



NAVAL Postgraduate School

OS4118
Statistical and Machine Learning

Clustering

Prof. Sam Buttrey
Fall AY 2020

The Nation's Premiere Defense Research University

Monterey, California WWW.NPS.EDU





- Techniques for finding structure in a set of measurements
- Group X's without knowing their y's
- Usually we don't know number of clusters
- Method 1: Visual
- Difficult because of (usually) complicated correlation structure in the data
- Particularly hard in high dimensions



Clustering as Classification

- Clustering is a classification problem in which the Y values have to be estimated
- Y_i | X_i is multinomial as before
- Most techniques give an assignment, but we can also get a probability vector
- Clustering remains under-developed
 - Model quality? Variable selection? Scaling? Transformations, interactions etc.? Model fit? Prediction?



Clustering by PCs

- Method 2: Principal Components
- If the PCs capture spread in a smart way, then "nearby" observations should have similar values on the PCs
- Plot 2 or 3 and look (e.g. state.x77)
- We know how to transform new (test set) observations into PC space
- We still need a rule for assigning observations to clusters



Our Dissimilarity Should Be...

- 1. Applicable to all types of data including data with mixed linear and categorical variables
- 2. **Invariant** to linear scaling, and robust to monotonic transformations, of numeric variables
- 3. Able to handle missing values and outliers
- 4. Capable of variable selection (ignoring noise variables, redundant variables), including weighting
- 5. Able to handle large data sets (in particular, we want to avoid computing all *n*-choose-2 pairwise distances when data sets are large)



Inter-point Distances

- Many clustering techniques rely on being able to measure distance
 - between two points;
 - between a point and a cluster; and
 - between two clusters.
- How do we...
 - define a distance that meets the criteria of the preceding page, especially weighting and selection, categorical values, and missing values?
- Our choices are Euclidean, Gower, etc...



Distance Between Clusters

- In addition to measuring distance between two observations, ...
- ...We also need to measure distance between a point and a cluster, and between two clusters
- Example: Euclidean between the two cluster averages
- Example: Manhattan between the two points farthest apart
- These choices may make a difference, and we don't have much guidance



A. Partition Methods

- Given number of clusters (!), try to find observations that are means or medians
- Goal: each observation should be closer to its cluster's center than to the center of another cluster; this partitions space
 - As we have seen, measuring "closer" requires some choices to be made
- Classic approach: k-means algorithm
 - R implementation predates daisy(),
 requires all numeric columns



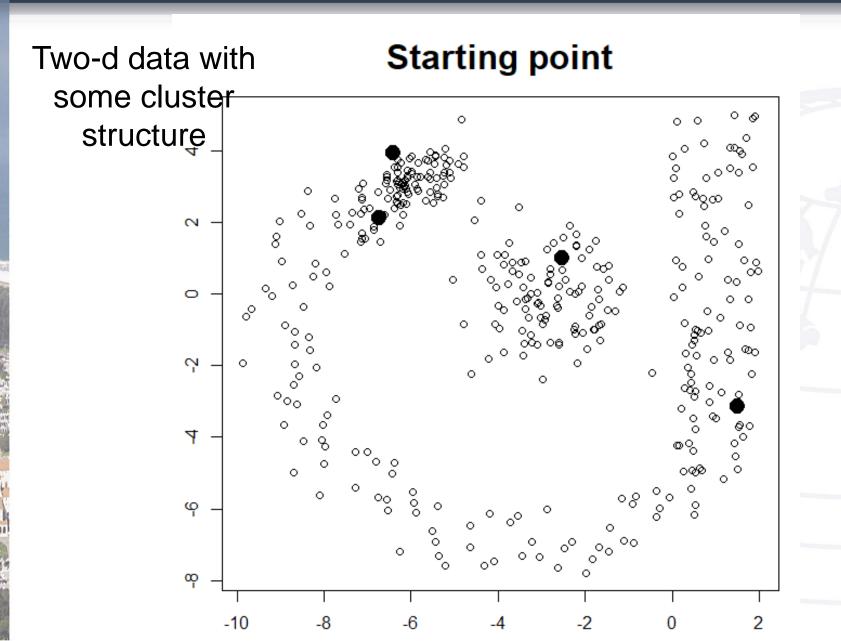
K-means Algorithm

- 1. Select *k* candidate cluster centers at random
- 2. Assign each observation to the nearest cluster center (w/Euclidean distance)
- 3. Recompute the cluster means
- 4. Repeat from 2. until convergence
- Guaranteed to converge, but not optimally; depends on step 1; k assumed known (try with many k's)



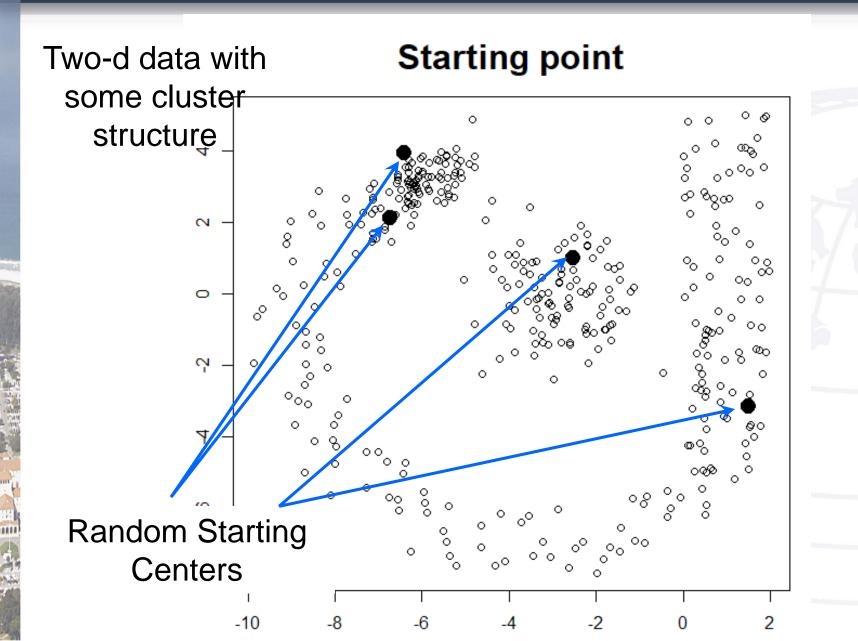
K-means Example (start)

10





K-means Example (start)



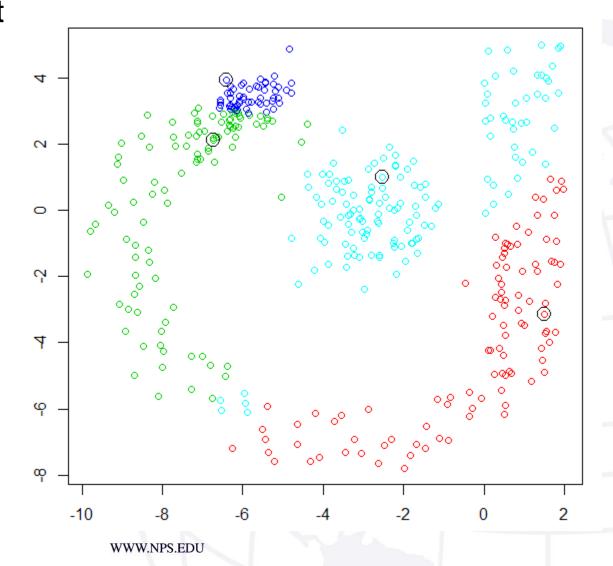


K-means Example (iteration 1)

Assign each point to the nearest center, using unweighted Euclidean distance

(Assignments shown here by color)

Iteration 1





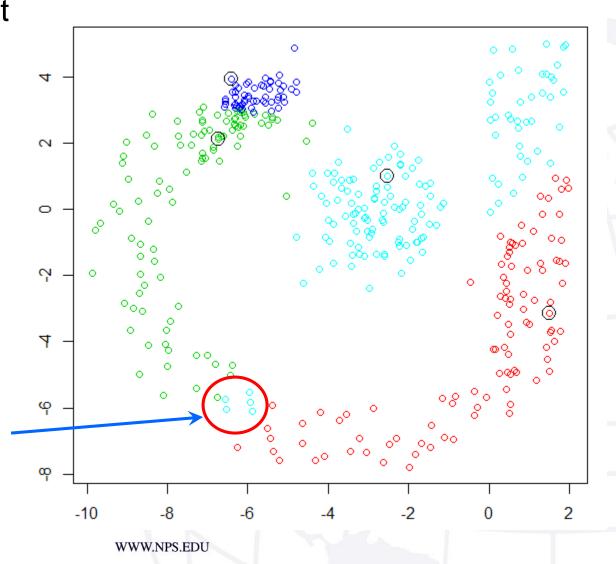
K-means Example (iteration 1)

Assign each point to the nearest center, using unweighted Euclidean distance

(Assignments shown here by color)

Check out these light blue points

Iteration 1

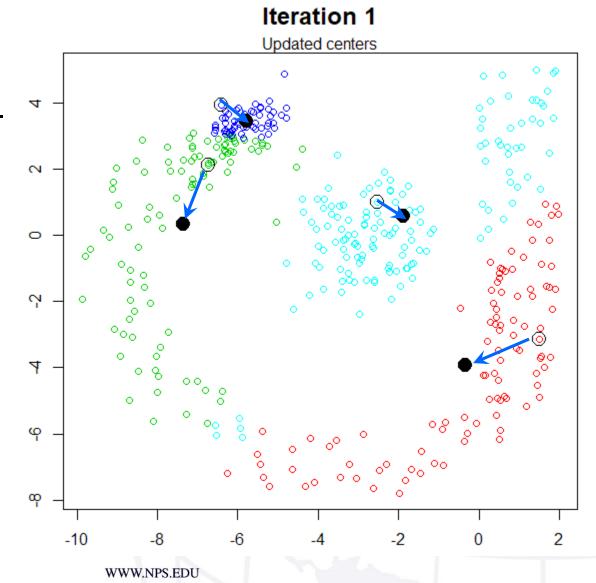




K-means example (iteration 1)

Use those assignments to recompute the cluster means, which causes them to change position

New positions are shown by black dots

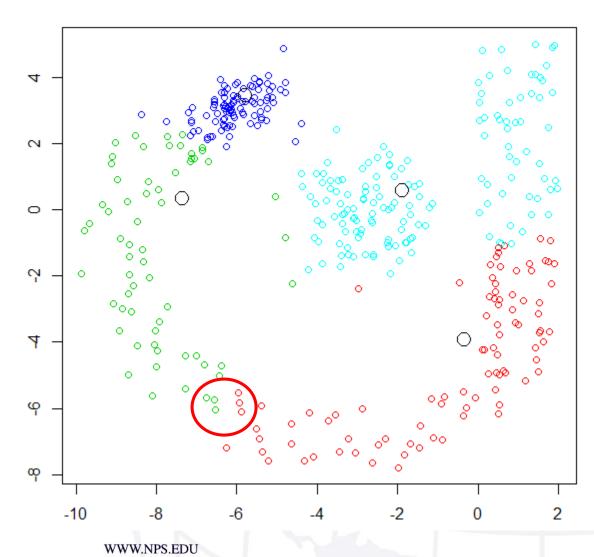




K-means Example (iteration 2)

Iteration 2

Now use those new positions to re-assign each observation to the closest center

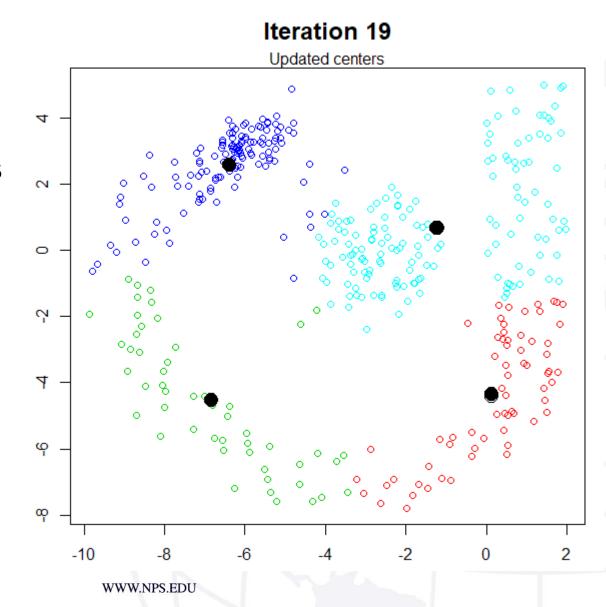




K-means Example (finish)

This example took
19 iterations – but
modern algorithms
are more clever
than the basic one
I laid out here

Starting points matter too!





K-means Stopping

- Stop when no assignment changes, or a pre-set max. number of iterations is reached
- One measure of quality: an R²-like thing
- Compute TotalSS = $\sum_{i} \sum_{j} (x_{ij} \bar{x}_{j})^{2}$
- Compute WithinSS for cluster 1 as

$$\sum_{\text{cluster 1}} \sum_{j} (x_{ij} - c_{1j})^2$$



K-means Stopping

- Stop when no assignment changes, or a pre-set max. number of iterations is reached
- One measure of quality: an R²-like thing
- Compute TotalSS = $\sum_{i} \sum_{j} (x_{ij} \bar{x}_{j})^{2}$
- Compute WithinSS for cluster 1 as

$$\sum_{\text{cluster 1}} \sum_{j} (x_{ij} - (c_{1j})^2)$$

Cluster 1's center

Now compute 1 – TotalWithin/Total SS





- Only kn (not n(n-1)/2) computations per iteration, helps with big data
- Well-suited to separated spherical clusters, not to narrow ellipses, snakes, linked chains, concentric spheres...
- Susceptible to influence from extreme outliers, which perhaps belong in their own clusters of size 1
- Example: state.x77 data





- Choosing k is important but hard
- Classical scheme: plot 1 TotWith/Tot, or just TotWith, against k for a bunch of different k values and identify...
- ...the knee in the curve
- Just as with principal components, the "knee" is not always easy to find





- pam (Kaufman & Rousseeuw, 1990) is k-means-like, but on medoids
 - A cluster medoid is the observation for which the sum of distances to other cluster members is the smallest in the cluster
 - Can use daisy() output, handle factors
 - Resistant to outliers
 - Expensive $(O(n^2)$ for time and memory)
- clara is pam's big sister
 - Operates on small subsets of the data
 - pamk() in {fpc} helps pick "best" k, but criteria can disagree



Cluster Validation

- K-means vs. pam
- How to evaluate how well we're doing?
 - Cluster validation is an open problem
 - Goals: ensure we're not just picking up sets of random fluctuations
 - If our clustering is "better" on our data than what we see with the same technique on random noise, do we feel better?
 - Determine which of two clusterings is "better"
 - Determine how many "real" clusters there are



Cluster Validity

- External Validity: Compare cluster labels to "truth," maybe in a classification context
 - True class labels often not known
 - We cluster without knowing classes
 - Classes can span clusters: f vs. f vs. f,so in any case...
 - True number of *clusters* rarely known, even if we knew how many *classes* there were



Cluster Validity

- Internal Validity: Measure something about "inherent" goodness
 - Perhaps R²-style, 1 SSW/SSB, using "sum of squares within" and "sum of squares between" as in k-means
 - Whatever metric the clustering algorithm optimizes will look good in our results
 - "Always" better than using our technique on noise
 - Not obvious how to use training/test set



The Silhouette Plot

- For each point, compute avg. distance to all points in its cluster (a), and avg. dist. to points in second-closest cluster (b)
- Silhouette coeff. is then (b a)/max(a, b)
 - Can be computed for individual observations, or averaged within clusters and overall
- Usually in [0,1]; larger better
- Drawn by plot.pam(), plot.clara()
- (Different from bannerplot!)





- K-means vs. pam (cont'd)
- How to evaluate how well we're doing?
 - For the moment let's measure agreement
 - One choice: Cramér's V
 - $-V = \sqrt{[\chi^2 / n (k-1)]}, k = \min(\#row, \#col)$
 - $-V \in [0, 1]$; more rows, cols \Rightarrow higher V
- Rules of thumb: .15 weak, .35 strong,
 .50+ "essentially measuring same thing"
 - Sorta kinda



B. Hierarchical Clustering

- Techniques to preserve hierarchy (so to get from the "best" six clusters to the best five, we join two existing clusters)
 - Advantages: hierarchy is good; nice pictures make it easier to choose number of clusters
 - Disadvantages: small data sets only
- Typically "agglomerative" or "divisive"
- Agglomerative, implemented in agnes(): each object starts as one cluster; keep "merging" the two closest clusters till there's one huge cluster





- Each step reduces the # of clusters by 1
- At each stage we need to know every entity's distance to every other
- We merge the two closest objects...
- ...Then compute distances of new object to all other entities
- As before, we need to be able to measure the distances between cluster, or between a point and a cluster



Hierarchical Clustering (cont'd)

- Divisive, implemented in diana():
 - Start with all objects in one group
 - At each step, find the largest cluster
 - Remove its "weirdest" observation
 - See if others from that parent want to join the splinter group
 - Repeat until each obs. is its own cluster
- Clustering techniques often don't agree!



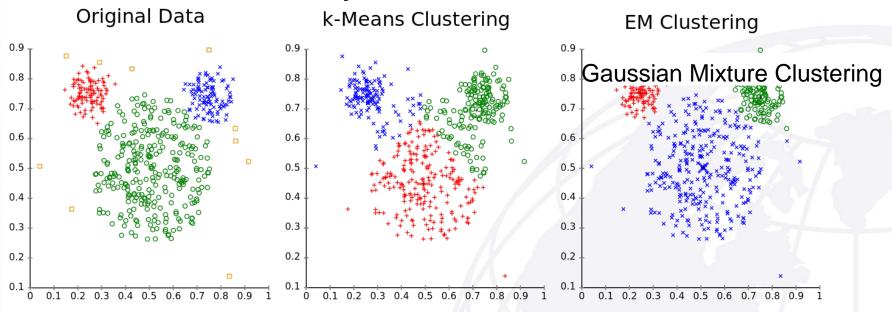


- The tree picture ("dendrogram") shows the merging distance vertically and the observations horizontally
- Any horizontal line specifies a number of clusters (implemented in cutree())
- Both Agnes + Diana require all n-choose-2 distances up front; ill-suited to large samples



Let's talk about K-means first

Different cluster analysis results on "mouse" data set:



It's not too good at finding clusters of different shapes.

It can't help identify the stray yellow anomalies

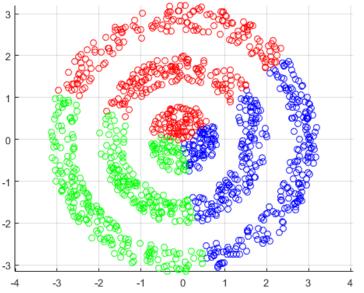
And like K-medoids (pam), you need to know the number of clusters.

https://en.wikipedia.org/wiki/K-means_clustering^{NPS.EDU}



Our methods can't cluster this

 Here the clusters are kind of silly, but the point is that they are not linearly separable



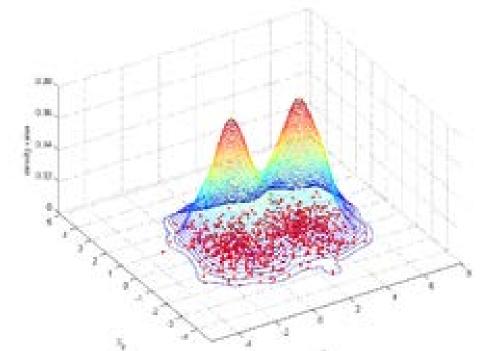
K-means clustering

https://stackoverflow.com/questions/40455334/matlab-kmeans-clustering-for-non-linearly-separable-data



Density Based Clustering

Density based clustering, an old idea of Hartigan (1975) i.e. cluster observations in high density regions. Observations in low density regions are allowed to be noise.



Does not require knowledge of the number of clusters or their shapes.

https://en.wikipedia.org/wiki/Multivariate_kernel_density_estimation



Density-Based Clustering

- The density-based algorithm DBSCAN of Ester, Kiegel, Sander, Xu (1996) is a very successful clustering algorithm of this type.
 - "Density-Based Spatial Clustering of Applications with Noise"
- The algorithm "scans" the data one time. Fast, scalable, intuitive, don't need to know the number of clusters, works with different shapes, and can assign observations to "noise" that is, some points don't get put into any cluster

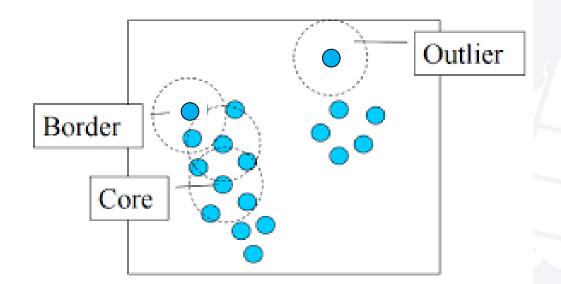


DBSCAN's Two Parameters

Pick a starting point (one of your observations) at random and specify two tuning parameters:

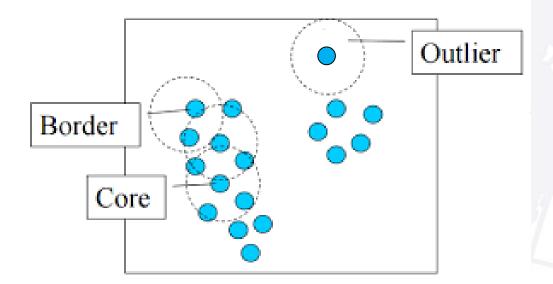
Epslion: The radius of a local neighborhood around a point.

Min Points: The minimum number of points that must be in that neighborhood for the point to be considered a "core point".





 When a cluster is formed, expand the cluster by checking all new points. Border points can belong to more than one cluster.

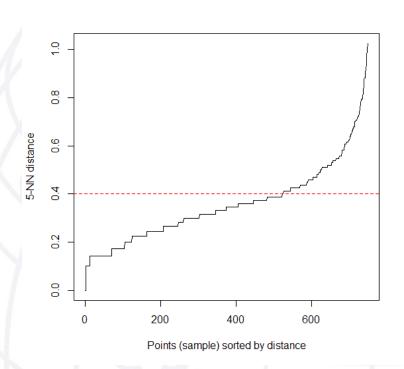


https://www.naftaliharris.com/blog/visualizing-dbscan-clustering/



Choosing Parameters

- One rule of thumb: choose minPoints = (# of columns + 1)...
 - But what if some columns are just noise?
- ...Choose Epsilon by plotting the sorted distances to the minPoints nearestneighbor and looking for the "knee"





Strengths and Weaknesses

DBSCAN Strengths:

- Can discover clusters of arbitrary shapes,
 whereas k-means likes spherical clusters
- Number of clusters need not be specified
- Scalable to very large data sets; only one scan through the data require
- Allows for anomalies (noise) that don't belong to any cluster

Weaknesses



Weaknesses:

- Can be defeated by clusters with different densities, because minPts and eps are held constant over the whole space
 - Newer OPTICS algorithm tries to address this
- Choosing epsilon can be difficult
- Curse of dimensionality in high dimensions,
 where observations are always far apart can produce lots of tiny clusters



Clustering Considerations

- Lots of other methods (e.g. mixture models) exist, including ensembles
- Scaling/weighting, transformation are not automatic (although methods are being proposed to do this)
- Hierarchical methods don't scale well
 - Must avoid computing all pairwise distances
- Validation and finding k are hard
 - Clustering is inherently much more harder than, say, linear regression