# CPSC 340: Machine Learning and Data Mining

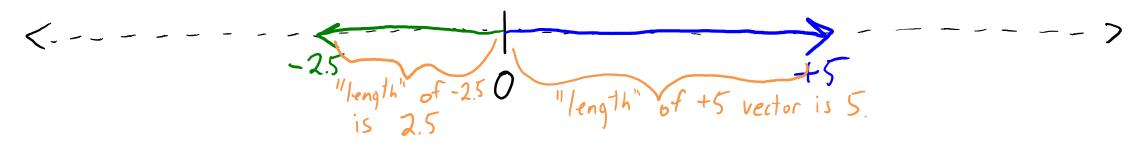
Density-Based Clustering Fall 2016

# Admin

- Assignment 1 :
  - 2 late days to hand it in before Wednesday's class.
  - 3 late days to hand it in before Friday's class.
  - 0 after that.
- Assignment 2 coming tonight.

# Norms in 1-Dimension

• We can view absolute value, |x|, as 'size' or 'length' of a number:



- It satisfies three intuitive properties of 'length':
  - 1. Only '0' has a 'length' of zero.
  - 2. Multiplying 'x' by constant ' $\alpha$ ' multiplies length by  $|\alpha|$ :
    - "Absolute homogeneity":  $|\alpha x| = |\alpha| |x|$ .
    - "If will twice as long if you multiply by 2".
  - 3. Length of 'x+y' is not more than length of 'x' plus length of 'y':

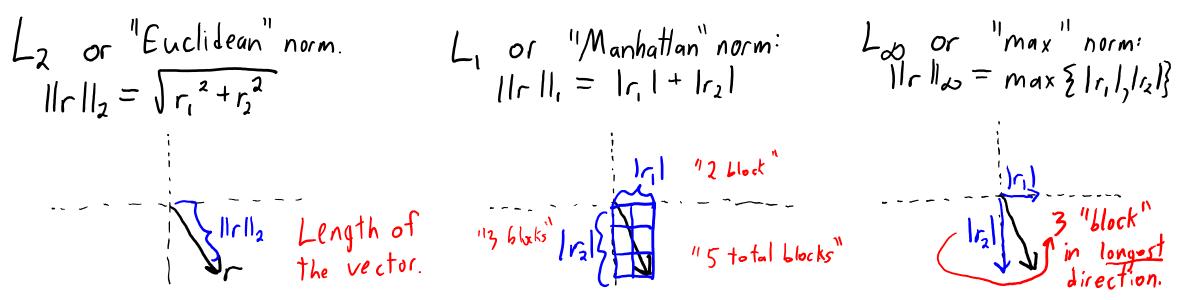
× y y

X + y

- "Triangle" inequality: |x + y| <= |x| + |y|.</li>
- Think of "how far you travel".

# Norms in 2-Dimensions

- In 1-dimension, only scaled absolute values satisfy the 3 properties.
- In 2-dimensions, there is no unique function satisfying them.
- We call any function satisfying them a norm:
  - Measures of "size" or "length" in 2-dimensions.
- Three most common examples:



## Norms as Measures of Distance

• By taking norm of difference, we get a "distance" between vectors:

$$\begin{aligned} \|x - y\|_{2} &= \sqrt{(x_{1} - y_{1})^{2} + (x_{2} - y_{2})^{2}} \\ \|x - y\|_{1} &= |x_{1} - y_{1}| + |x_{2} - y_{2}| \\ \|x - y\|_{0} &= \max \left\{ |x_{1} - y_{1}| \right\} + |x_{2} - y_{2}| \\ \|x - y\|_{\infty} &= \max \left\{ |x_{1} - y_{1}| \right\} + |x_{2} - y_{2}| \\ \|x - y\|_{\infty} &= \max \left\{ |x_{1} - y_{1}| \right\} + |x_{2} - y_{2}| \\ \|x - y\|_{\infty} &= \max \left\{ |x_{1} - y_{1}| \right\} + |x_{2} - y_{2}| \\ \|x - y\|_{\infty} &= \max \left\{ |x_{1} - y_{1}| \right\} + |x_{2} - y_{2}| \\ \|x - y\|_{\infty} &= \max \left\{ |x_{1} - y_{1}| \right\} + |x_{2} - y_{2}| \\ \|x - y\|_{\infty} &= \max \left\{ |x_{1} - y_{1}| \right\} + |x_{2} - y_{2}| \\ \|x - y\|_{\infty} &= \max \left\{ |x_{1} - y_{1}| \right\} + |x_{2} - y_{2}| \\ \|x - y\|_{\infty} &= \max \left\{ |x_{1} - y_{1}| \right\} + |x_{2} - y_{2}| \\ \|x - y\|_{\infty} &= \max \left\{ |x_{1} - y_{1}| \right\} + |x_{2} - y_{2}| \\ \|x - y\|_{\infty} &= \max \left\{ |x_{1} - y_{1}| \right\} + |x_{2} - y_{2}| \\ \|x - y\|_{\infty} &= \max \left\{ |x_{1} - y_{1}| \right\} + |x_{2} - y_{2}| \\ \|x - y\|_{\infty} &= \max \left\{ |x_{1} - y_{1}| \right\} + |x_{2} - y_{2}| \\ \|x - y\|_{\infty} &= \max \left\{ |x_{1} - y_{1}| \right\} + |x_{2} - y_{2}| \\ \|x - y\|_{\infty} &= \max \left\{ |x_{1} - y_{1}| \right\} + |x_{2} - y_{2}| \\ \|x - y\|_{\infty} &= \max \left\{ |x_{1} - y_{1}| \right\} + |x_{2} - y_{2}| \\ \|x - y\|_{\infty} &= \max \left\{ |x_{1} - y_{1}| \right\} + |x_{2} - y_{2}| \\ \|x - y\|_{\infty} &= \max \left\{ |x_{1} - y_{1}| \right\} + |x_{2} - y_{2}| \\ \|x - y\|_{\infty} &= \max \left\{ |x_{1} - y_{1}| \right\} + |x_{2} - y_{2}| \\ \|x - y\|_{\infty} &= \max \left\{ |x_{1} - y_{1}| \right\} + |x_{2} - y_{2}| \\ \|x - y\|_{\infty} &= \max \left\{ |x_{1} - y_{1}| \right\} + |x_{2} - y_{2}| \\ \|x - y\|_{\infty} &= \max \left\{ |x_{1} - y_{1}| \right\} + |x_{2} - y_{2}| \\ \|x - y\|_{\infty} &= \max \left\{ |x_{1} - y_{1}| \right\} + |x_{2} - y_{2}| \\ \|x - y\|_{\infty} &= \max \left\{ |x_{1} - y_{1}| \right\} + |x_{2} - y_{2}| \\ \|x - y\|_{\infty} &= \max \left\{ |x_{1} - y_{1}| \right\} + |x_{2} - y_{2}| \\ \|x - y\|_{\infty} &= \max \left\{ |x_{1} - y_{1}| \right\} + |x_{2} - y_{2}| \\ \|x - y\|_{\infty} &= \max \left\{ |x_{1} - y_{1}| \right\} + |x_{2} - y_{2}| \\ \|x - y\|_{\infty} &= \max \left\{ |x_{1} - y_{1}| \right\} + |x_{2} - y_{2}| \\ \|x - y\|_{\infty} &= \max \left\{ |x_{1} - y_{1}| \right\} + |x_{2} - y_{2}| \\ \|x - y\|_{\infty} &= \max \left\{ |x_{1} - y_{1}| \right\} + |x_{2} - y_{2}| \\ \|x - y\|_{\infty} &= \max \left\{ |x_{1} - y_{1}| \right\} + |x_{2} - y_{2}| \\ \|x - y\|_{\infty} &= \max \left\{ |x_{1} - y_{1}| \\ \|x - y\|_{\infty} &= \max \left\{ |x_{1} - y_{1}| \\ \|x - y\|_{\infty} &= \max \left\{ |x_{$$

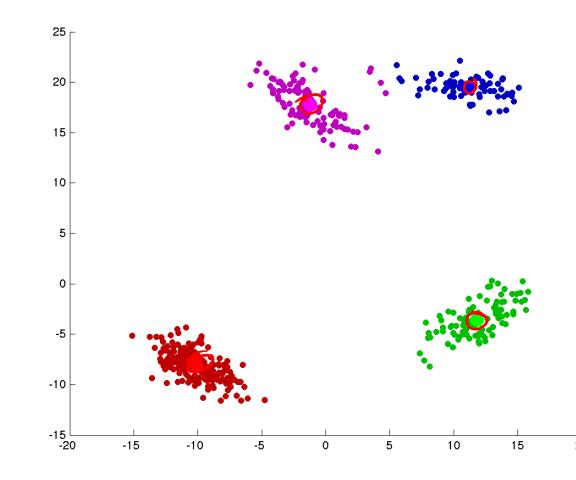
# Norms in d-Dimensions

• We can generalize these common norms to d-dimensional vectors:

- These norms place different weights
  - $-L_1$ : all values are equal.
  - $-L_2$ : bigger values are more important (because of squaring).
  - $-L_{\infty}$ : only biggest value is important.

# Last Time: K-Means Clustering

- We want to cluster data:
  - Assign objects to groups.
- K-means clustering:
  - Define groups by "means"
  - Assign objects to nearest mean.
     (Then update means during training.)
- Also used for vector quantization:
   Use means as prototypes of groups.



# **K-Means Initialization**

• K-means is fast but sensitive to initialization.

- Classic approach to initialization: random restarts.
  - Run to convergence using different random initializations.
  - Choose the one that minimizes average squared distance of data to means.

- Newer approach: k-means++
  - Random initialization that prefers means that are far apart.
  - Yields provable bounds on expected approximation ratio.

Steps of k-means++:

Expected

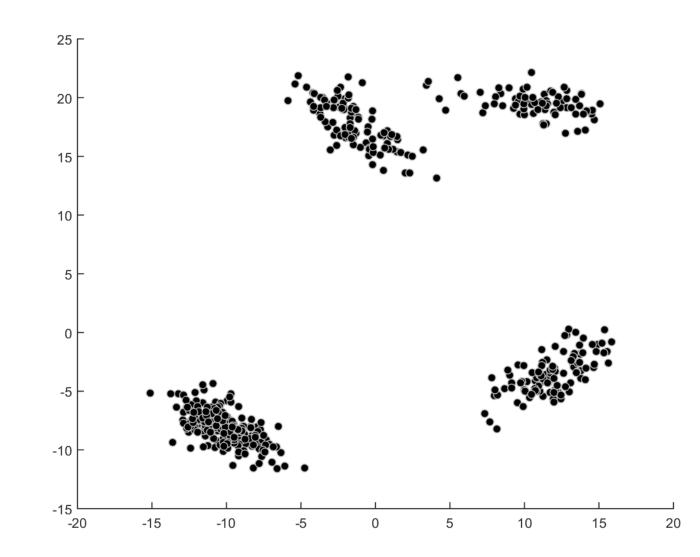
- 1. Select initial mean  $w_1$  as a random  $x_i$ .
- 2. Compute distance  $d_{ic}$  of each object  $x_i$  to each mean  $w_c$ .
- $d_{ic} = \sqrt{\frac{2}{2} (x_{ij} w_{cj})^2} = ||x_i w_c||_2$ 3. For each object 'i' set d, to the distance to the closest mean.

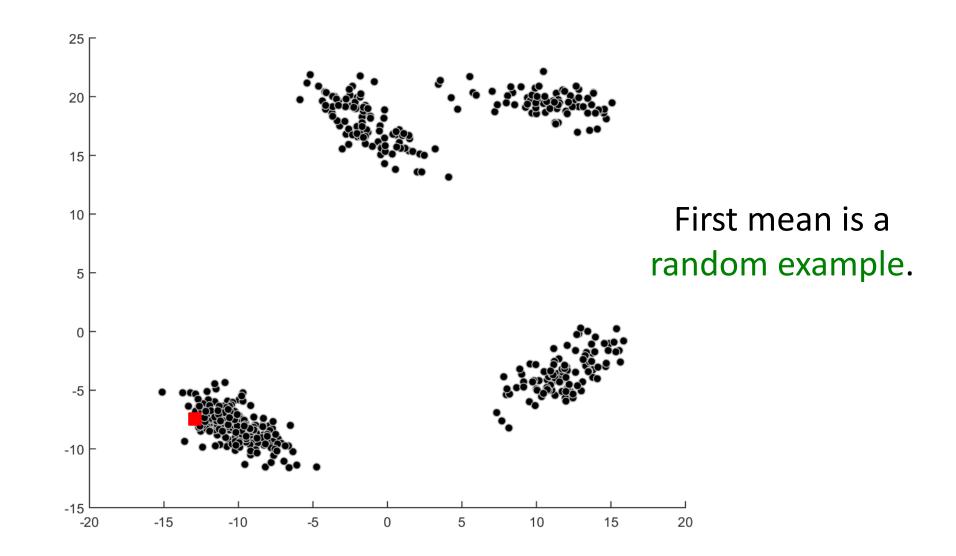
$$d_i = \min_{c} \{ d_i \}$$

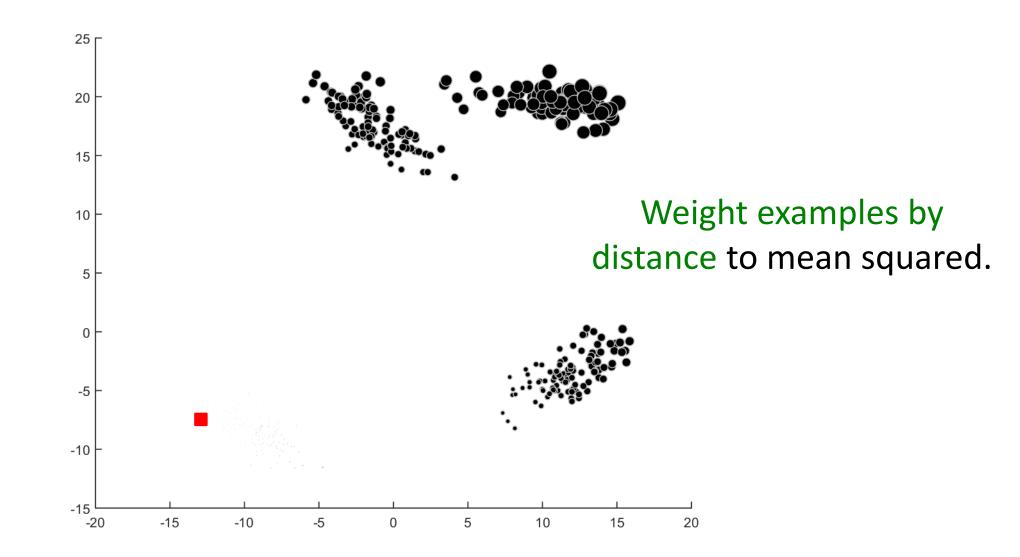
4. Choose next mean by sampling an example 'i' proportional to  $(d_i)^2$ .

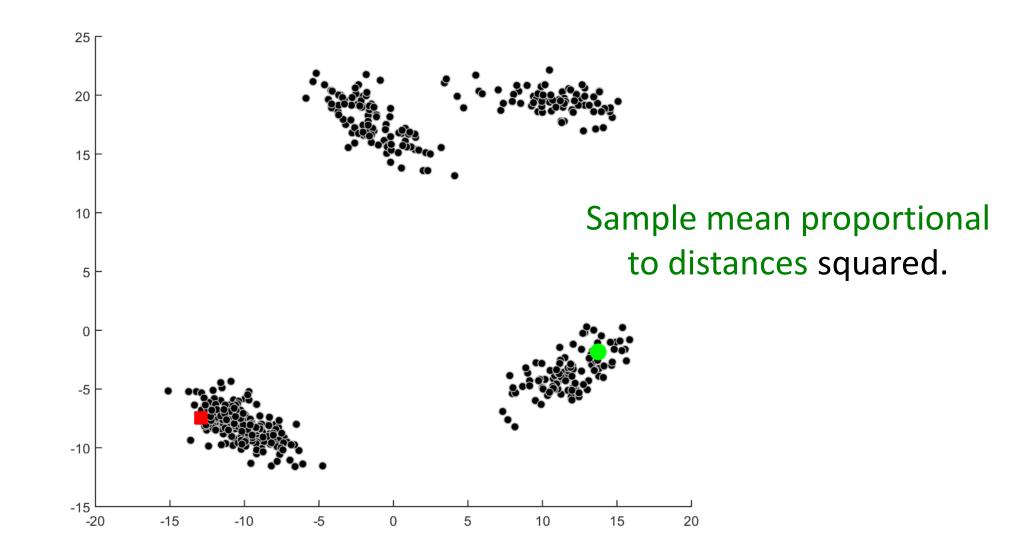
5. Keep returning to step 2 until we have k-means.  
Expected approximation ratio is O(log(k)).  

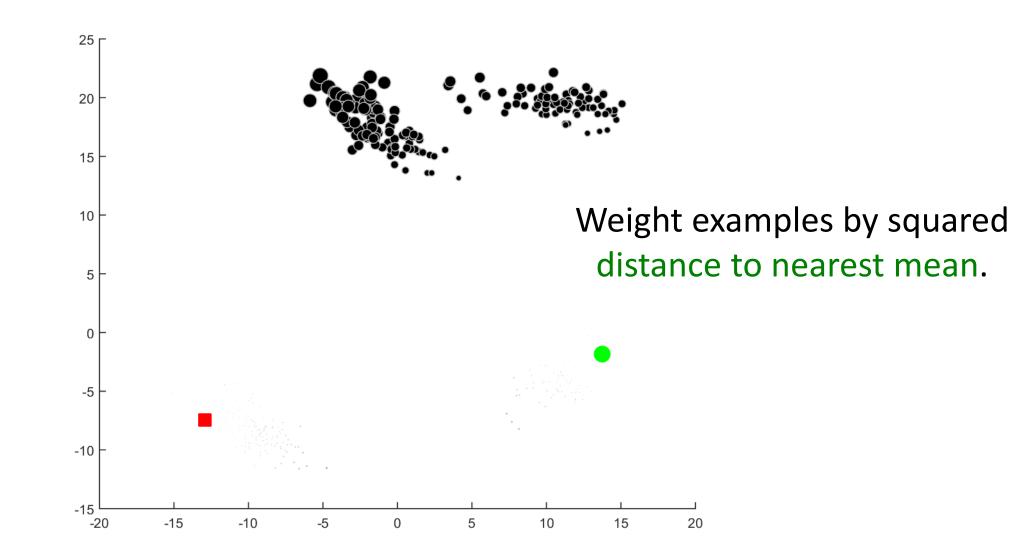
$$\int_{j=1}^{1} \alpha d_{j}^{2} = p_{j} = \frac{d_{j}^{2}}{2} \quad Can be done in for a be done in the beat do$$

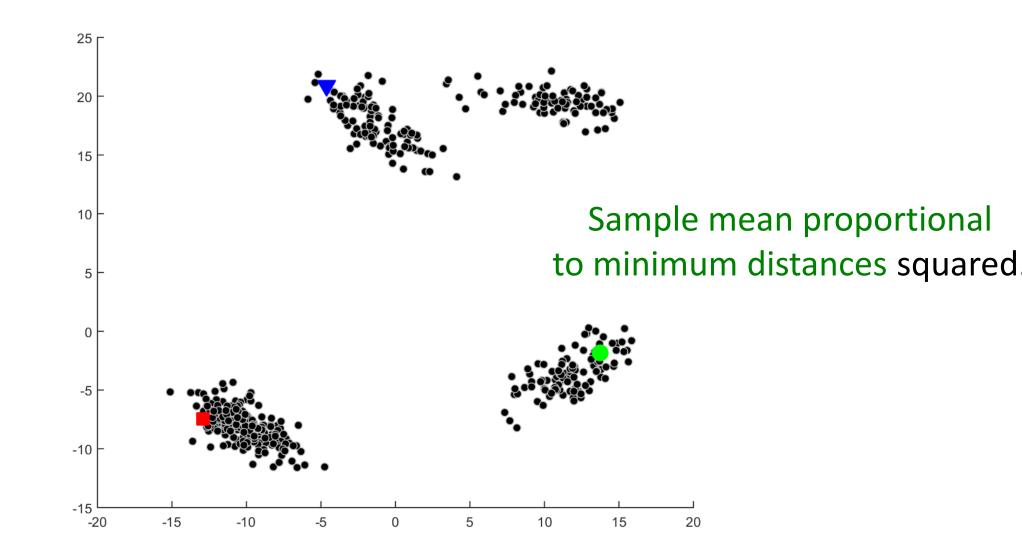


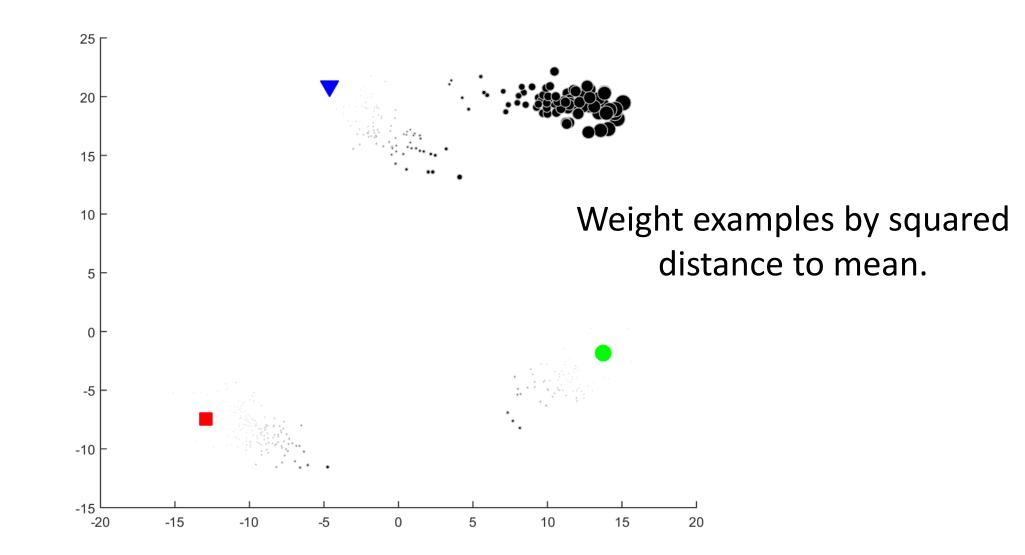


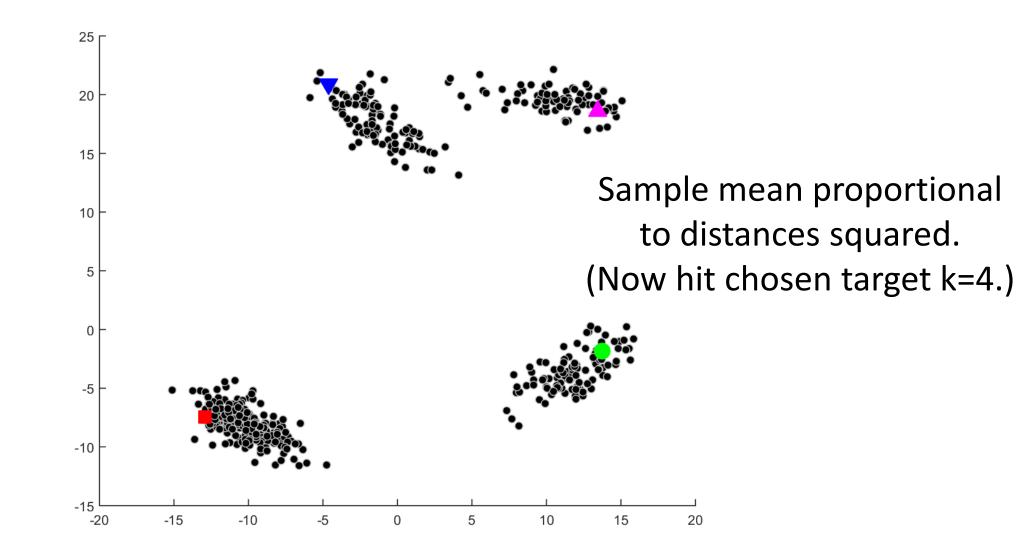


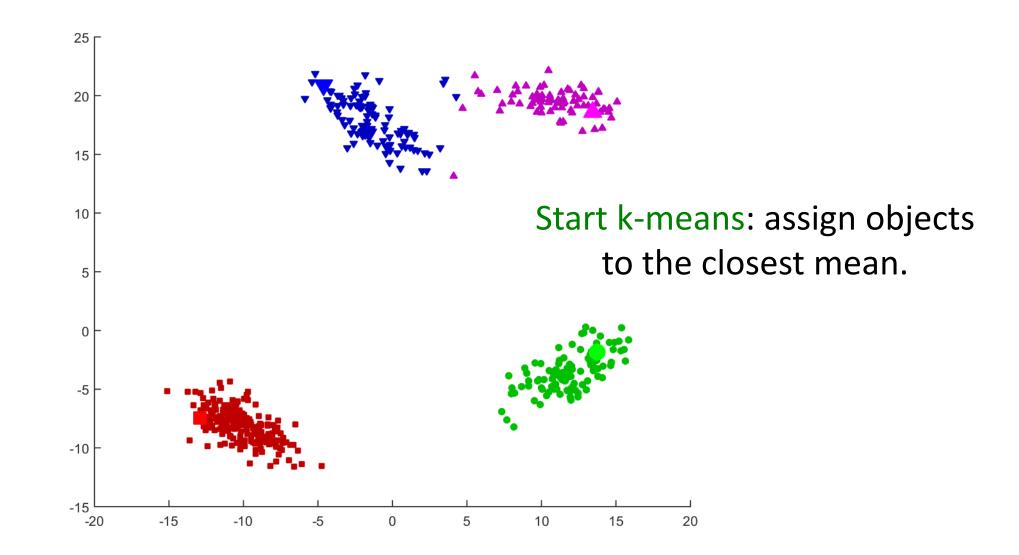


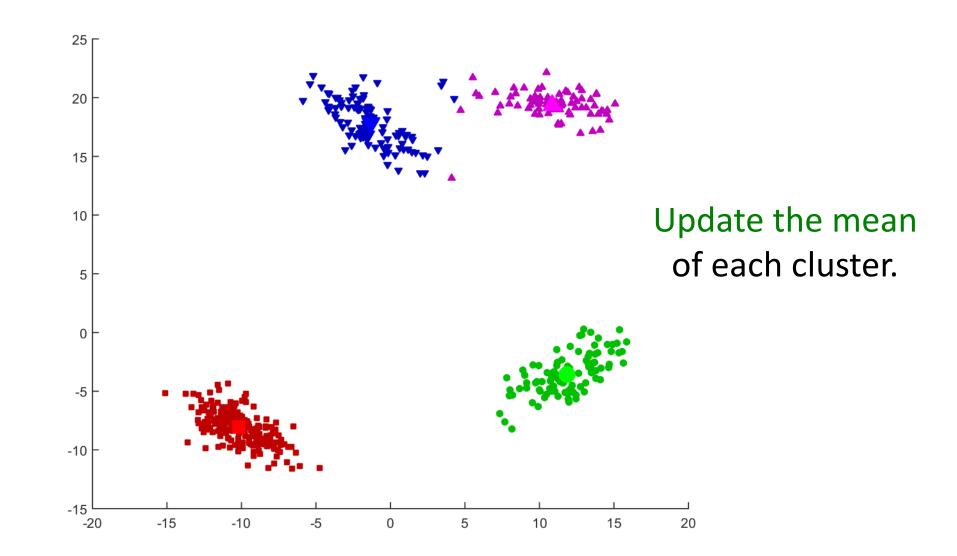


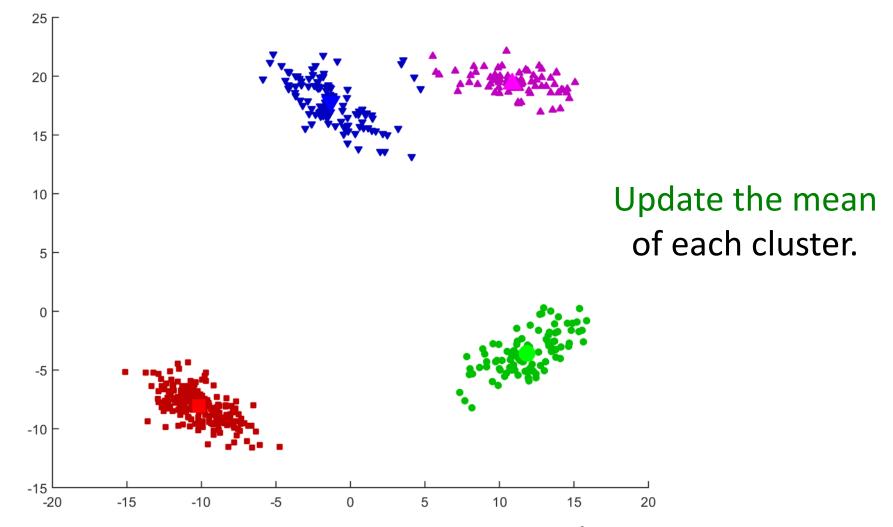












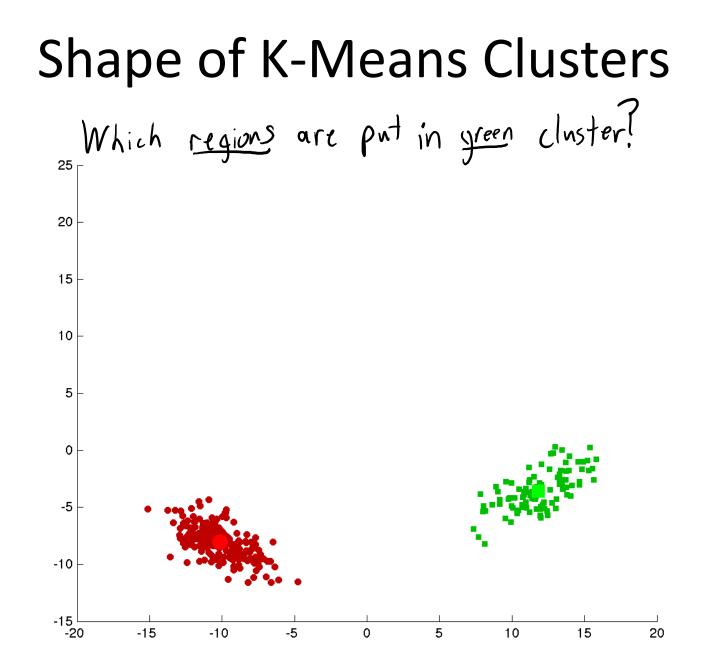
In this case: just 2 iterations!

K-means clusters are formed by the intersection of half-spaces.

Half-space is a Set of points (satifying a linear inequality, like 
$$\frac{2}{5}$$
 g; x;  $\leq b$   
Half-space

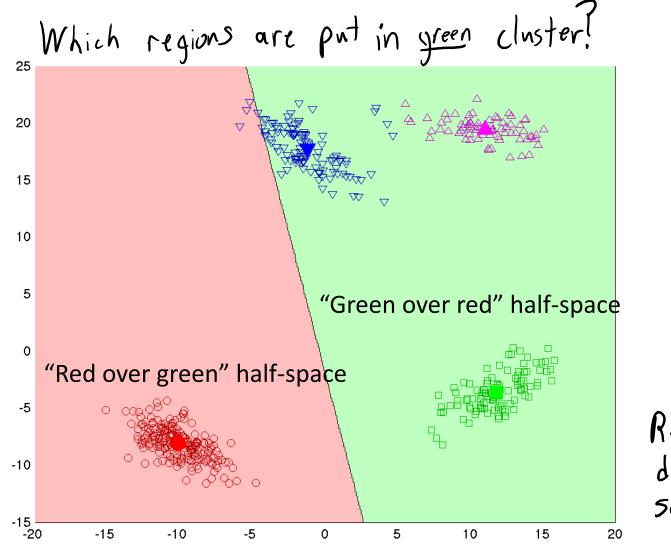
K-means clusters are formed by the intersection of half-spaces.

Hulf-space is a Set of points (satifying a linear inequality, like 
$$z_{j=1}$$
 aj xj  $\leq b$   
Hulf-space Half-space Half-space



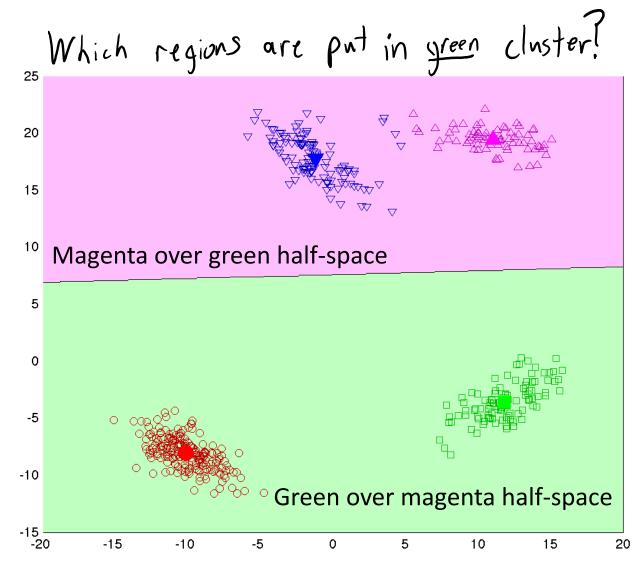
#### Shape of K-Means Clusters Which regions are put in green cluster? 25 20 15 10 "Closer to green" half-space 5 0 "Closer to red" half-space -5 -10 -15 ► -20 -15 -10 0 5 10 15 20 -5

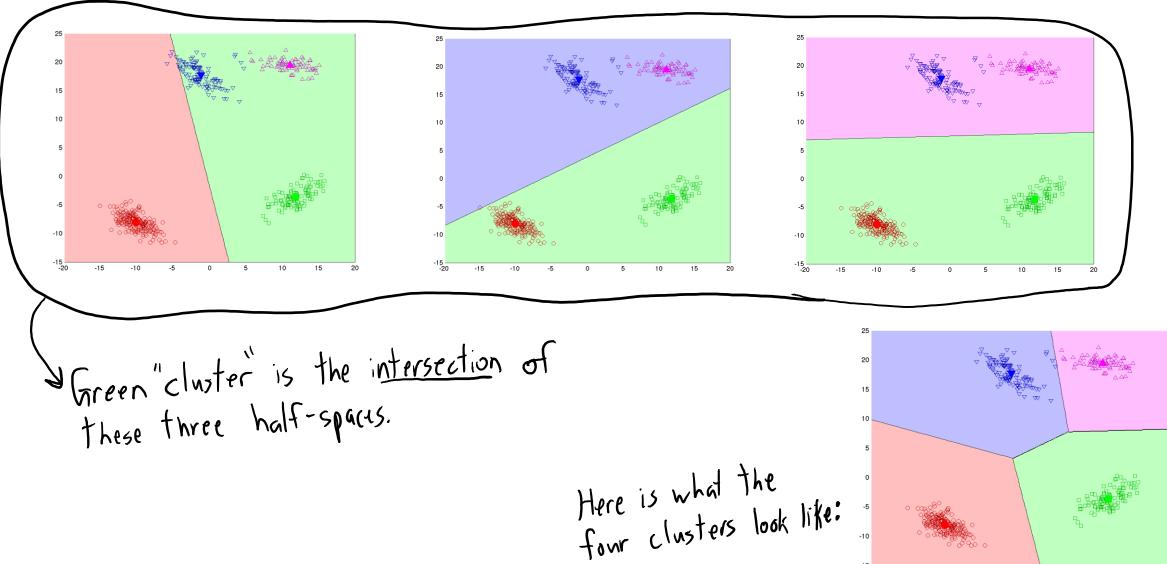
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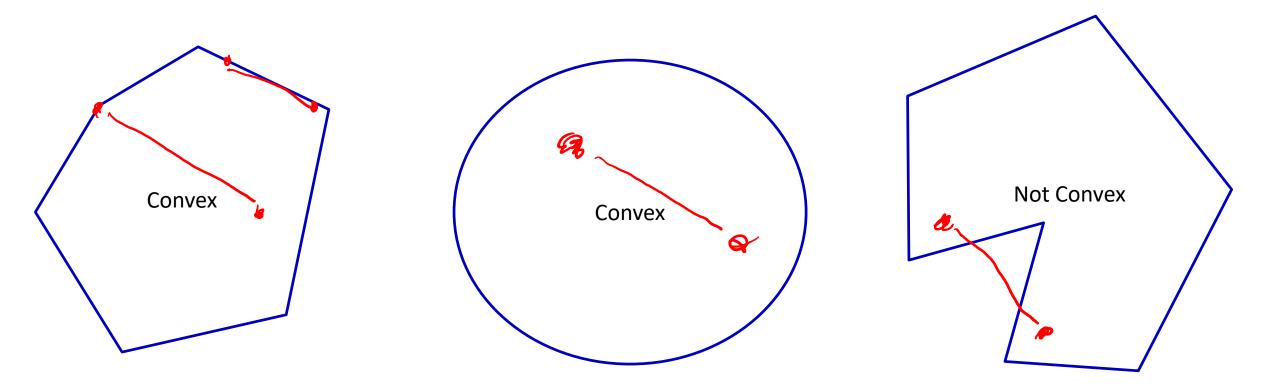
Red vs. green decision stays the some with more clusters.

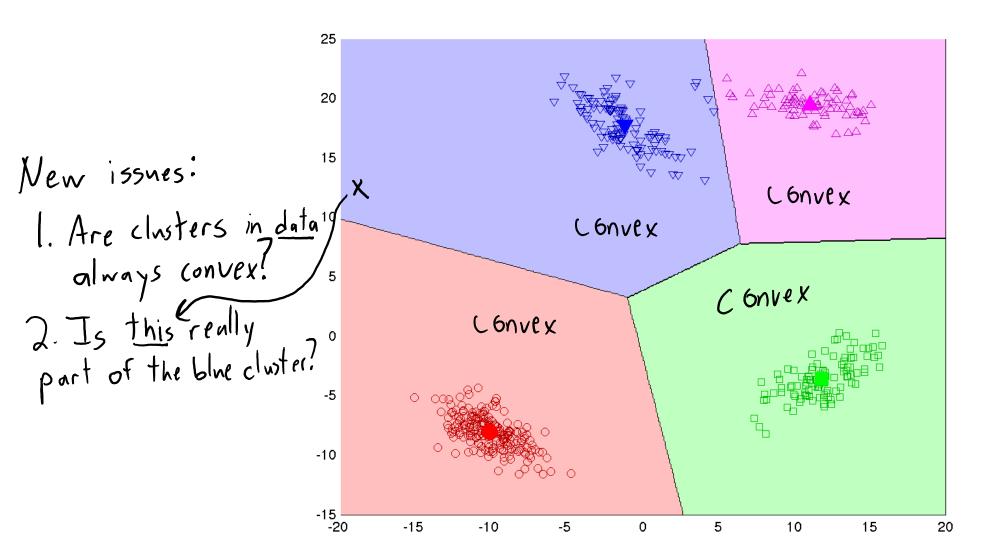
#### Shape of K-Means Clusters Which regions are put in green cluster! 25 $\overline{A}$ 20 15 10 Blue over green half-space 5 0 Blue vs. green decision defines different half-spaces. -5 -10 Green over blue half-space -15 ⊾ -20 -15 -10 10 15 20 5 -5 0



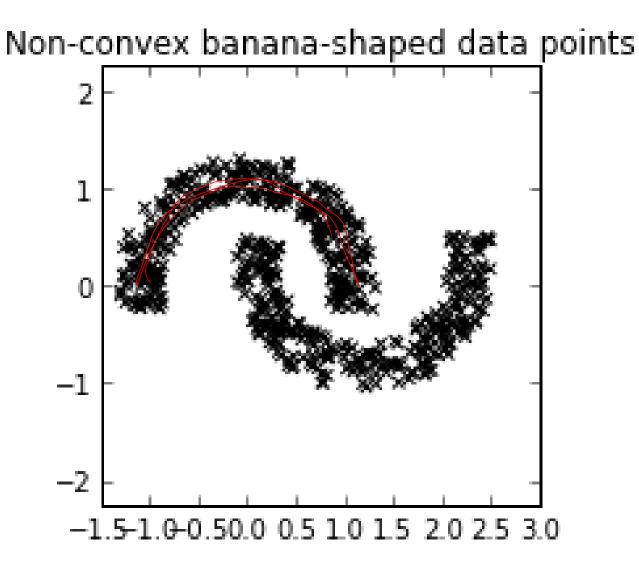


- Intersection of half-spaces form a convex set:
  - Line between any two points in the set stays in the set.

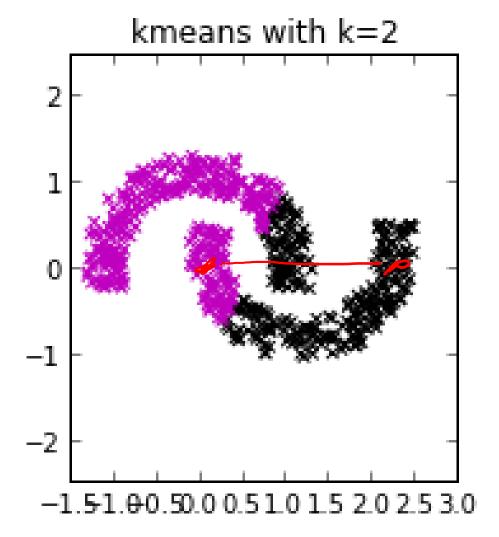




## K-Means with Non-Convex Clusters

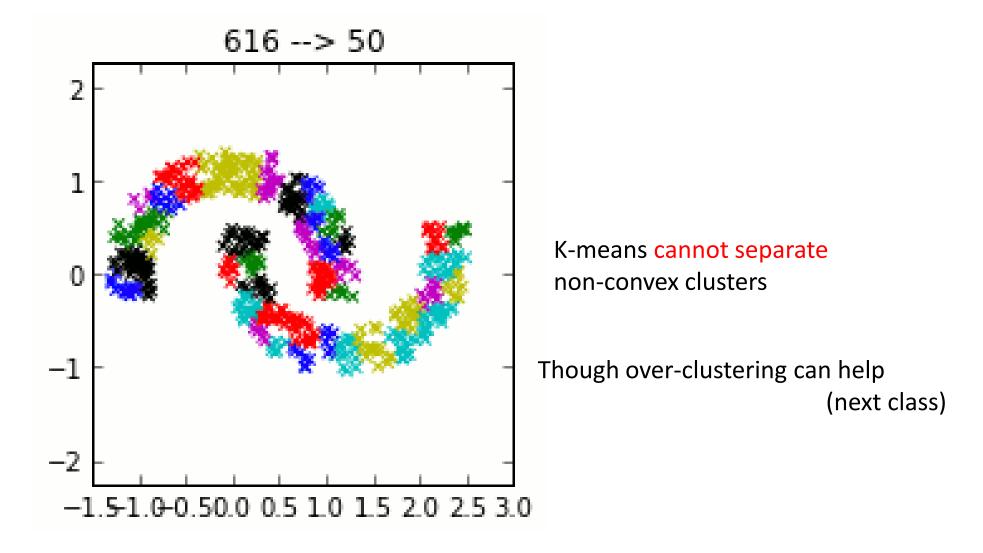


## K-Means with Non-Convex Clusters



K-means cannot separate non-convex clusters

# K-Means with Non-Convex Clusters



# **Application: Elephant Range Map**

- Find habitat area of African elephants.
  - Useful for assessing/protecting population.
- Build clusters from observations of locations.
- Clusters are non-convex:
  - affected by vegetation, mountains, rivers, water access, etc.
- We don't want to "partition" data:
  - Some points have no cluster.



# Motivation for Density-Based Clustering

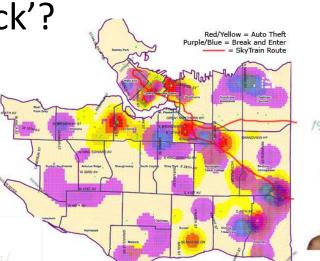
- Density-based clustering:
  - Clusters are defined by all the objects in "dense" regions.
  - Objects in non-dense regions don't get clustered.
- It's a non-parametric clustering method:
  - Clusters can become more complicated the more data we have.
  - No fixed number of clusters 'k'.

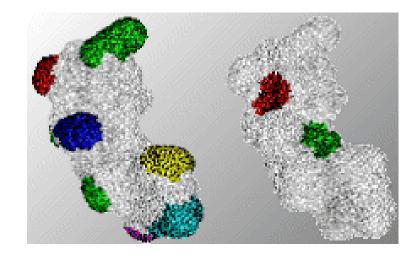


# **Other Potential Applications**

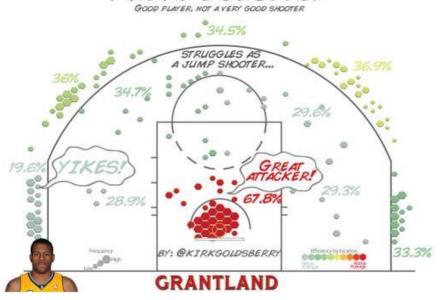
- Where are high crime regions of a city?
- Where should taxis patrol?
- Where does Iguodala make/miss shots?
- Which products are similar to this one?
- Which pictures are in the same place?
- Where can protein 'dock'?

https://en.wikipedia.org/wiki/Cluster\_analysis https://www.flickr.com/photos/dbarefoot/420194128/ http://letsgowarriors.com/replacing-jarrett-jack/2013/10/04/ http://www.dbs.informatik.uni-muenchen.de/Forschung/KDD/Clus

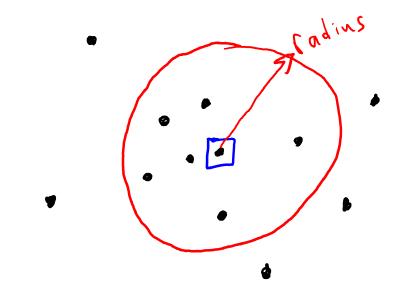




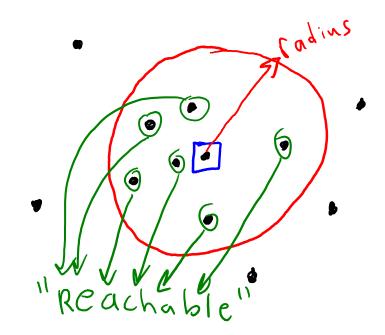
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- **Density-based clustering** algorithm (DBSCAN) has two parameters:
  - Radius: minimum distance between points to be considered 'close'.
    - Objects within this radius are called "reachable".



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- **Density-based clustering** algorithm (DBSCAN) has two parameters:
  - Radius: minimum distance between points to be considered 'close'.
    - Objects within this radius are called "reachable".
  - MinPoints: number of reachable points needed to define a cluster.
    - If you have minPoints "reachable points", you are called a "core" point.

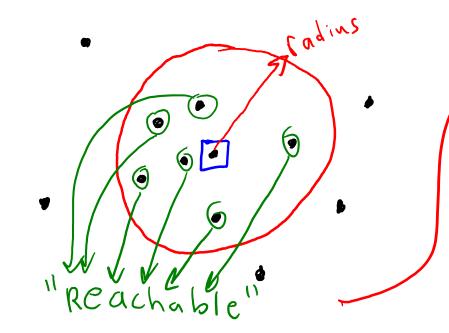
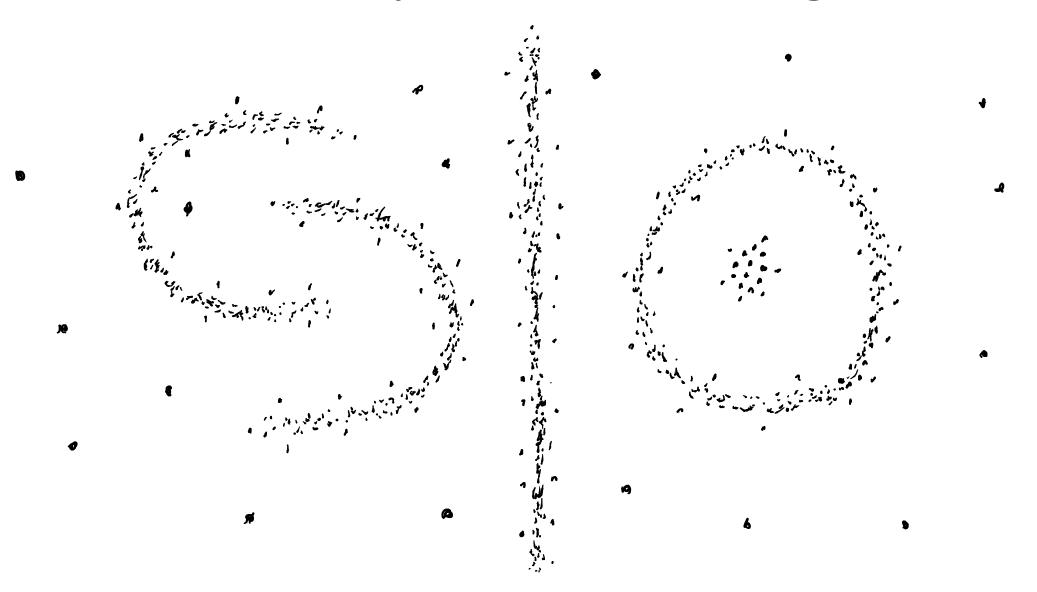
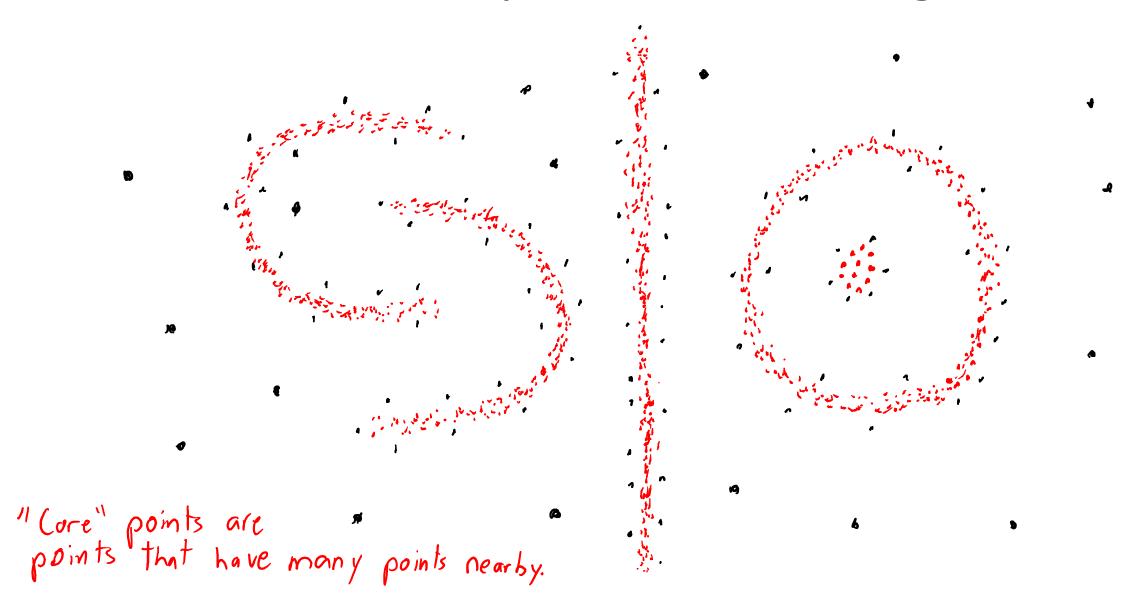
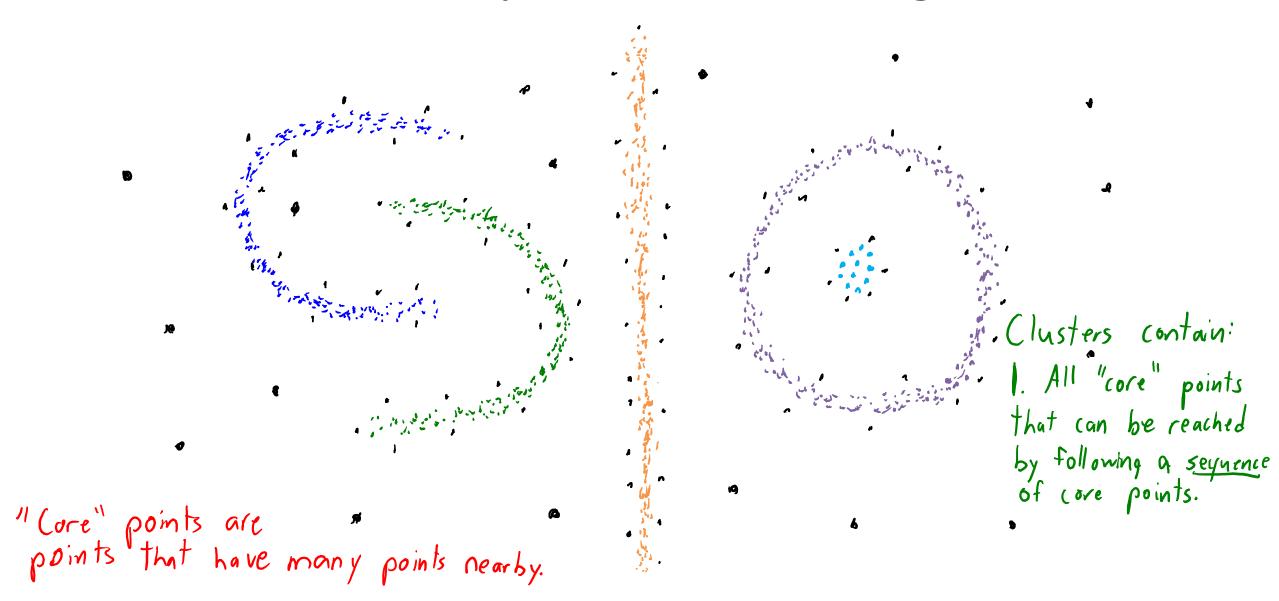
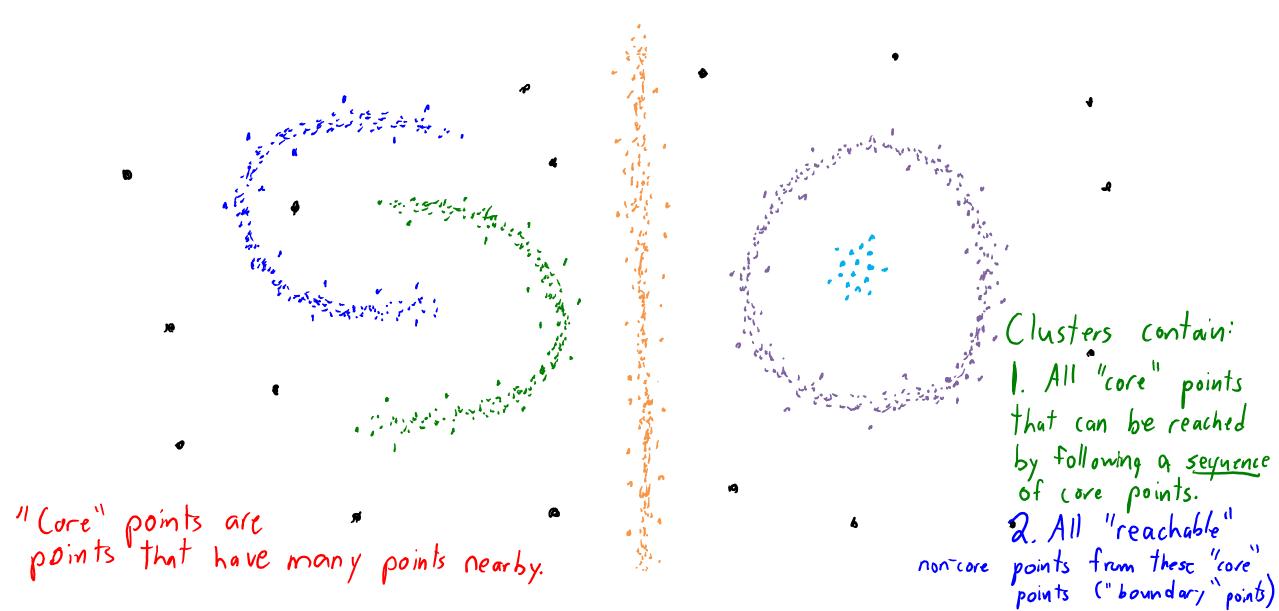


Fig., if min Points = 3
then this is a "core"
point since 6 points are
"reachable"

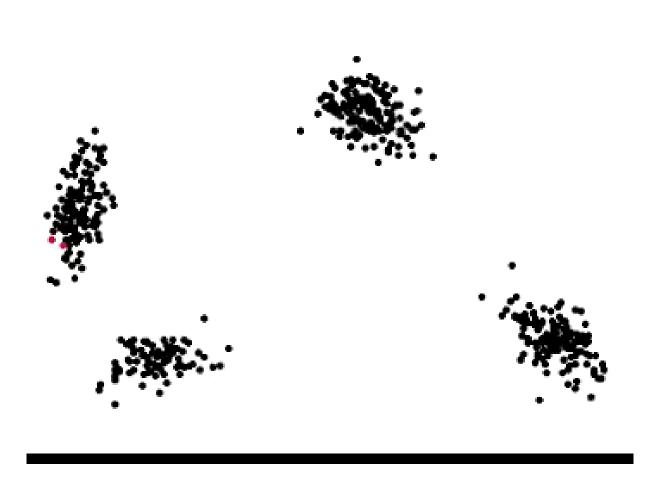








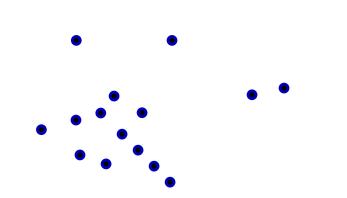
### **Density-Based Clustering in Action**



Interactive demo: <u>https://www.naftaliharris.com/blog/visualizing-dbscan-clustering</u>

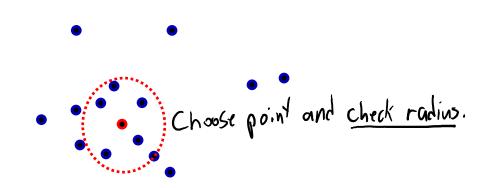
• Each "core" point defines a cluster:

- Consisting of "core" point and all its "reachable" points.



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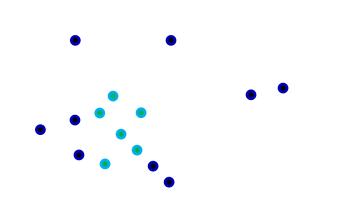
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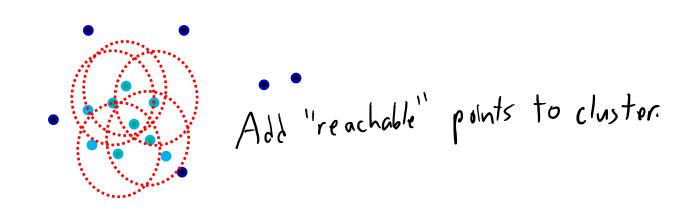
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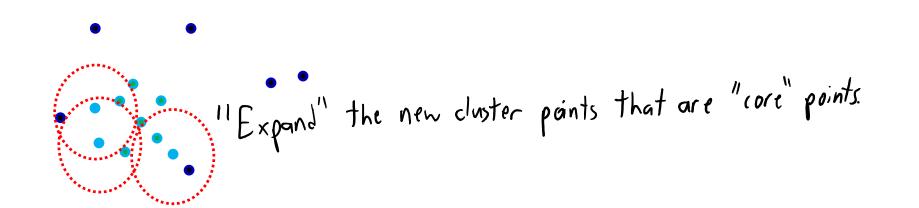
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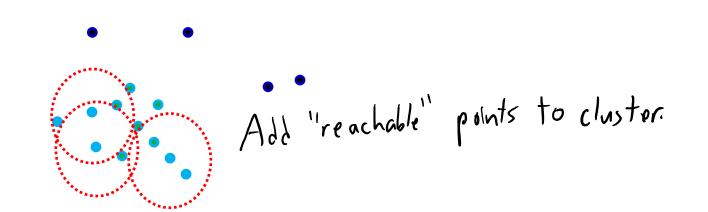
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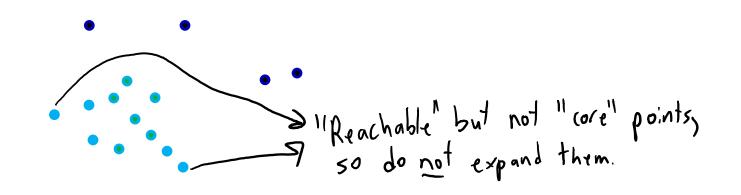
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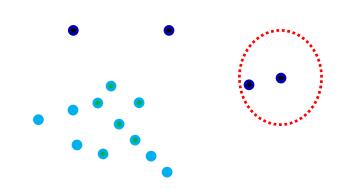


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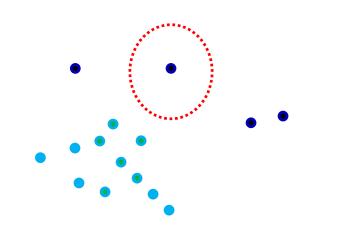
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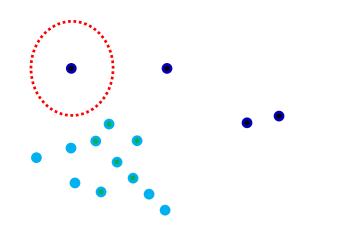
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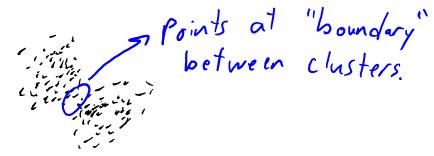
- Consisting of "core" point and all its "reachable" points.



- Pseudocode for DBSCAN:
  - For each example  $x_i$ :
    - If x<sub>i</sub> is already assigned to a cluster, do nothing.
    - Test whether xi is a 'core' point (less than minPoints neighbours with distances  $\leq$  'r').
      - If x<sub>i</sub> is not core point, do nothing.
      - If x<sub>i</sub> is a core point, "expand" cluster.
  - "Expand" cluster function:
    - Assign all  $x_i$  within distance 'r' of core point  $x_i$  to cluster.
    - For each newly-assigned neighbour x<sub>i</sub> that is a core point, "expand" cluster.

# **Density-Based Clustering Issues**

- Some points are not assigned to a cluster.
  - Good or bad, depending on the application.
- Ambiguity of "non-core" (boundary) points:



- Sensitive to the choice of radius and minPoints.
  - Otherwise, not sensitive to initialization (except for boundaries).
- If you get a new example, finding cluster is expensive.
  - Need to compute distances to training points.
- In high-dimensions, need a lot of points to 'fill' the space.

# Summary

- Norms:
  - Ways to measure "size" in higher dimensions.
- K-means++:
  - Randomized initialization of k-means with good expected performance.
- Shape of K-means clusters:
  - Intersection of half-spaces, which forms convex sets.
- Density-based clustering:
  - "Expand" and "merge" dense regions of points to find clusters.
  - Useful for finding non-convex connected clusters.
- Next time:
  - Discovering the tree of life.

### Bonus Slide: Lp-norms

• The  $L_1$ -,  $L_2$ -, and  $L_{\infty}$ -norms are special cases of Lp-norms:

$$\|x\|_{p} = \left(\sum_{j=1}^{d} x_{j}\right)^{r}$$

• This gives a norm for any (real-valued)  $p \ge 1$ .

– The L<sub> $\infty$ </sub>-norm is limit as 'p' goes to  $\infty$ .

• For p < 1, not a norm because triangle inequality not satisfied.

### Bonus Slide: Squared/Euclidean-Norm Notation

We're using the following conventions:

The subscript after the norm is used to denote the p-norm, as in these examples:

$$\|x\|_2 = \sqrt{\sum_{j=1}^d w_j^2}.$$
  
 $\|x\|_1 = \sum_{j=1}^d |w_j|.$ 

If the subscript is omitted, we mean the 2-norm:

 $||x|| = ||x||_2.$ 

If we want to talk about the squared value of the norm we use a superscript of "2":

$$\begin{split} \|x\|_2^2 &= \sum_{j=1}^d w_j^2 . \ \|x\|_1^2 &= \left(\sum_{j=1}^d |w_j|\right)^2. \end{split}$$

If we omit the subscript and have a superscript of "2", we're taking about the squared L2-norm:

$$\|x\|^2 = \sum_{j=1}^d w_j^2$$

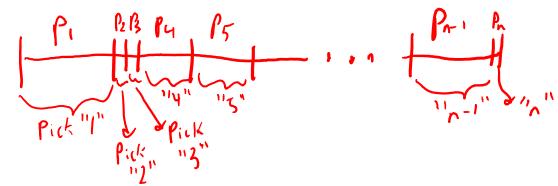
# **Bonus Slide: Uniform Sampling**

- Standard approach to generating a random number from {1,2,...,n}:
  - 1. Generate a uniform random number 'u' in the interval [0,1].
  - 2. Return the largest index 'i' such that  $u \leq i/n$ .
- Conceptually, this divides interval [0,1] into 'n' equal-size pieces:

This assumes p<sub>i</sub> = 1/n for all 'i'.
 probability of picking number 'i'.

# **Bonus Slide: Non-Uniform Sampling**

- Standard approach to generating a random number for general p<sub>i</sub>.
  - 1. Generate a uniform random number 'u' in the interval [0,1].
  - 2. Return the largest index 'i' such that  $u \leq \sum_{i=1}^{n} p_i$
- Conceptually, this divides interval [0,1] into non-equal-size pieces:



- Can sample from a generic discrete probability distribution in O(n).
- If you need to generate 'm' samples:
  - Cost is O(n + m log (n)) with binary search and storing cumulative sums.

## Bonus Slide: Discussion of K-Means++

• Recall the objective function k-means tries to minimize:

$$f(w, c) = \sum_{i=1}^{n} ||x_i - w_{c(i)}||_2^2$$

- Get good clustering with high probability by re-running.
- However, there is no guarantee that c<sup>\*</sup> is a good clustering.