

Department of Computer Science

CSCI 5622: Machine Learning

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Lecture 18: Unsupervised Learning II (Clustering)

Slides adapted from Jordan Boyd-Graber, Chris Ketelsen

Learning objectives

- Learn about general clustering
- Learn about the K-Means algorithm
- Learn about Gaussian Mixture Models

Supervised learning Unsupervised learning

Data: X

Labels: Y

Data: X

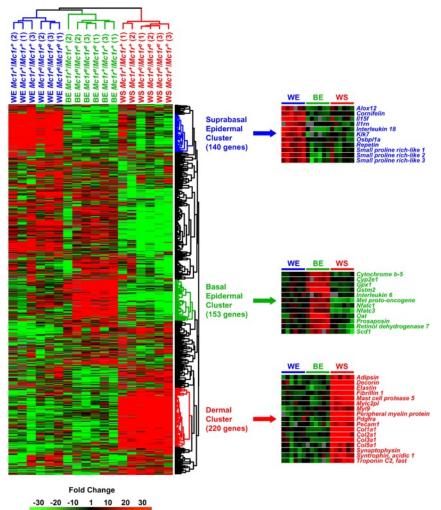
Latent structure: Z

Clustering

One important unsupervised method is clustering

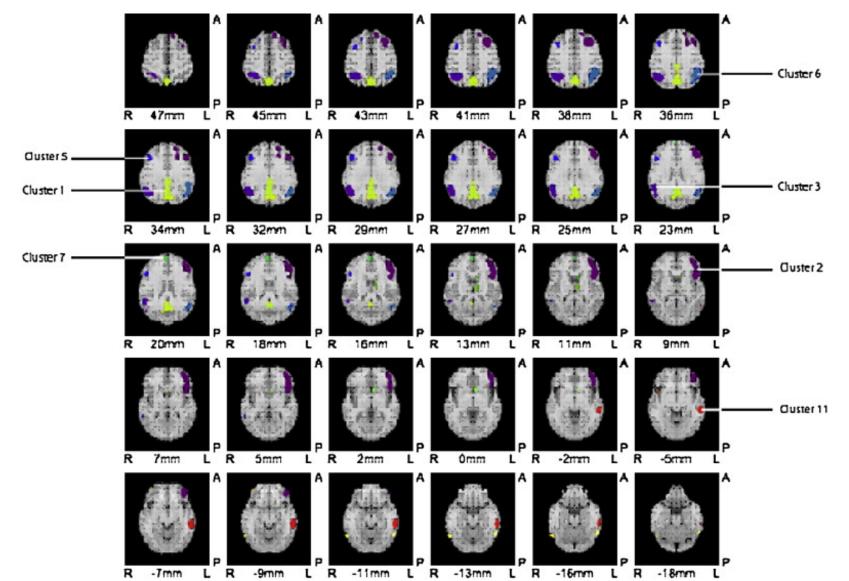
Goal: Organize data in classes

Clustering applications – Microarray Gene Expression data



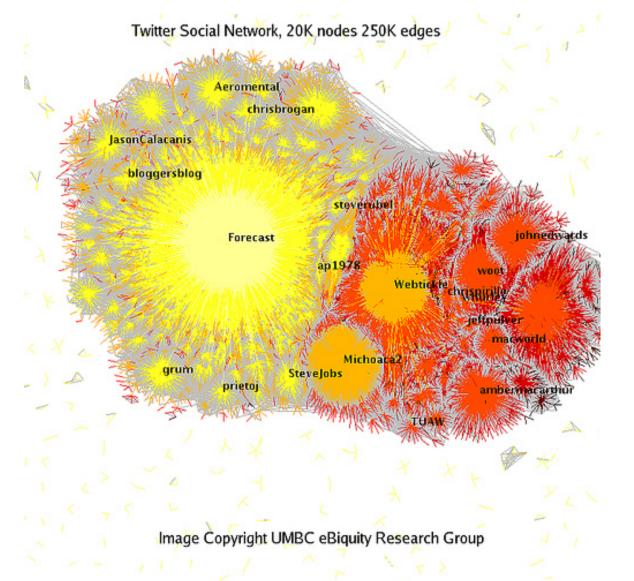
From: "Skin layer-specific transcriptional profiles in normal and recessive yellow (Mc1re/Mc1re) mice" by April and Barsh in Pigment Cell Research (2006)

Clustering applications – Medical Imaging



Clustering applications – Community

detection



News Media

The New York Times

The Washington Post











Mother Jones







theguardian

Clustering

- One important unsupervised method is clustering
- Goal: Organize data in classes
 - Classes are hard to define
 - Different data representation may lead to different clusterings

Clustering

- One important unsupervised method is clustering
- Goal: Organize data in classes
 - Data have high in-class similarity
 - Data have low out-of-class similarity

Clustering - Similarity

We'll call $d(\mathbf{x}, \mathbf{y})$ the similarity measure of \mathbf{x} and \mathbf{y}

Examples:

Euclidean Distance: $d(\mathbf{x}, \mathbf{y}) = ||\mathbf{x} - \mathbf{y}||^2$

Edit Distance: $d(\mathbf{x},\mathbf{y})=$ # replace, insert, deletes to turn \mathbf{x} into \mathbf{y}

$$d(kitten, sitting) = 3$$

kitten \rightarrow sitten \rightarrow sittin \rightarrow sitting

What properties make a good similarity measure?

Clustering - Similarity

We'll call $d(\mathbf{x}, \mathbf{y})$ the similarity measure of \mathbf{x} and \mathbf{y} Properties:

Symmetry
$$d(\mathbf{x}, \mathbf{y}) = d(\mathbf{y}, \mathbf{x})$$

Self-Consistency $d(\mathbf{x}, \mathbf{x}) = 0$
Positivity $d(\mathbf{x}, \mathbf{y}) = 0$ iff $\mathbf{x} = \mathbf{y}$
Triangle Inequality $d(\mathbf{x}, \mathbf{y}) \leq d(\mathbf{x}, \mathbf{z}) + d(\mathbf{z}, \mathbf{y})$

OK, so say we have a good similarity measure. How do we find clusters in the data?

- Simplest clustering method
- Iterative in nature
- Reasonably fast
- Very popular in practice (though with more bells and whistles)
- Requires real-valued data

General Idea:

pick *K* initial cluster means do until convergence ...

- associate examples closest to mean k with cluster k
- update cluster means with current examples in cluster k

Stop when:

cluster assignments don't change

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pick *K* initial cluster means do until convergence ...

- associate examples closest to mean k with cluster k
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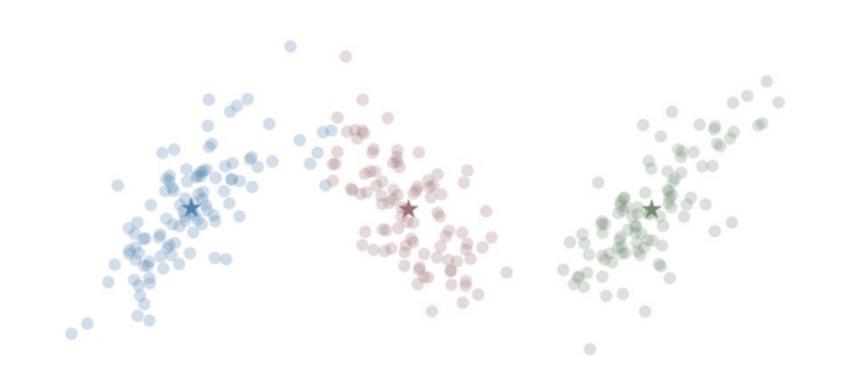
Stop when:

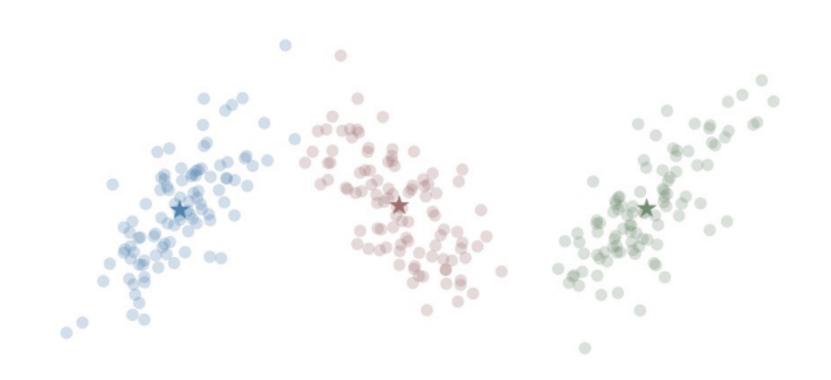
- cluster assignments don't change
- cluster means don't change (too much)

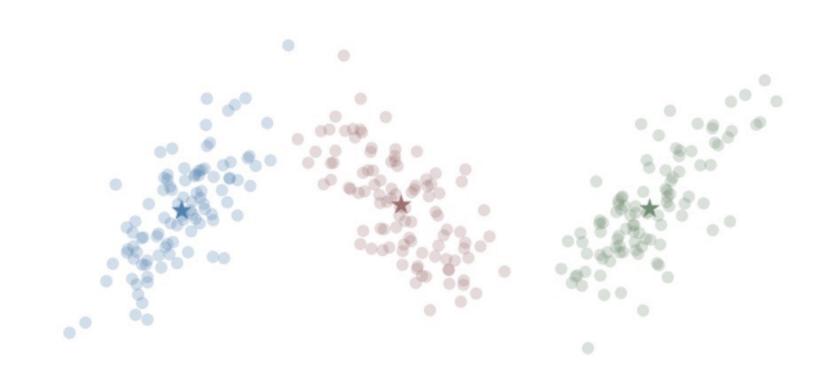














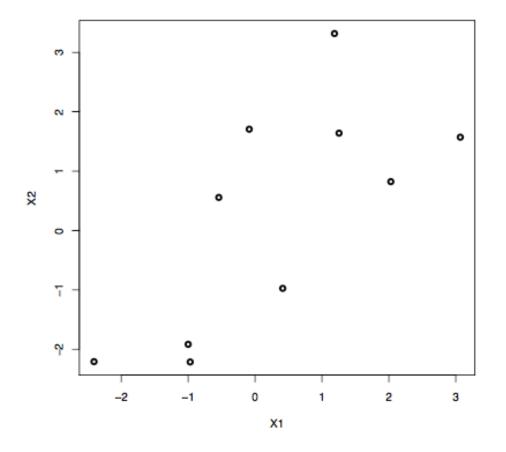
More K-means

Animations:

http://shabal.in/visuals/kmeans/4.html

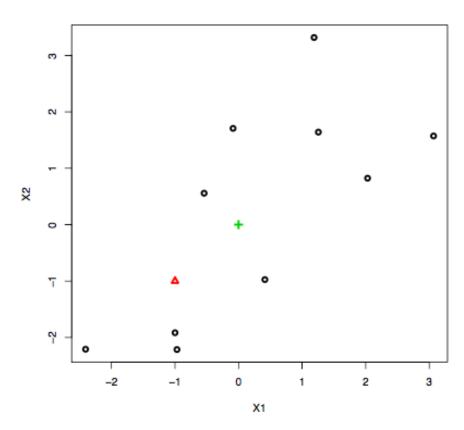
Data:

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	8.0



Pick *K* centers (randomly):

$$(-1,-1)$$
 and $(0,0)$



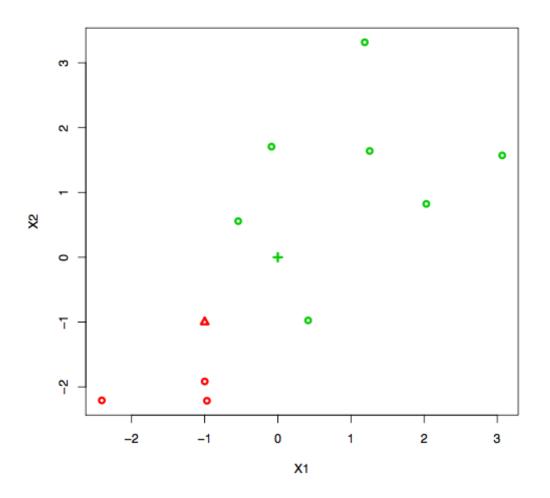
Calculate distance between points and those centers:

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	8.0
-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	8.0	3.5	2.2

Choose mean with smaller distance:

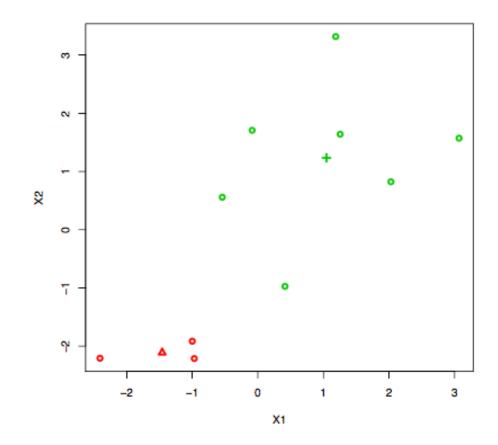
x_1	<i>x</i> ₂	(-1, -1)	(0,0)
0.4	-1.0	1.4	1.1
-1.0	-2.2	1.2	2.4
-2.4	-2.2	1.9	3.3
-1.0	-1.9	0.9	2.2
-0.5	0.6	1.6	8.0
-0.1	1.7	2.9	1.7
1.2	3.3	4.8	3.5
3.1	1.6	4.8	3.4
1.3	1.6	3.5	2.1
2.0	0.8	3.5	2.2

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)



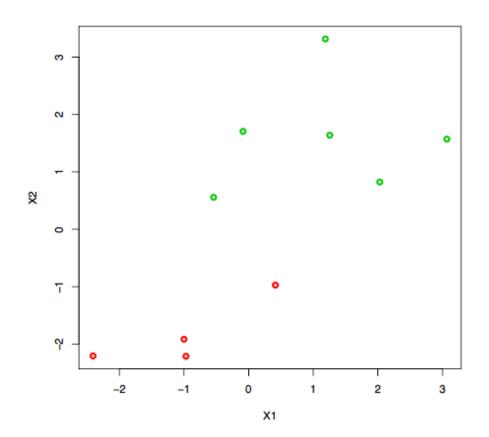
Recalculate distances for each cluster:

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

Choose mean with smaller distance:

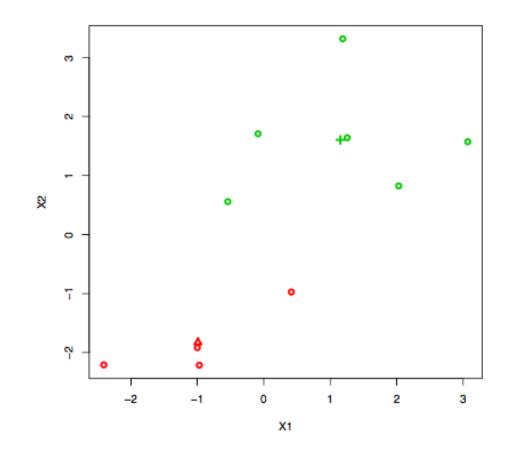
x_1	x_2	(-1.5, -2.1)	(1.0, 1.2)
0.4	-1.0	2.2	2.3
-1.0	-2.2	0.5	4.0
-2.4	-2.2	1.0	4.9
-1.0	-1.9	0.5	3.8
-0.5	0.6	2.8	1.7
-0.1	1.7	4.1	1.2
1.2	3.3	6.0	2.1
3.1	1.6	5.8	2.0
1.3	1.6	4.6	0.5
2.0	8.0	4.6	1.1

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

Strengths:

- Simple to understand
- Efficient time complexity $\mathcal{O}(dNKT)$ for $\mathbf{x} \in \mathbb{R}^d$
- Simple to implement

K-Means

```
def KMeans(X, K, max it=500):
    # Initialize cluster means to K samples from data
    rstart = choice(range(X.shape[0]), size=(K), replace=False)
    mu, muold = X[rstart,:], 1000*np.ones(X[rstart,:].shape)
    its = 0
    while its < max it and np.linalg.norm(mu-muold) > 1e-4:
        # compute distance b/w each point and centroid
        dist = np.array([[np.linalg.norm(x-m) for m in mu] for x in X]
        # compute new cluster assignments
        z = np.array([np.argmin(d) for d in dist])
        # move centroids
        muold = mu
        mu = np.array([np.mean(X[z==k, :], axis=0) for k in range(K)])
        its += 1
    return mu, z
```

K-Means

Weaknesses

- Doesn't really work with categorical data
- Usually only converges to local minimum
- Have to determine number of clusters
- Can be sensitive to outliers
- Only generates convex clusters

Doesn't really work with categorical data

- Doesn't really work with categorical data
- Fix: Do K-Modes instead

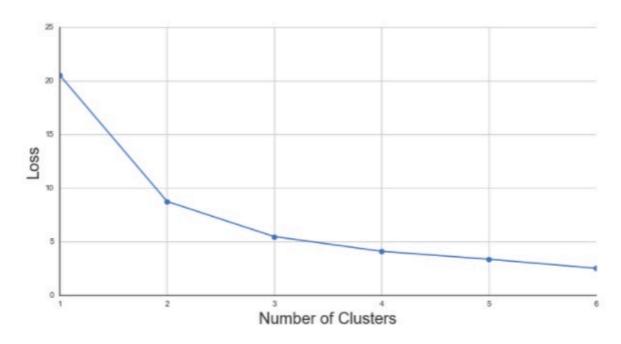
Usually only converges to local minimum

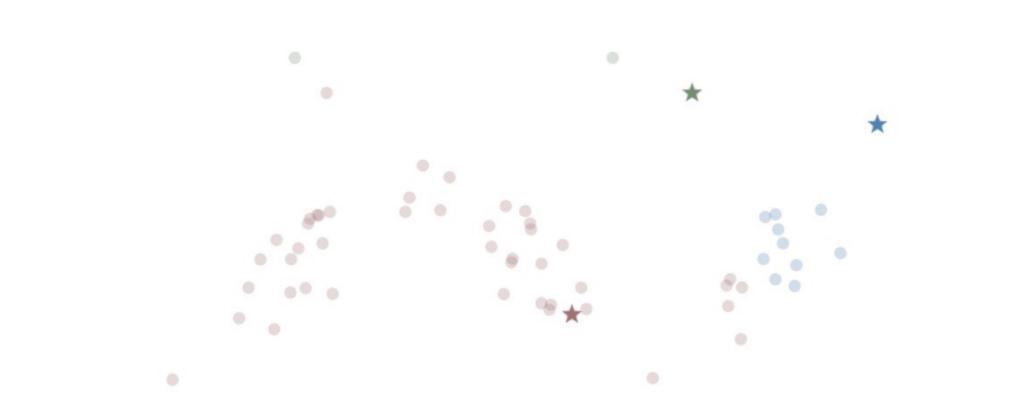
- Usually only converges to local minimum
- Fix: Do several runs with random inits, and choose best

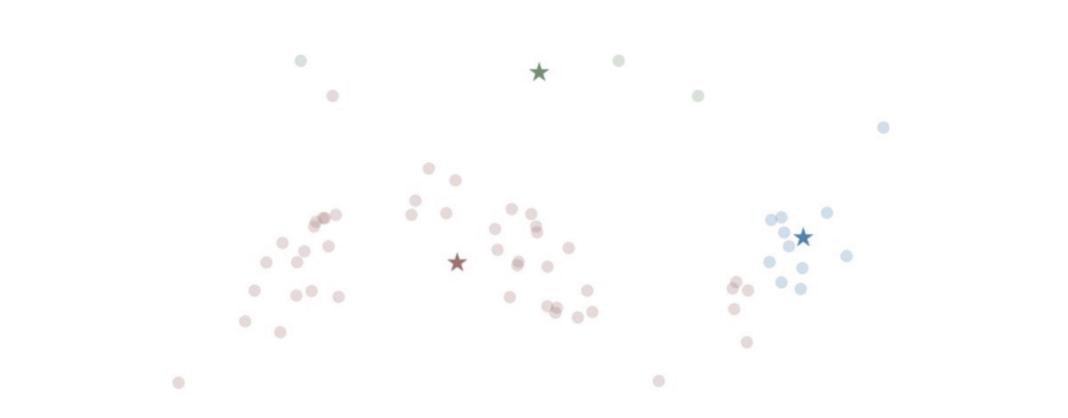
Have to determine number of clusters

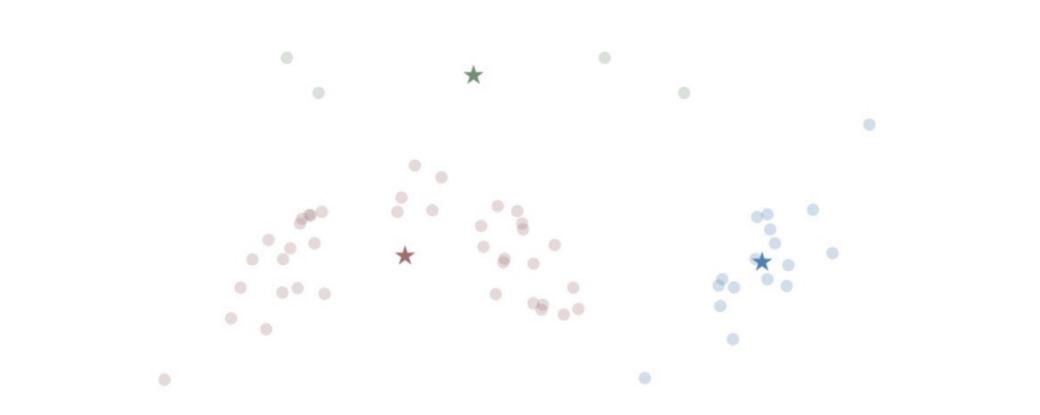
- Have to determine number of clusters
- Fix: Use the elbow method

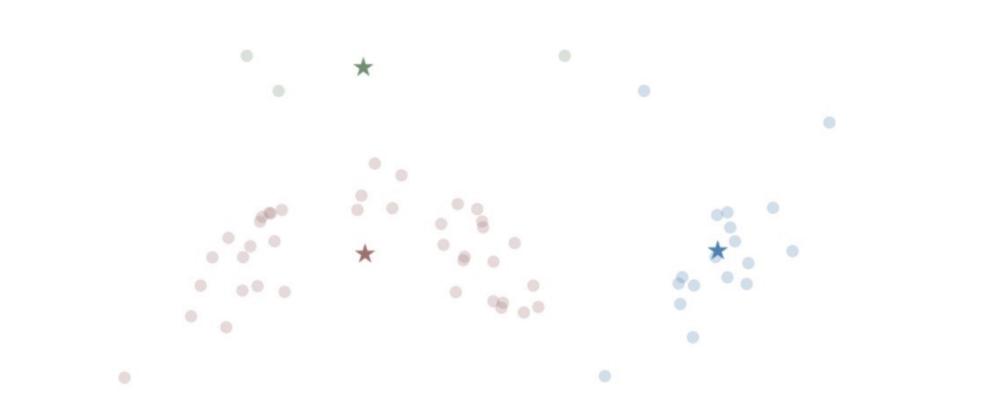
Run K-Means for different values of k and look at loss function



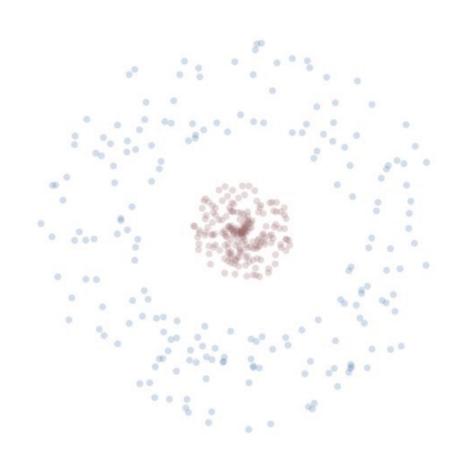




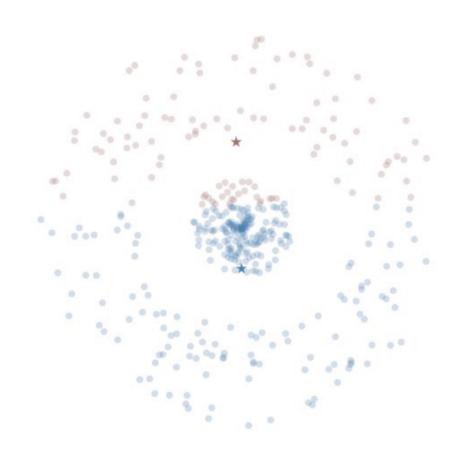




Weaknesses - Convex Clusters



Weaknesses - Convex Clusters



- Guassian Mixture Models (or GMMs) are a probabilistic generalization of K-means.
- In K-means we made **hard** cluster assignments.
- That is, we said \mathbf{x}_i definitely belongs to cluster k.
- GMM utilizes **soft** cluster assignments.
- That is, we'll say \mathbf{x}_i belongs to cluster $k = \{1, \dots, K\}$ with some probability.
- We can then estimate that probability for all k and, if need be, assign \mathbf{x}_i to the cluster with the highest probability.

The motivation behind GMMs is a generative one

The motivation behind GMMs is a generative one We'll impose on the data a distribution of the form

$$p(\mathbf{x}_i, z_i) = p(\mathbf{x}_i \mid z_i) \ p(z_i)$$

where here z_i is the cluster that \mathbf{x}_i belongs to (though, keep in mind that z_i is a random variable taking on all values in $\{1, \ldots, K\}$ We'll assume:

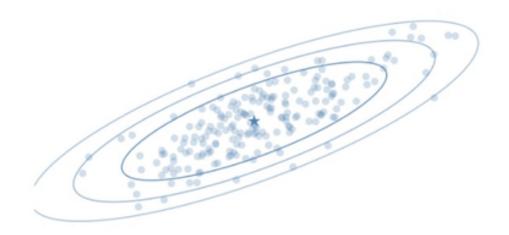
 z_i is multinomial (think rolling a die)

 $p(\mathbf{x}_i \mid z_i = k) \sim \mathcal{N}(\mu_k, \Sigma_k)$ (given a k, \mathbf{x}_i is Multivariate Gaussian)

 $p(\mathbf{x}_i \mid z_i = k) \sim \mathcal{N}(\ \mu_k, \Sigma_k)$ μ_k is a mean vector (just like in K-Means) Σ_k is a covariance matrix



 $p(\mathbf{x}_i \mid z_i = k) \sim \mathcal{N}(\ \mu_k, \Sigma_k)$ μ_k is a mean vector (just like in K-Means) Σ_k is a covariance matrix



 $p(\mathbf{x}_i \mid z_i = k) \sim \mathcal{N}(\ \mu_k, \Sigma_k)$ μ_k is a mean vector (just like in K-Means) Σ_k is a covariance matrix Density function for $\mathbf{x} \in \mathbb{R}^n$ and cluster k is given by

$$p(\mathbf{x} \mid z_i = k) = \frac{1}{(2\pi)^{n/2} |\Sigma_k|^{1/2}} \exp\left\{-\frac{1}{2} (\mathbf{x} - \mu_k)^T \Sigma_k^{-1} (\mathbf{x} - \mu_k)\right\}$$

Can generate data from model by marginalizing over *k*

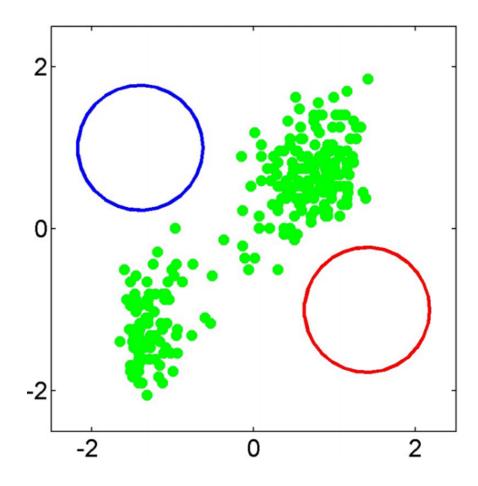
$$p(\mathbf{x}) = \sum_{k=1}^{K} p(\mathbf{x}, z = k) = \sum_{k=1}^{K} p(\mathbf{x} \mid z = k) p(z = k)$$

Recap

- K-Means is the most commonly used clustering algorithm
- We learned the Gaussian Mixture Model's generative story
 - We will learn EM-algorithm next week
 - But here's a quick preview (time permitting)

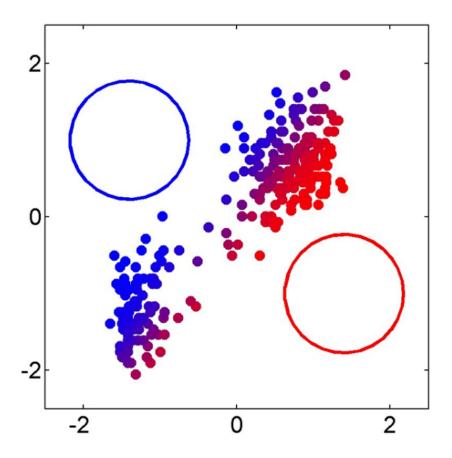
Expectation Maximization: an Intuitive Introduction

- Variables:
 - Data:
 - Data points **X** (known)
 - Cluster assignments Z (unknown)
 - Model:
 - Cluster assignment priors π (unknown)
 - Cluster means **µ** (unknown)
 - Cluster covariate matrices Σ (unknown)



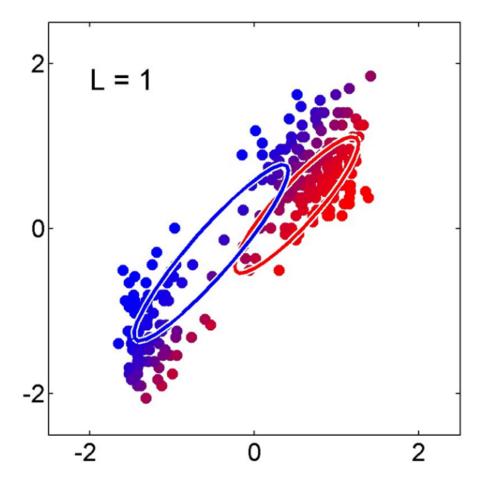
Expectation

Given the data points X and an estimate of the model parameters π, μ, Σ, it is easy to calculate expected cluster assignments z



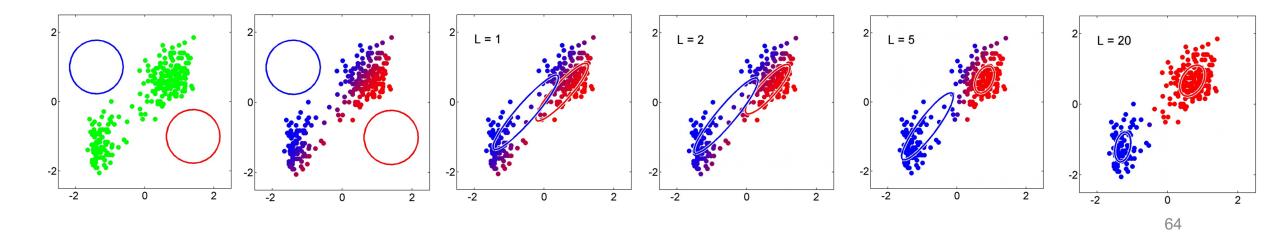
Maximization

Given the data points X and an estimate of the cluster assignments z, we can calculate the values of π, μ, and Σ that would maximize the likelihood of those clusters



EM algorithm

- Keep iterating between calculating the expected cluster assignments and finding the maximum likelihood model parameters until all variables converge
- Should seem familiar...



EM algorithm

- Black magic
- All over the place-shows up pretty much any time you want to do probabilistic modeling
- Proof boils down to "it can't hurt"

