## Outline

## Administrivia and Introduction

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Introduction
Principal Components Analysis
Singular Value Decomposition
Multidimensional Scaling
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Probabilistic Methods

## K-means

Partition methods seek to divide examples into a pre-assigned number of clusters $C_{1}, \ldots, C_{K}$ where for all $k, k^{\prime} \in\{1, \ldots, K\}$,

- $C_{k} \subset\left\{x_{1}, \ldots, x_{n}\right\}$
- $C_{k} \cap C_{k^{\prime}}=\emptyset \quad \forall k \neq k^{\prime}$
- $\cup_{k=1}^{K} C_{k}=\left\{x_{1}, \ldots, x_{n}\right\}$

For Euclidean space, we can assign a centre $r_{k}$ to each cluster in order to measure within-cluster deviance

$$
W_{C_{k}}\left(r_{k}\right)=\sum_{i: x_{i} \in C_{k}}\left\|x_{i}-r_{k}\right\|_{2}^{2} .
$$

## K-means

The overall objective is to choose both the cluster centres and allocation of points to minimize total within-cluster deviance given by

$$
W=\sum_{k=1}^{K} W_{C_{k}}\left(r_{k}\right) .
$$

Given the contents of a cluster, simple differentiation of $W_{C_{k}}\left(r_{k}\right)$ with respect to $r_{k}$ shows that within-cluster deviance is least when

$$
r_{k}=\frac{1}{\left|C_{k}\right|} \sum_{i: x_{i} \in C_{k}} x_{i},
$$

where $\left|C_{k}\right|=\#\left\{i: x_{i} \in C_{k}\right\}$ is the number of members of cluster $k$. The hard part is the combinatorial task of allocating points to clusters.

## K-means

The K-means algorithm is a well-known method that heuristically minimizes $W$ to partition $x_{1}, \ldots, x_{n}$ into $K$ clusters for some $K$.

1. Randomly fix $K$ cluster centres $r_{1}, \ldots, r_{K}$.
2. For each $i=1, \ldots, n$, assign each $x_{i}$ to the cluster with the nearest centre,

$$
x_{i} \in C_{k} \Leftrightarrow\left\|x_{i}-r_{k}\right\| \leq\left\|x_{i}-r_{k}^{\prime}\right\| \quad \forall k^{\prime} \neq k .
$$

3. Move cluster centres $r_{1}, \ldots, r_{K}$ to the average of the new clusters.
4. Repeat 2 and 3 until there is no change.
5. Return the partitions $C_{1}, \ldots, C_{K}$ at the end.

## Some Properties

Some notes about the K-means algorithm.

- The algorithm stops in a finite number of iterations. Between steps 2 and $3, W$ either stays constant -in which case we stop- or it decreases, this implies that we never revisit the same partition. As there are only finitely many partitions, the number of iterations cannot exceed this.
- The K-means algorithm need not converge to a globally optimal assignment. K-means is a heuristic search algorithm so it can get stuck at suboptimal configurations. The result depends on the starting configuration.
- Other partition based methods. There are many other partition based methods that employ related ideas for example K-medoids differs from K-means in requiring cluster centres $r_{i}$ to be an observation $x_{i}$.


## Example: Crabs

Looking at the Crabs data again.

```
library(MASS)
library(lattice)
data(crabs)
splom(~log(crabs[,4:8]),
    col=as.numeric(crabs[,1]),
    pch=as.numeric(crabs[,2]),
    main="circle/triangle is gender, black/red is species")
```


## Example: Crabs

circle/triangle is gender, black/red is species


Scatter Plot Matrix

## Example: Crabs

Apply kmeans with 2 clusters and plot results.

```
cl <- kmeans( log(crabs[,4:8]), 2, nstart=1, iter.max=10)
splom(~log(crabs[,4:8]),
    col=cl$cluster+2,
    main="blue/green is cluster finds big/small")
```


## Example: Crabs

## blue/green is cluster finds big/small

|  |  | $\begin{array}{\|ccc} \hline-3.0 & 2.5 & 3.0 \\ & 2.0 \\ -2.5 & \mathrm{BD} & 2.5- \\ 2.0 & 2.5 & 2.0 \\ \hline & 1 & \\ \hline \end{array}$ |
| :---: | :---: | :---: |
|  |  |  |
|  |  |  |
|  |  |  |
|  |  |  |

Scatter Plot Matrix

## Example: Crabs

Sphere the data.

```
pcp <- princomp( log(crabs[,4:8]) )
spc <- pcp$scores %*% diag(1/pcp$sdev)
splom( ~spc[,1:3],
    col=as.numeric(crabs[,1]),
    pch=as.numeric(crabs[,2]),
    main="circle/triangle is gender, black/red is species")
```


## Example: Crabs

circle/triangle is gender, black/red is species


## Example: Crabs

And apply K-means again.

```
cl <- kmeans(spc, 2, nstart=1, iter.max=20)
splom( ~spc[,1:3],
    col=cl$cluster+2, main="blue/green is cluster")
```


## Example: Crabs

blue/green is cluster


Scatter Plot Matrix

## Example: Crabs

circle/triangle is gender, black/red is species

blue/green is cluster


Scatter Plot Matrix

Discovers gender difference...
Results depends crucially on sphering the data first.

## Example: Crabs

Using 4 cluster centers.
colors are clusters


Scatter Plot Matrix

## Example: Crabs

circle/triangle is gender, black/red is species


Scatter Plot Matrix
colors are clusters


Scatter Plot Matrix

