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# Lecture 12

## Data Processing (2)

luhq at zju.edu.cn

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Zhejiang University, CKC

# Last Time

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- Data Processing 1
  - Statistical/Monte Carlo Simulation
  - Simulate the solution of real with less samples
  - How to write the corresponding code

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# Today

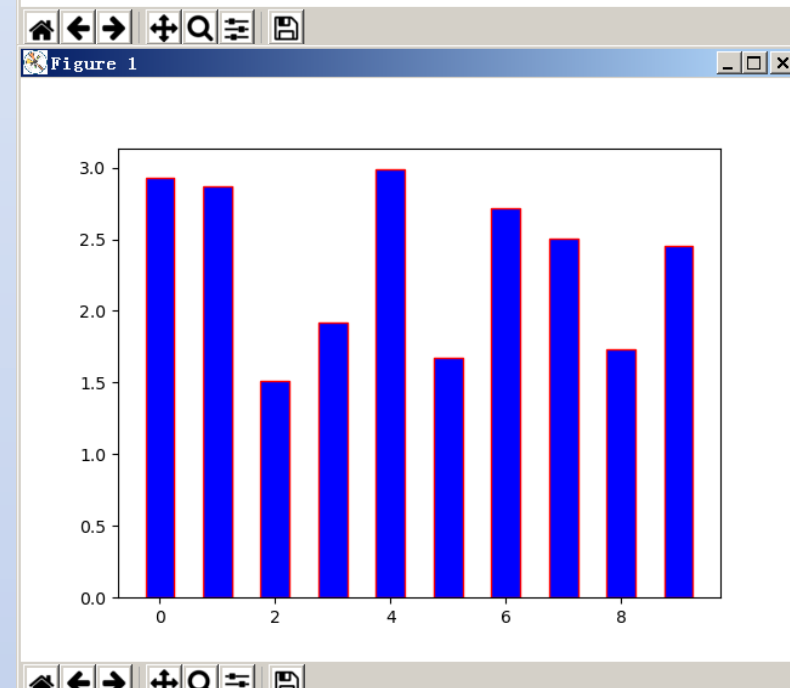
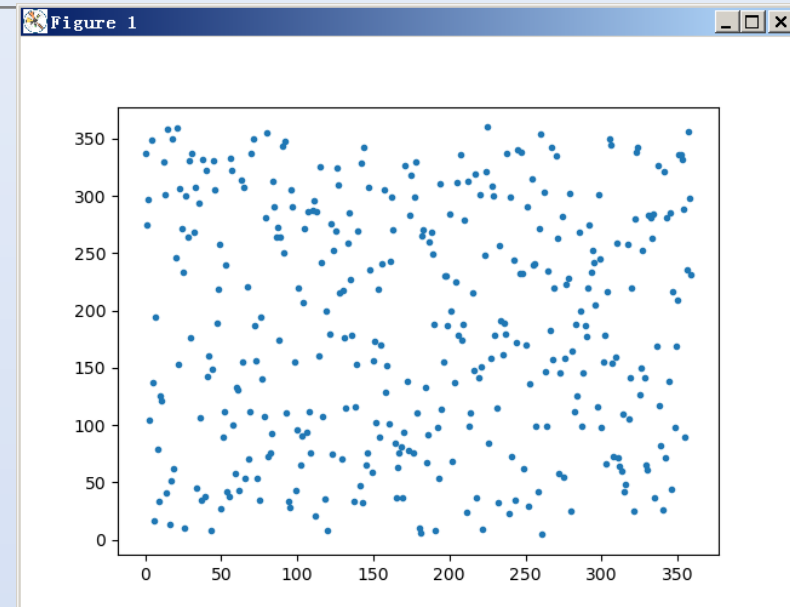
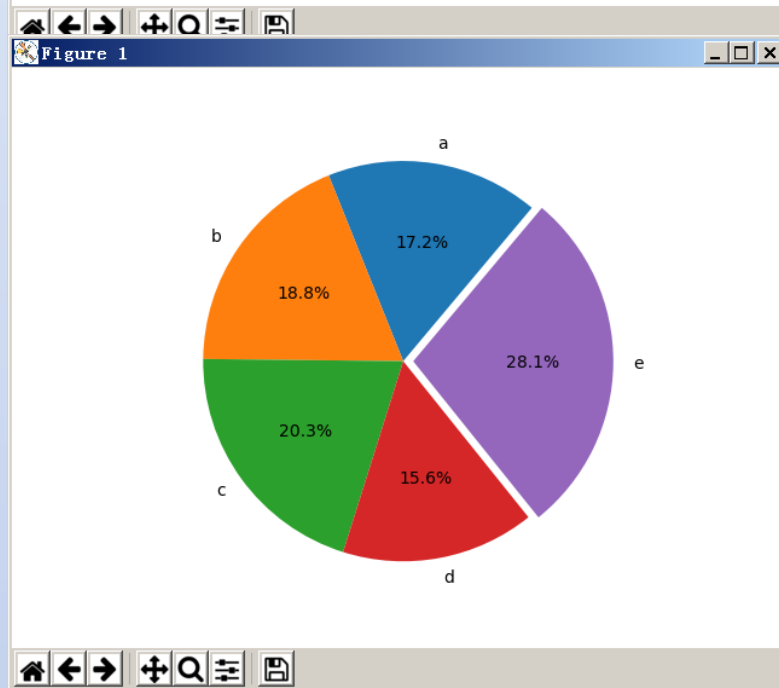
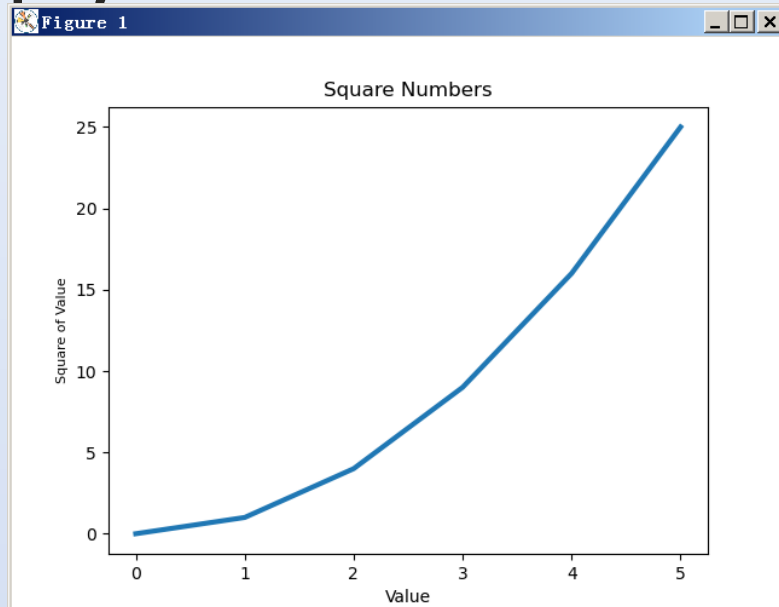
- Data Processing (Part 2)
  - Data visualization
  - Clustering
  - Classification

# Part 1: Data visualization

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- The data is represented as a graphical image
- Python pylab:
  - Draw the data into various 2D graphs (histogram, scatter chart, bar-chart, etc.).
  - This course requires the use of graphics in Project
  - **self-learning pylab**
- Install matplotlib from official website
  - pylab is its submodule
- Import pylab into your program
  - `import pylab`
  - `Import pylab as pl`      **# pl is the alias of pylab**

# pylab Demo: demopylab-line



# About Dada Processing

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- The Computer way
  1. Data processing Method (Need to find)
  2. Design Algorithm
    - procedural
  3. Implement in a programming language
    - paradigm

# Part 2 Clustering

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$$variability(c) = \sum_{e \in c} distance(mean(c), e)^2$$

$$dissimilarity(C) = \sum_{c \in C} variability(c)$$

- ◆ Why not divide variability by size of cluster?
  - Big and bad worse than small and bad
- ◆ Is optimization problem finding a C that minimizes  $dissimilarity(C)$ ?
  - No, otherwise could put each example in its own cluster
- **Clustering Is an Optimization Problem**

# Clustering

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- One of the data Processing **methods**
- Called:
  - Cluster analysis
  - Cluster method
- A "Cluster" is a set of similar data
  - **The data to be analyzed is divided into Clusters(簇)**
- Question is
  - **How to division?**
  - How to computerize
- .....



# Machine Learning Paradigm

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- Observe set of examples: **training data**
- Infer something about process that generated that data
- Use inference to make predictions about previously unseen data: **test data**
- Supervised: given a set of feature/label pairs, find a rule that predicts the label associated with a previously unseen input
- *Unsupervised*: given a set of feature vectors (without labels) group them into “natural clusters”

# Clustering Is an Optimization Problem

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- Need a constraint, e.g.,
  - Minimum distance between clusters
  - Number of clusters
- Two Popular Methods
  - Hierarchical clustering
  - K-means clustering

# Hiearchical Clustering

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1. Start by assigning each item to a cluster, so that if you have  $N$  items, you now have  $N$  clusters, each containing just one item.
2. Find the closest (most similar) pair of clusters and merge them into a single cluster, so that now you have one fewer cluster.
3. Continue the process until all items are clustered into a single cluster of size  $N$ .

What does distance mean?

# Linkage Metrics

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- *Single-linkage*: consider the distance between one cluster and another cluster to be equal to the shortest distance from any member of one cluster to any member of the other cluster
- *Complete-linkage*: consider the distance between one cluster and another cluster to be equal to the greatest distance from any member of one cluster to any member of the other cluster
- *Average-linkage*: consider the distance between one cluster and another cluster to be equal to the average distance from any member of one cluster to any member of the other cluster

# Example of Hierarchical Clustering

	BOS	NY	CHI	DEN	SF	SEA
BOS	0	206	963	1949	3095	2979
NY		0	802	1771	2934	2815
CHI			0	966	2142	2013
DEN				0	1235	1307
SF					0	808
SEA						0

{BOS} {NY}

{CHI}

{DEN}

{SF}

{SEA}

{BOS, NY}

{CHI}

{DEN}

{SF}

{SEA}

{BOS, NY, CHI}

{DEN}

{SF}

{SEA}

{BOS, NY, CHI}

{DEN}

{SF, SEA}

{BOS, NY, CHI, **DEN**}

{SF, SEA}

Single linkage

or

{BOS, NY, CHI}

{**DEN**, SF, SEA}

Complete linkage

# Clustering Algorithms

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- Hierarchical clustering
  - Can select number of clusters using dendrogram
  - Deterministic
  - Flexible with respect to linkage criteria
  - Slow
    - Naïve algorithm  $n^3$
    - $n^2$  algorithms exist for some linkage criteria
- K-means a much faster greedy algorithm
  - Most useful when you know how many clusters you want

# K-means Algorithm

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randomly chose k examples as initial centroids

**while true:**

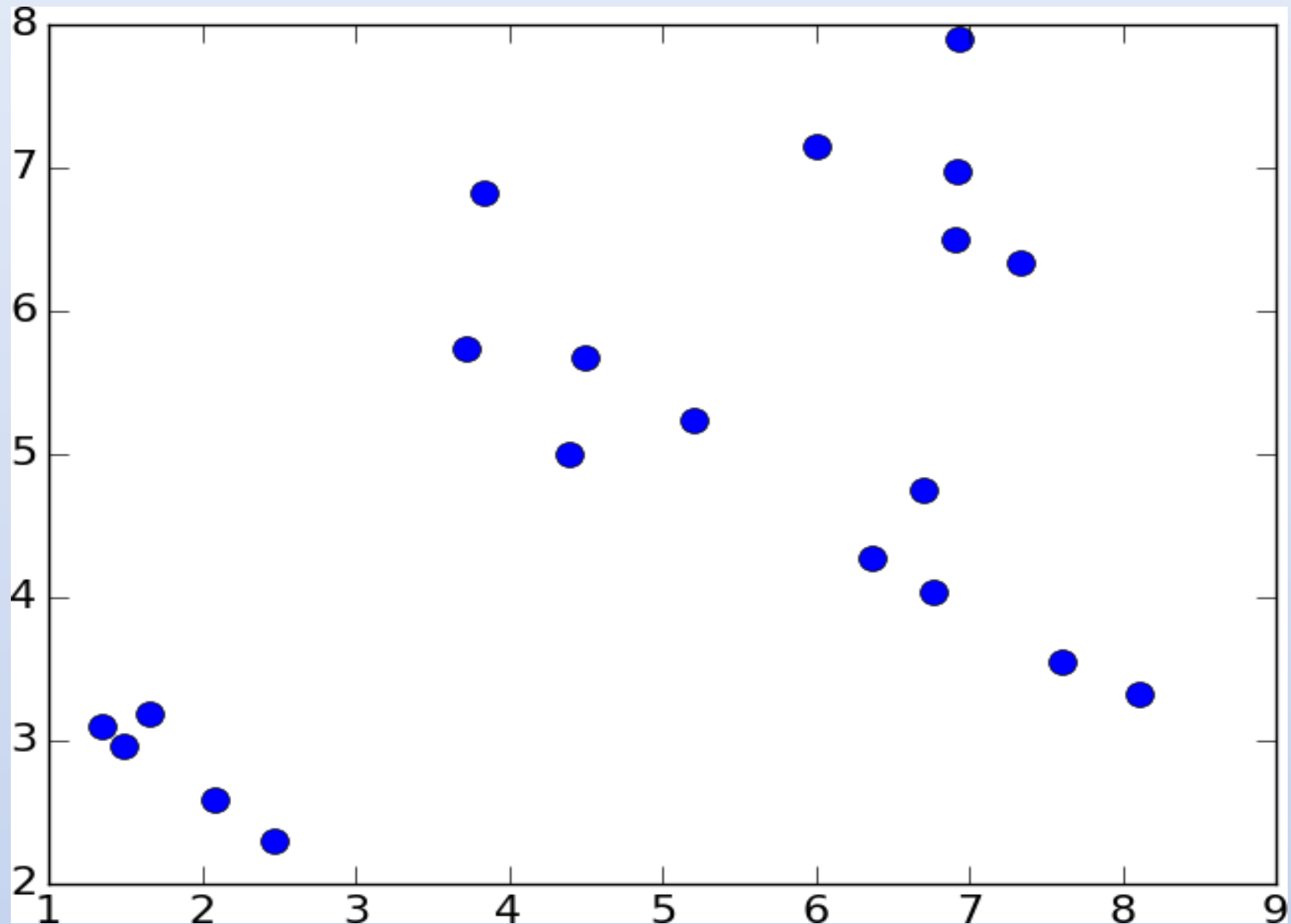
- create k clusters by assigning each example to closest centroid
- compute k new centroids by averaging examples in each cluster
- if centroids don't change:
  - break

What is complexity of one iteration?

$k*n*d$ , where n is number of points and d time required to compute the distance between a pair of points

# An Example

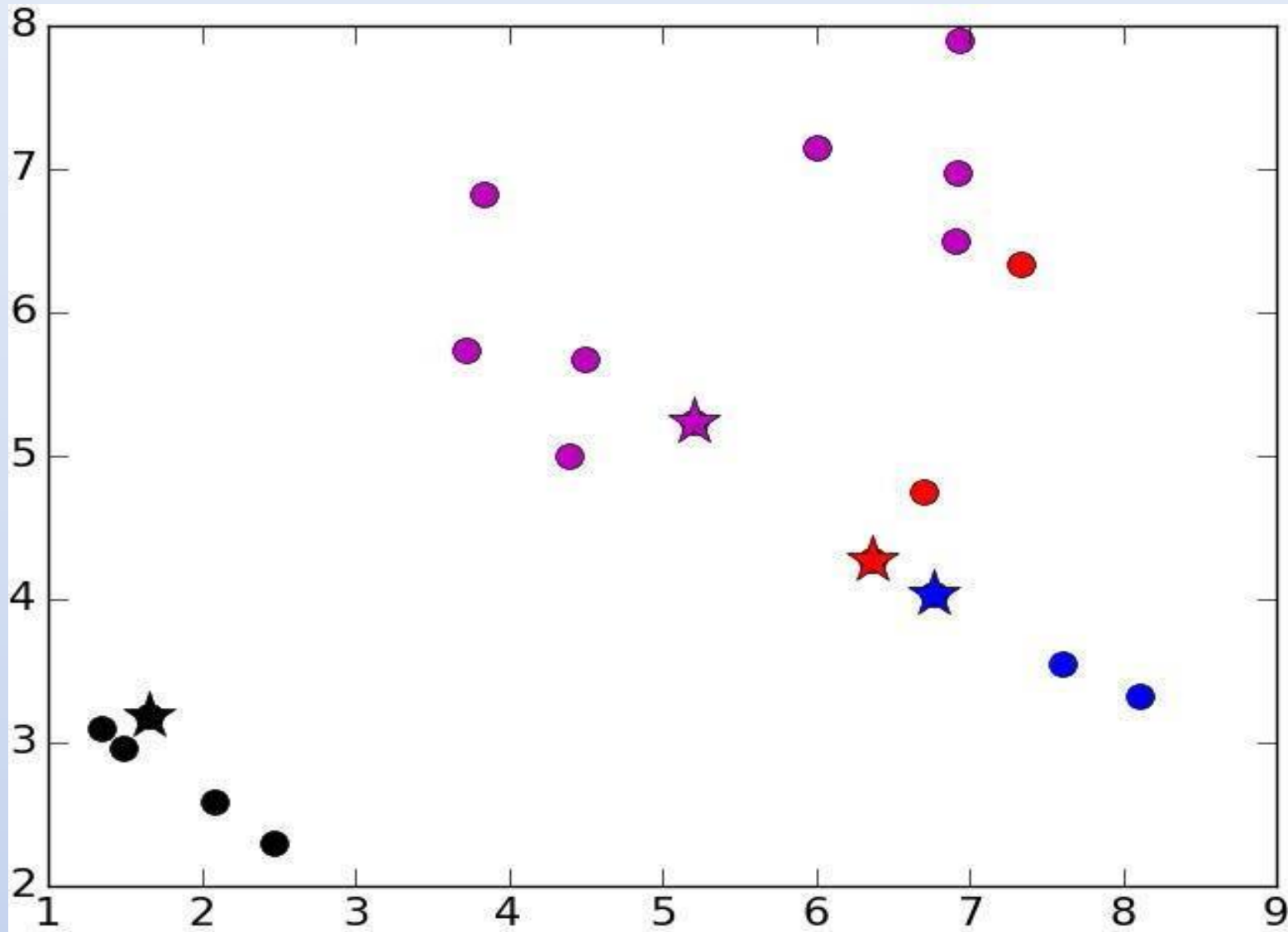
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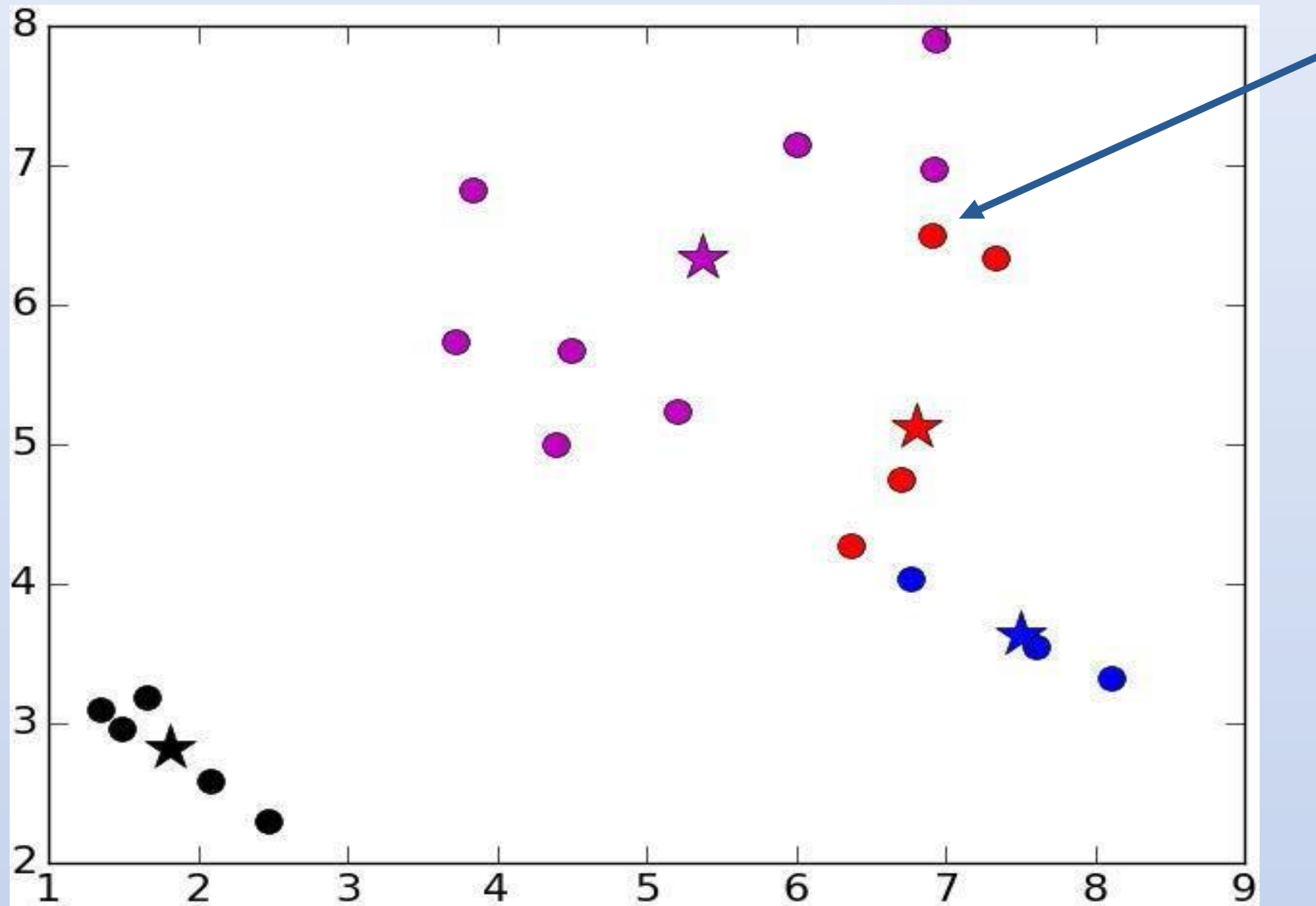
# K = 4, Initial Centroids

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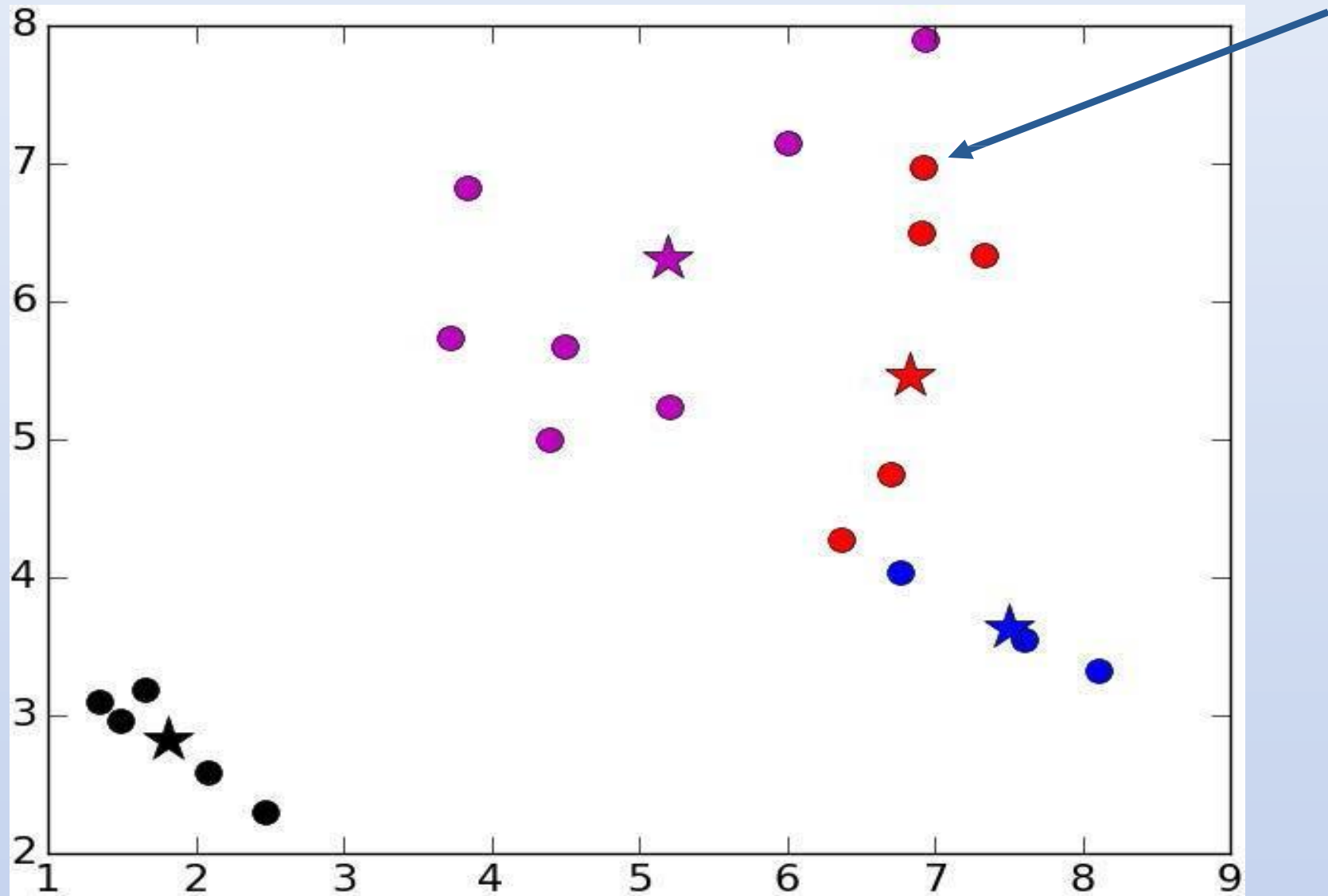
# Iteration 1

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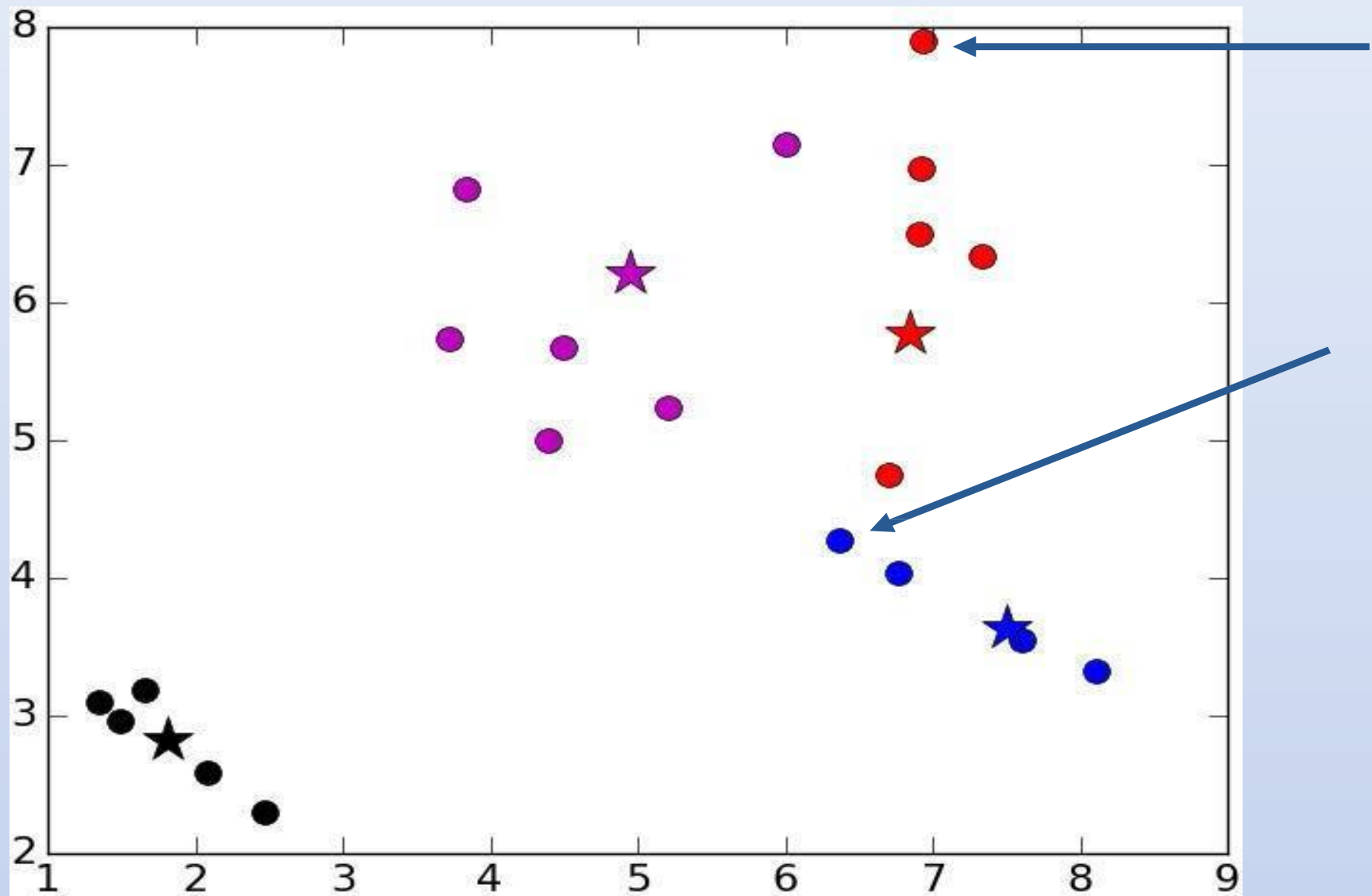
# Iteration 2

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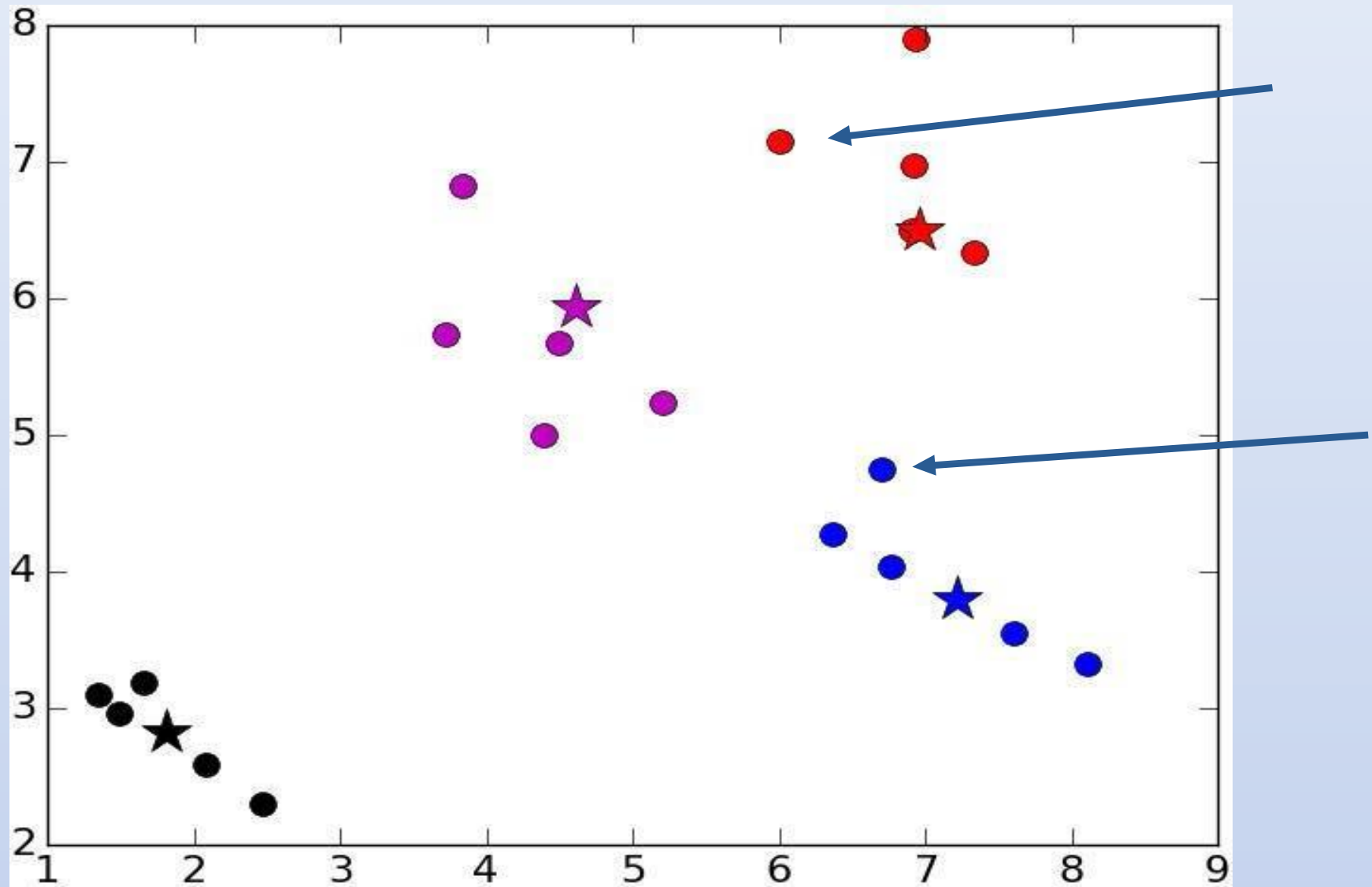
# Iteration 3

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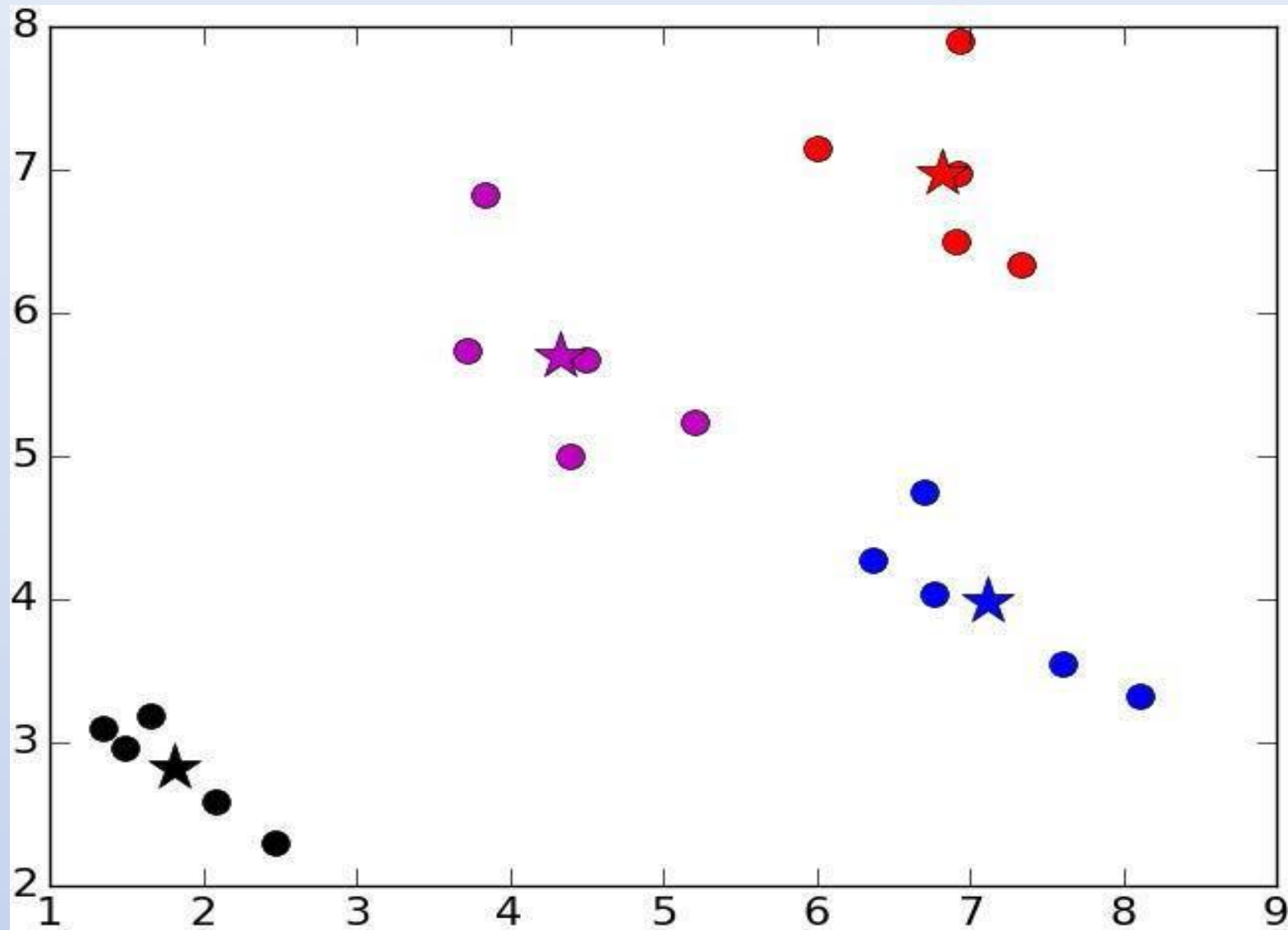
# Iteration 4

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# Iteration 5

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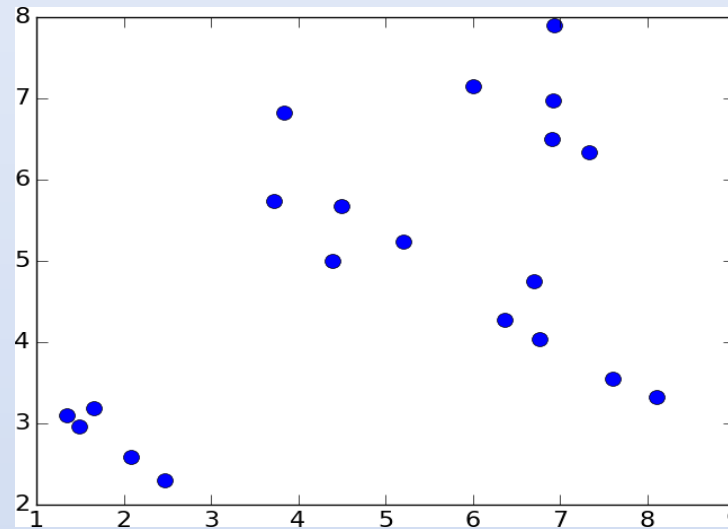


# Issues with k-means

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- Choosing the “wrong”  $k$  can lead to strange results

- Consider  $k = 3$



- Result can depend upon initial centroids

- Number of iterations
- Even final result
  - Greedy algorithm can find different local optimas

# How to Choose K

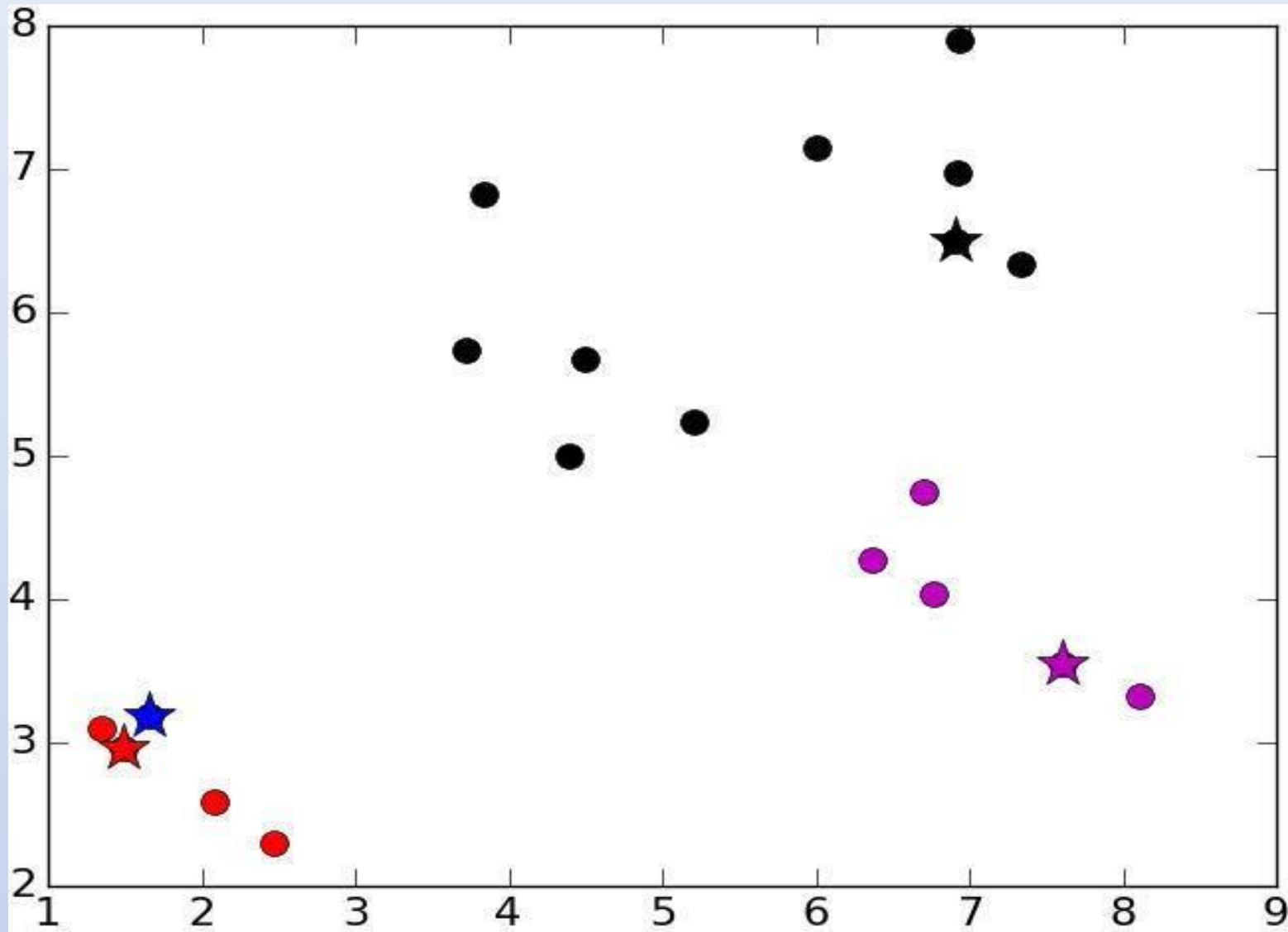
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- *A priori* knowledge about application domain
  - There are two kinds of people in the world:  $k = 2$
  - There are five different types of bacteria:  $k = 5$
- Search for a good  $k$ 
  - Try different values of  $k$  and evaluate quality of results
  - Run hierarchical clustering on subset of data



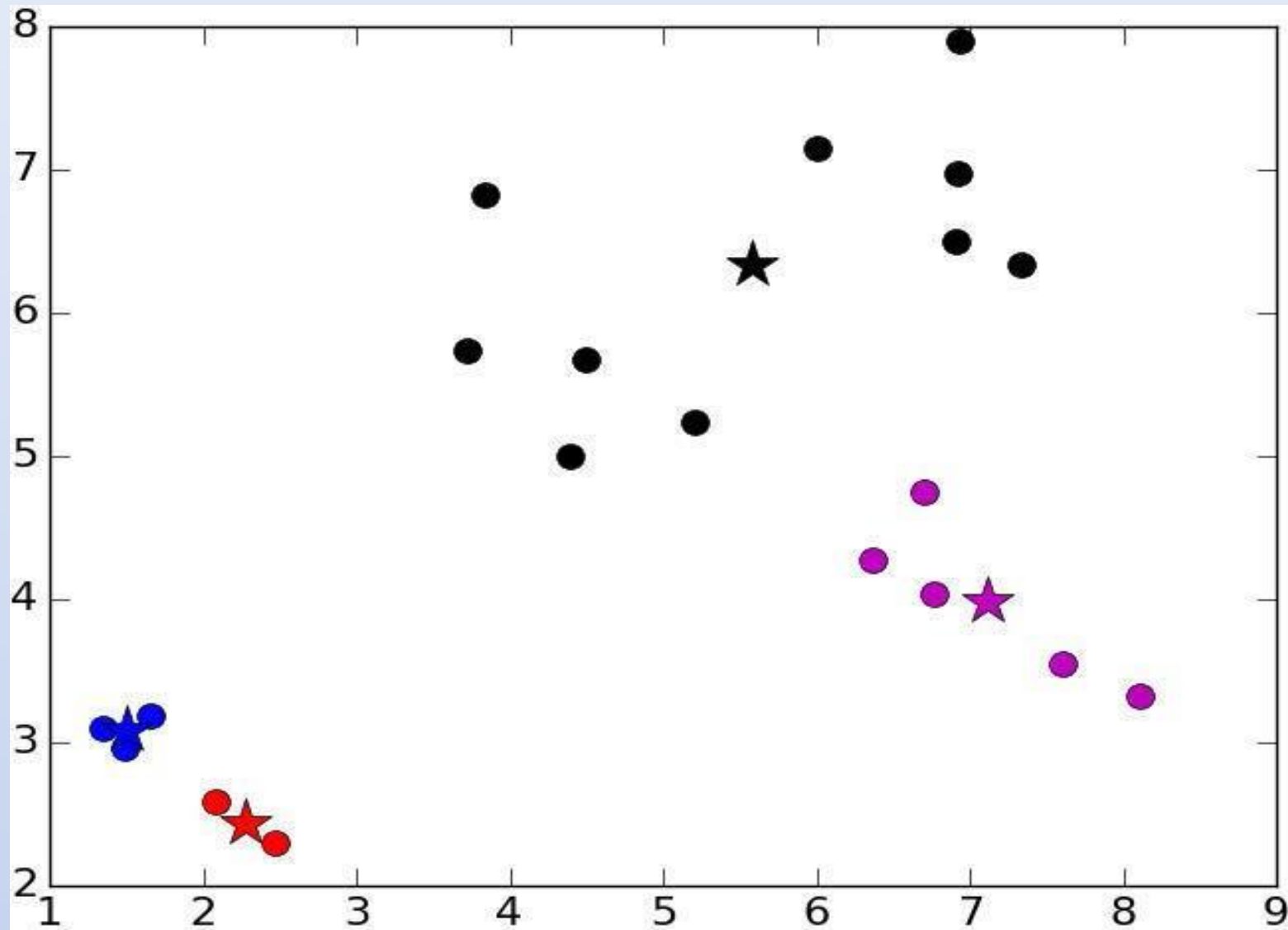
# Unlucky Initial Centroids

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# Converges On

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# Mitigating Dependence on Initial Centroids

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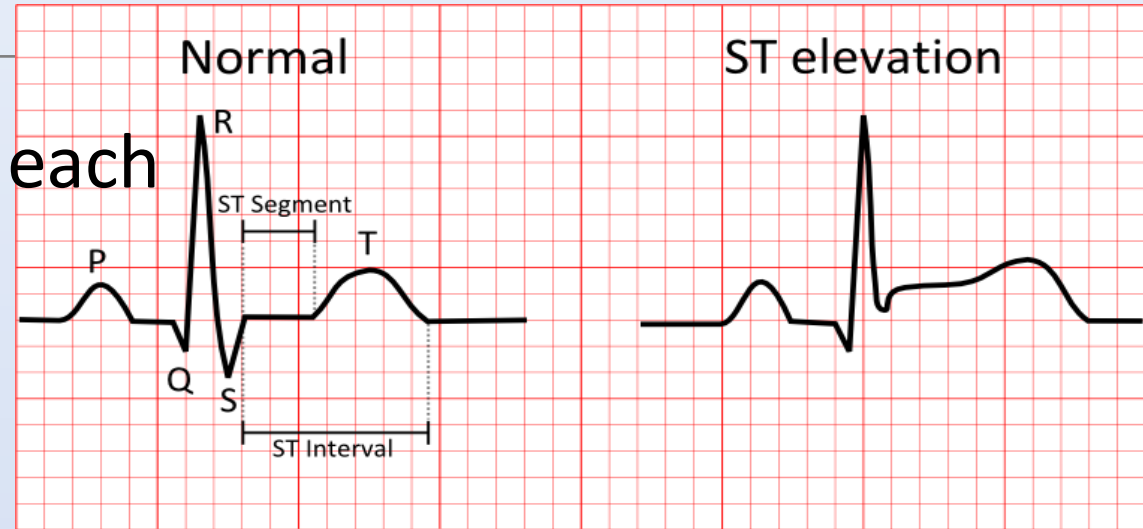
Try multiple sets of randomly chosen initial centroids

Select “best” result

```
best = kMeans(points)
for t in range(numTrials):
    C = kMeans(points)
    if dissimilarity(C) < dissimilarity(best):
        best = C
return best
```

# An Example

- Many patients with 4 features each
  - Heart rate in beats per minute
  - Number of past heart attacks
  - Age
  - ST elevation (binary)
- Outcome (death) based on features
  - Probabilistic, not deterministic
  - E.g., older people with multiple heart attacks at higher risk
- Cluster, and examine purity of clusters relative to outcomes



# Data Sample

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	<u>HR</u>	<u>Att</u>	<u>STE</u>	<u>Age</u>	<u>Outcome</u>
P000:	[ 89.]	1.	0.	66.]	: <b>1</b>
P001:	[ 59.]	0.	0.	72.]	: 0
P002:	[ 73.]	0.	0.	73.]	: 0
P003:	[ 56.]	1.	0.	65.]	: 0
P004:	[ 75.]	1.	1.	68.]	: <b>1</b>
P005:	[ 68.]	1.	0.	56.]	: 0
P006:	[ 73.]	1.	0.	75.]	: <b>1</b>
P007:	[ 72.]	0.	0.	65.]	: 0
P008:	[ 73.]	1.	0.	64.]	: <b>1</b>
P009:	[ 73.]	0.	0.	58.]	: 0
P010:	[ 100.]	0.	0.	75.]	: 0
P011:	[ 79.]	0.	0.	31.]	: 0
P012:	[ 81.]	0.	0.	58.]	: 0
P013:	[ 89.]	1.	0.	50.]	: <b>1</b>
P014:	[ 81.]	0.	0.	70.]	: 0

# Class Example

```
class Example(object):  
  
    def __init__(self, name, features, label = None):  
        #Assumes features is an array of floats  
        self.name = name  
        self.features = features  
        self.label = label  
  
    ...  
  
    def distance(self, other):  
        return minkowskiDist(self.features,  
                               other.getFeatures(), 2)
```

features : [hr, prevAC, stElev, age]

**Minkowski Distance:**

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

# class Cluster

```
class Cluster(object):

    def __init__(self, examples):
        """Assumes examples a non-empty list of Examples"""
        ...

    def update(self, examples):
        """Assume examples is a non-empty list of Examples
        Replace examples; return amount centroid has
        changed"""
        ...

    def computeCentroid(self):
        vals = pylab.array([0.0]*self.examples[0].\
                           dimensionality())
        for e in self.examples: #compute mean
            vals += e.getFeatures()
        centroid = Example('centroid', vals/len(self.examples))
        return centroid

    ...
```

# Class Cluster, cont.

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```
def variability(self):  
    totDist = 0  
    for e in self.examples:  
        totDist += (e.distance(self.centroid))**2  
    return totDist  
  
def members(self):  
    for e in self.examples:  
        yield e
```

...



# Evaluating a Clustering

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```
def dissimilarity(clusters):  
    """Assumes clusters a list of clusters  
    Returns a measure of the total dissimilarity of the  
    clusters in the list"""  
    totDist = 0  
    for c in clusters:  
        totDist += c.variability()  
    return totDist
```

# Patients

```
import cluster, pylab, numpy

class Patient(cluster.Example):
    pass

def scaleAttrs(vals):
    vals = pylab.array(vals)
    mean = sum(vals)/len(vals)
    sd = numpy.std(vals)
    vals = vals - mean
    return vals/sd

def getData(toScale = False):
    #read in data
    ...
    if toScale:
        hrList = scaleAttrs(hrList)
    ...
    #Build points
    ...
    return points
```

Z-Scaling

Mean = ?

Std = ?

# kmeans

```
def kmeans(examples, k, verbose = False):
    #Get k randomly chosen initial centroids,
    #create cluster for each
    ...
    #Iterate until centroids do not change
    ...
        #Associate each example with closest centroid
        ...
        for c in newClusters: #Avoid having empty clusters
            if len(c) == 0:
                raise ValueError('Empty Cluster')

        #Update each cluster; check if a centroid has changed
        ...

def trykmeans(examples, numClusters, numTrials, verbose=False):
    """Calls kmeans numTrials times and returns the result with
    the lowest dissimilarity"""
    ...
```

# Examining Results

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```
def printClustering(clustering):
    """Assumes: clustering is a sequence of clusters
    Prints information about each cluster
    Returns list of fraction of pos cases in each cluster"""
    ...

def testClustering(patients, numClusters, seed = 0,
                  numTrials = 5):
    random.seed(seed)
    bestClustering = trykmeans(patients, numClusters,
                              numTrials)
    posFracs = printClustering(bestClustering)
    return posFracs

patients = getData()
for k in (2,):
    print('\n      Test k-means (k = ' + str(k) + ')')
    posFracs = testClustering(patients, k)
```

# Result of Running It

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✓ Try `patients = getData( )`

Test k-means ( $k = 2$ )

Cluster of size 118 with fraction of positives = 0.3305

Cluster of size 132 with fraction of positives = 0.3333

Like it?

✓ Try `patients = getData(True)`

Test k-means ( $k = 2$ )

Cluster of size 224 with fraction of positives = 0.2902

Cluster of size 26 with fraction of positives = 0.6923

Happy with sensitivity?



# How Many Positives Are There?

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```
numPos = 0
for p in patients:
    if p.getLabel() == 1:
        numPos += 1
print('Total number of positive patients =', numPos)
```

Total number of positive patients = 83

Test k-means ( $k = 2$ )

Cluster of size 224 with fraction of positives = 0.2902

(Positive,  $0.2902 * 224 = 65$ )

Cluster of size 26 with fraction of positives = 0.6923

(Positive,  $0.6923 * 26 = 18$ )

# A Hypothesis

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- Different subgroups of positive patients have different characteristics
- How might we test this?
- Try some other values of k



True

```
patients = getData()
for k in (2,4,6):
    print('\n      Test k-means (k = ' + str(k) + ')')
    posFracs = testClustering(patients, k, 2)
```

# Testing Multiple Values of k

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Test k-means ( $k = 2$ )

Cluster of size 224 with fraction of positives = 0.2902

Cluster of size 26 with fraction of positives = 0.6923

Test k-means ( $k = 4$ )

Cluster of size 26 with fraction of positives = 0.6923

Cluster of size 86 with fraction of positives = 0.0814

Cluster of size 76 with fraction of positives = 0.7105

Cluster of size 62 with fraction of positives = 0.0645

Test k-means ( $k = 6$ )

Cluster of size 49 with fraction of positives = 0.0204

Cluster of size 26 with fraction of positives = 0.6923

Cluster of size 45 with fraction of positives = 0.0889

Cluster of size 54 with fraction of positives = 0.0926

Cluster of size 36 with fraction of positives = 0.7778

Cluster of size 40 with fraction of positives = 0.675

Pick a k,  
Which?



# Homework, DIY

1. Self-learning pylab, numpy  
Demo\_Pylab.py
2. Read the lect12.py and cluster.py  
comment the main code  
Prepare for the project

Project will be assigned next week

Next week's test: lect11, 12