
0.5	3.8
2.8	1.7
4.1	1.2
6.0	2.1
5.8	2.0
4.6	0.5
4.6	1.1

Outline

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K-Means in R

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K-Means vs Mixture Models

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Key Administrative Notes

 ${\tt R}$ has a function for K-means in the stats package; this is probably already loaded

- let's use this for the Old Faithful data
- > library(datasets)
- > faith.2 <- kmeans(faithful,2)</pre>
- > names(faith.2)
- > plot(faithful[,1],faithful[,2],col=faith.2\$cluster,
 - + pch=faith.2\$cluster,lwd=3)

K-means can be used for image segmentation

- partition image into multiple segments
- find boundaries of objects (useful for object recognition)
- make art



We can segment memes:



(4 segments on right)

To segment:

- ▶ load image, use jpeg package for .jpegs
- coerce input to matrix
- run K-means
- replace existing colors with mean values (or others!) for each cluster
- coerce into array
- save new image

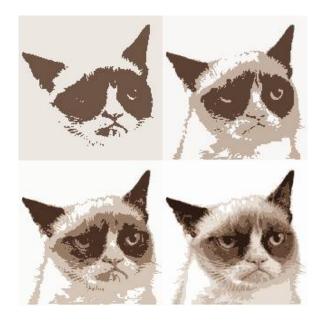
If you want to follow along, load the following packages:

- ▶ jpeg
- stats (probably already loaded)

K-Means in R

```
> grumpy <- readJPEG("GrumpyTrimmed.jpg")</pre>
> source("/DataMining/Lectures/Lecture22/k.means.to.image.R")
> grumpy.4 <- k.means.to.image(grumpy,4)</pre>
> writeJPEG(grumpy.4,"GrumpyK4.jpeg")
k.means.to.image <- function(im.mat.K){</pre>
# image im.mat, number of clusters K # coerce image into matrix
orig.dim <- dim(im.mat)</pre>
new.im <- im.mat.
dim(new.im) <- c(orig.dim[1]*orig.dim[2],3)</pre>
k.list <- kmeans(new.im,K) # Do K means!
out.im <- mat.or.vec(orig.dim[1]*orig.dim[2],3)</pre>
for (k in 1:K)
    out.im[(k.list$cluster==k),1] <- k.list$centers[k,1]</pre>
    out.im[(k.list$cluster==k),2] <- k.list$centers[k,2]
    out.im[(k.list$cluster==k),3] <- k.list$centers[k,3]}</pre>
# Re-coerce new image to original size
dim(out.im) <- orig.dim
return(out.im)
```

K-Means in R



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K-means is similar to the Gaussian mixture model

To generate data from a GMM:

- ▶ choose cluster with $C_i \sim Categorical(p_1, ..., p_p)$
- generate point x_i with $x_i|C_i=k\sim\mathcal{N}(\mu_k,\Sigma_k)$
- (μ_k is mean vector, Σ_k is covariance matrix)

As with K-Means, we generated data with:

- observation x_i in cluster C_i
- K clusters
- Our goal is use data to find μ_k (and Σ_k)

Mixture models are fit using the following iterative steps:

1. E-step:

$$\mathbb{P}(C_i = k \,|\, x_i) = \frac{\pi_k N(x_i \,|\, \mu_k, \Sigma_k)}{\sum_{\ell=1}^K \pi_\ell N(x_i \,|\, \mu_\ell, \Sigma_\ell)}$$

2. M-step:

$$\mu_k^{new} = \frac{1}{N_k} \sum_{i=1}^n \mathbb{P}(C_i = k \mid x_i) x_i$$

$$\pi_k^{new} = \frac{1}{N} \sum_{i=1}^n \mathbb{P}(C_i = k \mid x_i)$$

$$-\sum_{i=1}^n \mathbb{P}(C_i = k \mid x_i) (x_i - u_i^{new}) (x_i - u_i^{n$$

$$\Sigma_k^{new} = \frac{1}{N_k} \sum_{i=1}^n \mathbb{P}(C_i = k \,|\, x_i) (x_i - \mu_k^{new}) (x_i - \mu_k^{new})^\top$$

- (the Expectation-Maximization algorithm)
- ▶ Let's compare this conceptually to K-Means

Mixture models are closely related to:

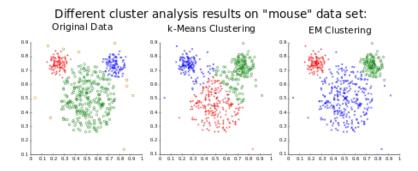
classification with linear/quadratic discriminate analysis

$$\mathbb{P}(y_i = k \,|\, x_i) = \frac{\pi_k N(x_i \,|\, \mu_k, \Sigma_k)}{\sum_{\ell=1}^K \pi_\ell N(x_i \,|\, \mu_\ell, \Sigma_\ell)}$$

▶ naive Bayes (if Σ_k is a diagonal matrix)

$$\mathbb{P}(y_i = k \mid x_i) = \frac{\pi_k \prod_{j=1}^p N(x_{ij} \mid \mu_{kj}, \sigma_{kj}^2)}{\sum_{\ell=1}^K \pi_\ell \prod_{j=1}^p N(x_{ij} \mid \mu_{\ell j}, \sigma_{\ell j}^2)}$$

Mixture models are more flexible than K-means: each component has Σ_k along with μ_k (how does this relate to LDA/QDA?)



Here, a mixture model is called "EM" after the algorithm used to fit the parameters 2

²Photo credit: Wikipedia

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Mixture Models vs K-Means

K-means is quite similar to a mixture model. Fit a simple mixture model, where

$$x_i \mid C_i = k \sim N(\mu_k, \Sigma_k)$$

Simplify the covariance model:

covariance matrices have only diagonal elements,

$$\Sigma_k = \begin{bmatrix} \sigma_{k1}^2 & 0 & \dots & 0 \\ 0 & \sigma_{k2}^2 & \dots & 0 \\ \dots & \dots & \dots & 0 \\ 0 & 0 & 0 & \sigma_{kp}^2 \end{bmatrix}$$

ightharpoonup set $\sigma_{k1}^2=\cdots=\sigma_{kp}^2$, suppose known and the same for all components

Mixture Models vs K-Means

This simplified mixture model then proceeds as:

- start with random cluster centers
- associate observations to clusters by (log-)likelihood,

$$\ell(x_i \mid C_i = k) = -\frac{p}{2}\log(2\pi) - \frac{1}{2}\log\left(\prod_{j=1}^p \sigma_{kj}^2\right) - \frac{1}{2}\sum_{j=1}^d (x_{ij} - \mu_{kj})^2 / \sigma_{kj}^2$$

$$\propto -p\log(\sigma_k) - \frac{1}{2\sigma_k^2}\sum_{j=1}^p (x_{ij} - \mu_{kj})^2$$

$$\propto -\sum_{j=1}^p (x_{i,j} - \mu_{kj})^2$$

- refit centers μ_1, \ldots, μ_K given clusters...
- recluster observations...
- stop when no change in clusters

Mixture Model vs K-Means

Compare mixture model with global variance to K-means:

clustering with K-means: minimize distance

$$d(x_i, \mu_k) = \sqrt{\sum_{j=1}^{p} (x_{ij} - \mu_{kj})^2}$$

clustering with single variance mixture model: maximize likelihood

$$\ell(x_i | C_i = k) \propto -\sum_{i=1}^{p} (x_{ij} - \mu_{kj})^2$$

update means with K-means: use average

$$\mu_{kj} = \frac{1}{n_k} \sum_{C = k} x_{ij}$$

update means in mixture model: use weighted average

$$\mu_{kj} = \frac{1}{N_k} \sum_{i=1}^n \mathbb{P}(C_i = k \mid x_i) x_{ij}$$

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So what about K? How do we find the right value?

- ▶ in general, there is no one accepted method
- some people choose it arbitrarily

To figure out evaluation methods, let's look at what happens when ${\cal K}$ increases

- all clustering models have an objective function (what is this for K-means? Mixture models?)
- when we add a cluster, the value in that objective function decreases (for 'minimize' objective functions or increases for 'maximize' objective functions)
- want to trade off number of clusters against objective function values

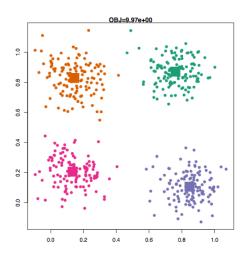


Figure 1: Division of data into four clusters

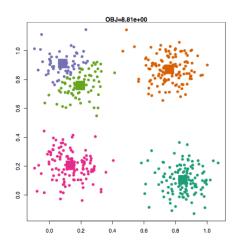


Figure 2: Division of data into five clusters

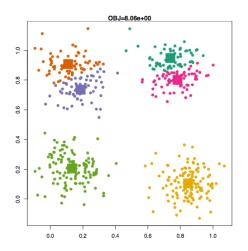


Figure 3: Division of data into six clusters

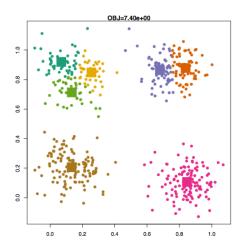


Figure 4: Division of data into seven clusters

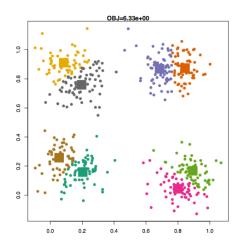


Figure 5: Division of data into eight clusters

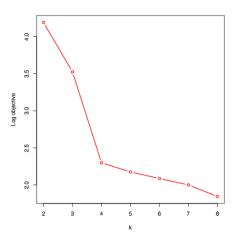


Figure 6: Plot of Log Objective function Vs. number of clusters

Other methods for choosing K:

Akaike Information Criterion (AIC):

$$AIC(K) = 2D_K - 2\log(L)$$

Bayesian Information Criterion (BIC):

$$BIC(K) = D_K \log(n) - 2\log(L)$$

- ▶ in both cases, L is the maximized value of the likelihood function for the model
- ▶ D_K is the number of parameters to be estimated with K clusters
- these work for clustering models with likelihoods

Practice for Final Exam

Use K-means to cluster the following data for K=1,2,3 with random initialization:

x_1	x_2
-1.0	-1.2
-1.2	-1.8
-2.1	-2.4
1.1	1.5
1.5	1.6
1.3	0.7

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Last 4 office hours

- ▶ TA: Tuesday Dec 1st and Thursday Dec 3rd, 8-9am in 903SSW
- ▶ Prof: Monday Dec 7, 5:30-6pm in 501 Schermerhorn
- ▶ Prof: Wednesday Dec 9, 6-7:30pm in 501 Schermerhorn

HW6

- will NOT cover SVM
- ▶ is due on Wednesday December 9 <u>BEFORE</u> 6:10pm

Final Exam

- ▶ Date: Wednesday December 16, 2015
- ▶ Time: 6 to 8:30pm
- ► Location: Here (501 Schermerhorn)
- Closed-book: TRUE
- Calculator: Good idea
- ► Electronic device (smart phone, tablet, laptop): strictly Forbidden