Stats for Data Science

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Regression, Classification, Clustering

Regression

1. Linear
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Classification

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4. Random Forest

Clustering

1. K-Means
2. Hierarchical
3. DBSCAN
4. HDBSCAN

Regression analysis is a statistical technique to assess the relationship between an predictor variable and one or more response factors.

Outcome Variable	GLM Family	Link	Mean to Variance
Continuous, unbounded	Normal or Standard Gaussian	Identity	
Continuous, non-negative	Gamma or inverse Gamma		
Discrete/ counts/ rate	Poisson Quassi-poisson or negative binomial	Log	Identity If not Identity
Count	Gamma		Over dispersion
Counts with multiple zero	Zero inflated poisson may be checked for fitting		
Binary	Binomial or Logistic regression		
Nominal	Multinomial regression		

Regression Model Selection Criteria

Three methods to classifier

1. model a classification rule - knn, decision tree, perceptron, svm
2. model the probability of class membership given input data - perceptron with cross-entropy cost
3. make a probabilistic model of data within each class - naive bayes 1 & 2 are discriminative classifications 3 is generative classification 2 & 3 probabilistic classification

“Help me understand our customers better so that we can market our products to them in a better manner!

Monothetic: Cluster members have some common property Expectation–Maximization (EM) Clustering using Gaussian Mixture Models (GMM)

Polythetic: Cluster members are similar to each other. Distance between elements define relationship

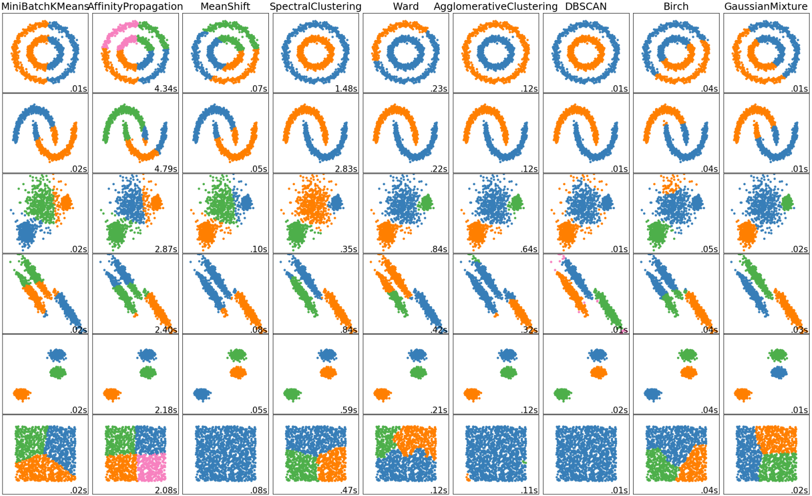
Hard Clustering: each data point either belongs to a cluster completely or not

Soft Clustering: a probability or likelihood of that data point to be in those clusters is assigned.

Clustering Models

Connectivity models	Distribution models	Centroid models	Density models
data points closer in data space exhibit more similarity to each other than the data points lying farther away	how probable is it that all data points in the cluster belong to the same distribution (e.g: Normal, Gaussian)	iterative clustering algorithms in which the notion of similarity is derived by the closeness of a data point to the centroid of the clusters	isolates various different density regions and assign the data points within these regions in the same cluster
hierarchical clustering	Expectation-maximization	K-Means, k-median	mean-shift, DBSCAN and OPTICS
Approaches: 1) Top-bottom, 2) bottom-up	EM uses multivariate normal distributions	DZA	DBSCAN uses radius ϵ and Center c
lacks scalability for handling big datasets, Time complexity: O(n^2)	These models often suffer from over-fitting. Prior knowledge to define num clusters	important to have prior knowledge of the dataset. results change in every trial	DBSCAN doesn't perform as well when the clusters are of varying density
Results are reproducible	more flexibility in terms of cluster covariance due to $\mu and \sigma$ (additional σ)	can handle big data , Time complexity: O(n)	DBSCAN identifies outliers as noises
chk1	elliptical shape (since we have a standard deviation in both the x and y directions	work well when the shape of the clusters is hyper spherical (like circle in 2D, sphere in 3D)	DBSCAN: can find arbitrarily sized and arbitrarily shaped clusters
Angola	GMMs support mixed membership since is probability based	AGO	DBSCAN: drawback in high-dimensional data since the distance threshold ϵ becomes challenging to estimate

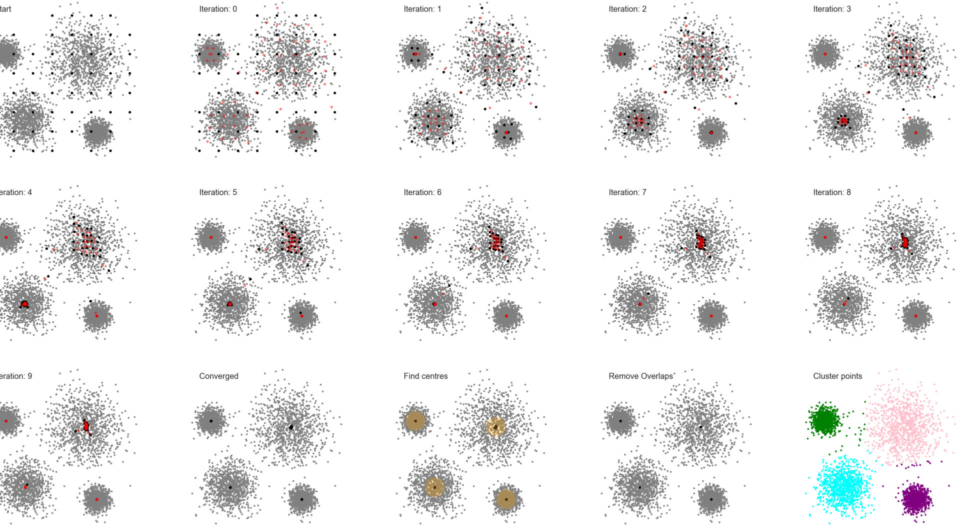
Clustering Types



mean-shift clustering

consider a set of points in two-dimensional space
a circular sliding window C centered and radius r as the kernel
hill-climbing algorithm that involves shifting this kernel iteratively to a higher density ($\propto$ number of points) region until convergence
At every iteration,
- shift the center point to the mean of the points within the window (hence the name)
-gradually move towards areas of higher point density
- until no longer increase in the density
- When multiple sliding windows overlap the window containing the most points is preserved. The data points are then clustered according to the sliding window in which they reside.

Density Models



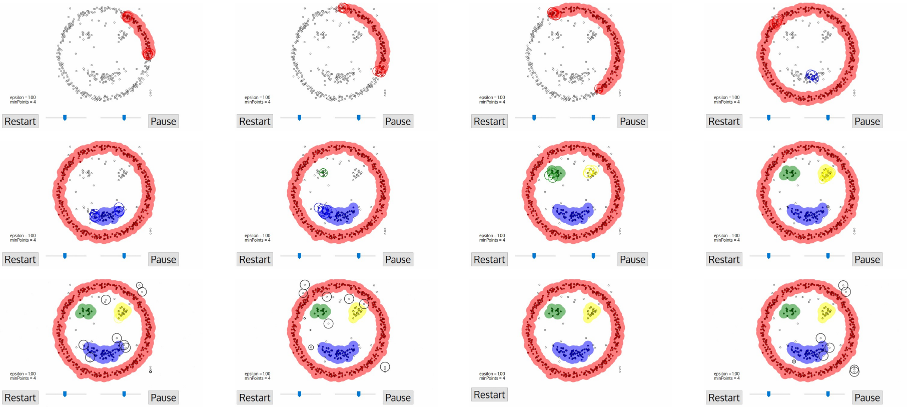
Density-Based Spatial Clustering of Applications with Noise-DBSCAN

-label all data point to be unvisited. For all unvisited points:

1. All points which are within the ϵ distance are neighborhood points (part of the same cluster)
2. If neighborhood points ¿= minPoints, then the clustering process starts and the current data point becomes the first point in the new cluster - Otherwise, mark the point as noise - In both cases that point is marked as "visited"
3. repeated for all of the new points in the cluster group
4. next an new unvisited point is retrieved and processed

Since at the end of this all points have been visited, each point will have been marked as either belonging to a cluster or being noise.

Density Models



hdbscan

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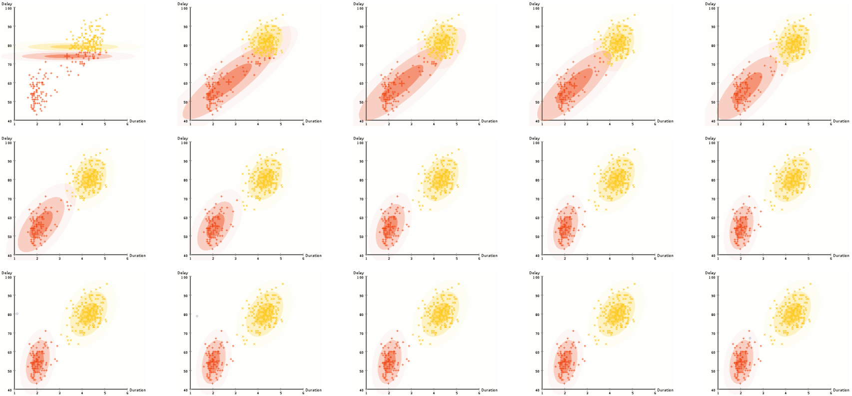
Gaussian Mixture Models (GMMs)

Assumption: the data points are Gaussian distributed (parameters: the mean and the standard deviation)! Each Gaussian distribution is assigned to a single cluster. To find the parameters of the Gaussian for each cluster, use an optimization algorithm called Expectation–Maximization (EM).

Expectation–Maximization (EM) using GMM

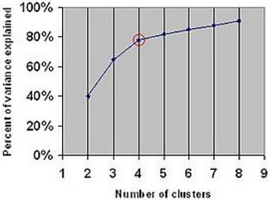
choose num of clusters
compute the probability that each data point belongs to a particular cluster. With a Gaussian distribution we are assuming that most of the data lies closer to the center of the cluster.
From probabilities $\rightarrow$ recompute set of parameters such that we maximize the probabilities of data points within the clusters
We compute these new parameters using a weighted sum of the data point positions, where the weights are the probabilities of the data point belonging in that particular cluster.
Repeat till convergence

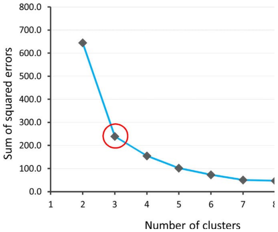
Distribution Models



K means

iterative clustering algorithm that aims to find local maxima in each iteration
take a quick look at the data and choose k (num clusters)
assign data points to the cluster $\leftrightarrow$ compute cluster centroid
repeat to reduce variation error
elbow method



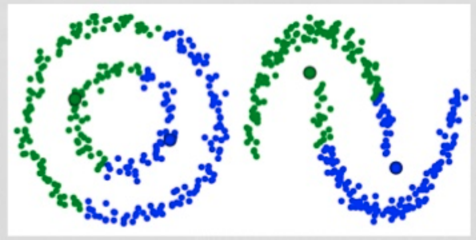


k-median

K median vs kmeans: instead of recomputing the group center points using the mean (like in K-Means) we use the median vector of the group. This method is **less sensitive to outliers** (because of using the Median) but is **much slower for larger datasets as sorting is required** on each iteration when computing the Median vector

mean-shift vs kmeans: Instead of selecting the number of clusters as mean-shift automatically discovers this (advantage), the selection of the window size/radius "r" can be non-trivial.

kmeans fail



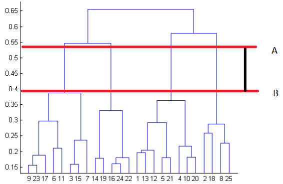
K-Means is actually a special case of GMM in which each cluster's covariance along all dimensions approaches 0

Agglomerative Hierarchical Clustering

The decision of dividing into or merging **two** clusters is taken on the basis of closeness of these clusters. Metrics for deciding the closeness of two clusters:
Euclidean distance: $||a-b||_2 = \sqrt{\sum(a_i - b_i)}$
Squared Euclidean distance: $||a-b||_2^2 = \sum(a_i - b_i)^2$
Manhattan distance: $||a-b||_1 = \sum |a_i - b_i|$
Maximum distance: $||a-b||_{INFINITY} = \max_i |a_i - b_i|$
Mahalanobis distance: $\sqrt{(a-b)^T S^{-1}(-b)}$
Maybe, use **average linkage** which defines the distance between two clusters to be the average distance between data points in the first cluster and data points in the second cluster.

hierarchical agglomerative clustering (HAC) or bottom-up

1. Each data point as a single cluster
2. select a distance metric
3. Iterate till convergence
   - combine two clusters with the smallest average linkage



The height in the dendrogram at which two clusters are merged represents the distance between two clusters in the data space. take 4 clusters as the red horizontal line in the dendrogram covers maximum vertical distance AB.

Life Time Value (LTV)

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Propensity of Cross-sell

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Thank You!