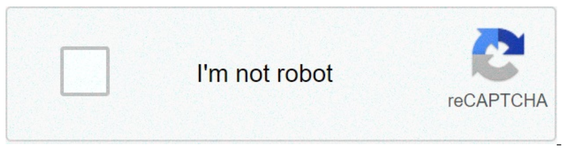

Continue

K means clustering steps

Steps involved in k means clustering. Briefly explain the steps of the k-means clustering algorithm. Four steps in the k-means clustering algorithm. K means clustering steps in sas. K-means clustering algorithm steps are in following order. Explain the steps of k-means clustering algorithm. K means clustering steps in r. Which of the following steps is not used in the k-means clustering algorithm.

The data clustering without label can be performed with the Sklearn.Cluster module. Each clustering algorithm is available in two variants: a class, which implements the adaptation method to learn the clusters on train data and a function, which were given train data, returns a series of interests corresponding to different Cluster. For the class, labels on training data can be found in the labels_ attribute. Input data An important thing to note is that the algorithms implemented in this module can take different types of matrix as input. All methods accept standard form matrices (N_SAMPLES, N_FEATURES). These can be obtained from classes in the Sklearn.feature_Extraction module. To rely on aging, SpectralCluster and DBScan can also insert forms of likeness of shape (n_samples, n_samples). These can be obtained from the functions in the Sklearn.metrics module. Pairwise. A comparison of clustering algorithms in the name of the SCIKIT-LEARN method "Parameters of the UseCase Geometry method (used metric) K-media number of very large clusters N_SAMPLES, MEDIUM N_CLUSTER with minibatch code General purpose, also cluster size, flat geometry, Not too many clusters, inductive distances between the damping points damping of the propagation, the sample preference is not scalable with N_SAMPLES many clusters, no uniform dimensions of the cluster, of the non-flat geometry, distance of the inductive graph (eg close graph) Media-shift bandwidth not scalable with N_SAMPLES Many cluster, irregular cluster size, non-flat geometry, inductive distances between spectral clustering number of medium cluster n_samples, small n_cluster few clusters, also cluster size, non-flat geometry, Transdutive graphic distance (eg closer neighborhood chart) Number of hierarchical clusters D I clusters or distance large threshold n_samples and n_cluster many clusters, possibly connectivity restrictions, is transductive nums between the points clustering number clustering of cluster or distance threshold, type of connection, large distance n_samples and n_cluster many clusters, possibly connectivity restrictions , Non-Euclidean Distances, Transdutive Any Torque Distance Dbscan Size of the DBScan district very large n_samples, medium n_cluster non-flat geometry, uneven cluster size, transducer distances between the most close points Ministry Ministry Registration of the very large cluster very large N_SAMples, geometry does not Flat n_cluster large, uneven cluster dimensions, variable cluster density, transductory distances between Gaussian mixtures very non-scalable flat geometry, good for inductive estimation, inductive Mahalanobis distances to center birch branching factor, the threshold , the globa cluster The optional ones. Large n_cluster and n_samples large data set, upper value removal, data reduction, euclidea inductive distance between non-flat geometry points clustering is useful when clusters have a specific form, ie a non-flat collector, and distance Standard Euclidea is not the right metric. This case rises in the two upper lines of the figure above. Gaussian mix models, useful for clustering, are described in another chapter of the documentation dedicated to mixing models. The Kmeans can be seen as a special case of Gaussian mixture model with equal covariance per component. The methods of transductive clustering (contrasting with inductive clustering methods) are not designed to be applied to new invisible data. Kmeans Cluster algorithms The data attempting to separate samples in N groups of equal variance, minimizing a known policy as inertia or summary within the (look down). This algorithm requires specifying the number of clusters. Scale well at the large number of samples and was used in a wide range of application areas in many different fields. The algorithm K-means divides a sample set (N) in (K) disjoint clusters (C), each described by the average (mu_j) of the samples in the bunch. The means are commonly called the â € >> From the import metrics Sklearn Sklearn labels_true = [0, 0, 0, 1, 1, 1] >>> labels_pred = [0, 0, 1, 1, 2, 2] >>> metric.adjusted_mutual_info_score (labels_true, labels_ped) 0.22504 ... a can Exchange 0 and 1 in the expected labels, renames from 2 to 3 and get the same score: >>> labels_pred = [1, 1, 0, 0, 3, 3] >>> metric.adjusted_mutual_info_score (labels_true, labels_ped) 0.22504. .. all, mutual_info_score, regulated_mutual_info_score and normalized_mutual_info_score are symmetrical: exchange the topic does not change the score. So they can be used as a consensus measure: >>> metric.adjusted_mutual_info_score (labels_pred, labels_true) 0.22504 ... perfect labeling is marked 1.0: >>> labels_pred = label_true [:] >>> metric.adjusted_mutual_info_score (labels_true , Labels_ped) 1.0 >>> metric. Normalized_mutual_info_score (labels_true, labels_ped) 1.0 This is not true for mutual_info_score, which is therefore more difficult to judge: >>> metric.mutual_info_score (labels_true, labels_ped) 0.69 ... bad (eg. Run independent labels) scores not Positive: >>> Labels_true = [0, 1, 2, 0, 3, 4, 5, 1] â € > Labels_Pred = [1, 1, 0, 0, 2, 2, 2, 2]> >> metrics.adjusted_mutual_info_score (labels_true, labels_pred) -0.10526 ... random assignments (uniforms) label assignments have a score you love near 0.0 for any value of n_cluster and n_samples (which is not the case for information Reciproco and V-measure for example). Toped upper than 1: the values close to zero indicate two label positions that are largely independent, while the values close to one indicate a significant agreement. Furthermore, a love exactly 1 indicates that the two tasks of labels are the same (with or without permutation). Contrary to the assistance, the measures based on me require the knowledge of the truth classes of the ground, while almost never available in practice or requires manual assignment by human annotators (as in the supervised learning setting). However, measures based on can also be useful in setting purely without supervision as a constitutive block for a consensus index that can be used for selecting the clustering model. NMI and I am not regulated against the possibility. Take two label positions (of the same objects as the N), (u) and (V). Their entropy is the quantity of uncertainty for a set of partitions, defined by: [H (u) = - sum_ {i = 1} ^ {| u |} p (i) log (p (i)) where (p (i) = | u_i | / n) is the probability that a randomly collected object from (u) falls into the Class (U_i). Likewise for (V): [H (V) = - sum_ {j = 1} ^ {| V |} P '(J) Log (P' (J)) with (P '(J) = | V_J | / N). The mutual information (MI) between (u) is calculated by: [text {mi} (u, v) = sm_ {i = 1} {| U |} sum_ {j = 1} ^ {| V |} P (I, J) Log (frac {p (i, j)} {p (i) p '(j)} right) where (p (i, j) = | u_i cap v_j | / n) It is the probability that a randomly collected object falls into both classes (u_i) and (v_j). It can also be expressed in the formulation of cardinality set: [text {mi} (u, v) = sum_ {i = 1} ^ {| U |} sum_ {j = 1} ^ {| V |} Frac {| u_i cork v_j |} {n} log left (frac {n | u_i cap v_j |} {| u_i || v_j |} right) Normalized reciprocal information is defined as [text {nmi} (u, v) = frac {text {mi} (u, v)} {text {sign} (h (u), h (v))} this value of the mutual information and also The normalized variant is not regulated for the case and tends to increase while the number of different labels (clusters) increases, regardless of the actual amount of Ã ¢ â,¬ Â Å "MUTUAL information" between the positions of the label. The value Expected for reciprocal information can be calculated using the following equation [VEB2009]. In this equation, (A_I = | u_i |) (the of elements in (u_i) and (b_j = | v_j |) (the number of elements in (v_j)). [And [text {mi} (u, v)] = sm_ {i = 1} ^ {| U |} sum_ {j = 1} ^ {| V |} sum_ {n_ {ij} = (a_i + b_j-n) ^ +} ^ {min (a_i, b_j)}} frac {n_ {ij}} {n}} log left (frac {n.n_ {ij}} {a_i b_j} right) frac {a_i! B_J! (N-a_i)! (N-B_J)!} {N! N_ {ij}! (A_i-n_ {ij})! (B_j-n_ {ij})! (N-a_i-b_j + n_ {ij})!} {Ij})!} Using the expected value, the rectified reciprocal information can then be calculated using a module similar to that of the Rand Rand index: [text {ami} = = - and [text {mi}]} {text {mes}} (h) {sign} (h (u), h (v)) - and [\ t text {mi}]} Normalized mutual information and regulated regulated information, normalization The value is generally some generalized media of the entrepreneies of each clustering. There are various generalized means and there are no rules companies by preferring one on others. The decision is largely a base Field-by-field; for example, in the detection of the community, the arithmetic average is more common. Each normalizing method provides Ã ¢ â,¬ Å "this similar behavior" [Yat2016]. In our implementation, this is controlled by the parameter medium_method. vinh et al. (2010) named nmi variants and love their average method [veb2010]. The averages is, Ã, â â â â â â â â â. â,¬ â "¢ and Ã ¢ â,¬ Â â â â â â â â â â â â â â â" averages are geometric and arithmetic means; we use these most widely common names. Veb2009 references Vinh, PPP and Bailey, (2009). Ã ¢ â,¬ "Information Theoretical measures for comparison of clustering ". Procedures of the 26th annual international conference on automatic learning - ICML Ã ¢ â,¬ ~ 09. Doi: 10,1145 / 1553374.1553511. ISBN 9781605585161. Veb2010 Vinh, PPP and Bailey, (2010). Ã ¢ â,¬ "Theoretical measures for the comparison of clusters: variants, properties, normalization and correction by chance. Jmlr < Yat2016 Yang , Algesheimer and Tessone, (2016). Ã ¢ â,¬ "A comparative analysis of community detection algorithms on artificial networks ... Scientific relationships 6: 30750. Doi: 10.1038 / srep30750. Given the knowledge of the class tasks of the earth truth of the samples, it is possible to define some intuitive metric using the conditional entropy analysis. In particular Rosenberg and Hirschberg (2007) define the following two desirable objectives for any cluster assignment: homogeneous: each cluster contains only a single class members. Completeness: All members of a specific class are assigned to the same cluster. We can transform those concepts as homogeneous scores _core and completeness_core. Both are limited below 0.0 and higher than 1.0 (higher it is better): >>> Sklearn import metrics >>> Labels_true = [0, 0, 0, 1, 1, 1] >>> Labels_PRED = [0, 0, 1, 1, 2, 2] >>> METRICS.HOMOGENEITY_SCORE (LATES_TRUE, LABELS_PED) 0.66 ... >>> METRICS.COMPLETE_CORE_CORE (LARGILS_TRUE, LABELS_PED) 0.42 ... their harmonic average called V -measure is calculated by v_measure_core: >>> metrics.v_measure_core (labels_true, labels_ped) 0.51 ... This function The formula is the following: [v = frac {(1 + beta) {(1 + beta) Vaults {homogenity} times {completeness}} {beta Text {}} + text {completeness})} {completeness})}} {complete})}} {complete})} Default at a value of 1.0, but for the use of a value of less than 1 per beta: >>> metric.v_measure_core (labels_true, labels_ped, beta = 0.6) 0.54 ... more weight will be attributed to homogenousness e Use a value higher than 1: >>> metric.v_measure_s core (labels_true, labels_pred, beta = 1.8) 0.48 ... more weight will be attributed to completeness. The measure V is actually equivalent to reciprocal information (NMI) discussed above, with the aggregation function is the arithmetic average [b2011]. The homogeneity, completeness and v-measure can be calculated simultaneously using homogeneity_completeny_v_measure as follows: >>> metric.homogeneity_completeny_v_measure (labels_true, labels_ped) (0.66 ..., 0.42 ..., 0.51 ...) The following assignment clustering is slightly better, since it is homogeneous but not complete: >>> labels_pred = [0, 0, 0, 1, 2, 2] >>> metric.homogeneity_completeny_v_measure (labels_true, labels_ped) (1.0, 0 , 68 ..., 0.81 ...) Note v_measure_core is symmetrical: it can be used to evaluate the agreement of two independent positions on the same data set. This is not the case for And homogeneity_core: both are bound by the report: homogeneous _core (A, b) == Completess_Score (B, a) Delimited scores: 0.0 is so bad that it can be, 1.0 is a perfect score. Intuitive interpretation: clustering with bad V-measure can be qualitatively analyzed in terms of homogeneous homogeneity Completeness to feel better that Ã ¢ â,¬ â â â â â â â â â errors is made by the assignment. No intake is carried out on the cluster structure: can be used to compare cluster algorithms such as k-media that presuppose isotropic blob shapes with spectral grouping algorithms that can find a cluster with Ã ¢ â,¬ Å "folded". The previously introduced metrics are not normalized with regard to random labeling: this means that depending on the number of samples, clusters and truthings of the land, a completely random labeling will always not produce the same values for homogeneous, the Completeness and therefore the measurement measure. In particular the random labeling won the zero-score yield especially when the number of clusters is great. This problem can easily be ignored when the number of samples is higher than a thousand and the Number of clusters is less than 10. For smaller sample sizes or more cluster is more secure. and a rectified index as the regulated Rand index (ARI). These metrics require the knowledge of the truth classes of the ground, while almost ever available in practice or requires manual assignment by human annotators (as in the supervised learning setting). The homogeneous scores and completeness are formally provided by: [H = 1 - frac {h (C | K)} {H (C)}} {H (C)}} {H (C)} [c = 1 - frac {h (k | c)} {h (k)} where (h (c | k) is the conditional entropy of classes assigned to cluster assignments and is date from: [h (c | k) = - sum_ {c = 1} ^ {| C |} SUM_ {K = 1} ^ {| k |} frac {n_ {c, k}} {n}}}} left (frac {n_ {c, k}} {n_k} right) and (h (c) is the class entropy and is given by: [h (c) = - sum_ {c = 1} ^ {| c |} frac {n_c} {n} clot log (frac {n_c} {n} right) with (n) the total number of samples, (n_c) e (N_K) The number of samples respectively belonging to the class (C) and the cluster (K), and finally (N_ {C, K}) The number of samples from class (C) Assigned to Cluster (K). The conditioning entropy of the clusters given the class (H (K | c)) and the cluster entropy (H (K) are defined symmetrically. Rosenberg and Hirschberg further define V-measure as a harmonious media of homogeneity and completeness: [v = 2 clot frac {h cdot c} {h + c clot c} {h + c} the index of Fowkes-alolls (sklearn.metrics.fowlkes_mallows_score) can be used when base sample truth class tasks are known. The Fowlkes-Mallows score is defined as the geometric average of the accuracy and call to torque: [text {IMF} = frac {text {tp}} {sqrt {} {sqrt {(text {tp} + text {fp}) (\ t text {tp} + text {fn})}}} {fn})}}}}}}})}}}}}})}}} {fn})}}} {fn})}}} {fn})}}} where tp is the number of positive true (ie the number of points of points belonging to the same clusters in both real labels and foreseen Labels), FP is the number of false positives (ie the number of points of which they belong to the same clusters in real labels and not in the expected labels) and Fn is the number of false negatives (ie the number of torque of Points that belong to the same clusters in the labels provided and not in the real labels). The score varies from 0 to 1. A high value indicates a good resemblance between two clusters. >>> From the import metrics Sklearn >>> Labels_true = [0, 0, 0, 1, 1, 1] >>> Labels_Pred = [0, 0, 1, 1, 2, 2] >>> Metrica.fowlkes_mallows_score (labels_true, labels_ped) 0.47140 ... you can exchange 0 and 1 in the expected labels, renames from 2 to 3 and get the same score: >>> labels_pred = [1, 1, 0, 0, 3, 3] >> > metrics.fowlkes_mallows_score (labels_true, labels_ped) 0.47140 ... The perfect labeling is dried 1.0: >>> labels_true [:] >>> metrics.fowlkes_mallows_core (labels_true, labels_ped) 1.0 bad (eg independent labels) have zero scores:> >> labels_true = [0, 1, 2, 0, 3, 4, 5, 1] â € > labels_pred = [1, 1, 0, 0, 2, 2, 2, 2] >>> metric.fowlkes_mallows_score (lebels_true, labels_pred) 0.0 assignments of random labels (uniforms) have An IMF score near 0.0 for any value of N_CLUSTER and N_SAMPLES (which is not the case of mutual reciprocal information or measurement V). Upper-limited to 1: values close to zero zero Two label positions that are largely independent, while values close to one indicate a significant agreement. Furthermore, the values of exactly 0 indicate assignments of purely independent labels and an IMF exactly 1 indicates that the two label tasks are the same (with or without permutation). No intake is carried out on the cluster structure: can be used to compare cluster algorithms such as k-media that presuppose isotropic blob shapes with spectral grouping algorithms that can find a cluster with Ã ¢ â,¬ Å "folded". Contrary to inertia, FMI-based measures require knowledge of the truth classes of the ground, while almost never available in practice or requires manual assignment by human annotators (as in the supervised learning setting). If the labels of Earth truth are not known, the evaluation must be performed using the model itself. The silhouette coefficient (Sklearn.metrics.silhouette_score) is an example of this assessment, in which a higher score of the silhouette coefficient refers to a Model with better defined clusters. The silhouette coefficient is defined for each sample and consists of two scores: A: The distance me Dia between a sample and all the other points in the same class. B: The average distance between a sample and all the other points in the closer closer cluster. The silhouette coefficient s for a single sample is then given as: [s = frac {b - a} {max (a, b)} the silhouette coefficient for a series of samples is given as the average of the Coefficient silhouette for each sample. >>> From the import metrics Sklearn >>> from Sklearn.metrics Import pairwise_distances >>> from Sklearn Import data set >>> x, y = data set.load_iris (return_x_y = true) in normal use, the coefficient of Silhouette is applied to the results of a cluster analysis. >>> Import number as np >>> from sklearn.cluster import kmeans >>> kmeans_model = kmeans (n_cluster = 3, random_state = 1) .fit (x) >>> labels = kmeans_model.labels_ >>> metricas.silhouette_core (X, labels, metric = 'Euclidean') 0.55 ... References Peter J. RousseEuw (1987). Ã ¢ â,¬ "Islhouettes: a graphic aid to the interpretation and validation of the cluster analysis ... Computational and applied mathematics 20: 53 - 65. doi: 10.1016 / 0377-0427 (87) 90125-7. Il Score is limited between -1 for incorrect clustering and +1 for a highly dense clustering. Scores around zero indicate superimposed clusters. The score is higher when clusters are dense and well separated, which refer to a standard concept Of a cluster. The silhouette coefficient is generally higher for convex clusters compared to other cluster concepts, such as density-based clusters like those obtained through DBScan. If the earth's truth labels are not known, the CALINSKI index -Harabasz (Sklearn.metrics.calinski_harabasz_score) - also known as a criterion of the ratio of variance - can be used to evaluate the model, where a higher calinski-harabasz score refers to a model with better defined clusters. The index is the R Input between the sum of the dispersion between cluster and dispersion within the cluster for all clusters (where the dispersion is defined as the sum of the square distances): >>> From the metrics of import Sklearn >>> of Sklearn.metrics Import pairwise_distanze >>> From the import data Sklearn >>> x, y = data set.load_iris (return_x_y = true) in normal use, the CALINSKI-HARABASZ index is applied to the results of a cluster analysis:> >> Import NUMPY as NP >> >> from sklearn.cluster import kmeans >>> kmeans_model = kmeans (n_cluster = 3, random_state = 1) .fit (x) >>> labels = kmeans_model.labels_ >>> metric.calinski_harabasz_core (x, labels) 561.62 ... The score is higher Clusters are dense and well separated, which refers to a standard concept of a cluster. The score is fast to calculate. The CALINSKI-HARABASZ index is generally higher for convex clusters than other cluster concepts, such as density-based clusters such as those obtained through DBScan. For a data set (and) (n_e) that was grouped in (k) cluster, the calinski-harabasz score is ã¨ Like the ratio between clusters dispersion of dispersion and dispersion inside the cluster: [S = frac {mathrm {tr} (b_k)} {mathrm {tr} (w_k)} times frac {n_e - k} {k - 1} where (mathrm {tr} (b_k) is track of the group dispersion matrix and (mathrm {tr} (w_k) is the trace of the 'Cluster dispersion intermersion defined by: [W_K = sum_ {q = 1} ^ k atm_ {x in c_q} (x - c_q) (x - c_q) ^ t] [b_k = sum_ {q = 1} ^ k n_q (c_q - c_e) (c_q - c_e) ^ t Cluster (C_E) The center of (and) is the number of points in cluster (q). If the truth labels are not known, the Davies-Boultin index (sklearn.metrics.davies_bouldin_score) can be used to evaluate the model, in which a lower index of Davies-Bouldin refers to a model with a better one Separation between clusters. This index meant the average Ã ¢ â,¬ Å "Similarity" between cluster, where the similarity is a measure that compares the distance between clusters with the size of the clusters themselves. Zero is the lowest possible score. The most values close to zero indicate a better partition. In normal use, the Davies-Boultin index is applied to the results of a cluster analysis as follows: >>> from the Sklearn import data set >>> Iris = datasets. Load_iris () >>> x = iris.data >>> from sklearn.cluster import kmeans >>> from sklearn.metrics import davies_bouldin_core >>> kmeans = kmeans (n_cluster = 3, random_state = 1) .fit (x)> >> labels = kmeans.labels_ >>> davies_bouldin_score (x, labels) 0.6619 ... the calculation of Davies-Bouldin is simpler than that of the scores of the silhouette. The index is calculated only quantities and functionality related to the set of data. The Davies-Bouting index is generally higher for convex clusters than other concepts Cluster, as clusters based on density like those obtained from DBScan. The use of the centerid distance limits the metric of distance to the Euclido space. The index is defined as the average similarity between each cluster (C_I) per (i = 1, ..., k) and its most similar (C_J). In the context of this index, the similarity is defined as a measure (r_ {ij}}) that exchanges: (s_i), the average distance between each cluster point and the center-center Cluster Ã ¢ â,¬ "Also know as the diameter of the cluster. (D_ {IJ}), the distance between the cluster centers (I). A simple choice to build (R_ {ij}) so that it is not negative and symmetrical is: [r_ {ij} = frac {s_i + s_j} {d_ {ij}}} {d_ {ij}} then the index of Davies-bouldin is defined as: [db = frac {1} {k} {1} {i = 1} ^ k max_ {i}} max_ {i}} j} r_ {ij}] Matrix contingency (sklearn.metrics.cluster.contingency_matrix) The intersection cardinality for each pair of True / expected clusters. The contingency matrix provides sufficient statistics for all clustering metrics in which samples are independent and identical distributed and one is not You must take some cases not in cluster into account. Here is an example: >>> from Sklearn.metrics.c Luster Import Import contingency_matrix >>> x = ["a", "a", "a", "b", "b", "b"] >>> y = [0, 0, 1, 1, 2, 2] >>> aray_matrix (x, y) array ([[2, 1, 0], [0, 1, 2]]) The first row of output array indicates that there are three samples whose real cluster is "" TO ". Of them, two are in cluster expected 0, one is in 1, and no one is in 2. and the second line indicates that there are three samples whose real cluster is "bÃ ¢ â,¬ of Ã ¢ Â, ¬. Of these, no one is in cluster expected 0, one is in 1 and two is in 2. a confusion matrix for the classification is a square contingency matrix in which the order of the rows and columns corresponds to a list of classes. It allows you to examine the dissemination of each true cluster through the clusters provided and The calculated quota table is typically used in the calculation of a statistic of similarities (like the others listed in this document) between the two clusters. The contingency matrix is easy to interpret for a small number of clusters, but it becomes very difficult to interpret for a large number of It does not give a single metric to use as a goal for clustering optimization. Wikipedia References Entry for Contingency Matrix The couple confusion matrix (sklearn.metrics.custer.pair_confusion_matrix) is a 2x2 resembly matrix [begin {split} c = {matrix} c_ {00} & C_ {01} In several clusters under real and expected clustering. It has the following items: (C_ {00}): Number of pairs with both clustering having unwrapped samples together But the other clustering does not have the samples grouped together (C_ {01}): the number of pairs with the real clustering of the label does not have the samples grouped together but the other clustering having grouped samples together (C_ { 11}: Number of pairs with both clustering with samples grouped together considering a pair of samples that is grouped together a positive torque, so as in binary classification the count of real negatives is (c_ {00}) , the false negatives is (c_ {10}), the real positives are (c_ {11}) and false positives is (c_ {01}). The perfectly combined labels have all the voices not zero on the diagonal regardless of the actual values of the label: >>> from sklearn.metrics.Cluster Import pair_confusion_matrix >>> pair_confusion_matrix ([0, 0, 1, 1], [0, 0 , 1, 1]) Array ([[8, 0], [0, 4]]] >>> pair_confusion_matrix ([0, 0, 1, 1], [1, 1, 0, 0]) Array ([[[8, 0], [0, 4]]) Labels that assign all classes The members of the same clusters are complete but may not always be pure, then penalized and have some non-zero off-diagonal voices: >>> pair_confusion_matrix ([0, 0, 1, 2], [0, 0, 1, 1]) Array ([[8, 2], [0, 2]]) The matrix is not symmetrical: >>> parac_confusion_matrix ([0 , 0, 1, 1], [0, 0, 1, 2]) Array ([[[[8, 0], [2, 2]]] If class members are completely divided into different clusters, assignment It's totally incomplete, from here the Matrix has all the zero diagonal voices: >>> pair_confusion_matrix ([0, 0, 0, 0], [0, 1, 2, 3]) Array ([[0, 0], [12, 0]]) Show this source of origin of the page

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