

# Package ‘FCPS’

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**Type** Package

**Title** Fundamental Clustering Problems Suite

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**Maintainer** Michael Thrun <m. thrun@gmx.net>

**Description** Over sixty clustering algorithms are provided in this package with consistent input and output, which enables the user to try out algorithms swiftly. Additionally, 26 statistical approaches for the estimation of the number of clusters as well as the mirrored density plot (MD-plot) of clusterability are implemented. The package is published in Thrun, M.C., Stier Q.: “Fundamental Clustering Algorithms Suite” (2021), SoftwareX, <DOI:10.1016/j.softx.2020.100642>. Moreover, the fundamental clustering problems suite (FCPS) offers a variety of clustering challenges any algorithm should handle when facing real world data, see Thrun, M.C., Ultsch A.: “Clustering Benchmark Datasets Exploiting the Fundamental Clustering Problems” (2020), Data in Brief, <DOI:10.1016/j.dib.2020.105501>.

**Imports** mclust, ggplot2, DataVisualizations

**Suggests** mlpack, kernlab, cclust, dbscan, kohonen, MCL, ADPclust, cluster, DatabionicSwarm, orclus, subspace, flexclust, ABCanalysis, apcluster, pracma, EMCluster, pdfCluster, parallelDist, plotly, ProjectionBasedClustering, GeneralizedUmatrix, mstknncust, densityClust, parallel, energy, R.utils, tclust, Spectrum, genie, protoclust, fastcluster, clusterability, signal, reshape2, PPCI, clustrd, smacof, rgl, prclust, CEC, dendextend, moments, prabclus, VarSelLCM, sparcl, mixtools, HDclassif, clustvarsel, yardstick, knitr, rmarkdown, igraph, leiden, clustMixType, clusterSim, NetworkToolbox

**Depends** R (>= 3.5.0)

**License** GPL-3

**LazyData** TRUE

**LazyLoad** yes

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**BugReports** <https://github.com/Mthrun/FCPS/issues>

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**VignetteBuilder** knitr

**SystemRequirements** Pandoc ( $\geq 1.12.3$ )

**NeedsCompilation** no

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FCPS-package

*Fundamental Clustering Problems Suite*


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## Description

Over sixty clustering algorithms are provided in this package with consistent input and output, which enables the user to try out algorithms swiftly. Additionally, 26 statistical approaches for the estimation of the number of clusters as well as the mirrored density plot (MD-plot) of clusterability are implemented. The package is published in Thrun, M.C., Stier Q.: "Fundamental Clustering Algorithms Suite" (2021), SoftwareX, <DOI:10.1016/j.softx.2020.100642>. Moreover, the fundamental clustering problems suite (FCPS) offers a variety of clustering challenges any algorithm should handle when facing real world data, see Thrun, M.C., Ultsch A.: "Clustering Benchmark Datasets Exploiting the Fundamental Clustering Problems" (2020), Data in Brief, <DOI:10.1016/j.dib.2020.105501>.

The package consists of many algorithms and fundamental datasets for clustering published in [Thrun/Stier, 2021]. Originally, the 'Fundamental Clustering Problems Suite' (FCPS) offered a variety of clustering problems any algorithm shall be able to handle when facing real world data. Nine of the here presented artificial datasets were priorly named FCPS with a fixed sample size in Ultsch, A.: "Clustering with SOM: U\*C", In Workshop on Self-Organizing Maps, 2005. FCPS often served in the paper as an elementary benchmark for clustering algorithms. The FCPS package extends datasets, enables variable sample sizes for these datasets, and provides a standardized and easy access to many clustering algorithms.

<https://www.deepbionics.org/>

## Details

FCPS datasets consists of data sets with known a priori classification to be reproduced by the algorithms. All data sets are intentionally created to be simple and might be visualized in two or three dimensions. Each data sets represents a certain problem that is solved by known clustering algorithms with varying success. This is done in order to reveal benefits and shortcomings of algorithms in question. Standard clustering methods, e.g. single-linkage, ward and k-means, are not able to solve all FCPS problems satisfactorily. "Lsun3D and each of the nine artificial data sets of "Fundamental Clustering Problems Suite" (FCPS) were defined separately for a specific clustering problem as cited (in [Thrun/Ultsch, 2020]). The original sample size defined in the respective first publication mentioning the data was used in [Thrun/Ultsch, 2020], but using the R function

"ClusterChallenge" (...) any sample size can be drawn for all artificial data sets. [Thrun/Ultsch, 2020]

Index: This package was not yet installed at build time.

### Author(s)

NA

Maintainer: Michael Thrun <m.thrun@gmx.net>

### References

[Thrun/Ultsch, 2020] Thrun, M. C., & Ultsch, A.: Clustering Benchmark Datasets Exploiting the Fundamental Clustering Problems, Data in Brief, Vol. 30(C), pp. 105501, doi:10.1016/j.dib.2020.105501, 2020.

[Thrun/Stier, 2021] Thrun, M. C., & Stier, Q.: Fundamental Clustering Algorithms Suite SoftwareX, Vol. 13(C), in press, pp. 100642. doi:10.1016/j.softx.2020.100642, 2021.

[Ultsch, 2005] Ultsch, A.: Clustering with SOM: U\*C, In Proc. Workshop on Self-Organizing Maps, pp. 75-82, Paris, France, 2005.

---

ADPclustering	<i>(Adaptive) Density Peak Clustering algorithm using automatic parameter selection</i>
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---

### Description

The algorithm was introduced in [Rodriguez/Laio, 2014] and here implemented by [Wang/Xu, 2017]. The algorithm is adaptive in the sense that only ClusterNo has to be set instead of the parameters of [Rodriguez/Laio, 2014] implemented in [ADPclustering](#).

### Usage

```
ADPclustering(Data,ClusterNo=NULL,PlotIt=FALSE,...)
```

### Arguments

Data	[1:n,1:d] matrix of dataset to be clustered. It consists of n cases of d-dimensional data points. Every case has d attributes, variables or features.
ClusterNo	Optional, either: A number k which defines k different Clusters to be build by the algorithm, or a range of ClusterNo to let the algorithm choose from.
PlotIt	default: FALSE, If TRUE plots the first three dimensions of the dataset with colored three-dimensional data points defined by the clustering stored in Cls
...	Further arguments to be set for the clustering algorithm, if not set, default arguments are used.

**Details**

The ADP algorithm decides the k number of clusters. This is contrary to the other version of the algorithm from another package which can be called with [DensityPeakClustering](#).

**Value**

List of

`Cls` [1:n] numerical vector with n numbers defining the classification as the main output of the clustering algorithm. It has k unique numbers representing the arbitrary labels of the clustering.

`Object` Object defined by clustering algorithm as the other output of this algorithm

**Author(s)**

Michael Thrun

**References**

[Rodriguez/Laio, 2014] Rodriguez, A., & Laio, A.: Clustering by fast search and find of density peaks, *Science*, Vol. 344(6191), pp. 1492-1496. 2014.

[Wang/Xu, 2017] Wang, X.-F., & Xu, Y.: Fast clustering using adaptive density peak detection, *Statistical methods in medical research*, Vol. 26(6), pp. 2800-2811. 2017.

**See Also**

[DensityPeakClustering](#)

[adpclus](#)

**Examples**

```
data('Hepta')
out=ADPclustering(Hepta$Data,PlotIt=FALSE)
```

---

AgglomerativeNestingClustering  
*AGNES clustering*

---

**Description**

Agglomerative hierarchical clustering (AGNES)of [Rousseeuw/Kaufman, 1990, pp. 199-252]

**Usage**

```
AgglomerativeNestingClustering(DataOrDistances, ClusterNo,
PlotIt = FALSE, Standardization = TRUE, ...)
```

**Arguments**

DataOrDistances	[1:n,1:d] matrix of dataset to be clustered. It consists of n cases or d-dimensional data points. Every case has d attributes, variables or features. Alternatively, symmetric [1:n,1:n] distance matrix
ClusterNo	A number k which defines k different clusters to be built by the algorithm. if ClusterNo=0, the dendrogram is generated instead of a clustering to estimate the numbers of clusters.
PlotIt	Default: FALSE if codeClusterNo!=0, If TRUE or codeClusterNo=0 plots the first three dimensions of the dataset with colored three-dimensional data points defined by the clustering stored in Cls
Standardization	DataOrDistances is standardized before calculating the dissimilarities. Measurements are standardized for each variable (column), by subtracting the variable's mean value and dividing by the variable's mean absolute deviation. If DataOrDistances is already a distance matrix, then this argument will be ignored.
...	Further arguments to be set for the clustering algorithm, if not set, default arguments are used.

**Value**

List of	
Cls	[1:n] numerical vector with n numbers defining the classification as the main output of the clustering algorithm. It has k unique numbers representing the arbitrary labels of the clustering.
Dendrogram	Dendrogram of hierarchical clustering algorithm
Object	Object defined by clustering algorithm as the other output of this algorithm

**Author(s)**

Michael Thrun

**References**

- [Rousseeuw/Kaufman, 1990] Rousseeuw, P. J., & Kaufman, L.: Finding groups in data, Belgium, John Wiley & Sons Inc., ISBN: 0471735787, doi 10.1002/9780470316801, Online ISBN: 9780470316801, 1990.
- [Struyf et al., 1996] Struyf, A., Hubert, M. and Rousseeuw, Peter J.: Clustering in an Object-Oriented Environment, Journal of Statistical Software, Vol. 1, doi: 10.18637/jss.v001.i04, 1996.
- [Struyf et al., 1997] Struyf, A., Hubert, M. and Rousseeuw, P.J.: Integrating Robust Clustering Techniques in S-PLUS, Computational Statistics and Data Analysis, Vol. 26, pp. 17–37, 1997.

**See Also**

[agnes](#)

**Examples**

```

data('Hepta')
CA=AgglomerativeNestingClustering(Hepta$Data,ClusterNo=7,PlotIt=FALSE)
## Not run:
ClusterDendrogram(CA$Dendrogram,7,main='AGNES clustering')

print(CA$Object)
plot(CA$Object)

## End(Not run)

```

---

APclustering

*Affinity Propagation Clustering*


---

**Description**

Affinity propagation clustering published by [Frey/Dueck, 2007] and implemented by [Bodenhofer et al., 2011].

**Usage**

```

APclustering(DataOrDistances,

InputPreference=NA,ExemplarPreferences=NA,

DistanceMethod="euclidean",

Seed=7568,PlotIt=FALSE,Data,...)

```

**Arguments**

DataOrDistances	[1:n,1:d] with: if d=n and symmetric then distance matrix assumed, otherwise: [1:n,1:d] matrix of dataset to be clustered. It consists of n cases or d-dimensional data points. Every case has d attributes, variables or features. In the latter case the Euclidean distances will be calculated.
InputPreference	Default parameter set, see <b>apcluster</b>
ExemplarPreferences	Default parameter set, see <b>apcluster</b>
DistanceMethod	DistanceMethod as in <a href="#">dist</a> for <a href="#">similarities</a> .
Seed	Set as integervalue to have reproducible results, see <b>apcluster</b>
PlotIt	Default: FALSE, If TRUE and dataset of [1:n,1:d] dimensions then a plot of the first three dimensions of the dataset with colored three-dimensional data points defined by the clustering stored in CIs will be generated.



Data	[1:n,1:d] data matrix in the case that DataOrDistances is missing and partial matching does not work.
...	Further arguments to be set for the clustering algorithm, if not set, default arguments are used.

### Details

Distancematrix D is converted to similarity matrix S with  $S = -(D^2)$ .

If data matrix is used, then euclidean similarities are calculated by `similarities` and a specified distance method.

The AP algorithm decides the k number of clusters.

### Value

List of

`Cls` [1:n] numerical vector with n numbers defining the classification as the main output of the clustering algorithm. It has k unique numbers representing the arbitrary labels of the clustering.

`Object` Object defined by clustering algorithm as the other output of this algorithm

### Author(s)

Michael Thrun

### References

[Frey/Dueck, 2007] Frey, B. J., & Dueck, D.: Clustering by passing messages between data points, *Science*, Vol. 315(5814), pp. 972-976, <doi:10.1126/science.1136800>, 2007.

[Bodenhofer et al., 2011] Bodenhofer, U., Kothmeier, A., & Hochreiter, S.: APCluster: an R package for affinity propagation clustering, *Bioinformatics*, Vol. 27(17), pp, 2463-2464, 2011.

Further details in <http://www.bioinf.jku.at/software/apcluster/>

### See Also

`apcluster`

### Examples

```
data('Hepta')
res=APclustering(Hepta$Data, PlotIt = FALSE)
```

Atom

*Atom introduced in [Ultsch, 2004].*

---

**Description**

Two nested spheres with different variances that are not linear not separable. Detailed description of dataset and its clustering challenge is provided in [Thrun/Ultsch, 2020].

**Usage**

```
data("Atom")
```

**Details**

Size 800, Dimensions 3, stored in Atom\$Data

Classes 2, stored in Atom\$Cls

**References**

[Ultsch, 2004] Ultsch, A.: Strategies for an artificial life system to cluster high dimensional data, Abstracting and Synthesizing the Principles of Living Systems, GWAL-6, U. Brggemann, H. Schaub, and F. Detje, Eds, pp. 128-137. 2004.

[Thrun/Ultsch, 2020] Thrun, M. C., & Ultsch, A.: Clustering Benchmark Datasets Exploiting the Fundamental Clustering Problems, Data in Brief, Vol. 30(C), pp. 105501, doi:10.1016/j.dib.2020.105501, 2020.

**Examples**

```
data(Atom)
str(Atom)
```

---

AutomaticProjectionBasedClustering*Automatic Projection-Based Clustering*

---

**Description**

Projection-based clustering [AutomaticProjectionBasedClustering](#) projects the data (nonlinear) into two dimensions and tries only to preserve relevant neighborhoods prior to clustering. The cluster analysis itself includes the high-dimensional distances in the clustering process. Performs non-interactive projection-based clustering based on non-linear projection methods [Thrun/Ultsch, 2017], [Thrun/Ultsch, 2020a].

**Usage**

```
AutomaticProjectionBasedClustering(DataOrDistances, ClusterNo, Type="NerV",
StructureType = TRUE, PlotIt=FALSE, PlotTree=FALSE, PlotMap=FALSE, ...)
```

**Arguments**

DataOrDistances	Either nonsymmetric [1:n,1:d] numerical matrix of a dataset to be clustered. It consists of n cases of d-dimensional data points. Every case has d attributes, variables or features. or symmetric [1:n,1:n] distance matrix, e.g. as <code>matrix(dist(Data, method))</code>
ClusterNo	A number k which defines k different clusters to be built by the algorithm.
Type	Type of Projection method, either NerV [Venna et al., 2010] Pswarm [Thrun/Ultsch, 2020b] MDS [Torgerson, 1952] Uwot [McInnes et al., 2018] CCA [Demartines/Herault, 1995] Sammon [Sammon, 1969] t-SNE [Van der Maaten/Hinton, 2008]
StructureType	Either compact (TRUE) or connected (FALSE), see discussion in [Thrun, 2018]
PlotIt	Default: FALSE, if TRUE plots the first three dimensions of the dataset with colored three-dimensional data points defined by the clustering stored in C1s
PlotTree	TRUE: Plots the dendrogram, FALSE: no plot
PlotMap	Plots the topographic map [Thrun et al., 2016].
...	Further arguments to be set for the clustering algorithm, if not set, default arguments are used.

**Details**

The first idea of using non-PCA projections for clustering was published by [Bock, 1987] as a definition. However, to the knowledge of the author, it was not applied to any data. The coexistence of projection and clustering was introduced in [Thrun/Ultsch, 2017].

Projection-based clustering is based on a nonlinear projection of high-dimensional data into a two-dimensional space [Thrun/Ultsch, 2020b]. Typical projection-methods like t-distributed stochastic neighbor embedding (t-SNE) [Van der Maaten/Hinton, 2008], or neighbor retrieval visualizer (NerV) [Venna et al., 2010] are used project data explicitly into two dimensions disregarding the subspaces of higher dimension than two and preserving only relevant neighborhoods in high-dimensional data. In the next step, the Delaunay graph [Delaunay, 1934] between the projected points is calculated, and each vertex between two projected points is weighted with the high-dimensional distance between the corresponding high-dimensional data points. Thereafter the shortest path between every pair of points is computed using the Dijkstra algorithm [Dijkstra, 1959]. The shortest paths are then used in the clustering process, which involves two choices depending on

the structure type in the high-dimensional data [Thrun/Ultsch, 2020b]. This Boolean choice can be decided by looking at the topographic map of high-dimensional structures [Thrun/Ultsch, 2020a]. In a benchmarking of 34 comparable clustering methods, projection-based clustering was the only algorithm that always was able to find the high-dimensional distance or density-based structure of the dataset [Thrun/Ultsch, 2020b].

It should be noted that it is preferable to use a visualization for the Generalized U-Matrix like the topographic map `plotTopographicMap` of [Thrun et al., 2016] to evaluate the choice of the boolean parameter `StructureType` and the clustering, improve it or set the number of clusters appropriately. A comparison with 32 clustering algorithms showed that PBC is always able to find the correct cluster structure while the best of the 32 clustering algorithms varies depending on the dataset [Thrun/Ultsch, 2020].

The first systematic comparison to other DR clustering methods like Projection-Pursuit Methods `ProjectionPursuitClustering`, supspace clustering methods `SubspaceClustering`, and CA-based clustering methods can be found in [Thrun/Ultsch, 2020a]. For PCA-based clustering methods please see `TandemClustering`.

### Value

List of

<code>Cls</code>	[1:n] numerical vector with n numbers defining the classification as the main output of the clustering algorithm. It has k unique numbers representing the arbitrary labels of the clustering. . Points which cannot be assigned to a cluster will be reported with 0.
<code>Object</code>	Object defined by clustering algorithm as the other output of this algorithm

### Author(s)

Michael Thrun

### References

- [Bock, 1987] Bock, H.: On the interface between cluster analysis, principal component analysis, and multidimensional scaling, *Multivariate statistical modeling and data analysis*, (pp. 17-34), Springer, 1987.
- [Thrun/Ultsch, 2017] Thrun, M. C., & Ultsch, A.: Projection based Clustering, *Proc. International Federation of Classification Societies (IFCS)*, pp. 250-251, Tokai University, Japanese Classification Society (JCS), Tokyo, Japan August 7-10, 2017.
- [Thrun/Ultsch, 2020a] Thrun, M. C., & Ultsch, A.: Using Projection based Clustering to Find Distance and Density based Clusters in High-Dimensional Data, *Journal of Classification*, in press, doi 10.1007/s00357-020-09373-2, 2020.
- [Thrun et al., 2016] Thrun, M. C., Lerch, F., Loetsch, J., & Ultsch, A.: Visualization and 3D Printing of Multivariate Data of Biomarkers, in Skala, V. (Ed.), *International Conference in Central Europe on Computer Graphics, Visualization and Computer Vision (WSCG)*, Vol. 24, pp. 7-16, Plzen, <http://wscg.zcu.cz/wscg2016/short/A43-full.pdf>, 2016.
- [McInnes et al., 2018] McInnes, L., Healy, J., & Melville, J.: Umap: Uniform manifold approximation and projection for dimension reduction, arXiv preprint arXiv:1802.03426, 2018.

[Demartines/Herault, 1995] Demartines, P., & Herault, J.: CCA:" Curvilinear component analysis", Proc. 15 Colloque sur le traitement du signal et des images, Vol. 199, GRETSI, Groupe d Etudes du Traitement du Signal et des Images, France 18-21 September, 1995.

[Sammon, 1969] Sammon, J. W.: A nonlinear mapping for data structure analysis, IEEE Transactions on computers, Vol. 18(5), pp. 401-409. doi doi:10.1109/t-c.1969.222678, 1969.

[Thrun/Ultsch, 2020b] Thrun, M. C., & Ultsch, A.: Swarm Intelligence for Self-Organized Clustering, Journal of Artificial Intelligence, Vol. in press, pp. doi 10.1016/j.artint.2020.103237, 2020.

[Torgerson, 1952] Torgerson, W. S.: Multidimensional scaling: I. Theory and method, Psychometrika, Vol. 17(4), pp. 401-419. 1952.

[Venna et al., 2010] Venna, J., Peltonen, J., Nybo, K., Aidos, H., & Kaski, S.: Information retrieval perspective to nonlinear dimensionality reduction for data visualization, The Journal of Machine Learning Research, Vol. 11, pp. 451-490. 2010.

[Van der Maaten/Hinton, 2008] Van der Maaten, L., & Hinton, G.: Visualizing Data using t-SNE, Journal of Machine Learning Research, Vol. 9(11), pp. 2579-2605. 2008.

## Examples

```
data('Hepta')
out=AutomaticProjectionBasedClustering(Hepta$Data,ClusterNo=7,PlotIt=FALSE)
```

---

Chainlink

*Chainlink introduced in [Ultsch et al., 1994; Ultsch, 1995].*

---

## Description

Two chains of rings. Detailed description of dataset and its clustering challenge is provided in [Thrun/Ultsch, 2020].

## Usage

```
data("Chainlink")
```

## Details

Size 1000, Dimensions 3, stored in Chainlink\$Data

Classes 2, stored in Chainlink\$Cls

## References

[Ultsch et al., 1994] Ultsch, A., Guimaraes, G., Korus, D., & Li, H.: Knowledge extraction from artificial neural networks and applications, *Parallele Datenverarbeitung mit dem Transputer*, (pp. 148-162), Springer, 1994.

[Ultsch, 1995] Ultsch, A.: Self organizing neural networks perform different from statistical k-means clustering, *Proc. Society for Information and Classification (GFKL)*, Vol. 1995, Basel 8th-10th March 1995.

[Thrun/Ultsch, 2020] Thrun, M. C., & Ultsch, A.: Clustering Benchmark Datasets Exploiting the Fundamental Clustering Problems, *Data in Brief*, Vol. 30(C), pp. 105501, [doi:10.1016/j.dib.2020.105501](https://doi.org/10.1016/j.dib.2020.105501), 2020.

## Examples

```
data(Chainlink)
str(Chainlink)
```

---

ClusterabilityMDplot *Clusterability MDplot*

---

## Description

Clusterability mirrored-density plot. Clusterability aims to quantify the degree of cluster structures [Adolfsson et al., 2019]. A dataset has a high probability to possess cluster structures, if the first component of the PCA projection is multimodal [Adolfsson et al., 2019]. As the dip test is less exact than the MDplot [Thrun et al., 2020], p-values above 0.05 can be given for MDplots which are clearly multimodal.

An alternative investigation of clusterability can be performed by inspecting the topographic map of the Generalized U-Matrix for a specific projection method using the **ProjectionBasedClustering** and **GeneralizedUmatrix** packages on CRAN, see [Thrun/Ultsch, 2021] for details.

## Usage

```
ClusterabilityMDplot(DataOrDistance, Method,
na.rm=FALSE, PlotIt=TRUE, ...)
```

## Arguments

DataOrDistance	Either a dataset[1:n,1:d] of n cases and d features or a symmetric distance matrix [1:d,1:d] or multiple data sets or distances in a list
Method	"none" performs no dimension reduction. "pca" uses the scores from the first principal component. "distance" computes pairwise distances (using distance_metric as the metric).
na.rm	Statistical testing will not work with missing values, if TRUE values are imputed with averages

PlotIt	TRUE: print plot, otherwise do not plot directly, instead use Handle for further adjustment
...	Further arguments for functionMDplot4multiplevectors of package <b>DataVisualizations</b> like "main", and "Ordering"

### Details

Use the method of [Adolfsson et al., 2019] specified as `pca` plus `dip-test` (PCA dip) per default without scaling or standardization of data because this step should never be done automatically. In [Thrun, 2020] the standardization and scaling did not improve the results.

If `list` is named, than the names of the list will be used and the MDplots will be re-ordered according to multimodality in the plot, otherwise only the pvalues of [Adolfsson et al., 2019] will be the names and the ordering of the MDplots is the same as the list.

Beware, as shown below, this test fails for almost touching clusters of Tetra and is difficult to interpret on WingNut but with overlaid with a robustly estimated unimodal Gaussian distribution it can be interpreted as multimodal). However, it does not fail for chaining data contrary to the claim in [Adolfsson et al., 2019].

Based on [Thrun, 2020], the author of this function disagrees with [Adolfsson et al., 2019] as to the preference which clusterability method should be used because the approach "distance" is not preferable for density-based cluster structures.

### Value

List of	
Handle	GGobject, plotter handle of <b>ggplot2</b>
Pvalue	One or more p-values of dip test depending on <code>DataOrDistance</code>

### Note

"none" seems to call `dip.test` in `clusterabilitytest` with high-dimensional data. In that case `dip.test` just vectorizes the matrix of the data which does not make any sense. Since this could be a bug, the "none" option should not be used.

Imputation does not work for distance matrices. Imputation is still experimental. It is advised to impute missing values before using this function

### Author(s)

Michael Thrun

### References

- [Adolfsson et al., 2019] Adolfsson, A., Ackerman, M., & Brownstein, N. C.: To cluster, or not to cluster: An analysis of clusterability methods, *Pattern Recognition*, Vol. 88, pp. 13-26, 2019.
- [Thrun et al., 2020] Thrun, M. C., Gehlert, T. & Ultsch, A.: Analyzing the Fine Structure of Distributions, *PLoS ONE*, Vol. 15(10), pp. 1-66, DOI [doi:10.1371/journal.pone.0238835](https://doi.org/10.1371/journal.pone.0238835), 2020.
- [Thrun/Ultsch, 2021] Thrun, M. C., and Ultsch, A.: Swarm Intelligence for Self-Organized Clustering, *Artificial Intelligence*, Vol. 290, pp. 103237, [doi:10.1016/j.artint.2020.103237](https://doi.org/10.1016/j.artint.2020.103237), 2021.

[Thrun, 2020] Thrun, M. C.: Improving the Sensitivity of Statistical Testing for Clusterability with Mirrored-Density Plot, in Archambault, D., Nabney, I. & Peltonen, J. (eds.), Machine Learning Methods in Visualisation for Big Data, The Eurographics Association, <https://diglib.eg.org:443/handle/10.2312/mlvis20201102>, Norrkoping, Sweden, May, 2020.

### See Also

[MDplot](#)

### Examples

```
##one dataset
data(Hepta)

ClusterabilityMDplot(Hepta$Data)

##multiple datasets
data(Atom)
data(Chainlink)
data(Lsun3D)
data(GolfBall)
data(EngyTime)
data(Target)
data(Tetra)
data(WingNut)
data(TwoDiamonds)

DataV = list(
  Atom = Atom$Data,
  Chainlink = Chainlink$Data,
  Hepta = Hepta$Data,
  Lsun3D = Lsun3D$Data,
  GolfBall = GolfBall$Data,
  EngyTime = EngyTime$Data,
  Target = Target$Data,
  Tetra = Tetra$Data,
  WingNut = WingNut$Data,
  TwoDiamonds = TwoDiamonds$Data
)

ClusterabilityMDplot(DataV)
```

---

ClusterApply

*Applies a function over grouped data*

---

### Description

Applies a given function to each dimension d of data separately for each cluster



**Usage**

```
ClusterApply(DataOrDistances,FUN,Cls,Simple=FALSE,...)
```

**Arguments**

DataOrDistances	[1:n,1:d] with: if d=n and symmetric then distance matrix assumed, otherwise: [1:n,1:d] matrix of defining the dataset that consists of n cases or d-dimensional data points. Every case has d attributes, variables or features.
FUN	Function to be applied to each cluster of data and each column of data
Cls	[1:n] numerical vector with n numbers defining the classification as the main output of the clustering algorithm. It has k unique numbers representing the arbitrary labels of the clustering.
Simple	Boolean, if TRUE, simplifies output
...	Additional parameters to be passed on to FUN

**Details**

Applies a given function to each feature of each cluster of data using the clustering stored in CIs which is the cluster identifiers for all rows in data. If missing, all data are in first cluster, The main output is FUNPerCluster[i] which is the result of FUN for the data points in cluster of UniqueClusters[i] named with the function's name used.

In case of a distance matrix an automatic classical multidimensional scaling transformation of distances to data is computed. Number of dimensions is selected by the minimal stress w.r.t. the possible output dimensions of cmdscale.

If FUN has not function name, then ResultPerCluster is given back.

**Value**

if(Simple==FALSE) List with

UniqueClusters The unique clusters in CIs

FUNPerCluster a matrix of [1:k,1:d] of d features and k clusters, the list element is named by the function FUN used

if(Simple==TRUE)

a matrix of [1:k,1:d] of d features and k clusters

**Author(s)**

Felix Pape, Michael Thrun

**Examples**

```

##one dataset
data(Hepta)
Data=Hepta$Data
Cls=Hepta$Cls
#mean per cluster
ClusterApply(Data,mean,Cls)

#Simplified
ClusterApply(Data,mean,Cls,Simple=TRUE)

# Mean per cluster of MDS transformation
# Beware, this is not the same!

ClusterApply(as.matrix(dist(Data)),mean,Cls)

## Not run:
Iris=datasets::iris
Distances=as.matrix(Iris[,1:4])
SomeFactors=Iris$Species
V=ClusterCreateClassification(SomeFactors)
Cls=V$Cls
V$ClusterNames
ClusterApply(Distances,mean,Cls)

## End(Not run)
#special case of identity
## Not run:
suppressPackageStartupMessages(library('prabclus',quietly = TRUE))
data(tetragonula)
#Generated Specific Distance Matrix
ta <- alleleconvert(strmatrix=as.matrix(tetragonula[1:236,]))
tai <- alleleinit(allelematrix=ta,distance="none")
Distance=alleledist((unbuild.charmatrix(tai$charmatrix,236,13)),236,13)

MDStrans=ClusterApply(Distance,identity)$identityPerCluster

## End(Not run)

```

---

ClusterChallenge

*Generates a Fundamental Clustering Challenge based on specific artificial datasets.*


---

**Description**

Lsun3D and FCPS datasets were introduced in various publications for a specific fixed size. This function generalizes them for any sample size.

**Usage**

```
ClusterChallenge(Name, SampleSize,
PlotIt=FALSE, PointSize=1, Plotter3D="rgl", ...)
```

**Arguments**

Name	string, either 'Atom', 'Chainlink', 'EngyTime', 'GolfBall', 'Hepta', 'Lsun3D', 'Target', 'Tetra', 'TwoDiamonds', 'WingNut'
SampleSize	Size of Sample higher than 300, preferable above 500
PlotIt	TRUE: Plots the challenge with <a href="#">ClusterPlotMDS</a>
PointSize	If PlotIt=TRUE: see <a href="#">ClusterPlotMDS</a>
Plotter3D	If PlotIt=TRUE: see <a href="#">ClusterPlotMDS</a>
...	If PlotIt=TRUE: further arguments for <a href="#">ClusterPlotMDS</a>

**Details**

A detailed description of the datasets can be found in [Thrun/Ultsch 2020]. Sampling works by combining Pareto Density Estimation with rejection sampling.

**Value**

LIST, with	
Name	[1:SampleSize, 1:d] data matrix
Cls	[1:SampleSize] numerical vector of classification

**Author(s)**

Michael Thrun

**References**

[Thrun/Ultsch, 2020] Thrun, M. C., & Ultsch, A.: Clustering Benchmark Datasets Exploiting the Fundamental Clustering Problems, Data in Brief, Vol. in press, pp. 105501, [doi:10.1016/j.dib.2020.105501](https://doi.org/10.1016/j.dib.2020.105501), 2020.

**See Also**

[ClusterPlotMDS](#)

**Examples**

```
## Not run:
ClusterChallenge("Chainlink", 2000, PlotIt=TRUE)

## End(Not run)
```

---

ClusterCount

*ClusterCount*


---

**Description**

Calculates statistics for clustering in each group of the data points

**Usage**

```
ClusterCount(Cls, Ordered=TRUE, NonFinite=9999)
```

**Arguments**

Cls	1:n numerical vector of numbers defining the classification as the main output of the clustering algorithm for the n cases of data. It has k unique numbers representing the arbitrary labels of the clustering.
Ordered	Optional, boolean, if TRUE: the output is ordered increasingly by cluster labels in UniqueClusters.
NonFinite	Optional, If non finite values are given in the numerical vector, they are set to the scalar value defined here

**Details**

The ordering of the output is defined by the first occurrence of every cluster label in CIs in the setting of Ordered=FALSE.

The function can be overloaded with non-numerical vectors. In this case, a cast via `as.character()` is applied to CIs, a warning is stated, and the statistics are still computed.

**Value**

UniqueClusters	[1:k] numerical vector of the k unique clusters in CIs
CountPerCluster	Named vector [1:k] with the number of data points in the corresponding unique clusters. Names are the UniqueClusters
NumberOfClusters	The number of clusters k
ClusterPercentages	[1:k] numerical vector of the percentages of datapoints belonging to a cluster for each cluster

**Author(s)**

Michael Thrun

**Examples**

```
data('Hepta')
Cls=Hepta$Cls
ClusterCount(Cls)
```

---

ClusterCreateClassification

*Create Classification for Cluster.. functions*

---

**Description**

Creates a Cls from arbitrary list of objects

**Usage**

```
ClusterCreateClassification(Objects,Decreasing)
```

**Arguments**

Objects	Listed objects, for example factor
Decreasing	Boolean that can be missing. If given, sorts ClusterNames with either decreasing or increasing.

**Details**

ClusterNames can be sorted before the classification stored Cls is created. See example.

**Value**

LIST, with

Cls [1:n] numerical vector with n numbers defining the labels of the classification. It has 1 to k unique numbers representing the arbitrary labels of the classification.

ClusterNames ClusterNames defined which names belongs to which unique number

**Author(s)**

Michael Thrun

**Examples**

```
## Not run:
Iris=datasets::iris
SomeFactors=Iris$Species
V=ClusterCreateClassification(SomeFactors)
Cls=V$Cls
V$ClusterNames
```

```

table(Cls,SomeFactors)

#Increasing alphabetical order
V=ClusterCreateClassification(SomeFactors,Decreasing=FALSE)
Cls=V$Cls
V$ClusterNames
table(Cls,SomeFactors)

## End(Not run)

```

---

ClusterDaviesBouldinIndex

*Davies Bouldin Index*


---

### Description

Internal (i.e. without prior classification) cluster quality measure called Davies Bouldin index for a given clustering published in [Davies/Bouldin, 1979].

### Usage

```
ClusterDaviesBouldinIndex(Cls, Data, ...)
```

### Arguments

Cls	[1:n] numerical vector of numbers defining the classification as the main output of the clustering algorithm for the n cases of data. It has k unique numbers representing the arbitrary labels of the clustering.
Data	matrix, [1:d,1:n] dataset of d variables and n cases
...	Further arguments passed on to the <a href="#">index.DB</a> function of clusterSim

### Details

Wrapper for [index.DB](#). Davies Bouldin index is defined in [Davies/Bouldin, 1979]. Best clustering scheme essentially minimizes the Davies-Bouldin index because it is defined as the function of the ratio of the within cluster scatter, to the between cluster separation.[Davies/Bouldin, 1979].

### Value

List of	
DaviesBouldinIndex	scalar,Davies Bouldin index
Object	further information stored in <a href="#">index.DB</a>

### Author(s)

Michael Thrun

## References

[Davies/Bouldin, 1979] Davies, D. L., & Bouldin, D. W.: A cluster separation measure, IEEE Transactions on Pattern Analysis and Machine Intelligence, Vol. 1(2), pp. 224-227. doi 10.1109/TPAMI.1979.4766909, 1979.

## Examples

```
data("Hepta")
Cls=kmeansClustering(Hepta$Data,ClusterNo = 7,Type="Hartigan")$Cls
ClusterDaviesBouldinIndex(Cls,Hepta$Data)[1]
```

```
data("Hepta")
ClsWellSeperated=kmeansClustering(Hepta$Data,ClusterNo = 7,Type="Steinley")$Cls
ClusterDaviesBouldinIndex(ClsWellSeperated,Hepta$Data)[1]
```

---

ClusterDendrogram	<i>Cluster Dendrogram</i>
-------------------	---------------------------

---

## Description

Presents a dendrogram of a given tree using a colorsequence for the branches defined from the highest cluster size to the lowest cluster size.

## Usage

```
ClusterDendrogram(TreeOrDendrogram, ClusterNo,
  Colorsequence,main='Name of Algorithm')
```

## Arguments

TreeOrDendrogram	Either object of hclust defining the tree, third list element of hierarchical cluster algorithms of this package or Object of class dendrogram, second list element of hierarchical cluster algorithms.
ClusterNo	k number of clusters for cutree.
Colorsequence	[1:k] character vector of colors, per default the colorsequence defined in the <b>DataVisualizations</b> is used
main	Title of plot

## Details

Requires the package **dendextend** to work correctly.

**Value**

In mode invisible:

[1:n] numerical vector defining the clustering of k clusters; this classification is the main output of the algorithm.

**Author(s)**

Michael Thrun

**See Also**

[cutree](#), [hclust](#)

**Examples**

```
data(Lsun3D)
listofh=HierarchicalClustering(Lsun3D$Data,0,'SingleL')
Tree=listofh$Object
#given colors are per default:
#"magenta" "yellow" "black" "red"
ClusterDendrogram(Tree, 4,main='Single Linkage Clustering')

listofh=HierarchicalClustering(Lsun3D$Data,4)
ClusterCount(listofh$Cls)
#c1 is magenta, c2 is red, c3 is yellow, c4 is black
#because the order of the cluster sizes is
#c1,c3,c4,c2
```

---

ClusterDistances

*ClusterDistances*

---

**Description**

Computes intra-cluster distances which are the distance in-between each cluster.

**Usage**

```
ClusterDistances(FullDistanceMatrix, Cls,
Names, PlotIt = FALSE)

ClusterIntraDistances(FullDistanceMatrix, Cls,
Names, PlotIt = FALSE)
```



**Arguments**

FullDistanceMatrix	[1:n,1:n] symmetric distance matrix
Cls	[1:n] numerical vector of k classes
Names	Optional [1:k] character vector naming k classes
PlotIt	Optional, Plots if TRUE

**Details**

Cluster distances are given back as a matrix, one column per cluster and the vector of the full distance matrix without the diagonal elements and the upper half of the symmetric matrix. Details and definitions can be found in [Thrun, 2021].

**Value**

Matrix [1:m,1:(k+1)] of k clusters, each column consists of the distances in a cluster, filled up with NaN at the end to be of the same length as the vector of the upper triangle of the complete distance matrix.

**Author(s)**

Michael Thrun

**References**

[Thrun, 2021] Thrun, M. C.: The Exploitation of Distance Distributions for Clustering, International Journal of Computational Intelligence and Applications, Vol. 20(3), pp. 2150016, DOI: [doi:10.1142/S1469026821500164](https://doi.org/10.1142/S1469026821500164), 2021.

**See Also**

[MDplot](#)

[ClusterInterDistances](#)

**Examples**

```
data(Hepta)
Distance=as.matrix(dist(Hepta$Data))

interdists=ClusterDistances(Distance,Hepta$Cls)
```

---

ClusterDunnIndex      *Dunn Index*

---

### Description

Internal (i.e. without prior classification) cluster quality measure called Dunn index for a given clustering published in [Dunn, 1974].

### Usage

```
ClusterDunnIndex(Cls,DataOrDistances,
DistanceMethod="euclidean",Silent=TRUE,Force=FALSE,...)
```

### Arguments

Cls	[1:n] numerical vector of numbers defining the classification as the main output of the clustering algorithm for the n cases of data. It has k unique numbers representing the arbitrary labels of the clustering.
DataOrDistances	matrix, DataOrDistance[1:n,1:n] symmetric matrix of dissimilarities, if variable unsymmetric DataOrDistance[1:d,1:n] is assumed as a dataset and the euclidean distances are calculated of d variables and n cases
DistanceMethod	Optional, one of 39 distance methods of parDist of package parallelDist, if Data matrix is chosen above
Silent	TRUE: Warnings are shown
Force	TRUE: force computing in case of numerical instability
...	Further arguments passed on to the parDist function, e.g. user_defined distance functions

### Details

Dunn index is defined as  $Dunn = \min(InterDist) / \max(IntraDist)$ . Well separated clusters have usually a dunn index above 1, for details please see [Dunn, 1974].

### Value

List of	
Dunn	scalar, Dunn Index
IntraDist	[1:k] numerical vector of minimal intra cluster distances per given cluster
InterDist	[1:k] numerical vector of minimal inter cluster distances per given cluster

### Author(s)

Michael Thrun

## References

[Dunn, 1974] Dunn, J. C.: Well\_separated clusters and optimal fuzzy partitions, Journal of cybernetics, Vol. 4(1), pp. 95-104. 1974.

## Examples

```
data("Hepta")
Cls=kmeansClustering(Hepta$Data,ClusterNo = 7,Type="Hartigan")$Cls
ClusterDunnIndex(Cls,Hepta$Data)
```

```
data("Hepta")
ClsWellSeperated=kmeansClustering(Hepta$Data,ClusterNo = 7,Type="Steinley")$Cls
ClusterDunnIndex(ClsWellSeperated,Hepta$Data)
```

---

ClusterEqualWeighting *ClusterEqualWeighting*

---

## Description

Weights clusters equally

## Usage

```
ClusterEqualWeighting(Cls, Data, MinClusterSize)
```

## Arguments

Cls	1:n numerical vector of numbers defining the classification as the main output of the clustering algorithm for the n cases of data. It has k unique numbers representing the arbitrary labels of the clustering.
Data	Optional, [1:n,1:d] matrix of dataset consisting of n cases of d-dimensional data points. Every case has d attributes, variables or features.
MinClusterSize	Optional, scalar defining the number of cases m that each cluster should have

## Details

Balance clusters such that their sizes are the same by subsampling the larger cluster. If `MinClusterSize` is missing the number of cases per cluster is set to the smallest cluster size. For clusters sizes smaller than `MinClusterSize`, sampling with replacement is turned on, i.e. up sampling. For clusters sizes equal to `MinClusterSize`, no sampling is performed.

**Value**

List of

BalancedCls	Vector of Cls such that all clusters have the same sizes spezified by MinClusterSize
BalancedInd	index such that BalancedCls = Cls[BalancedInd]
BalancedData	NULL if missing, otherwise, Data[BalancedInd,]

**Author(s)**

Alfred Ultsch (matlab), reimplemented by Michael Thrun

**Examples**

```
data(Hepta)
ClusterEqualWeighting(Hepta$Cls,Hepta$Data,5)
```

---

ClusteringAccuracy      *ClusterAccuracy*

---

**Description**

ClusterAccuracy

**Usage**

```
ClusterAccuracy(PriorCls,CurrentCls,K=9)
```

**Arguments**

PriorCls	Ground truth,[1:n] numerical vector with n numbers defining the classification. It has k unique numbers representing the arbitrary labels of the clustering.
CurrentCls	Main output of the clustering, [1:n] numerical vector with n numbers defining the classification. It has k unique numbers representing the arbitrary labels of the clustering.
K	Maximal number of classes for computation.

**Details**

Here, accuracy is defined as the normalized sum over all true positive labeled data points of a clustering algorithm. The best of all permutation of labels with the highest accuracy is selected in every trial because algorithms arbitrarily define the labels [Thrun et al., 2018]. Beware that in contrast to [ClusterMCC](#), the labels can be arbitrary. However, accuracy is a only a valid quality measure if the clusters are balanced (of) nearly equal size). Ohterwise please use [ClusterMCC](#).

In contrast to the F-measure, "Accuracy tends to be naturally unbiased, because it can be expressed in terms of a binomial distribution: A success in the underlying Bernoulli trial would be defined as sampling an example for which a classifier under consideration makes the right prediction. By

definition, the success probability is identical to the accuracy of the classifier. The i.i.d. assumption implies that each example of the test set is sampled independently, so the expected fraction of correctly classified samples is identical to the probability of seeing a success above. Averaging over multiple folds is identical to increasing the number of repetitions of the Binomial trial. This does not affect the posterior distribution of accuracy if the test sets are of equal size, or if we weight each estimate by the size of each test set." [Forman/Scholz, 2010]

**Value**

Single scalar of Accuracy between zero and one

**Author(s)**

Michael Thrun

**References**

[Thrun et al., 2018] Michael C. Thrun, Felix Pape, Alfred Ultsch: Benchmarking Cluster Analysis Methods in the Case of Distance and Density-based Structures Defined by a Prior Classification Using PDE-Optimized Violin Plots, ECDA, Potsdam, 2018

[Forman/Scholz, 2010] Forman, G., and Scholz, M.: Apples-to-apples in cross-validation studies: pitfalls in classifier performance measurement, ACM SIGKDD Explorations Newsletter, Vol. 12(1), pp. 49-57. 2010.

**See Also**

[ClusterMCC](#)

**Examples**

```
#Influence of random sets/ random starts on k-means

data('Hepta')
Cls=kmeansClustering(Hepta$Data,7,Type = "Hartigan",nstart=1)
table(Cls$Cls,Hepta$Cls)
ClusterAccuracy(Hepta$Cls,Cls$Cls)

data('Hepta')
Cls=kmeansClustering(Hepta$Data,7,Type = "Hartigan",nstart=100)
table(Cls$Cls,Hepta$Cls)
ClusterAccuracy(Hepta$Cls,Cls$Cls)
```

---

**ClusterInterDistances** *Computes Inter-Cluster Distances*

---

**Description**

Computes inter-cluster distances which are the distance between each cluster and all other clusters

**Usage**

```
ClusterInterDistances(FullDistanceMatrix, Cls,  
Names,PlotIt=FALSE)
```

**Arguments**

FullDistanceMatrix	[1:n,1:n] symmetric distance matrix
Cls	[1:n] numerical vector of numbers defining the classification as the main output of the clustering algorithm for the n cases of data. It has k unique numbers representing the arbitrary labels of the clustering.
Names	Optional [1:k] character vector naming k classes
PlotIt	Optional, Plots if TRUE

**Details**

Cluster distances are given back as a matrix, one column per cluster and the vector of the full distance matrix without the diagonal elements and the upper half of the symmetric matrix. Details and definitons can be found in [Thrun, 2021].

**Value**

Matrix [1:m,1:(k+1)] of k clusters, each columns consists of the distances between a cluster and all other clusters, filled up with NaN at the end to be of the same lenght as the vector of the upper triangle of the complete distance matrix.

**Author(s)**

Michael Thrun

**References**

[Thrun, 2021] Thrun, M. C.: The Exploitation of Distance Distributions for Clustering, International Journal of Computational Intelligence and Applications, Vol. 20(3), pp. 2150016, DOI: [doi:10.1142/S1469026821500164](https://doi.org/10.1142/S1469026821500164), 2021.

**See Also**[MDplot](#)

ClusterDistances

**Examples**

```

data(Hepta)
Distance=as.matrix(dist(Hepta$Data))

interdists=ClusterInterDistances(Distance,Hepta$Cls)

```

ClusterMCC

*Matthews Correlation Coefficient (MCC)***Description**

Matthews correlation coefficient eneralized to the multiclass case (a.k.a. R\_K statistic).

**Usage**

```
ClusterMCC(PriorCls, CurrentCls,Force=TRUE)
```

**Arguments**

PriorCls	Ground truth,[1:n] numerical vector with n numbers defining the classification. It has k unique numbers representing the labels of the clustering.
CurrentCls	Main output of the clustering, [1:n] numerical vector with n numbers defining the classification. It has k unique numbers representing the labels of the clustering.
Force	Boolean, if is TRUE: forces code even if one or more than one of the k numbers given in PriorCls is missing in CurrentCls or vice versa. In this case, one label per missing number is added ad the end of the vectors.

**Details**

Contrary to accuracy, the MCC is balanced measure which can be used even if the classes are of very different sizes. When there are more than two labels the MCC will no longer range between -1 and +1. Instead the minimum value will be between -1 and 0 depending on the true distribution. The maximum value is always +1. Beware that in contrast to [ClusterAccuracy](#), the labels cannot be arbitrary. Instead each label of PriorCls and CurrentCls has to be mapped to the same cluster of data points. Typically this has to be ensured manually.

**Value**

Single scalar of MCC in a range described in details.

**Note**

If No. of Clusters is not equivalent, internally the number is alligned with zero datapoints belonging to the missing clusters.

**Author(s)**

Michael Thrun

**References**

Matthews, B. W.: Comparison of the predicted and observed secondary structure of T4 phage lysozyme, *Biochimica et Biophysica Acta (BBA), Protein Structure*, Vol. 405(2), pp. 442-451, 1975.

Boughorbel, S.B: Optimal classifier for imbalanced data using Matthews Correlation Coefficient metric, *PLOS ONE*, Vol. 12(6), pp. e0177678, 2017.

Chicco, D.; Toetsch, N. and Jurman, G.: The Matthews correlation coefficient (MCC) is more reliable than balanced accuracy, bookmaker informedness, and markedness in two\_class confusion matrix evaluation. *BioData Mining*. Vol. 14., 2021.

**See Also**

[ClusterAccuracy](#)

**Examples**

```
#Beware that algorithm arbitrary defines the labels
data(Hepta)
V=kmeansClustering(Hepta$Data,Type = "Hartigan",7)
table(V$Cls,Hepta$Cls)
#result is only valid if the above issue is resolved manually
ClusterMCC(Hepta$Cls,V$Cls)
```

---

ClusterNoEstimation     *Estimates Number of Clusters using up to 26 Indicators*

---

**Description**

Calculation of up to 26 indicators and the recommendations based on them for the number of clusters in data sets. For a given dataset and clusterings for this dataset, key indicators mentioned in details are calculated and based on this a recommendation regarding the number of clusters is given for each indicator.

An alternative estimation of the cluster number can be done by counting the valleys of the topographic map of the generalized U-Matrix for a specific projection method using the **ProjectionBasedClustering** and **GeneralizedUmatrix** packages on CRAN, see [Thrun/Ultsch, 2021] for details.



**Usage**

```
ClusterNoEstimation(DataOrDistances, ClsMatrix = NULL, MaxClusterNo,
ClusterIndex = "all", Method = NULL, MinClusterNo = 2,
Silent = TRUE, PlotIt=FALSE, SelectByABC=TRUE, Colorsequence, ...)
```

**Arguments**

DataOrDistances	Either [1:n,1:d] matrix of dataset to be clustered. It consists of n cases of d-dimensional data points. Every case has d attributes, variables or features. or Symmetric [1:n,1:n] distance matrix
ClsMatrix	[1:n,1:(MaxClusterNo)] matrix of clusterings each columns is defined as: 1:n numerical vector of numbers defining the classification as the main output of the clustering algorithm for the n cases of data. It has k unique numbers representing the arbitrary labels of the clustering. (see also details (2) and (3)), must be specified if method = NULL
MaxClusterNo	Highest number of clusters to be checked
Method	Cluster procedure, with which the clusterings are created (see details (4) for possible methods), must be specified if ClsMatrix = NULL
Optional:	
ClusterIndex	String or vector of strings with the indicators to be calculated (see details (1)), default = "all"
MinClusterNo	Lowest number of clusters to be checked, default = 2
Silent	If TRUE status messages are output, default = FALSE
PlotIt	If TRUE plots fanplot with proposed cluster numbers
SelectByABC	If PlotIt=TRUE, TRUE: Plots group A of ABCanalysis of the most important ones (highest overlap in indicators), FALSE: plots all indicators
Colorsequence	Optional, character vector of sufficient length of colors for the fan plot.If the sequence is too long the first part of the sequence is used.
...	Optional, further arguents used if clustering methods if Method is set.

**Details**

Each column of ClsMatrix has to have at least two unqiue clusters defined. Otherwise the function will stop.

(1)

The following 26 indicators can be calculated: "ball", "beale", "calinski", "ccc", "cindex", "db", "duda", "dunn", "frey", "friedman", "hartigan", "kl", "marriot", "mcclain", "pseudot2", "ptbiserial", "ratkowsky", "rubin", "scott", "sdbw", "sdindex", "silhouette", "ssi", "tracew", "trcovw", "xuindex".

These can be specified individually or as a vector via the parameter index. If you enter 'all', all key figures are calculated.

(2)

The indicators kl, duda, pseudot2, beale, frey and mclain require a clustering for MaxClusterNo+1 clusters. If these key figures are to be calculated, this clustering must be specified in cls.

(3)

The indicator kl requires a clustering for MinClusterNo-1 clusters. If this key figure is to be calculated, this clustering must also be specified in cls. For the case MinClusterNo = 2 no clustering for 1 has to be given.

(4)

The following methods can be used to create clusterings:

"kmeans," "DBSclustering", "DivisiveAnalysisClustering", "FannyClustering", "ModelBasedClustering", "SpectralClustering" or all methods found in [HierarchicalClustering](#).

(5)

The indicators duda, pseudot2, beale and frey are only intended for use in hierarchical cluster procedures.

If a distances matrix is given, then **ProjectionBasedClustering** is required to be accessible.

### Value

Indicators	A table of the calculated indicators except Duda, Pseudot2 and Beale
ClusterNo	The recommended number of clusters for each calculated indicator
ClsMatrix	[1:n,MinClusterNo:(MaxClusterNo)] Output of the clusterings used for the calculation
HierarchicalIndicators	Either NULL or the values for the indicators Duda, Pseudot2 and Beale in case of hierarchical cluster procedures, if calculated

### Note

Code of "calinski", "cindex", "db", "hartigan", "ratkowsky", "scott", "marriot", "ball", "trcovw", "tracew", "friedman", "rubin", "ssi" of package cclust ist adapted for the purpose of this function.

Colorsequence works if **DataVisualizations** 1.1.13 is installed (currently only on github available).

### Author(s)

Peter Nahrgang, revised by Michael Thrun (2021)

### References

Charrad, Malika, et al. "Package 'NbClust', J. Stat. Soft Vol. 61, pp. 1-36, 2014.

Dimtriadou, E. "cclust: Convex Clustering Methods and Clustering Indexes." R package version 0.6-16, URL <https://CRAN.R-project.org/package=cclust>, 2009.

[Thrun/Ultsch, 2021] Thrun, M. C., and Ultsch, A.: Swarm Intelligence for Self-Organized Clustering, Artificial Intelligence, Vol. 290, pp. 103237, doi:10.1016/j.artint.2020.103237, 2021.

**Examples**

```

# Reading the iris dataset from the standard R-Package datasets
data <- as.matrix(iris[,1:4])
MaxClusterNo = 7
# Creating the clusterings for the data set
#(here with method complete) for the number of clusters 2 to 8
hc <- hclust(dist(data), method = "complete")
clsm <- matrix(data = 0, nrow = dim(data)[1],

ncol = MaxClusterNo)
for (i in 2:(MaxClusterNo+1)) {
  clsm[,i-1] <- cutree(hc,i)
}

# Calculation of all indicators and recommendations for the number of clusters
indicatorsList=ClusterNoEstimation(Data = data,

ClsMatrix = clsm, MaxClusterNo = MaxClusterNo)

# Alternatively, the same calculation as above can be executed with the following call
ClusterNoEstimation(Data = data, MaxClusterNo = 7, Method = "CompleteL")
# In this variant, the function clusternumbers also takes over the clustering

```

---

ClusterNormalize

*Cluster Normalize*


---

**Description**

Values in Cls are consistently recoded to positive consecutive integers

**Usage**

```
ClusterNormalize(Cls)
```

**Arguments**

Cls [1:n numerical vector of numbers defining the classification as the main output of the clustering algorithm for the n cases of data. It has k unique numbers representing the arbitrary labels of the clustering.

**Details**

For recoding depending on cluster size please see [ClusterRenameDescendingSize](#).

**Value**

The renamed classification. A vector of clusters recoded to positive consecutive integers.

**Author(s)**

.

**See Also**[ClusterRenameDescendingSize](#)**Examples**

```

data('Lsun3D')
Cls=Lsun3D$Cls
#not descending cluster numbers
Cls[Cls==1]=543
Cls[Cls==4]=1

# Now ordered consecutively
ClusterNormalize(Cls)

```

ClusterPlotMDS

*Plot Clustering using Dimensionality Reduction by MDS***Description**

This function uses a projection method to perform dimensionality reduction (DR) on order to visualize the data as 3D data points colored by a clustering.

**Usage**

```

ClusterPlotMDS(DataOrDistances, Cls, main = "Clustering",
DistanceMethod = "euclidean", OutputDimension = 3,
PointSize=1,Plotter3D="rgl",Colorsequence, ...)

```

**Arguments**

DataOrDistances	Either nonsymmetric [1:n,1:d] datamatrix of n cases and d features or symmetric [1:n,1:n] distance matrix
Cls	1:n numerical vector of numbers defining the classification as the main output of the clustering algorithm for the n cases of data. It has k unique numbers representing the arbitrary labels of the clustering.
main	String, title of plot
DistanceMethod	Method to compute distances, default "euclidean"
OutputDimension	Either two or three depending on user choice

PointSize	Scalar defining the size of points
Plotter3D	In case of 3 dimensions, choose either "plotly" or "rgl",
Colorsequence	[1:k] character vector of colors, per default the colorsquence defined in the <b>DataVisualizations</b> is used
...	Please see <a href="#">Plot3D</a> in <b>DataVisualizations</b>

### Details

If dataset has more than 3 dimensions, mds is performed as defined in the **smacof** [De Leeuw/Mair, 2011]. If **smacof** package is not installed, classical metric MDS (see Def. in [Thrun, 2018]) is performed. In both cases, the first OutputDimension are visualized. Points are colored by the labels (Cls).

In the special case that the dataset has not more than 3 dimensions, all dimensions are visualized and no DR is performed.

### Value

The rgl or plotly plot handler depending on Plotter3D

### Note

If **DataVisualizations** is not installed a 2D plot using native plot function is shown.

If **MASS** is not installed, classical metric MDS is used, see [Thrun, 2018] for definition.

### Author(s)

Michael Thrun

### References

[De Leeuw/Mair, 2011] De Leeuw, J., & Mair, P.: Multidimensional scaling using majorization: SMACOF in R, Journal of statistical Software, Vol. 31(3), pp. 1-30. 2011.

[Thrun, 2018] Thrun, M. C.: Projection Based Clustering through Self-Organization and Swarm Intelligence, doctoral dissertation 2017, Springer, ISBN: 978-3-658-20539-3, Heidelberg, 2018.

### See Also

[Plot3D](#)

### Examples

```
data(Hepta)
ClusterPlotMDS(Hepta$Data,Hepta$Cls)
```

```
data(Leukemia)
ClusterPlotMDS(Leukemia$DistanceMatrix,Leukemia$Cls)
```

---

ClusterRedefine      *Redefines Clustering*

---

### Description

Redefines some or all Clusters of Clustering such that the names of the numerical vectors are defined by

### Usage

```
ClusterRedefine(Cls, NewLabels, OldLabels)
```

### Arguments

Cls	1:n numerical vector of numbers defining the classification as the main output of the clustering algorithm for the n cases of data. It has k unique numbers representing the arbitrary labels of the clustering.
NewLabels	[1:p], p<=k labels (identifiers) of clusters to be changed with
OldLabels	Optional, [1:p], p<=k labels(identifiers) of clusters to be changed, default [1:k] unique cluster Ids of Cls

### Details

The same ordering of NewLabels and OldLabels is assumed, i.e., the mapping is defined by OldLabels[i] -> NewLabels[i] with i in [1:p]. NewLabels can also be a vector for strings, for example for plotting.

### Value

Cls[1:n] numerical vector named after the row names of data

### Author(s)

Michael Thrun

### Examples

```
data('Lsun3D')
Cls=Lsun3D$Cls
Data=Lsun3D$Data#
#prior
ClsNew=unique(Cls)+10
#Redfined Clustering
NewCls=ClusterRedefine(Cls,ClsNew)

table(Cls,NewCls)

#require(DataVisualizations)
```

```

n=length(unique(Cls))
NewCls=ClusterRedefine(Cls,LETTERS[1:n])
#DataVisualizations package required
if(requireNamespace("DataVisualizations"))
  DataVisualizations::Classplot(Data[,1],Data[,2],
  Cls,Names=NewCls,Plotter="ggplot",Size =1.5)

```

---

ClusterRename

*Renames Clustering*


---

### Description

Renames Clustering such that the names of the numerical vectors are the row names of DataOrDistances

### Usage

```
ClusterRename(Cls, DataOrDistances)
```

### Arguments

Cls	1:n numerical vector of numbers defining the classification as the main output of the clustering algorithm for the n cases of data. It has k unique numbers representing the arbitrary labels of the clustering.
DataOrDistances	Either nonsymmetric [1:n,1:d] datamatrix of n cases and d features or symmetric [1:n,1:n] distance matrix

### Details

If DataOrDistances is missing or if inconsistent length, nothing is done.

### Value

Cls[1:n] numerical vector named after the row names of data

### Author(s)

Michael Thrun

### Examples

```

data('Hepta')
Cls=Hepta$Cls
Data=Hepta$Data#
#prior
Cls
#Named Clustering
ClusterRename(Cls,Data)

```

---

ClusterRenameDescendingSize  
*Cluster Rename Descending Size*

---

### Description

Renames the clusters of a classification in descending order.

### Usage

```
ClusterRenameDescendingSize(Cls,  

  ProvideClusterNames=FALSE)
```

### Arguments

**Cls** [1:n numerical vector of numbers defining the classification as the main output of the clustering algorithm for the n cases of data. It has k unique numbers representing the arbitrary labels of the clustering.

**ProvideClusterNames**  
 TRUE: Provides in separate output new and old k numbers, FALSE: simple output

### Details

Beware: output changes in this function depending on ProvideClusterNames in order to be congruent to prior code in a large variety of other packages.

### Value

ProvideClusterNames==FALSE:

**RenamedCls** The renamed classification. A vector of clusters, were the largest cluster is C1 and so forth

ProvideClusterNames==TRUE: List V with

**RenamedCls** The renamed classification. A vector of clusters, were the largest cluster is C1 and so forth

**ClusterName** [1:k,1:2] matrix of k new numbers and prior numbers

### Author(s)

Michael Thrun, Alfred Ultsch

### See Also

[ClusterNormalize](#)



**Examples**

```

data('Lsun3D')
Cls=Lsun3D$Cls
#not descending cluster numbers
Cls[Cls==1]=543
Cls[Cls==4]=1

# Now ordered per cluster size and descending
ClusterRenameDescendingSize(Cls)

```

---

ClusterShannonInfo      *Shannon Information*

---

**Description**

Shannon Information [Shannon, 1948] for each column in ClsMatrix.

**Usage**

```
ClusterShannonInfo(ClsMatrix)
```

**Arguments**

**ClsMatrix**      [1:n,1:C] matrix of C clusterings each columns is defined as:  
 1:n numerical vector of numbers defining the classification as the main output of the clustering algorithm for the n cases of data. It has k unique numbers representing the arbitrary labels of the clustering.

**Details**

$\text{Info}[1:d] = \sum(-p * \log(p)/\text{MaxInfo})$  for all unique cases with probability p in ClsMatrix[,c] for a column with k clusters  $\text{MaxInfo} = -(1/k)*\log(1/k)$

**Value**

**Info**      [1:max.nc,1:C] matrix of Shannin informaton as defined in details, each column represents one Cls of ClsMatrix,each row yields the information of one cluster up the ClusterNo k, if k<max.nc (highest number of clusters) then NaN are filled.

**ClusterNo**      Number of Clusters k found for each Cls respectively

**MaxInfo**      max per column of Info

**MinInfo**      min per column of Info

**MedianInfo**      median per column of Info

**MeanInfo**      mean per column of Info

**Note**

reimplemented from Alfred's Ultsch Matlab version but not verified yet.

**Author(s)**

Michael Thrun

**References**

[Shannon, 1948] Shannon, C. E.: A Mathematical Theory of Communication, Bell System Technical Journal, Vol. 27(3), pp. 379-423. doi doi:10.1002/j.1538-7305.1948.tb01338.x, 1948.

**Examples**

```
# Reading the iris dataset from the standard R-Package datasets
data <- as.matrix(iris[,1:4])
max.nc = 7
# Creating the clusterings for the data set
#(here with method complete) for the number of classes 2 to 8
hc <- hclust(dist(data), method = "complete")
clsm <- matrix(data = 0, nrow = dim(data)[1],

ncol = max.nc)
for (i in 2:(max.nc+1)) {
  clsm[,i-1] <- cutree(hc,i)
}

ClusterShannonInfo(clsm)
```

---

ClusterUpsamplingMinority

*Cluster Up Sampling using SMOTE for minority cluster*

---

**Description**

Wrapper for one specific internal function of L. Torgo who implemented there the relevant part of the SMOTE algorithm [Chawla et al., 2002].

**Usage**

```
ClusterUpsamplingMinority(Cls, Data, MinorityCluster,

Percentage = 200, knn = 5, PlotIt = FALSE)
```

**Arguments**

Cls	1:n numerical vector of numbers defining the classification as the main output of the clustering algorithm for the n cases of data. It has k unique numbers representing the arbitrary labels of the clustering.
Data	[1:n,1:d] datamatrix of n cases and d features
MinorityCluster	scalar defining the number of the cluster to be upsampeled
Percentage	percentage above 100 of who many samples should be taken
knn	k nearest neighbors of SMOTE algorithm
PlotIt	TRUE: plots the result using <a href="#">ClusterPlotMDS</a>

**Details**

the number of items m is defined by the scalar Percentage and the up sampling is combined with the Data and the Cls to DataExt and ClsExt such that the sample is placed thereafter.

**Value**

List with	
ClsExt	1:(n+m) numerical vector of numbers defining the classification as the main output of the clustering algorithm for the n cases of data. It has k unique numbers representing the arbitrary labels of the clustering.
DataExt	[1:(n+m),1:d] datamatrix of n cases and d features

**Author(s)**

L. Torgo

**References**

[Chawla et al., 2002] Chawla, N. V., Bowyer, K. W., Hall, L. O., & Kegelmeyer, W. P.: SMOTE: synthetic minority over-sampling technique, Journal of artificial intelligence research, Vol. 16, pp. 321-357. 2002.

**Examples**

```
data(Lsun3D)
Data=Lsun3D$Data
Cls=Lsun3D$Cls
table(Cls)

V=ClusterUpsamplingMinority(Cls,Data,4,1000)
table(V$ClsExt)
```

---

 CrossEntropyClustering

*Cross-Entropy Clustering*


---

### Description

Cross-entropy clustering published by [Tabor/Spurek, 2014] and implemented by [Spurek et al., 2017].

### Usage

```
CrossEntropyClustering(Data, ClusterNo, PlotIt=FALSE, ...)
```

### Arguments

Data	[1:n,1:d] matrix of dataset to be clustered. It consists of n cases of d-dimensional data points. Every case has d attributes, variables or features.
ClusterNo	A number k which defines k different clusters to be built by the algorithm.
PlotIt	Default: FALSE, If TRUE plots the first three dimensions of the dataset with colored three-dimensional data points defined by the clustering stored in Cls
...	Further arguments to be set for the clustering algorithm, if not set, default arguments are used.

### Details

Contrary to most of the other implemented algorithms in this package, the results on the easiest clustering challenge of Hepta are unstable for cross-entropy clustering in the sense that the clustering is not always correct. Reproducibility experiments should be performed (see [Tabor/Spurek, 2014]).

### Value

List of	
Cls	[1:n] numerical vector with n numbers defining the classification as the main output of the clustering algorithm. It has k unique numbers representing the arbitrary labels of the clustering.
Object	Object defined by clustering algorithm as the other output of this algorithm

### Author(s)

Michael Thrun

## References

[Spurek et al., 2017] Spurek, P., Kamieniecki, K., Tabor, J., Misztal, K., & Śmieja, M.: R package cec, Neurocomputing, Vol. 237, pp. 410-413. 2017.

[Tabor/Spurek, 2014] Tabor, J., & Spurek, P.: Cross-entropy clustering, Pattern Recognition, Vol. 47(9), pp. 3046-3059. 2014.

## Examples

```
data('Hepta')
out=CrossEntropyClustering(Hepta$Data,ClusterNo=7,PlotIt=FALSE)
```

---

DBSCAN

*DBSCAN*

---

## Description

Density-Based Spatial Clustering of Applications with Noise of [Ester et al., 1996].

## Usage

```
DBSCAN(Data,Radius,minPts,Rcpp=TRUE,
PlotIt=FALSE,UpperLimitRadius,...)
```

## Arguments

Data	[1:n,1:d] matrix of dataset to be clustered. It consists of n cases of d-dimensional data points. Every case has d attributes, variables or features.
Radius	Eps [Ester et al., 1996, p. 227] neighborhood in the R-ball graph/unit disk graph), size of the epsilon neighborhood. If NULL, automatic estimation is performed using insights of [Ultsch, 2005].
minPts	Number of minimum points in the eps region (for core points). In principle minimum number of points in the unit disk, if the unit disk is within the cluster (core) [Ester et al., 1996, p. 228]. If NULL, 2.5 percent of points is selected.
Rcpp	If TRUE: fast Rcpp implementation of mlpack is used. FALSE uses dbscan package.
PlotIt	Default: FALSE, If TRUE plots the first three dimensions of the dataset with colored three-dimensional data points defined by the clustering stored in Cls
UpperLimitRadius	Limit for radius search, experimental
...	Further arguments to be set for the clustering algorithm, if not set, default arguments are used.



```

        BestAcc[i] = 50
    }
    max(BestAcc)
    which.max(BestAcc)
    parameters <- DBSGrid[13,]

    Cls9 = DBSCAN(
        Data,
        minPts = parameters$minPTs,
        Radius = parameters$Radius,
        UpperLimitRadius = parameters$Radius,
        PlotIt = TRUE
    )$Cls

    ## End(Not run)

```

---

DBScusteringAndVisualization

*Databionic Swarm (DBS) Clustering and Visualization*

---

### Description

Swarm-based clustering by exploiting self-organization, emergence, swarm intelligence and game theory published in [Thrun/Ultsch, 2021].

### Usage

```

DatabionicSwarmClustering(DataOrDistances, ClusterNo = 0,
    StructureType = TRUE, DistancesMethod = NULL,
    PlotTree = FALSE, PlotMap = FALSE, PlotIt=FALSE,
    Parallel = FALSE)

```

### Arguments

DataOrDistances	Either nonsymmetric [1:n,1:d] numerical matrix of a dataset to be clustered. It consists of n cases of d-dimensional data points. Every case has d attributes, variables or features. or symmetric [1:n,1:n] distance matrix, e.g. as <code>matrix(dist(Data,method))</code>
ClusterNo	Number of Clusters, if zero a the topographic map is plotted. Number of valleys equals number of clusters.
StructureType	Either TRUE or FALSE, has to be tested against the visualization. If colored points of clusters a divided by mountain ranges, parameter is incorrect.

DistancesMethod	Optional, if data matrix given, anonon Euclidean distance can be selected
PlotTree	Optional, if TRUE: dendrogram is plotted.
PlotMap	Optional, if TRUE: topographic map is plotted if <b>GeneralizedUmatrix</b> is installed.
PlotIt	Default: FALSE, If TRUE and dataset of [1:n,1:d] dimensions then a plot of the first three dimensions of the dataset with colored three-dimensional data points defined by the clustering stored in Cls will be generated.
Parallel	FALSE: default implementation, TRUE faster Cpp parallel implementation, for this the subsequent packages have to be installed from github, as they are not available on CRAN yet.

### Details

This function does not enable the user first to project the data and then to test the Boolean parameter defining the type of structure contrary to the **DatabionicSwarm** which is an inappropriate approach in case of exploratory data analysis.

Instead, this function is implemented for the purpose of automatic benchmarking because in such a case nobody will investigate many trials with one visualization per trial.

If one would like to perform a clustering exploratively (in the sense that a prior clustering is not given for evaluation purposes), then please use the **DatabionicSwarm** package directly and read the vignette there. Databionic swarm is like k-means a stochastic algorithm meaning that the clustering and visualization may change between trials.

### Value

List of	
Cls	1:n numerical vector of numbers defining the classification as the main output of the clustering algorithm for the n cases of data. It has k unique numbers representing the arbitrary labels of the clustering.
Object	List of further output of DBS

### Note

Current implementation is not efficient enough to cluster more than N=4000 cases as in that case it takes longer than a day for a result.

### Author(s)

Michael Thrun

### References

[Thrun/Ultsch, 2021] Thrun, M. C., and Ultsch, A.: Swarm Intelligence for Self-Organized Clustering, Artificial Intelligence, Vol. 290, pp. 103237, doi:10.1016/j.artint.2020.103237, 2021.



[Thrun/Ultsch, 2021] Thrun, M. C., & Ultsch, A.: Swarm Intelligence for Self-Organized Clustering (Extended Abstract), in Bessiere, C. (Ed.), 29th International Joint Conference on Artificial Intelligence (IJCAI), Vol. IJCAI-20, pp. 5125–5129, doi:10.24963/ijcai.2020/720, Yokohama, Japan, Jan., 2021.

### See Also

[Pswarm](#), [DBScustering](#), [GeneratePswarmVisualization](#)

### Examples

```
# Generate random but small non-structured data set
data = cbind(
  sample(1:100, 300, replace = TRUE),
  sample(1:100, 300, replace = TRUE),
  sample(1:100, 300, replace = TRUE)
)
# Make sure there are no structures
# (sample size is small and still could generate structures randomly)
if(requireNamespace('DatabionicSwarm', quietly = TRUE)){
  Data = DatabionicSwarm::RobustNormalization(data, Centered = TRUE)
  #DataVisualizations::Plot3D(Data)

  # No structures are visible
  # Topographic map looks like "egg carton"
  # with every point in its own valley
  Cls = DatabionicSwarmClustering(Data, 0, PlotMap = TRUE)
}else{
  # only for testing purposes of CRAN!
  # in case CRAN tests with no suggest packages available
  # please use always some kind of standardization!
  Cls = DatabionicSwarmClustering(data, 0, PlotMap = TRUE)
}

# Distance based cluster structures
# 7 valleys are visible, thus ClusterNo=7

data(Hepta)
#DataVisualizations::Plot3D(Hepta$Data)

Cls = DatabionicSwarmClustering(Hepta$Data, 0, PlotMap = TRUE)

#entangled, complex, and non-linear separable structures
## Not run:
#takes too long for CRAN tests
data(Chainlink)
#DataVisualizations::Plot3D(Chainlink$Data)

# 2 valleys are visible, thus ClusterNo=2
```

```

Cls = DatabionicSwarmClustering(Chainlink$Data, 0, PlotMap = TRUE)

# Experiment with parameter StructureType only
# reveals that clustering is appropriate
# if StructureType=FALSE
Cls = DatabionicSwarmClustering(Chainlink$Data,
                                2,
                                StructureType = FALSE,
                                PlotMap = TRUE)

# Here clusters (colored points)
# are not seperated by valleys
Cls = DatabionicSwarmClustering(Chainlink$Data,
                                2,
                                StructureType = TRUE,
                                PlotMap = TRUE)

## End(Not run)

```

---

DensityPeakClustering *Density Peak Clustering algorithm using the Decision Graph*

---

## Description

Density peaks clustering of [Rodriguez/Laio, 2014] is here implemented by [Pedersen et al., 2017] with estimation of [Wang et al, 2015] meaning its non adaptive in the sense of [ADPclustering](#).

## Usage

```

DensityPeakClustering(DataOrDistances, Rho,Delta,Dc,Knn=7,
DistanceMethod = "euclidean", PlotIt = FALSE, Data, ...)

```

## Arguments

DataOrDistances	Either [1:n,1:n] symmetric distance matrix or [1:n,1:d] non symmetric data matrix of n cases and d variables
Rho	Local density of a point, see [Rodriguez/Laio, 2014] for explanation
Delta	Minimum distance between a point and any other point, see [Rodriguez/Laio, 2014] for explanation
Dc	Optional, cutoff distance, will either be estimated by [Pedersen et al., 2017] or [Wang et al, 2015] (see example below)
Knn	Optional k nearest neighbors
DistanceMethod	Optional distance method of data, default is euclid, see <a href="#">parDist</a> for details
PlotIt	Optional TRUE: Plots 2d or 3d result with clustering

Data	[1:n,1:d] data matrix in the case that DataOrDistances is missing and partial matching does not work.
...	Optional, further arguments for <a href="#">densityClust</a>

### Details

The densityClust algorithm does not decide the k number of clusters, this has to be done by the parameter setting. This is contrary to the other version of the algorithm from another package which can be called with [ADPclustering](#).

The plot shows the density peaks (Cluster centers). Set Rho and Delta as boundaries below the number of relevant cluster centers for your problem. (see example below).

### Value

If Rho and Delta are set:

list of

Cls [1:n numerical vector of numbers defining the classification as the main output of the clustering algorithm for the n cases of data. It has k unique numbers representing the arbitrary labels of the clustering.

Object output of [Pedersen et al., 2017] algorithm

If Rho and Delta are missing:

p object of [plot\\_ly](#) for the decision graph is returned

### Author(s)

Michael Thrun

### References

[Wang et al., 2015] Wang, S., Wang, D., Li, C., & Li, Y.: Comment on " Clustering by fast search and find of density peaks", arXiv preprint arXiv:1501.04267, 2015.

[Pedersen et al., 2017] Thomas Lin Pedersen, Sean Hughes and Xiaojie Qiu: densityClust: Clustering by Fast Search and Find of Density Peaks. R package version 0.3. <https://CRAN.R-project.org/package=densityClust>, 2017.

[Rodriguez/Laio, 2014] Rodriguez, A., & Laio, A.: Clustering by fast search and find of density peaks, Science, Vol. 344(6191), pp. 1492-1496. 2014.

### See Also

[ADPclustering](#)

[densityClust](#)

**Examples**

```

data(Hepta)
H=EntropyOfDataField(Hepta$Data, seq(from=0,to=1.5,by=0.05),PlotIt=FALSE)
Sigmamin=names(H)[which.min(H)]
Dc=3/sqrt(2)*as.numeric(names(H)[which.min(H)])
# Look at the plot and estimate rho and delta

DensityPeakClustering(Hepta$Data, Knn = 7,Dc=Dc)
Cls=DensityPeakClustering(Hepta$Data,Dc=Dc,Rho = 0.028,

Delta = 22,Knn = 7,PlotIt = TRUE)$Cls

```

---

DivisiveAnalysisClustering

*Large DivisiveAnalysisClustering Clustering*

---

**Description**

Divisive Analysis Clustering (diana) of [Rousseeuw/Kaufman, 1990, pp. 253-279]

**Usage**

```

DivisiveAnalysisClustering(DataOrDistances, ClusterNo,
PlotIt=FALSE,Standardization=TRUE,PlotTree=FALSE,Data,...)

```

**Arguments**

DataOrDistances	[1:n,1:d] matrix of dataset to be clustered. It consists of n cases of d-dimensional data points. Every case has d attributes, variables or features. Alternatively, symmetric [1:n,1:n] distance matrix
ClusterNo	A number k which defines k different clusters to be build by the algorithm. if ClusterNo=0 and PlotTree=TRUE, the dendrogram is generated instead of a clustering to estimate the numbers of clusters.
PlotIt	Default: FALSE, If TRUE plots the first three dimensions of the dataset with colored three-dimensional data points defined by the clustering stored in Cls
Standardization	DataOrDistances Is standardized before calculating the dissimilarities. Measurements are standardized for each variable (column), by subtracting the variable's mean value and dividing by the variable's mean absolute deviation.If DataOrDistances Is already a distance matrix, then this argument will be ignored.
PlotTree	TRUE: Plots the dendrogram, FALSE: no plot

Data	[1:n,1:d] data matrix in the case that DataOrDistances is missing and partial matching does not work.
...	Further arguments to be set for the clustering algorithm, if not set, default arguments are used.

**Value**

List of	
Cls	[1:n] numerical vector with n numbers defining the classification as the main output of the clustering algorithm. It has k unique numbers representing the arbitrary labels of the clustering.
Dendrogram	Dendrogram of hierarchical clustering algorithm
Object	Object defined by clustering algorithm as the other output of this algorithm

**Author(s)**

Michael Thrun

**References**

[Rousseeuw/Kaufman, 1990] Rousseeuw, P. J., & Kaufman, L.: Finding groups in data, Belgium, John Wiley & Sons Inc., ISBN: 0471735787, doi: 10.1002/9780470316801, Online ISBN: 9780470316801, 1990.

**Examples**

```
data('Hepta')
CA=DivisiveAnalysisClustering(Hepta$Data,ClusterNo=7,PlotIt=FALSE)

print(CA$Object)
plot(CA$Object)
ClusterDendrogram(CA$Dendrogram,7,main='DIANA')
```

---

EngyTime

*EngyTime introduced in [Baggenstoss, 2002].*

---

**Description**

Gaussian mixture. Detailed description of dataset and its clustering challenge is provided in [Thrun/Ultsch, 2020].

**Usage**

```
data("EngyTime")
```

**Details**

Size 4096, Dimensions 2, stored in EngyTime\$Data

Classes 2, stored in EngyTime\$Cls

**References**

[Baggenstoss, 2002] Baggenstoss, P. M.: Statistical modeling using gaussian mixtures and hmms with matlab, Naval Undersea Warfare Center, Newport RI, 2002.

[Thrun/Ultsch, 2020] Thrun, M. C., & Ultsch, A.: Clustering Benchmark Datasets Exploiting the Fundamental Clustering Problems, Data in Brief, Vol. 30(C), pp. 105501, doi:10.1016/j.dib.2020.105501, 2020.

**Examples**

```
data(EngyTime)
str(EngyTime)
```

---

EntropyOfDataField      *Entropy Of a Data Field [Wang et al., 2011].*

---

**Description**

Calculates the Potential Entropy Of a Data Field for a given ranges of impact factors sigma

**Usage**

```
EntropyOfDataField(Data,
sigmarange = c(0.01, 0.1, 0.5, 1, 2, 5, 8, 10, 100)
, PlotIt = FALSE)
```

**Arguments**

Data	[1:n,1:d] data matrix
sigmarange	Numeric vector [1:s] of relevant sigmas
PlotIt	FALSE: disable plot, TRUE: Plot with upper boundary of H after [Wang et al., 2011].

**Details**

In theory there should be a curve with a clear minimum of Entropy [Wang et al.,2011]. Then the choice for the impact factor sigma is the minimum of the entropy to define the correct data field. It follows, that the influence radius is  $3/\sqrt{2} \cdot \sigma$  (3B rule of gaussian distribution) for clustering algorithms like density peak clustering [Wang et al.,2011].

**Value**

[1:s] named vector of the Entropy of data field. The names are the impact factor sigma.

**Author(s)**

Michael Thrun

**References**

[Wang et al., 2015] Wang, S., Wang, D., Li, C., & Li, Y.: Comment on " Clustering by fast search and find of density peaks", arXiv preprint arXiv:1501.04267, 2015.

[Wang et al., 2011] Wang, S., Gan, W., Li, D., & Li, D.: Data field for hierarchical clustering, International Journal of Data Warehousing and Mining (IJDWM), Vol. 7(4), pp. 43-63. 2011.

**Examples**

```
data(Hepta)
H=EntropyOfDataField(Hepta$Data,PlotIt=FALSE)
Sigmamin=names(H)[which.min(H)]
Dc=3/sqrt(2)*as.numeric(names(H)[which.min(H)])
```

---

EstimateRadiusByDistance

*Estimate Radius By Distance*

---

**Description**

Published in [Thrun et al, 2016] for the case of automatically estimating the radius of the P-matrix. Can also be used to estimate the radius parameter for distance based clustering algorithms.

**Usage**

```
EstimateRadiusByDistance(DistanceMatrix)
```

**Arguments**

DistanceMatrix [1:n,1:n] symmetric distance Matrix of n cases

**Details**

For density-based clustering algorithms like [DBSCAN](#) it is not always usefull.

**Value**

Numerical scalar defining the radius

**Note**

Symmetric matrix is assumed.

**Author(s)**

Michael Thrun

**References**

[Thrun et al., 2016] Thrun, M. C., Lerch, F., Loetsch, J., & Ultsch, A.: Visualization and 3D Printing of Multivariate Data of Biomarkers, in Skala, V. (Ed.), International Conference in Central Europe on Computer Graphics, Visualization and Computer Vision (WSCG), Vol. 24, pp. 7-16, Plzen, <http://wscg.zcu.cz/wscg2016/short/A43-full.pdf>, 2016.

**See Also**

[GeneratePmatrix](#)

**Examples**

```
data('Hepta')
DistanceMatrix=as.matrix(dist(Hepta$Data))
Radius=EstimateRadiusByDistance(DistanceMatrix)
```

---

FannyClustering

*Fuzzy Analysis Clustering [Rousseeuw/Kaufman, 1990, p. 253-279]*

---

**Description**

...

**Usage**

```
FannyClustering(DataOrDistances,ClusterNo,
PlotIt=FALSE,Standardization=TRUE,...)
```

**Arguments**

DataOrDistances

[1:n,1:d] matrix of dataset to be clustered. It consists of n cases or d-dimensional data points. Every case has d attributes, variables or features. Alternatively, symmetric [1:n,1:n] distance matrix

ClusterNo

A number k which defines k different clusters to be build by the algorithm.

PlotIt

Default: FALSE, If TRUE plots the first three dimensions of the dataset with colored three-dimensional data points defined by the clustering stored in C1s



**Standardization**

DataOrDistances is standardized before calculating the dissimilarities. Measurements are standardized for each variable (column), by subtracting the variable's mean value and dividing by the variable's mean absolute deviation. If DataOrDistances is already a distance matrix, then this argument will be ignored.

...

Further arguments to be set for the clustering algorithm, if not set, default arguments are used.

**Details**

...

**Value**

List of

Cls

[1:n] numerical vector with n numbers defining the classification as the main output of the clustering algorithm. It has k unique numbers representing the arbitrary labels of the clustering. Points which cannot be assigned to a cluster will be reported with 0.

Object

Object defined by clustering algorithm as the second output of this algorithm

**Author(s)**

Michael Thrun

**References**

[Rousseeuw/Kaufman, 1990] Rousseeuw, P. J., & Kaufman, L.: Finding groups in data, Belgium, John Wiley & Sons Inc., ISBN: 0471735787, doi: 10.1002/9780470316801, Online ISBN: 9780470316801, 1990.

**Examples**

```
data('Hepta')
out=FannyClustering(Hepta$Data,ClusterNo=7,PlotIt=FALSE)
```

---

 GapStatistic

*Gap Statistic*


---

**Description**

Gap Statistic

**Usage**

```
GapStatistic(Data, ClusterNoMax, ClusterFun, ...)
```

**Arguments**

Data [1:n,1:d] data matrix  
ClusterNoMax max no of clusters to be investigated  
ClusterFun which clustering algorithm to investigate  
... further arguments passed on

**Details**

does not work on hepta, see example

**Value**

tobedocumented

**Note**

Wrapper only

**Author(s)**

Michael Thrun

**References**

Tibshirani, R., Walther, G. and Hastie, T: Estimating the number of data clusters via the Gap statistic, Journal of the Royal Statistical Society B, Vol. 63, pp. 411-423, 2003.

**Examples**

```
data(Hepta)
#GapStatistic(Hepta$Data,10,ClusterFun = kmeans)
```

---

GenieClustering      *Genie Clustering by Gini Index*

---

**Description**

Outlier Resistant Hierarchical Clustering Algorithm of [Gagolewski/Bartoszuk, 2016].

**Usage**

```
GenieClustering(DataOrDistances, ClusterNo = 0,  
DistanceMethod="euclidean", ColorTreshold = 0,...)
```

**Arguments**

DataOrDistances	[1:n,1:d] matrix of dataset to be clustered. It consists of n cases of d-dimensional data points. Every case has d attributes, variables or features. Alternatively, symmetric [1:n,1:n] distance matrix
ClusterNo	A number k which defines k different clusters to be build by the algorithm.
DistanceMethod	See <a href="#">parDist</a> , for example 'euclidean', 'mahalanobis', 'manhattan' (cityblock), 'fJaccard', 'binary', 'canberra', 'maximum'. Any unambiguous substring can be given.
ColorTreshold	Draws cutline w.r.t. dendrogram y-axis (height), height of line as scalar should be given
...	furter argument to genie like: thresholdGini Single numeric value in [0,1], threshold for the Gini index, 1 gives the standard single linkage algorithm

**Details**

Wrapper for Genie algorithm.

**Value**

List of	
Cls	If, ClusterNo>0: [1:n] numerical vector with n numbers defining the classification as the main output of the clustering algorithm. It has k unique numbers representing the arbitrary labels of the clustering. Otherwise for ClusterNo=0: NULL
Dendrogram	Dendrogram of hierarchical clustering algorithm
Object	Ultrametric tree of hierarchical clustering algorithm

**Author(s)**

Michael Thrun

**References**

[Gagolewski/Bartoszuk, 2016] Gagolewski M., Bartoszuk M., Cena A., Genie: A new, fast, and outlier-resistant hierarchical clustering algorithm, Information Sciences, Vol. 363, pp. 8-23, 2016.

**See Also**

[HierarchicalClustering](#)

**Examples**

```
data('Hepta')
Clust=GenieClustering(Hepta$Data,ClusterNo=7)
```

---

GolfBall

*GolfBall introduced in [Ultsch, 2005]*

---

**Description**

No clusters at all. Detailed description of dataset and its clustering challenge is provided in [Thrun/Ultsch, 2020].

**Usage**

```
data("GolfBall")
```

**Details**

Size 4002, Dimensions 3, stored in GolfBall\$Data

Classes 1, stored in GolfBall\$Cls

**References**

[Ultsch, 2005] Ultsch, A.: Clustering with SOM: U\* C, Proc. Proceedings of the 5th Workshop on Self-Organizing Maps, Vol. 2, pp. 75-82, 2005.

[Thrun/Ultsch, 2020] Thrun, M. C., & Ultsch, A.: Clustering Benchmark Datasets Exploiting the Fundamental Clustering Problems, Data in Brief, Vol. 30(C), pp. 105501, doi:10.1016/j.dib.2020.105501, 2020.

**Examples**

```
data(GolfBall)
str(GolfBall)
```

---

HCLclustering

*On-line Update (Hard Competitive learning) method*

---

**Description**

Hard Competitive learning clustering published by [Ripley, 2007].

**Usage**

```
HCLclustering(Data, ClusterNo, PlotIt=FALSE, ...)
```

**Arguments**

Data	[1:n,1:d] matrix of dataset to be clustered. It consists of n cases of d-dimensional data points. Every case has d attributes, variables or features.
ClusterNo	A number k which defines k different clusters to be build by the algorithm.
PlotIt	Default: FALSE, If TRUE plots the first three dimensions of the dataset with colored three-dimensional data points defined by the clustering stored in C1s
...	Further arguments to be set for the clustering algorithm, if not set, default arguments are used.

**Value**

List of	
C1s	[1:n] numerical vector with n numbers defining the classification as the main output of the clustering algorithm. It has k unique numbers representing the arbitrary labels of the clustering.
Object	Object defined by clustering algorithm as the other output of this algorithm

**Author(s)**

Michael Thrun

**References**

- [Dimitriadou, 2002] Dimitriadou, E.: cclust-convex clustering methods and clustering indexes. R package, 2002,
- [Ripley, 2007] Ripley, B. D.: Pattern recognition and neural networks, Cambridge university press, ISBN: 0521717701, 2007.

**Examples**

```
data('Hepta')
out=HCLclustering(Hepta$Data,ClusterNo=7,PlotIt=FALSE)
```

---

HDDClustering	<i>HDD clustering is a model-based clustering method of [Bouveyron et al., 2007].</i>
---------------	---

---

**Description**

HDD clustering is based on the Gaussian Mixture Model and on the idea that the data lives in subspaces with a lower dimension than the dimension of the original space. It uses the EM algorithm to estimate the parameters of the model [Berge et al., 2012].

**Usage**

```
HDDClustering(Data, ClusterNo, PlotIt=F,...)
```

**Arguments**

Data	[1:n,1:d] matrix of dataset to be clustered. It consists of n cases of d-dimensional data points. Every case has d attributes, variables or features.
ClusterNo	Optional, Numeric indicating either the number of cluster or a vector of 1:k to indicate the maximal expected number of clusters.
PlotIt	(optional) Boolean. Default = FALSE = No plotting performed.
...	Further arguments to be set for the clustering algorithm, if not set, default arguments are used, see <a href="#">hddc</a> for details.

**Details**

HDD clustering maximises the BIC criterion for a range of possible number of cluster up to ClusterNo. Per default the most general model is used, alternatively the parameter `model="ALL"` can be used to evaluate all possible models with BIC [Berge et al., 2012]. If specific properties of Data are known priorly please see [hddc](#) for specific model selection.

**Value**

List of	
Cls	[1:n] numerical vector with n numbers defining the classification as the main output of the clustering algorithm. It has k unique numbers representing the arbitrary labels of the clustering.
Object	Object defined by clustering algorithm as the other output of this algorithm

**Author(s)**

Quirin Stier

**References**

[Berge et al., 2012] L. Berge, C. Bouveyron and S. Girard, HDclassif: an R Package for Model-Based Clustering and Discriminant Analysis of High-Dimensional Data, Journal of Statistical Software, vol. 42 (6), pp. 1-29, 2012.

[Bouveyron et al., 2007] Bouveyron, C. Girard, S. and Schmid, C: High-Dimensional Data Clustering, Computational Statistics and Data Analysis, vol. 52 (1), pp. 502-519, 2007.

**Examples**

```
# Hepta
data("Hepta")
Data = Hepta$Data
#Non-default parameter model
#can be set to evaluate all possible models
V = HDDClustering(Data=Data,ClusterNo=7,model="ALL")
Cls = V$Cls

ClusterAccuracy(Hepta$Cls, Cls)
```

```
## Not run:  
library(HDclassif)  
data(Crabs)  
Data = Crabs[,-1]  
V = HDDClustering(Data=Data,ClusterNo=4,com_dim=1)  
  
## End(Not run)
```

---

Hepta

*Hepta introduced in [Ultsch, 2003]*

---

### Description

Clearly defined clusters, different variances. Detailed description of dataset and its clustering challenge is provided in [Thrun/Ultsch, 2020].

### Usage

```
data("Hepta")
```

### Details

Size 212, Dimensions 3, stored in Hepta\$Data

Classes 7, stored in Hepta\$Cls

### References

[Ultsch, 2003] Ultsch, A.: Maps for the visualization of high-dimensional data spaces, Proc. Workshop on Self organizing Maps (WSOM), pp. 225-230, Kyushu, Japan, 2003.

[Thrun/Ultsch, 2020] Thrun, M. C., & Ultsch, A.: Clustering Benchmark Datasets Exploiting the Fundamental Clustering Problems, Data in Brief, Vol. 30(C), pp. 105501, doi:10.1016/j.dib.2020.105501, 2020.

### Examples

```
data(Hepta)  
str(Hepta)
```

---

HierarchicalClusterData

*Internal function of Hierarchical Clusterering of Data*


---

### Description

Please use [HierarchicalClustering](#). Hierarchical cluster analysis on a set of dissimilarities and methods for analyzing it. Uses stats package function 'hclust'.

### Usage

```
HierarchicalClusterData(Data,ClusterNo=0,
Type="ward.D2",DistanceMethod="euclidean",
ColorTreshold=0,Fast=FALSE,Cls=NULL,...)
```

### Arguments

Data	[1:n,1:d] matrix of dataset to be clustered. It consists of n cases of d-dimensional data points. Every case has d attributes, variables or features.
ClusterNo	A number k which defines k different clusters to be build by the algorithm.
Type	Methode der Clustering: "ward.D", "ward.D2", "single", "complete", "average", "mcquitty", "median" or "centroid".
DistanceMethod	see <a href="#">parDist</a> , for example 'euclidean', 'mahalanobis', 'manhattan' (cityblock), 'fJaccard', 'binary', 'canberra', 'maximum'. Any unambiguous substring can be given.
ColorTreshold	Draws cutline w.r.t. dendrogram y-axis (height), height of line as scalar should be given
Fast	If TRUE and fastcluster installed, then a faster implementation of the methods above can be used
Cls	[1:n] classification vector for coloring of dendrogram in plot
...	In case of plotting further argument for plot, see <a href="#">as.dendrogram</a>

### Value

List of	
Cls	If, ClusterNo>0: [1:n] numerical vector with n numbers defining the classification as the main output of the clustering algorithm. It has k unique numbers representing the arbitrary labels of the clustering. Otherwise for ClusterNo=0: NULL
Dendrogram	Dendrogram of hierarchical clustering algorithm
Object	Ultrametric tree of hierarchical clustering algorithm



**Author(s)**

Michael Thrun

**See Also**[HierarchicalClusterData](#)[HierarchicalClusterDists](#)[HierarchicalClustering](#)**Examples**

```
data('Hepta')
#out=HierarchicalClusterData(Hepta$Data,ClusterNo=7)
```

---

 HierarchicalClusterDists

*Internal Function of Hierarchical Clustering with Distances*


---

**Description**

Please use [HierarchicalClustering](#). Cluster analysis on a set of dissimilarities and methods for analyzing it. Uses stats package function 'hclust'.

**Usage**

```
HierarchicalClusterDists(pDist,ClusterNo=0,Type="ward.D2",
ColorTreshold=0,Fast=FALSE,...)
```

**Arguments**

pDist	Distances as either matrix [1:n,1:n] or dist object
ClusterNo	A number k which defines k different clusters to be built by the algorithm.
Type	Method of cluster analysis: "ward.D", "ward.D2", "single", "complete", "average", "mcquitty", "median" or "centroid".
ColorTreshold	Draws outline w.r.t. dendrogram y-axis (height), height of line as scalar should be given
Fast	If TRUE and fastcluster installed, then a faster implementation of the methods above can be used
...	In case of plotting further argument for plot, see <a href="#">as.dendrogram</a>

**Value**

List of	
Cls	If, ClusterNo>0: [1:n] numerical vector with n numbers defining the classification as the main output of the clustering algorithm. It has k unique numbers representing the arbitrary labels of the clustering. Otherwise for ClusterNo=0: NULL
Dendrogram	Dendrogram of hierarchical clustering algorithm
Object	Ultrametric tree of hierarchical clustering algorithm

**Author(s)**

Michael Thrun

**See Also**

[HierarchicalClusterData](#)

[HierarchicalClusterDists](#)

[HierarchicalClustering](#)

**Examples**

```
data('Hepta')
#out=HierarchicalClusterDists(as.matrix(dist(Hepta$Data)),ClusterNo=7)
```

---

HierarchicalClustering

*Hierarchical Clustering*

---

**Description**

Wrapper for various agglomerative hierarchical clustering algorithms.

**Usage**

```
HierarchicalClustering(DataOrDistances,ClusterNo,Type='SingleL',Fast=TRUE,Data,...)
```

**Arguments**

DataOrDistances	Either nonsymmetric [1:n,1:d] numerical matrix of a dataset to be clustered. It consists of n cases of d-dimensional data points. Every case has d attributes, variables or features. or symmetric [1:n,1:n] distance matrix, e.g. <code>as.matrix(dist(Data,method))</code>
ClusterNo	A number k which defines k different clusters to be built by the algorithm.

Type	Method of cluster analysis: "Ward", "SingleL", "CompleteL", "AverageL" (UP-GMA), "WPGMA" (mcquitty), "MedianL" (WPGMC), "CentroidL" (UPGMC), "Minimax", "MinEnergy", "Gini", "HDBSCAN", or "Sparse"
Fast	If TRUE and fastcluster installed, then a faster implementation of the methods above can be used except for "Minimax", "MinEnergy", "Gini" or "HDBSCAN"
Data	[1:n,1:d] data matrix in the case that DataOrDistances is missing and partial matching does not work.
...	Further arguments passed on to either <a href="#">HierarchicalClusterData</a> , <a href="#">HierarchicalClusterDists</a> , <a href="#">MinimalEnergyClustering</a> or <a href="#">GenieClustering</a> (for "Gini"), <a href="#">HierarchicalDBSCAN</a> (for HDBSCAN) or <a href="#">SparseClustering</a> (for Sparse).

### Details

Please see [HierarchicalClusterData](#) and [HierarchicalClusterDists](#) or the other functions listed above.

It should be noted that in case of "HDBSCAN" the number of clusters is manually selected by cutree to have the same convention as the other algorithms. Usually, "HDBSCAN" selects the number of clusters automatically.

### Value

List of	
Cls	If, ClusterNo>0: [1:n] numerical vector with n numbers defining the classification as the main output of the clustering algorithm. It has k unique numbers representing the arbitrary labels of the clustering. Otherwise for ClusterNo=0: NULL
Dendrogram	Dendrogram of hierarchical clustering algorithm
Object	Ultrametric tree of hierarchical clustering algorithm

### Author(s)

Michael Thrun

### See Also

[HierarchicalClusterData](#)  
[HierarchicalClusterDists](#),  
[MinimalEnergyClustering](#).

### Examples

```
data('Hepta')
out=HierarchicalClustering(Hepta$Data,ClusterNo=7)
```

---

HierarchicalDBSCAN      *Hierarchical DBSCAN*

---

### Description

Hierarchical DBSCAN clustering [Campello et al., 2015].

### Usage

```
HierarchicalDBSCAN(DataOrDistances,minPts=4,
PlotTree=FALSE,PlotIt=FALSE,...)
```

### Arguments

DataOrDistances	Either a [1:n,1:d] matrix of dataset to be clustered. It consists of n cases of d-dimensional data points. Every case has d attributes, variables or features. or a [1:n,1:n] symmetric distance matrix.
minPts	Classic smoothing factor in density estimates [Campello et al., 2015, p.9]
PlotIt	Default: FALSE, If TRUE plots the first three dimensions of the dataset with colored three-dimensional data points defined by the clustering stored in C1s
PlotTree	Default: FALSE, If TRUE plots the dendrogram. If minPts is missing, PlotTree is set to TRUE.
...	Further arguments to be set for the clustering algorithm, if not set, default arguments are used.

### Details

"Computes the hierarchical cluster tree representing density estimates along with the stability-based flat cluster extraction proposed by Campello et al. (2013). HDBSCAN essentially computes the hierarchy of all DBSCAN\* clusterings, and then uses a stability-based extraction method to find optimal cuts in the hierarchy, thus producing a flat solution." [Hahsler et al., 2019]

It is claimed by the inventors that the minPts parameter is noncritical [Campello et al., 2015, p.35]. minPts is reported to be set to 4 on all experiments [Campello et al., 2015, p.35].

### Value

List of	
C1s	[1:n] numerical vector defining the clustering; this classification is the main output of the algorithm. Points which cannot be assigned to a cluster will be reported as members of the noise cluster with 0.
Dendrogram	Dendrogram of hierarchical clustering algorithm
Tree	Ultrametric tree of hierarchical clustering algorithm
Object	Object defined by clustering algorithm as the other output of this algorithm

**Author(s)**

Michael Thrun

**References**

[Campello et al., 2015] Campello, R. J., Moulavi, D., Zimek, A., & Sander, J.: Hierarchical density estimates for data clustering, visualization, and outlier detection, ACM Transactions on Knowledge Discovery from Data (TKDD), Vol. 10(1), pp. 1-51. 2015.

[Hahsler et al., 2019] Hahsler M, Piekenbrock M, Doran D: dbscan: Fast Density-Based Clustering with R. Journal of Statistical Software, 91(1), pp. 1-30. doi: 10.18637/jss.v091.i01, 2019

**Examples**

```
data('Hepta')

out=HierarchicalDBSCAN(Hepta$Data,PlotIt=FALSE)

data('Leukemia')
set.seed(1234)
CA=HierarchicalDBSCAN(Leukemia$DistanceMatrix)
#ClusterCount(CA$Cls)
#ClusterDendrogram(CA$Dendrogram,5,main='H-DBscan')
```

---

kmeansClustering

*K-Means Clustering*

---

**Description**

Perform k-means clustering on a data matrix.

**Usage**

```
kmeansClustering(DataOrDistances, ClusterNo,
  Type = 'LBG',RandomNo=5000, CategoricalData,
  PlotIt=FALSE, Verbose = FALSE, ... )
```

**Arguments**

DataOrDistances

Either nonsymmetric [1:n,1:d] datamatrix of n cases and d numerical features or symmetric [1:n,1:n] distance matrix

ClusterNo

A number k which defines k different clusters to be built by the algorithm.

Type	Choice of Kmeans algorithm, currently either "Hartigan" [Hartigan/Wong, 1979], "LBG" [Linde et al., 1980], "Sparse" sparse k-means proposed in [Witten/Tibshirani, 2010], "Steinley" best method of [Steinley/Brusco, 2007] proposed in Steinley 2003, "Lloyd" [Lloyd, 1982], "Forgy" [Forgy, 1965], MacQueen [MacQueen, 1967], kcentroids [Leisch, 2006], "kprototypes" [Szepannek, 2018], "Pelleg-moore" [Pelleg & Moors, 2000], Elkan" [Elkan, 2003], Hamerly" [Hamerly, 2010], "Dualtree" or Dualtree-covertree [Curtin, 2017]"
RandomNo	Only for "Steinley" or in case of distance matrix, number of random initializations with searching for minimal SSE, see [Steinley/Brusco, 2007]
CategoricalData	Only for "kprototypes", [1:n,1:m] matrix of categorical features]
PlotIt	Default: FALSE, If TRUE plots the first three dimensions of the dataset with colored three-dimensional data points defined by the clustering stored in Cls
Verbose	Print details, if true
...	Further arguments like iter.max, nstart, for kcentroids please see kcca function of the <b>flexclust</b> package, or <a href="#">KMeansSparseCluster</a>

### Details

Uses either **stats** package function 'kmeans', **clust** package implementation, **flexclust** package implementation or own code. In case of a distance matrix, RandomNo should be significantly lower than 5000, otherwise a long computation time is to be expected.

### Value

List V of

Cls	[1:n] numerical vector with n numbers defining the classification as the main output of the clustering algorithm. It has k unique numbers representing the arbitrary labels of the clustering.
Object	Object of the clustering algorithm used if existent, otherwise SumDistsToCentroids: Vector of within-cluster sum of squares, one component per cluster
Centroids	the final cluster centers.

### Note

The version using a distance matrix is still in the test phase and not yet verified.

### Author(s)

Michael Thrun

## References

- [Hartigan/Wong, 1979] Hartigan, J. A., & Wong, M. A.: Algorithm AS 136: A k-means clustering algorithm, *Journal of the Royal Statistical Society. Series C (Applied Statistics)*, Vol. 28(1), pp. 100-108. 1979.
- [Linde et al., 1980] Linde, Y., Buzo, A., & Gray, R.: An algorithm for vector quantizer design, *IEEE Transactions on communications*, Vol. 28(1), pp. 84-95. 1980.
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- [Hamerly, 2010] Hamerly, Greg: Making k-means even faster, *Proceedings of the 2010 SIAM international conference on data mining*, Society for Industrial and Applied Mathematics, pp. 130-140, 2010.
- [Szepannek, 2018] Szepannek, G.: clustMixType: User-Friendly Clustering of Mixed-Type Data in R, *The R Journal*, Vol. 10/2, pp. 200-208, doi:10.32614/RJ2018048, 2018.
- [Curtin, 2017] Curtin, Ryan R: A dual-tree algorithm for fast k-means clustering with large k, *Proceedings of the 2017 SIAM International Conference on Data Mining*, Society for Industrial and Applied Mathematics, 2017.

## Examples

```
data('Hepta')
out=kmeansClustering(Hepta$Data,ClusterNo=7,PlotIt=FALSE)
```

```
data('Leukemia')
# As expected does not perform well
# For non-spherical cluster structures:
out=kmeansClustering(Leukemia$DistanceMatrix,ClusterNo=6,RandomNo =10,PlotIt=TRUE)
```

```
data('Hepta')
out=kmeansClustering(Hepta$Data,ClusterNo=7,PlotIt=FALSE,Type="Steinley")
```

```
data('Hepta')
out=kmeansClustering(Hepta$Data,ClusterNo = 7,
Type = "kprototypes",CategoricalData = as.matrix(Hepta$Cls))
```

---

kmeansDist

*k-means Clustering using a distance matrix*


---

### Description

Perform k-means clustering on a distance matrix

### Usage

```
kmeansDist(Distance, ClusterNo=2,Centers=NULL,
RandomNo=1,maxIt = 2000,
PlotIt=FALSE,verbose = F)
```

### Arguments

Distance	Distance matrix. For n data points of the dimension n x n
ClusterNo	A number k which defines k different clusters to be built by the algorithm.
Centers	Default(NULL) a set of initial (distinct) cluster centres.
RandomNo	If>1: Number of random initializations with searching for minimal SSE is defined by this scalar
maxIt	Optional: Maximum number of iterations before the algorithm terminates.
PlotIt	Default: FALSE, If TRUE plots the first three dimensions of the dataset with colored three-dimensional data points defined by the clustering stored in Cls
verbose	Optional: Algorithm always outputs current iteration.

### Value

Cls[1:n]	[1:n] numerical vector with n numbers defining the classification as the main output of the clustering algorithm. It has k unique numbers representing the arbitrary labels of the clustering.
centerids[1:k]	Indices of the centroids from which the cluster Cls was created



**Note**

Currently an experimental version

**Author(s)**

Felix Pape, Michael Thrun

**Examples**

```
data('Hepta')
#out=kmeansDist(as.matrix(dist(Hepta$Data)),ClusterNo=7,PlotIt=FALSE,RandomNo = 10)

## Not run:
data('Leukemia')
#as expected does not perform well
#for non-spherical cluster structures:
#out=kmeansDist(Leukemia$DistanceMatrix,ClusterNo=6,PlotIt=TRUE,RandomNo=10)

## End(Not run)
```

---

LargeApplicationClustering

*Large Application Clustering*

---

**Description**

Clustering Large Applications (clara) of [Rousseeuw/Kaufman, 1990, pp. 126-163]

**Usage**

```
LargeApplicationClustering(Data, ClusterNo,
PlotIt=FALSE,Standardization=TRUE,Samples=50,Random=TRUE,...)
```

**Arguments**

Data	[1:n,1:d] matrix of dataset to be clustered. It consists of n cases of d-dimensional data points. Every case has d attributes, variables or features.
ClusterNo	A number k which defines k different clusters to be built by the algorithm.
PlotIt	Default: FALSE, If TRUE plots the first three dimensions of the dataset with colored three-dimensional data points defined by the clustering stored in C1s
Standardization	Data is standardized before calculating the dissimilarities. Measurements are standardized for each variable (column), by subtracting the variable's mean value and dividing by the variable's mean absolute deviation.
Samples	Integer, say N, the number of samples to be drawn from the dataset. Default value set as recommended by documentation of <a href="#">clara</a>

Random	Logical indicating if R's random number generator should be used instead of the primitive <code>clara()</code> -builtin one.
...	Further arguments to be set for the clustering algorithm, if not set, default arguments are used.

### Details

It is recommended to use `set.seed` if clustering output should be always the same instead of setting `Random=FALSE` in order to use the primitive `clara()`-builtin random number generator.

### Value

List of	
<code>Cls</code>	[1:n] numerical vector with n numbers defining the classification as the main output of the clustering algorithm. It has k unique numbers representing the arbitrary labels of the clustering.
Object	Object defined by clustering algorithm as the other output of this algorithm

### Author(s)

Michael Thrun

### References

[Rousseeuw/Kaufman, 1990] Rousseeuw, P. J., & Kaufman, L.: Finding groups in data, Belgium, John Wiley & Sons Inc., ISBN: 0471735787, doi 10.1002/9780470316801, Online ISBN: 9780470316801, 1990.

### Examples

```
data('Hepta')
out=LargeApplicationClustering(Hepta$Data,ClusterNo=7,PlotIt=FALSE)
```

---

Leukemia

*Leukemia distance matrix and classification used in [Thrun, 2018]*

---

### Description

Data is anonymized. Original dataset was published in [Haferlach et al., 2010]. Original dataset had around 12.000 dimensions. Detailed description of preprocessed dataset and its clustering challenge is provided in [Thrun/Ultsch, 2020].

### Usage

```
data("Leukemia")
```

## Details

554x554 distance matrix. Cls defines the following clusters:

1= APL Outlier

2=APL

3=Healthy

4=AML

5=CLL

6=CLL Outlier

## References

[Thrun, 2018] Thrun, M. C.: Projection Based Clustering through Self-Organization and Swarm Intelligence, doctoral dissertation 2017, Springer, Heidelberg, ISBN: 978-3-658-20539-3, [doi:10.1007/9783658205409](https://doi.org/10.1007/9783658205409), 2018.

[Haferlach et al., 2010] Haferlach, T., Kohlmann, A., Wieczorek, L., Basso, G., Te Kronnie, G., Bene, M.-C., . . . Mills, K. I.: Clinical utility of microarray-based gene expression profiling in the diagnosis and subclassification of leukemia: report from the International Microarray Innovations in Leukemia Study Group, *Journal of Clinical Oncology*, Vol. 28(15), pp. 2529-2537. 2010.

[Thrun/Ultsch, 2020] Thrun, M. C., & Ultsch, A.: Clustering Benchmark Datasets Exploiting the Fundamental Clustering Problems, *Data in Brief*, Vol. 30(C), pp. 105501, [doi:10.1016/j.dib.2020.105501](https://doi.org/10.1016/j.dib.2020.105501), 2020.

## Examples

```
data(Leukemia)
str(Leukemia)
Cls=Leukemia$Cls
Distance=Leukemia$DistanceMatrix
isSymmetric(Distance)
```

---

Lsun3D

*Lsun3D inspired by FCPS introduced in [Thrun, 2018]*

---

## Description

Clearly defined clusters, different variances. Detailed description of dataset and its clustering challenge is provided in [Thrun/Ultsch, 2020].

## Usage

```
data("Lsun3D")
```

**Details**

Size 404, Dimensions 3

Dataset defines discontinuities, where the clusters have different variances. Three main clusters, and four outliers (in cluster 4). For a more detailed description see [Thrun, 2018].

**References**

[Thrun, 2018] Thrun, M. C.: Projection Based Clustering through Self-Organization and Swarm Intelligence, doctoral dissertation 2017, Springer, Heidelberg, ISBN: 978-3-658-20539-3, doi:10.1007/9783658205409, 2018.

[Thrun/Ultsch, 2020] Thrun, M. C., & Ultsch, A.: Clustering Benchmark Datasets Exploiting the Fundamental Clustering Problems, Data in Brief, Vol. 30(C), pp. 105501, doi:10.1016/j.dib.2020.105501, 2020.

**Examples**

```
data(Lsun3D)
str(Lsun3D)
Cls=Lsun3D$Cls
Data=Lsun3D$Data
```

---

MarkovClustering

*Markov Clustering*

---

**Description**

Graph clustering algorithm introduced by [van Dongen, 2000].

**Usage**

```
MarkovClustering(DataOrDistances=NULL,Adjacency=NULL,
Radius=TRUE,DistanceMethod="euclidean",addLoops = TRUE,PlotIt=FALSE,...)
```

**Arguments**

DataOrDistances	NULL or: Either [1:n,1:n] symmetric distance matrix or [1:n,1:d] not symmetric data matrix of n cases and d variables
Adjacency	Used if Data is NULL, matrix [1:n,1:n] defining which points are adjacent to each other by the number 1; not adjacent: 0
Radius	Scalar, Radius for unit disk graph (r-ball graph) if adjacency matrix is missing. Automatic estimation can be done either with =TRUE [Ultsch, 2005] or FALSE [Thrun et al., 2016] if Data instead of Distances are given.
DistanceMethod	Optional distance method of data, default is euclid, see <a href="#">parDist</a> for details

<code>addLoops</code>	Logical; if TRUE, self-loops with weight 1 are added to each vertex of <code>x</code> (see <code>mcl</code> of CRAN package <code>MCL</code> ).
<code>PlotIt</code>	Default: FALSE, If TRUE plots the first three dimensions of the dataset with colored three-dimensional data points defined by the clustering stored in <code>Cls</code>
<code>...</code>	Further arguments to be set for the clustering algorithm, if not set, default arguments are used.

### Details

`DataOrDistances` is used to compute the Adjacency matrix if this input is missing. Then a unit-disk (R-ball) graph is calculated.

### Value

List of	
<code>Cls</code>	[1:n] numerical vector with <code>n</code> numbers defining the classification as the main output of the clustering algorithm. It has <code>k</code> unique numbers representing the arbitrary labels of the clustering. Points which cannot be assigned to a cluster will be reported with 0.
Object	Object defined by clustering algorithm as the other output of this algorithm

### Author(s)

Michael Thrun

### References

- [van Dongen, 2000] van Dongen, S.M. Graph Clustering by Flow Simulation. Ph.D. thesis, University of Utrecht. Utrecht University Repository: <http://dspace.library.uu.nl/handle/1874/848>, 2000
- [Thrun et al., 2016] Thrun, M. C., Lerch, F., Loetsch, J., & Ultsch, A. : Visualization and 3D Printing of Multivariate Data of Biomarkers, in Skala, V. (Ed.), International Conference in Central Europe on Computer Graphics, Visualization and Computer Vision (WSCG), Vol. 24, Plzen, 2016.
- [Ultsch, 2005] Ultsch, A.: Pareto density estimation: A density estimation for knowledge discovery, In Baier, D. & Werrnecke, K. D. (Eds.), Innovations in classification, data science, and information systems, (Vol. 27, pp. 91-100), Berlin, Germany, Springer, 2005.

### Examples

```
data('Hepta')
out=MarkovClustering(Data=Hepta$Data,PlotIt=FALSE)
```

---

MeanShiftClustering    *Mean Shift Clustering*


---

**Description**

Mean Shift Clustering of [Cheng, 1995]

**Usage**

```
MeanShiftClustering(Data,
PlotIt=FALSE,...)
```

**Arguments**

Data	[1:n,1:d] matrix of dataset to be clustered. It consists of n cases of d-dimensional data points. Every case has d attributes, variables or features.
PlotIt	Default: FALSE, If TRUE plots the first three dimensions of the dataset with colored three-dimensional data points defined by the clustering stored in Cls
...	Further arguments to be set for the clustering algorithm, if not set, default arguments are used.

**Details**

the radius used for search can be specified with the "radius" parameter. The maximum number of iterations before algorithm termination is controlled with the "max\_iterations" parameter.

If the distance between two centroids is less than the given radius, one will be removed. A radius of 0 or less means an estimate will be calculated and used for the radius. Default value "0" (numeric).

**Value**

List of	
Cls	[1:n] numerical vector with n numbers defining the classification as the main output of the clustering algorithm. It has k unique numbers representing the arbitrary labels of the clustering.
Object	Object defined by clustering algorithm as the other output of this algorithm

**Author(s)**

Michael Thrun

**References**

[Cheng, 1995] Cheng, Yizong: Mean Shift, Mode Seeking, and Clustering, IEEE Transactions on Pattern Analysis and Machine Intelligence, Vol. 17 (8), pp. 790-799, doi:10.1109/34.400568, 1995.

**Examples**

```
data('Hepta')
out=MeanShiftClustering(Hepta$Data,PlotIt=FALSE,radius=1)
```

---

MinimalEnergyClustering

*Minimal Energy Clustering*


---

**Description**

Hierarchical Clustering using the minimal energy approach of [Szekely/Rizzo, 2005].

**Usage**

```
MinimalEnergyClustering(DataOrDistances, ClusterNo = 0,
DistanceMethod="euclidean", ColorTreshold = 0,Data,...)
```

**Arguments**

DataOrDistances	[1:n,1:d] matrix of dataset to be clustered. It consists of n cases of d-dimensional data points. Every case has d attributes, variables or features. Alternatively, symmetric [1:n,1:n] distance matrix
ClusterNo	A number k which defines k different clusters to be build by the algorithm.
DistanceMethod	See <a href="#">parDist</a> , for example 'euclidean', 'mahalanobis', 'manhattan' (cityblock), 'fJaccard', 'binary', 'canberra', 'maximum'. Any unambiguous substring can be given.
ColorTreshold	Draws outline w.r.t. dendrogram y-axis (height), height of line as scalar should be given
Data	[1:n,1:d] data matrix in the case that DataOrDistances is missing and partial matching does not work.
...	In case of plotting further argument for plot, see <a href="#">as.dendrogram</a>

**Value**

List of	
Cls	If ClusterNo>0: [1:n] numerical vector with n numbers defining the classification as the main output of the clustering algorithm. It has k unique numbers representing the arbitrary labels of the clustering. Otherwise ClusterNo=0: NULL
Dendrogram	Dendrogram of hierarchical clustering algorithm
Object	Ultrametric tree of hierarchical clustering algorithm

**Author(s)**

Michael Thrun

**References**

[Szekely/Rizzo, 2005] Szekely, G. J. and Rizzo, M. L.: Hierarchical Clustering via Joint Between-Within Distances: Extending Ward's Minimum Variance Method, *Journal of Classification*, 22(2) 151-183.<http://dx.doi.org/10.1007/s00357-005-0012-9>, 2005.

**See Also**

[HierarchicalClustering](#)

**Examples**

```
data('Hepta')
out=MinimalEnergyClustering(Hepta$Data,ClusterNo=7)
```

---

MinimaxLinkageClustering

*Minimax Linkage Hierarchical Clustering*

---

**Description**

In the minimax linkage hierarchical clustering every cluster has an associated prototype element that represents that cluster [Bien/Tibshirani, 2011].

**Usage**

```
MinimaxLinkageClustering(DataOrDistances, ClusterNo = 0,
DistanceMethod="euclidean", ColorTreshold = 0,...)
```

**Arguments**

DataOrDistances	[1:n,1:d] matrix of dataset to be clustered. It consists of n cases or d-dimensional data points. Every case has d attributes, variables or features. Alternatively, symmetric [1:n,1:n] distance matrix
ClusterNo	A number k which defines k different clusters to be build by the algorithm.
DistanceMethod	See <a href="#">parDist</a> , for example 'euclidean', 'mahalanobis', 'manhattan' (cityblock), 'fJaccard', 'binary', 'canberra', 'maximum'. Any unambiguous substring can be given.
ColorTreshold	Draws outline w.r.t. dendrogram y-axis (height), height of line as scalar should be given
...	In case of plotting further argument for plot, see <a href="#">as.dendrogram</a>



**Value**

List of

Cls	If, ClusterNo>0: [1:n] numerical vector with n numbers defining the classification as the main output of the clustering algorithm. It has k unique numbers representing the arbitrary labels of the clustering. Otherwise for ClusterNo=0: NULL
Dendrogram	Dendrogram of hierarchical clustering algorithm
Object	Ultrametric tree of hierarchical clustering algorithm

**Author(s)**

Michael Thrun

**References**

[Bien/Tibshirani, 2011] Bien, J., and Tibshirani, R.: Hierarchical Clustering with Prototypes via Minimax Linkage, The Journal of the American Statistical Association, Vol. 106(495), pp. 1075-1084, 2011.

**See Also**

[HierarchicalClustering](#)

**Examples**

```
data('Hepta')
out=MinimaxLinkageClustering(Hepta$Data,ClusterNo=7)
```

---

ModelBasedClustering    *Model Based Clustering*

---

**Description**

Calls Model based clustering of [Fraley/Raftery, 2006] which models a Mixture Of Gaussians (MoG).

**Usage**

```
ModelBasedClustering(Data,ClusterNo=2,PlotIt=FALSE,...)
```

**Arguments**

Data	[1:n,1:d] matrix of dataset to be clustered. It consists of n cases of d-dimensional data points. Every case has d attributes, variables or features.
ClusterNo	A number k which defines k different clusters to be built by the algorithm.
PlotIt	Default: FALSE, If TRUE plots the first three dimensions of the dataset with colored three-dimensional data points defined by the clustering stored in Cls
...	Further arguments to be set for the clustering algorithm, if not set, default arguments are used.

**Details**

see [Thrun, 2017, p. 23] or [Fraley/Raftery, 2002] and [Fraley/Raftery, 2006].

**Value**

List of	
Cls	[1:n] numerical vector with n numbers defining the classification as the main output of the clustering algorithm. It has k unique numbers representing the arbitrary labels of the clustering.
Object	Object defined by clustering algorithm as the other output of this algorithm

**Note**

MoGclustering used in [Thrun, 2017] was renamed to [ModelBasedClustering](#) in this package.

**Author(s)**

Michael Thrun

**References**

[Thrun, 2017] Thrun, M. C.:A System for Projection Based Clustering through Self-Organization and Swarm Intelligence, (Doctoral dissertation), Philipps-Universitaet Marburg, Marburg, 2017.

[Fraley/Raftery, 2002] Fraley, C., and Raftery, A. E.: Model-based clustering, discriminant analysis, and density estimation, Journal of the American Statistical Association, Vol. 97(458), pp. 611-631. 2002.

[Fraley/Raftery, 2006] Fraley, C., and Raftery, A. E.MCLUST version 3: an R package for normal mixture modeling and model-based clustering,DTIC Document, 2006.

**See Also**

[MoGclustering](#)

**Examples**

```
data('Hepta')
out=ModelBasedClustering(Hepta$Data,PlotIt=FALSE)
```

---

ModelBasedVarSelClustering

*Model Based Clustering with Variable Selection*


---

### Description

Model-based clustering with variable selection and estimation of the number of clusters which is either based on [Marbac/Sedki, 2017],[Marbac et al., 2020], or on [Scrucca and Raftery, 2014].

### Usage

```
ModelBasedVarSelClustering(Data,ClusterNo,Type,PlotIt=FALSE, ...)
```

### Arguments

Data	[1:n,1:d] matrix of dataset to be clustered. It consists of n cases of d-dimensional data points. Every case has d attributes, variables or features.
ClusterNo	Numeric which defines number of cluster to search for.
Type	String, either VarSelLCM [Marbac/Sedki, 2017],[Marbac et al., 2020], or clustvarsel [Scrucca and Raftery, 2014].
PlotIt	(optional) Boolean. Default = FALSE = No plotting performed.
...	Further arguments passed on to <a href="#">VarSelCluster</a> or <a href="#">clustvarsel</a> .

### Value

List of	
Cls	[1:n] numerical vector with n numbers defining the classification as the main output of the clustering algorithm. It has k unique numbers representing the arbitrary labels of the clustering.
Object	Object defined by clustering algorithm as the other output of this algorithm

### Author(s)

Quirin Stier, Michael Thrun

### References

[Marbac/Sedki, 2017] Marbac, M. and Sedki, M.: Variable selection for model-based clustering using the integrated complete-data likelihood. *Statistics and Computing*, 27(4), pp. 1049-1063, 2017.

[Marbac et al., 2020] Marbac, M., Sedki, M., & Patin, T.: Variable selection for mixed data clustering: application in human population genomics, *Journal of Classification*, Vol. 37(1), pp. 124-142. 2020.

**Examples**

```

# Hepta
data("Hepta")
Data = Hepta$Data
V = ModelBasedVarSelClustering(Data, ClusterNo=7, Type="VarSelLCM")
Cls = V$Cls
ClusterAccuracy(Hepta$Cls, Cls, K = 7)

V = ModelBasedVarSelClustering(Data, ClusterNo=7, Type="clustvarsel")
Cls = V$Cls
ClusterAccuracy(Hepta$Cls, Cls, K = 7)

## Not run:
# Hearts
heart=VarSelLCM::heart
ztrue <- heart[, "Class"]
Data <- heart[, -13]
V <- ModelBasedVarSelClustering(Data, 2, Type="VarSelLCM")
Cls = V$Cls
ClusterAccuracy(ztrue, Cls, K = 2)

## End(Not run)

```

MoGclustering

*Mixture of Gaussians Clustering using EM***Description**

MixtureOfGaussians (MoG) clustering based on Expectation Maximization (EM) of [Chen et al., 2012] or algorithms closely resembling EM of [Benaglia/Chauveau/Hunter, 2009].

**Usage**

```
MoGclustering(Data, ClusterNo=2, Type, PlotIt=FALSE, Silent=TRUE, ...)
```

**Arguments**

Data	[1:n,1:d] matrix of dataset to be clustered. It consists of n cases of d-dimensional data points. Every case has d attributes, variables or features.
ClusterNo	A number k which defines k different clusters to be built by the algorithm.
Type	string defining approach to select: initialization approach of "EM" or "kmeans" of [Chen et al., 2012], or other methods "mvnormalmixEM" [McLachlan/Peel, 2000], "npEM"[Benaglia et al., 2009] or its extension "mvnpEM" [Chauveau/Hoang, 2016].
PlotIt	Default: FALSE, if TRUE plots the first three dimensions of the dataset with colored three-dimensional data points defined by the clustering stored in Cls
Silent	(optional) Boolean: print output or not (Default = FALSE = no output)
...	Further arguments to be set for the clustering algorithm, if not set, default arguments are used, see package mixtools <b>EMCluster</b> or <b>mixtools</b> for details.

**Details**

Algorithms for clustering through EM or its close resembles.

**Value**

List of

`Cls` [1:n] numerical vector with n numbers defining the classification as the main output of the clustering algorithm. It has k unique numbers representing the arbitrary labels of the clustering.

`Object` Object defined by clustering algorithm as the other output of this algorithm

**Note**

MoG used in [Thrun, 2017] was renamed to [ModelBasedClustering](#) in this package. Type="mvnormalmixEM" sometimes fails

**Author(s)**

Michael Thrun

**References**

[Chen et al., 2012] Chen, W., Maitra, R., & Melnykov, V.: EMCluster: EM Algorithm for Model-Based Clustering of Finite Mixture Gaussian Distribution, R Package, URL <http://cran.r-project.org/package=EMCluster>, 2012.

[Chauveau/Hoang, 2016] Chauveau, D., & Hoang, V. T. L.: Nonparametric mixture models with conditionally independent multivariate component densities, Computational Statistics & Data Analysis, Vol. 103, pp. 1-16. 2016.

[Benaglia et al., 2009] Benaglia, T., Chauveau, D., and Hunter, D. R.: An EM-like algorithm for semi-and nonparametric estimation in multivariate mixtures. Journal of Computational and Graphical Statistics, 18(2), pp. 505-526, 2009.

[McLachlan/Peel, 2000] D. McLachlan, G. J. and Peel, D.: Finite Mixture Models, John Wiley and Sons, Inc, 2000.

**See Also**

[ModelBasedClustering](#)

**Examples**

```
data('Hepta')
Data = Hepta$Data
out=MoGclustering(Data,ClusterNo=7,Type="EM",PlotIt=FALSE)
V=out$Cls
```

```
V1 = MoGclustering(Data,ClusterNo=7,Type="mvnpEM")
Cls1 = V1$Cls
```

```

V2 = MoGclustering(Data,ClusterNo=7,Type="npEM")
Cls2 = V2$Cls

## Not run:
#does not work always
  V3 = MoGclustering(Data,ClusterNo=7,Type="mvnormalmixEM")
  Cls3 = V3$Cls

## End(Not run)

```

---

MSTclustering

*MST-kNN clustering algorithm [Inostroza-Ponta, 2008].*


---

### Description

Performs the MST-kNN clustering algorithm which generate a clustering solution with automatic k determination using two proximity graphs: Minimal Spanning Tree (MST) and k-Nearest Neighbor (kNN) which are recursively intersected.

### Usage

```
MSTclustering(DataOrDistances, DistanceMethod = "euclidean",PlotIt=FALSE, ...)
```

### Arguments

DataOrDistances	Either [1:n,1:n] symmetric distance matrix or [1:n,1:d] not symmetric data matrix of n cases and d variables
DistanceMethod	Optional distance method of data, default is euclid, see <a href="#">parDist</a> for details
PlotIt	Default: FALSE, if TRUE plots the first three dimensions of the dataset with colored three-dimensional data points defined by the clustering stored in Cls
...	Optional, further arguments for <a href="#">mst.knn</a>

### Details

Does not work on Hepta with euclidean distances.

### Value

List of	
Cls	[1:n] numerical vector with n numbers defining the classification as the main output of the clustering algorithm. It has k unique numbers representing the arbitrary labels of the clustering.
Object	Object defined by clustering algorithm as the other output of this algorithm

**Author(s)**

Michael Thrun

**References**

[Inostroza-Ponta, 2008] Inostroza-Ponta, M.: An integrated and scalable approach based on combinatorial optimization techniques for the analysis of microarray data, University of Newcastle, ISBN, 2008

**See Also**

[mst.knn](#)

**Examples**

```
data(Hepta)

MSTclustering(Hepta$Data)
```

---

NetworkClustering      *Network Clustering*

---

**Description**

Either leiden [Traag et al., 2019] or louvain [Blondel et al., 2008] clustering

**Usage**

```
NetworkClustering(DataOrDistances=NULL,Adjacency=NULL,
Type="louvain",Radius=FALSE,PlotIt=FALSE,...)
```

**Arguments**

DataOrDistances	NULL or: [1:n,1:d] matrix of dataset to be clustered. It consists of n cases or d-dimensional data points. Every case has d attributes, variables or features. Alternatively, symmetric [1:n,1:n] distance matrix
Adjacency	Used if DataOrDistances is NULL, matrix [1:n,1:n] defining which points are adjacent to each other by the number 1; not adjacent: 0
Type	Either "louvain" or "leiden"
Radius	Scalar, Radius for unit disk graph (r-ball graph) if adjacency matrix is missing. Automatic estimation can be done either with =TRUE [Ultsch, 2005] or FALSE [Thrun et al., 2016]
PlotIt	Default: FALSE, If TRUE plots the first three dimensions of the dataset with colored three-dimensional data points defined by the clustering stored in C1s

... Further arguments to be set for the clustering algorithm, if not set, default arguments are used.

### Details

DataOrDistances is used to compute the Adjacency matrix if this input is missing. Then a unit-disk (R-ball) graph is calculated. Radius=TRUE only works if data matrix is given.

### Value

List of

Cls [1:n] numerical vector with n numbers defining the classification as the main output of the clustering algorithm. It has k unique numbers representing the arbitrary labels of the clustering. Points which cannot be assigned to a cluster will be reported with 0.

Object Object defined by clustering algorithm as the other output of this algorithm

### Note

leiden requires igraph package and an installed python version. automatic installation may not work. manual call in console has to be in this case `conda install -c conda-forge leidenalg`

### Author(s)

Michael Thrun

### References

[Blondel et al., 2008] Blondel, V. D., Guillaume, J.-L., Lambiotte, R., & Lefebvre, E.: Fast unfolding of communities in large networks, *Journal of statistical mechanics: theory and experiment*, Vol. 2008(10), pp. P10008. 2008.

[Traag et al., 2019] Traag, V. A., Waltman, L., & van Eck, N. J.: From Louvain to Leiden: guaranteeing well-connected communities, *Scientific reports*, Vol. 9(1), pp. 1-12. 2019.

### Examples

```
data('Hepta')
#out=NetworkClustering(Hepta$Data,PlotIt=FALSE)
```



---

NeuralGasClustering    *Neural gas algorithm for clustering*

---

**Description**

Neural gas clustering published by [Martinetz et al., 1993] and implemented by [Bodenhofer et al., 2011].

**Usage**

```
NeuralGasClustering(Data, ClusterNo, PlotIt=FALSE, ...)
```

**Arguments**

Data	[1:n,1:d] matrix of dataset to be clustered. It consists of n cases of d-dimensional data points. Every case has d attributes, variables or features.
ClusterNo	A number k which defines k different clusters to be built by the algorithm.
PlotIt	Default: FALSE, If TRUE plots the first three dimensions of the dataset with colored three-dimensional data points defined by the clustering stored in C1s
...	Further arguments to be set for the clustering algorithm, if not set, default arguments are used.

**Value**

List of	
C1s	[1:n] numerical vector with n numbers defining the classification as the main output of the clustering algorithm. It has k unique numbers representing the arbitrary labels of the clustering.
Object	Object defined by clustering algorithm as the other output of this algorithm

**Author(s)**

Michael Thrun

**References**

[Dimitriadou, 2002] Dimitriadou, E.: cclust-convex clustering methods and clustering indexes. R package, 2002,

[Martinetz et al., 1993] Martinetz, T. M., Berkovich, S. G., & Schulten, K. J.: 'Neural-gas' network for vector quantization and its application to time-series prediction, IEEE Transactions on Neural Networks, Vol. 4(4), pp. 558-569. 1993.

**Examples**

```
data('Hepta')
out=NeuralGasClustering(Hepta$Data,ClusterNo=7,PlotIt=FALSE)
```

---

OPTICSclustering      *OPTICS Clustering*

---

### Description

OPTICS (Ordering points to identify the clustering structure) clustering algorithm [Ankerst et al.,1999].

### Usage

```
OPTICSclustering(Data, MaxRadius,RadiusThreshold, minPts = 5, PlotIt=FALSE,...)
```

### Arguments

Data	[1:n,1:d] matrix of dataset to be clustered. It consists of n cases of d-dimensional data points. Every case has d attributes, variables or features.
MaxRadius	Upper limit neighborhood in the R-ball graph/unit disk graph), size of the epsilon neighborhood (eps) [Ester et al., 1996, p. 227]. If NULL, automatic estimation is done using insights of [Ultsch, 2005].
RadiusThreshold	Threshold to identify clusters (RadiusThreshold <= MaxRadius), if NULL 0.9*MaxRadius is set.
minPts	Number of minimum points in the eps region (for core points). In principle minimum number of points in the unit disk, if the unit disk is within the cluster (core) [Ester et al., 1996, p. 228]. If NULL, its 2.5 percent of points.
PlotIt	Default: FALSE, If TRUE plots the first three dimensions of the dataset with colored three-dimensional data points defined by the clustering stored in Cls
...	Further arguments to be set for the clustering algorithm, if not set, default arguments are used.

### Details

...

### Value

List of	
Cls	[1:n] numerical vector defining the clustering; this classification is the main output of the algorithm. Points which cannot be assigned to a cluster will be reported as members of the noise cluster with 0.
Object	Object defined by clustering algorithm as the other output of this algorithm

### Author(s)

Michael Thrun

## References

[Ankerst et al.,1999] Mihael Ankerst, Markus M. Breunig, Hans-Peter Kriegel, Joerg Sander: OPTICS: Ordering Points To Identify the Clustering Structure, ACM SIGMOD international conference on Management of data, ACM Press, pp. 49-60, 1999.

[Ester et al., 1996] Ester, M., Kriegel, H.-P., Sander, J., & Xu, X.: A density-based algorithm for discovering clusters in large spatial databases with noise, Proc. Kdd, Vol. 96, pp. 226-231, 1996.

[Ultsch, 2005] Ultsch, A.: Pareto density estimation: A density estimation for knowledge discovery, In Baier, D. & Wernicke, K. D. (Eds.), Innovations in classification, data science, and information systems, (Vol. 27, pp. 91-100), Berlin, Germany, Springer, 2005.

## See Also

[optics](#)

## Examples

```
data('Hepta')
out=OPTICSclustering(Hepta$Data,MaxRadius=NULL,RadiusThreshold=NULL,minPts=NULL,PlotIt = FALSE)
```

---

PAMclustering

*Partitioning Around Medoids (PAM)*

---

## Description

Partitioning (clustering) of the data into k clusters around medoids, a more robust version of k-means [Rousseeuw/Kaufman, 1990, p. 68-125] .

## Usage

```
PAMclustering(DataOrDistances,ClusterNo,
PlotIt=FALSE,Standardization=TRUE,Data,...)
```

## Arguments

DataOrDistances	[1:n,1:d] matrix of dataset to be clustered. It consists of n cases of d-dimensional data points. Every case has d attributes, variables or features. Alternatively, symmetric [1:n,1:n] distance matrix
ClusterNo	A number k which defines k different clusters to be built by the algorithm.
PlotIt	Default: FALSE, If TRUE plots the first three dimensions of the dataset with colored three-dimensional data points defined by the clustering stored in C1s

**Standardization**

DataOrDistances is standardized before calculating the dissimilarities. Measurements are standardized for each variable (column), by subtracting the variable's mean value and dividing by the variable's mean absolute deviation. If DataOrDistances is already a distance matrix, then this argument will be ignored.

**Data**

[1:n,1:d] data matrix in the case that DataOrDistances is missing and partial matching does not work.

**...**

Further arguments to be set for the clustering algorithm, if not set, default arguments are used.

**Details**

[Rousseeuw/Kaufman, 1990, chapter 2] or [Reynolds et al., 1992].

**Value****List of****Cls**

[1:n] numerical vector with n numbers defining the classification as the main output of the clustering algorithm. It has k unique numbers representing the arbitrary labels of the clustering.

**Object**

Object defined by clustering algorithm as the other output of this algorithm

**Author(s)**

Michael Thrun

**References**

[Rousseeuw/Kaufman, 1990] Rousseeuw, P. J., & Kaufman, L.: Finding groups in data, Belgium, John Wiley & Sons Inc., ISBN: 0471735787, doi:10.1002/9780470316801, Online ISBN: 9780470316801, 1990.

[Reynolds et al., 1992] Reynolds, A., Richards, G., de la Iglesia, B. and Rayward-Smith, V.: Clustering rules: A comparison of partitioning and hierarchical clustering algorithms, Journal of Mathematical Modelling and Algorithms 5, 475-504, DOI:10.1007/s10852-005-9022-1, 1992.

**Examples**

```
data('Hepta')
out=PAMclustering(Hepta$Data,ClusterNo=7,PlotIt=FALSE)
```

---

pdfClustering	<i>Probability Density Distribution Clustering</i>
---------------	--

---

**Description**

Clustering via non parametric density estimation

**Usage**

```
pdfClustering(Data, PlotIt = FALSE, ...)
```

**Arguments**

Data	[1:n,1:d] matrix of dataset to be clustered. It consists of n cases of d-dimensional data points. Every case has d attributes, variables or features.
PlotIt	Default: FALSE, if TRUE plots the first three dimensions of the dataset with colored three-dimensional data points defined by the clustering stored in C1s
...	Further arguments to be set for the clustering algorithm, if not set, default arguments are used.

**Details**

Cluster analysis is performed by the density-based procedures described in Azzalini and Torelli (2007) and Menardi and Azzalini (2014), and summarized in Azzalini and Menardi (2014).

**Value**

List of	
C1s	[1:n] numerical vector with n numbers defining the classification as the main output of the clustering algorithm. It has k unique numbers representing the arbitrary labels of the clustering.
Object	Object defined by clustering algorithm as the other output of this algorithm

**Author(s)**

Michael Thrun

**References**

Azzalini, A., Menardi, G. (2014). Clustering via nonparametric density estimation: the R package pdfCluster. *Journal of Statistical Software*, 57(11), 1-26, URL <http://www.jstatsoft.org/v57/i11/>.

Azzalini A., Torelli N. (2007). Clustering via nonparametric density estimation. *Statistics and Computing*. 17, 71-80.

Menardi, G., Azzalini, A. (2014). An advancement in clustering via nonparametric density estimation. *Statistics and Computing*. DOI: 10.1007/s11222-013-9400-x.

**Examples**

```
data('Hepta')
out=pdfClustering(Hepta$Data,PlotIt=FALSE)
```

---

 PenalizedRegressionBasedClustering

*Penalized Regression-Based Clustering of [Wu et al., 2016].*

---

**Description**

Clustering is performed through penalized regression with grouping pursuit

**Usage**

```
PenalizedRegressionBasedClustering(Data, FirstLambda,
  SecondLambda, Tau, PlotIt = FALSE, ...)
```

**Arguments**

Data	[1:n,1:d] matrix of dataset to be clustered. It consists of n cases of d-dimensional data points. Every case has d attributes, variables or features.
FirstLambda	Set 1 for quadratic penalty based algorithm, 0.4 for revised ADMM.
SecondLambda	The magnitude of grouping penalty.
Tau	Tuning parameter: tau, related to grouping penalty.
PlotIt	Default: FALSE, if TRUE plots the first three dimensions of the dataset with colored three-dimensional data points defined by the clustering stored in Cls
...	Further arguments for <a href="#">PRclust</a> , enables also usage of [Pan et al., 2013].

**Details**

Parameters are rather challenging to choose.

**Value**

List of	
Cls	[1:n] numerical vector with n numbers defining the classification as the main output of the clustering algorithm. It has k unique numbers representing the arbitrary labels of the clustering.
Object	Object defined by clustering algorithm as the other output of this algorithm

**Note**

Data matrix is internally transposed in order to fit the definition of the algorithm.

**Author(s)**

Michael Thrun

**References**

[Pan et al., 2013] Pan, W., Shen, X., & Liu, B.: Cluster analysis: unsupervised learning via supervised learning with a non-convex penalty, *The Journal of Machine Learning Research*, Vol. 14(1), pp. 1865-1889. 2013.

[Wu et al., 2016] Wu, C., Kwon, S., Shen, X., & Pan, W.: A new algorithm and theory for penalized regression-based clustering, *The Journal of Machine Learning Research*, Vol. 17(1), pp. 6479-6503. 2016.

**Examples**

```
data(Hepta)
Data=Hepta$Data
out=PenalizedRegressionBasedClustering(Data,0.4,1,2,PlotIt=FALSE)
table(out$Cls,Hepta$Cls)
```

---

 ProjectionPursuitClustering

*Cluster Identification using Projection Pursuit as described in [Hofmeyr/Pavlidis, 2019].*

---

**Description**

Summarizes recent projection pursuit methods for clustering based on [Hofmeyr/Pavlidis, 2015], [Hofmeyr, 2016] and [Pavlidis et al., 2016] .

**Usage**

```
ProjectionPursuitClustering(Data,ClusterNo,Type="MinimumDensity",
PlotIt=FALSE,PlotSolution=FALSE,...)
```

**Arguments**

Data	[1:n,1:d] matrix of dataset to be clustered. It consists of n cases of d-dimensional data points. Every case has d attributes, variables or features.
ClusterNo	A number k which defines k different clusters to be built by the algorithm.
Type	Either MinimumDensity[Pavlidis et al., 2016] MaximumClusterbility[Hofmeyr/Pavlidis, 2015], or NormalisedCut [Hofmeyr, 2016] or KernelPCA [Hofmeyr/Pavlidis, 2019].
PlotIt	Default: FALSE, if TRUE plots the first three dimensions of the dataset with colored three-dimensional data points defined by the clustering stored in Cls
PlotSolution	Plots the partitioning solution as a tree as described in
...	Further arguments to be set for the clustering algorithm, if not set, default arguments are used.

**Details**

The details of the options for projection pursuit and partitioning of data are defined in [Hofmeyr/Pavlidis, 2019].

"KernelPCA" uses additionally the package kernlab and is implemented as given in the fifth example on page 21, section "extension" of [Hofmeyr/Pavlidis, 2019].

The first idea of using non-PCA projections for clustering was published by [Bock, 1987] as an definition. However, to the knowledge of the author it was not applied to any data. The first systematic comparison to Projection-Pursuit Methods [ProjectionPursuitClustering](#) and [AutomaticProjectionBasedClustering](#) can be found in [Thrun/Ultsch, 2018]. For PCA-based clustering methods please see [TandemClustering](#)

**Value**

List of

`cls` [1:n] numerical vector with n numbers defining the classification as the main output of the clustering algorithm. It has k unique numbers representing the arbitrary labels of the clustering. Points which cannot be assigned to a cluster will be reported with 0.

`Object` Object defined by clustering algorithm as the other output of this algorithm

**Author(s)**

Michael Thrun

**References**

[Hofmeyr/Pavlidis, 2015] Hofmeyr, D., & Pavlidis, N.: Maximum clusterability divisive clustering, Proc. 2015 IEEE Symposium Series on Computational Intelligence, pp. 780-786, IEEE, 2015.

[Hofmeyr/Pavlidis, 2019] Hofmeyr, D., & Pavlidis, N.: PPCI: an R Package for Cluster Identification using Projection Pursuit, The R Journal, 2019.

[Hofmeyr, 2016] Hofmeyr, D. P.: Clustering by minimum cut hyperplanes, IEEE Transactions on Pattern Analysis and Machine Intelligence, Vol. 39(8), pp. 1547-1560. 2016.

[Pavlidis et al., 2016] Pavlidis, N. G., Hofmeyr, D. P., & Tasoulis, S. K.: Minimum density hyperplanes, The Journal of Machine Learning Research, Vol. 17(1), pp. 5414-5446. 2016.

[Thrun/Ultsch, 2018] Thrun, M. C., & Ultsch, A.: Using Projection based Clustering to Find Distance and Density based Clusters in High-Dimensional Data, Journal of Classification, Vol. in revision, 2018.

[Bock, 1987] Bock, H.: On the interface between cluster analysis, principal component analysis, and multidimensional scaling, Multivariate statistical modeling and data analysis, (pp. 17-34), Springer, 1987.

**Examples**

```
data('Hepta')
out=ProjectionPursuitClustering(Hepta$Data,ClusterNo=7,PlotIt=FALSE)
```



---

 QTclustering

*Stochastic QT Clustering*


---

**Description**

Stochastic quality clustering of [Heyer et al., 1999] with an improved implementation by [Scharl/Leisch, 2006].

**Usage**

```
QTclustering(Data,Radius,PlotIt=FALSE,...)
```

**Arguments**

Data	[1:n,1:d] matrix of dataset to be clustered. It consists of n cases of d-dimensional data points. Every case has d attributes, variables or features.
Radius	Maximum radius of clusters. If NULL, automatic estimation can be done with [Thrun et al., 2016] if not otherwise set.
PlotIt	Default: FALSE, if TRUE plots the first three dimensions of the dataset with colored three-dimensional data points defined by the clustering stored in Cls
...	Further arguments to be set for the clustering algorithm, if not set, default arguments are used.

**Value**

List of	
Cls	[1:n] numerical vector with n numbers defining the classification as the main output of the clustering algorithm. It has k unique numbers representing the arbitrary labels of the clustering. Points which cannot be assigned to a cluster will be reported with 0.
Object	Object defined by clustering algorithm as the other output of this algorithm

**Author(s)**

Michael Thrun

**References**

[Heyer et al., 1999] Heyer, L. J., Kruglyak, S., & Yooseph, S.: Exploring expression data: identification and analysis of coexpressed genes, *Genome research*, Vol. 9(11), pp. 1106-1115. 1999.

[Scharl/Leisch, 2006] Scharl, T., & Leisch, F.: The stochastic QT-clust algorithm: evaluation of stability and variance on time-course microarray data, in Rizzi, A. & Vichi, M. (eds.), *Proc. Proceedings in Computational Statistics (Compstat)*, pp. 1015-1022, Physica Verlag, Heidelberg, Germany, 2006.

[Thrun et al., 2016] Thrun, M. C., Lerch, F., Loetsch, J., & Ultsch, A. : Visualization and 3D Printing of Multivariate Data of Biomarkers, in Skala, V. (Ed.), International Conference in Central Europe on Computer Graphics, Visualization and Computer Vision (WSCG), Vol. 24, Plzen, 2016.

[Ultsch, 2005] Ultsch, A.: Pareto density estimation: A density estimation for knowledge discovery, In Baier, D. & Werrnecke, K. D. (Eds.), Innovations in classification, data science, and information systems, (Vol. 27, pp. 91-100), Berlin, Germany, Springer, 2005.

## Examples

```
data('Hepta')
out=QTclustering(Hepta$Data,Radius=NULL,PlotIt=FALSE)
```

---

```
RobustTrimmedClustering
      Robust Trimmed Clustering
```

---

## Description

Robust Trimmed Clustering invented by [Garcia-Escudero et al., 2008] and implemented by [Fritz et al., 2012].

## Usage

```
RobustTrimmedClustering(Data, ClusterNo,
Alpha=0.05,PlotIt=FALSE,...)
```

## Arguments

Data	[1:n,1:d] matrix of dataset to be clustered. It consists of n cases of d-dimensional data points. Every case has d attributes, variables or features.
ClusterNo	A number k which defines k different clusters to be built by the algorithm.
PlotIt	Default: FALSE, if TRUE plots the first three dimensions of the dataset with colored three-dimensional data points defined by the clustering stored in C1s
Alpha	No trimming is done equals to alpha =0, otherwise proportion of datapoints to be trimmed, <code>tclust</code> uses 0.05 as default.
...	Further arguments to be set for the clustering algorithm, e.g. <code>.nstart</code> (number of random initializations), <code>iter.max</code> (maximum number of concentration steps), <code>restr</code> and <code>restr.fact</code> described in details. If not set, default arguments are used.

**Details**

"This iterative algorithm initializes k clusters randomly and performs "concentration steps" in order to improve the current cluster assignment. The number of maximum concentration steps to be performed is given by iter.max. For approximately obtaining the global optimum, the system is initialized nstart times and concentration steps are performed until convergence or iter.max is reached. When processing more complex data sets higher values of nstart and iter.max have to be specified (obviously implying extra computation time). ... The larger restr.fact is chosen, the looser is the restriction on the scatter matrices, allowing for more heterogeneity among the clusters. On the contrary, small values of restr.fact close to 1 imply very equally scattered clusters. This idea of constraining cluster scatters to avoid spurious solutions goes back to Hathaway (1985), who proposed it in mixture fitting problems" [Fritz et al., 2012]. The type of constraint restr can be set to "eigen", "deter" or "sigma.". Please see [tclust](#) for further parameter description.

**Value**

List of

cls [1:n] numerical vector with n numbers defining the classification as the main output of the clustering algorithm. It has k unique numbers representing the arbitrary labels of the clustering.

Object Object defined by clustering algorithm as the other output of this algorithm

**Author(s)**

Michael Thrun

**References**

[Garcia-Escudero et al., 2008] Garcia-Escudero, L. A., Gordaliza, A., Matran, C., & Mayo-Iscar, A.: A general trimming approach to robust cluster analysis, *The annals of Statistics*, Vol. 36(3), pp. 1324-1345. 2008.

[Fritz et al., 2012] Fritz, H., Garcia-Escudero, L. A., & Mayo-Iscar, A.: tclust: An R package for a trimming approach to cluster analysis, *Journal of statistical Software*, Vol. 47(12), pp. 1-26. 2012.

**Examples**

```
data('Hepta')
out=RobustTrimmedClustering(Hepta$Data,ClusterNo=7,Alpha=0,PlotIt=FALSE)
```

---

SharedNearestNeighborClustering  
*SNN clustering*

---

**Description**

Shared Nearest Neighbor Clustering of [Ertoz et al., 2003].

**Usage**

```
SharedNearestNeighborClustering(Data,Knn,
Radius,minPts,PlotIt=FALSE,
UpperLimitRadius,...)
```

**Arguments**

Data	[1:n,1:d] matrix of dataset to be clustered. It consists of n cases of d-dimensional data points. Every case has d attributes, variables or features.
Knn	Number of neighbors to consider to calculate the shared nearest neighbors.
Radius	Eps [Ester et al., 1996, p. 227] neighborhood in the R-ball graph/unit disk graph), size of the epsilon neighborhood. If NULL, automatic estimation is done using insights of [Ultsch, 2005].
minPts	Number of minimum points in the eps region (for core points). In principle minimum number of points in the unit disk, if the unit disk is within the cluster (core) [Ester et al., 1996, p. 228]. if NULL, its 2.5 percent of points.
PlotIt	Default: FALSE, if TRUE plots the first three dimensions of the dataset with colored three-dimensional data points defined by the clustering stored in C1s
UpperLimitRadius	Limit for radius search, experimental
...	Further arguments to be set for the clustering algorithm, if not set, default arguments are used.

**Details**

..

**Value**

List of	
C1s	[1:n] numerical vector defining the clustering; this classification is the main output of the algorithm. Points which cannot be assigned to a cluster will be reported as members of the noise cluster with 0.
Object	Object defined by clustering algorithm as the other output of this algorithm

**Author(s)**

Michael Thrun

**References**

[Ertoz et al., 2003] Levent Ertoz, Michael Steinbach, Vipin Kumar: Finding Clusters of Different Sizes, Shapes, and Densities in Noisy, High Dimensional Data, SIAM International Conference on Data Mining, 47-59, 2003.

**See Also**[sNNclust](#)**Examples**

```
data('Hepta')
out=SharedNearestNeighborClustering(
Hepta$Data, Knn=7,Radius=NULL,minPts=NULL,PlotIt = FALSE)
```

---

SOMclustering	<i>self-organizing maps based clustering implemented by [Wherens, Buydens, 2017].</i>
---------------	---

---

**Description**

Either the variant k-batch or k-online is possible in which every unit can be seen approximately as an cluster.

**Usage**

```
SOMclustering(Data,LC=c(1,2),ClusterNo=NULL,
Mode="online",PlotIt=FALSE,rln=100,alpha = c(0.05, 0.01),...)
```

**Arguments**

Data	[1:n,1:d] matrix of dataset to be clustered. It consists of n cases of d-dimensional data points. Every case has d attributes, variables or features.
LC	Lines and Columns of a very small SOM, usually every unit is a cluster, will be ignored if ClusterNo is not NULL.
ClusterNo	Optional, A number k which defines k different clusters to be built by the algorithm. LC will then be set accordingly.
Mode	Either "batch" or "online"
PlotIt	Default: FALSE, if TRUE plots the first three dimensions of the dataset with colored three-dimensional data points defined by the clustering stored in Cls
rln	Please see <a href="#">supersom</a>
alpha	Please see <a href="#">supersom</a>
...	Further arguments to be set for the clustering algorithm in <a href="#">somgrid</a> , if not set, default arguments are used.

**Details**

This clustering algorithm is based on very small maps and, hence, not emergent (c.f. [Thrun, 2018, p.37]). A 3x3 map means 9 units leading to 9 clusters.

Batch is a deterministic clustering approach whereas online is a stochastic clustering approach and research indicates that online should be preferred (c.f. [Thrun, 2018, p.37]).

**Value**

List of	
Cls	[1:n] numerical vector defining the classification as the main output of the clustering algorithm
Object	Object defined by clustering algorithm as the other output of this algorithm

**Author(s)**

Michael Thrun

**References**

[Wehrens, Buydens, 2017] R. Wehrens and L.M.C. Buydens, J. Stat. Softw. 21 (5), 2007; R. Wehrens and J. Kruisselbrink, submitted, 2017.

[Thrun, 2018] Thrun, M.C., Projection Based Clustering through Self-Organization and Swarm Intelligence. 2018, Heidelberg: Springer.

**Examples**

```
data('Hepta')
out=SOMclustering(Hepta$Data,ClusterNo=7,PlotIt=FALSE)
```

---

SOTAclustering

*SOTA Clustering*

---

**Description**

Self-organizing Tree Algorithm (SOTA) introduced by [Herrero et al., 2001].

**Usage**

```
SOTAclustering(Data, ClusterNo,PlotIt=FALSE,UnrestGrowth,...)
```

**Arguments**

Data	[1:n,1:d] matrix of dataset to be clustered. It consists of n cases of d-dimensional data points. Every case has d attributes, variables or features.
ClusterNo	A number k which defines k different clusters to be built by the algorithm.
PlotIt	Default: FALSE, if TRUE plots the first three dimensions of the dataset with colored three-dimensional data points defined by the clustering stored in Cls
UnrestGrowth	TRUE: forces the ClusterNo option to uphold. FALSE: enables the algorithm to find its own number of clusters, in this cases ClusterNo should contain a high number because it is internally set as the number of iterations which is either reached or the max diversity criteria is satisfied priorly.
...	Further arguments to be set for the clustering algorithm, if not set, default arguments are used.

**Value**

List of	
Cls	[1:n] numerical vector with n numbers defining the classification as the main output of the clustering algorithm. It has k unique numbers representing the arbitrary labels of the clustering.
sotaObject	Object defined by clustering algorithm as the other output of this algorithm

**Note**

\*Luis Winckelman intergrated several function from clValid because it's ORPHANED.

**Author(s)**

Luis Winckelmann\*, Vasyl Pihur, Guy Brock, Susmita Datta, Somnath Datta

**References**

[Herrero et al., 2001] Herrero, J., Valencia, A., & Dopazo, J.: A hierarchical unsupervised growing neural network for clustering gene expression patterns, *Bioinformatics*, Vol. 17(2), pp. 126-136. 2001.

**Examples**

```
#Does Work
data('Hepta')
out=SOTAClustering(Hepta$Data,ClusterNo=7)
table(Hepta$Cls,out$Cls)
```

```
#Does not work well
data('Lsun3D')
out=SOTAClustering(Lsun3D$Data,ClusterNo=100,PlotIt=FALSE,UnrestGrowth=FALSE)
```

---

SparseClustering      *Sparse Clustering*

---

**Description**

Implements the sparse clustering methods of [Witten/Tibshirani, 2010].

**Usage**

```
SparseClustering(DataOrDistances, ClusterNo, Type="Hierarchical",
PlotIt=F,Silent=FALSE, NoPerms=10,Wbounds, ...)
```

**Arguments**

DataOrDistances	Either a [1:n,1:d] matrix of dataset to be clustered. It consists of n cases of d-dimensional data points. Every case has d attributes, variables or features. or a [1:n,1:n] symmetric distance matrix.
ClusterNo	Numeric indicating number to cluster to find in Tree/ Dendrogramm in case of Type="Hierachical" or numer of cluster to use in Type="kmeans"
Type	(optional) Char selecting methods Hierarchical or kmeans. Default: "Hierarchical"
PlotIt	(optional) Boolean. Default = FALSE = No plotting performed.
Silent	(optional) Boolean: print output or not (Default = FALSE = no output)
NoPerms	(optional), numeric scalar, Number of permutations.
Wbounds	(optional) numeric vector, range of tuning parameters to consider. This is the L1 bound on w, the feature weights [Witten/Tibshirani, 2010].
...	Further arguments passed on to sparse <a href="#">HierarchicalSparseCluster</a> or <a href="#">KMeansSparseCluster</a> depending on Type.

**Value**

List of	
Cls	[1:n] numerical vector with n numbers defining the classification as the main output of the clustering algorithm. It has k unique numbers representing the arbitrary labels of the clustering.
Object	Object defined by clustering algorithm as the other output of this algorithm
Tree	Object Tree if Type="Hierachical" is used.

**Note**

Quality of clustering results varies between sparse hierarchical if data is given in comparison to the case that distances are given.

**Author(s)**

Quirin Stier, Michael Thrun

**References**

[Witten/Tibshirani, 2010] Witten, D. and Tibshirani, R.: A Framework for Feature Selection in Clustering. Journal of the American Statistical Association, Vol. 105(490), pp. 713-726, 2010.



**Examples**

```

# Hepta
data("Hepta")
Data = Hepta$Data
V1 = SparseClustering(Data, ClusterNo=7, Type="kmeans")
Cls1 = V1$Cls

V2 = SparseClustering(Data, ClusterNo=7, Type="Hierarchical")
Cls2 = V2$Cls

InputDistances = parallelDist::parDist(Data, method="euclidean")
DistanceMatrix = as.matrix(InputDistances)
V3 = SparseClustering(DistanceMatrix, ClusterNo=7, Type="Hierarchical")
Cls3 = V3$Cls

## Not run:
set.seed(1)
Data = matrix(rnorm(100*50),ncol=50)
y = c(rep(1,50),rep(2,50))
Data[y==1,1:25] = Data[y==1,1:25]+2

V1 = SparseClustering(Data, ClusterNo=2, Type="kmeans")
Cls1 = V1$Cls

## End(Not run)

```

---

SpectralClustering      *Spectral Clustering*

---

**Description**

Clusters the Data into "ClusterNo" different clusters using the Spectral Clustering method

**Usage**

```
SpectralClustering(Data, ClusterNo, PlotIt=FALSE, ...)
```

**Arguments**

Data	[1:n,1:d] matrix of dataset to be clustered. It consists of n cases of d-dimensional data points. Every case has d attributes, variables or features.
ClusterNo	A number k which defines k different clusters to be built by the algorithm.
PlotIt	default: FALSE, if TRUE plots the first three dimensions of the dataset with colored three-dimensional data points defined by the clustering stored in Cls

... Further arguments to be set for the clustering algorithm, if not set, default arguments are used. e.g.:

kernel : Kernelmethod, possible options: rbf`dot` Radial Basis kernel function "Gaussian" poly`dot` Polynomial kernel function vanill`dot` Linear kernel function tanh`dot` Hyperbolic tangent kernel function laplace`dot` Laplacian kernel function bess`dot` Bessel kernel function anova`dot` ANOVA RBF kernel function splin`dot` Spline kernel string`dot` String kernel

kpar : Kernelparameter: a character string or the list of hyper-parameters (kernel parameters). The default character string "automatic" uses a heuristic to determine a suitable value for the width parameter of the RBF kernel. "local" (local scaling) uses a more advanced heuristic and sets a width parameter for every point in the data set. A list can also be used containing the parameters to be used with the kernel function.

### Value

List of

Cls [1:n] numerical vector with n numbers defining the classification as the main output of the clustering algorithm. It has k unique numbers representing the arbitrary labels of the clustering.

Object Object defined by clustering algorithm as the other output of this algorithm

### Author(s)

Michael Thrun

### References

[Ng et al., 2002] Ng, A. Y., Jordan, M. I., & Weiss, Y.: On spectral clustering: Analysis and an algorithm, *Advances in neural information processing systems*, Vol. 2, pp. 849-856. 2002.

### Examples

```
data('Hepta')
out=SpectralClustering(Hepta$Data,ClusterNo=7,PlotIt=FALSE)
```

### Description

Spectrum is a self-tuning spectral clustering method for single or multi-view data. In this wrapper restricted to the standard use in other clustering algorithms.

**Usage**

```
Spectrum(Data, Type = 2, ClusterNo = NULL,
PlotIt = FALSE, Silent = TRUE, PlotResults = FALSE, ...)
```

**Arguments**

Data	1:n,1:d] matrix of dataset to be clustered. It consists of n cases of d-dimensional data points. Every case has d attributes, variables or features.
Type	Type=1: default eigengap method (Gaussian clusters) Type=2: multimodality gap method (Gaussian/ non-Gaussian clusters) Type=3: Allows to setClusterNo
ClusterNo	Optional, A number k which defines k different clusters to be built by the algorithm. For default ClusterNo=NULL please see details.
PlotIt	Default: FALSE, If TRUE plots the first three dimensions of the dataset with colored three-dimensional data points defined by the clustering stored in Cls
Silent	Silent progress of algorithm=TRUE
PlotResults	Plots result of spectrum with plot function
...	Method: numerical value: 1 = default eigengap method (Gaussian clusters), 2 = multimodality gap method (Gaussian/ non-Gaussian clusters), 3 = no automatic method (see fixk param) Other parameters defined in Spectrum packages

**Details**

Spectrum is a partitioning algorithm and either uses the eigengap or multimodality gap heuristics to determine the number of clusters, please see Spectrum package for details

**Value**

List of	
Cls	[1:n] numerical vector with n numbers defining the classification as the main output of the clustering algorithm. It has k unique numbers representing the arbitrary labels of the clustering.
Object	Object defined by clustering algorithm as the other output of this algorithm

**Author(s)**

Michael Thrun

**References**

[John et al, 2020] John, C. R., Watson, D., Barnes, M. R., Pitzalis, C., & Lewis, M. J.: Spectrum: Fast density-aware spectral clustering for single and multi-omic data. *Bioinformatics*, Vol. 36(4), pp. 1159-1166, 2020.

**See Also**[Spectrum](#)**Examples**

```
data('Hepta')
out=Spectrum(Hepta$Data,PlotIt=FALSE)

out=Spectrum(Hepta$Data,PlotIt=TRUE)
```

---

StatPDEdensity

*Pareto Density Estimation*

---

**Description**

Density estimation for ggplot with a clear model behind it.

**Format**

The format is: Classes 'StatPDEdensity', 'Stat', 'ggproto' <ggproto object: Class StatPDEdensity, Stat> aesthetics: function compute\_group: function compute\_layer: function compute\_panel: function default\_aes: uneval extra\_params: na.rm finish\_layer: function non\_missing\_aes: parameters: function required\_aes: x y retransform: TRUE setup\_data: function setup\_params: function super: <ggproto object: Class Stat>

**Details**

PDE was published in [Ultsch, 2005], short explanation in [Thrun, Ultsch 2018] and the PDE optimized violin plot was published in [Thrun et al., 2018].

**References**

[Ultsch,2005] Ultsch, A.: Pareto density estimation: A density estimation for knowledge discovery, in Baier, D.; Wernicke, K. D., (Eds), Innovations in classification, data science, and information systems, Proc Gfkl 2003, pp 91-100, Springer, Berlin, 2005.

[Thrun, Ultsch 2018] Thrun, M. C., & Ultsch, A. : Effects of the payout system of income taxes to municipalities in Germany, in Papiez, M. & Smiech,, S. (eds.), Proc. 12th Professor Aleksander Zelias International Conference on Modelling and Forecasting of Socio-Economic Phenomena, pp. 533-542, Cracow: Foundation of the Cracow University of Economics, Cracow, Poland, 2018.

[Thrun et al, 2018] Thrun, M. C., Pape, F., & Ultsch, A. : Benchmarking Cluster Analysis Methods using PDE-Optimized Violin Plots, Proc. European Conference on Data Analysis (ECDA), accepted, Paderborn, Germany, 2018.

### Description

Subspace (projected) clustering is a technique which finds clusters within different subspaces (a selection of one or more dimensions).

### Usage

```
SubspaceClustering(Data,ClusterNo,DimSubspace,
Type='Orclus',PlotIt=FALSE,OrclusInitialClustersNo=ClusterNo+2,...)
```

### Arguments

Data	[1:n,1:d] matrix of dataset to be clustered. It consists of n cases or d-dimensional data points. Every case has d attributes, variables or features.
ClusterNo	A number k which defines k different clusters to be built by the proclus or orclus algorithm.
DimSubspace	Numerical number defining the dimensionality in which clusters should be search in in the orclus algorithm, for proclus it is an optional parameter
Type	'Orclus', subspace clustering based on arbitrarily oriented projected cluster generation [Aggarwal and Yu, 2000] 'ProClus' ProClus algorithm for subspace clustering [Aggarwal/Wolf, 1999] 'Clique' ProClus algorithm finds subspaces of high-density clusters [Agrawal et al., 1999] and [Agrawal et al., 2005] 'SubClu' SubClu algorithm is a density-connected approach for subspace clustering [Kailing et al.,2004]
PlotIt	Default: FALSE, if TRUE plots the first three dimensions of the dataset with colored three-dimensional data points defined by the clustering stored in Cls
OrclusInitialClustersNo	Only for Orclus algorithm: Initial number of clusters (that are computed in the entire data space) must be greater than k. The number of clusters is iteratively decreased by a factor until the final number of k clusters is reached.
...	Further arguments to be set for the clustering algorithm, if not set, default arguments are used. For Subclue: "epsilon" and "minSupport", see <a href="#">DBSCAN</a> For Clique: "xi" (number of intervals for each dimension) and "tau" (Density Threshold), see <a href="#">DBSCAN</a>

**Details**

Subspace clustering algorithms have the goal to find one or more subspaces with the assumption that sufficient dimensionality reduction is dimensionality reduction without loss of information. Hence subspace clustering aims at finding a linear subspace such that the subspace contains as much predictive information as the input space. The subspace is usually higher than two but lower than the input space. In contrast, projection-based clustering [AutomaticProjectionBasedClustering](#) projects the data (nonlinear) into two dimensions and tries only to preserve relevant neighborhoods.

**Value**

List of

`Cls` [1:n] numerical vector with n numbers defining the classification as the main output of the clustering algorithm. It has k unique numbers representing the arbitrary labels of the clustering.

`Object` Object defined by clustering algorithm as the other output of this algorithm

**Note**

`JAVA_HOME` has to be set for rJava to the ProClus algorithm (in windows set `PATH` env. variable to `.../bin` path of Java. The architecture of R and Java have to match. Java automatically downloads the Java version of the browser which may not be installed in the architecture in R. In such a case choose a Java version manually.

**Author(s)**

Michael Thrun

**References**

[Aggarwal/Wolf et al., 1999] Aggarwal, C. C., Wolf, J. L., Yu, P. S., Procopiuc, C., & Park, J. S.: Fast algorithms for projected clustering, Proc. ACM SIGMoD Record, Vol. 28, pp. 61-72, ACM, 1999.

[Aggarwal/Yu, 2000] Aggarwal, C. C., & Yu, P. S.: Finding generalized projected clusters in high dimensional spaces, (Vol. 29), ACM, ISBN: 1581132174, 2000.

[Agrawal et al., 1999]: Rakesh Agrawal, Johannes Gehrke, Dimitrios Gunopulos, and Prabhakar Raghavan: Automatic Subspace Clustering of High Dimensional Data for Data Mining Applications, In Proc. ACM SIGMOD, 1999.

[Agrawal et al., 2005] Agrawal, R., Gehrke, J., Gunopulos, D., & Raghavan, P.: Automatic subspace clustering of high dimensional data, Data Mining and Knowledge Discovery, Vol. 11(1), pp. 5-33. 2005.

[Kailing et al., 2004] Kailing, Karin, Hans-Peter Kriegel, and Peer Kroeger: Density-connected subspace clustering for high-dimensional data, Proceedings of the 2004 SIAM international conference on data mining. Society for Industrial and Applied Mathematics, 2004

**Examples**

```
data('Hepta')
out=SubspaceClustering(Hepta$Data,ClusterNo=7,PlotIt=FALSE)
```

---

TandemClustering	<i>Tandem Clustering</i>
------------------	--------------------------

---

**Description**

Summarizes clustering methods that combine k-means and pca

**Usage**

```
TandemClustering(Data,ClusterNo,Type="Reduced",PlotIt=FALSE,...)
```

**Arguments**

Data	[1:n,1:d] matrix of dataset to be clustered. It consists of n cases of d-dimensional data points. Every case has d attributes, variables or features.
ClusterNo	A number k which defines k different clusters to be built by the algorithm.
Type	Reduced: Reduced k-means (RKM) [De Soete/Carroll, 1994]. Factorial: Factorial k-mean (FKM) [Vichi/Kiers, 2001] KernelPCA: Kernel PCA with minimum normalised cut hyperplanes [Hofmeyr/Pavlidis, 2019]
PlotIt	Default: FALSE, if TRUE plots the first three dimensions of the dataset with colored three-dimensional data points defined by the clustering stored in Cls
...	Further arguments to be set for the clustering algorithm, if not set, default arguments are used.

**Details**

If the ClusterNo exceeds the number of dimensions, than the function is called recursively with ClusterNo=2. In each iteration the cluster with the highest number of overall points is clustered again, until the number of clusters is met.

"KernelPCA" uses additionally the package kernlab and is implemented as given in the fifth example on page 18, section "extension" of [Hofmeyr/Pavlidis, 2019]

The first idea of using non-PCA projections for clustering was published by [Bock, 1987] as an definition. However, to the knowledge of the author it was not applied to any data. The first systematic comparison to Projection-Pursuit Methods [ProjectionPursuitClustering](#) and [AutomaticProjectionBasedClustering](#) can be found in [Thrun/Ultsch, 2018].

**Value**

List of	
Cls	[1:n] numerical vector with n numbers defining the classification as the main output of the clustering algorithm. It has k unique numbers representing the arbitrary labels of the clustering. Points which cannot be assigned to a cluster will be reported with 0.
Object	Object defined by clustering algorithm as the other output of this algorithm

**Author(s)**

Michael Thrun

**References**

- [De Soete/Carroll, 1994] De Soete, G., & Carroll, J. D.: K-means clustering in a low-dimensional Euclidean space, *New approaches in classification and data analysis*, (pp. 212-219), Springer, 1994.
- [Hofmeyr/Pavlidis, 2019] Hofmeyr, D., & Pavlidis, N.: PPCI: an R Package for Cluster Identification using Projection Pursuit, *The R Journal*, 2019.
- [Vichi/Kiers, 2001] Vichi, M., & Kiers, H. A.: Factorial k-means analysis for two-way data, *Computational Statistics & Data Analysis*, Vol. 37(1), pp. 49-64. 2001.
- [Thrun/Ultsch, 2018] Thrun, M. C., & Ultsch, A.: Using Projection based Clustering to Find Distance and Density based Clusters in High-Dimensional Data, *Journal of Classification*, Vol. in revision, 2018.
- [Bock, 1987] Bock, H.: On the interface between cluster analysis, principal component analysis, and multidimensional scaling, *Multivariate statistical modeling and data analysis*, (pp. 17-34), Springer, 1987.

**Examples**

```
data('Hepta')
out=TandemClustering(Hepta$Data,ClusterNo=7,PlotIt=FALSE)
```

---

Target

*Target introduced in [Ultsch, 2005].*

---

**Description**

Detailed description of dataset and its clustering challenge of outliers is provided in [Thrun/Ultsch, 2020]

**Usage**

```
data("Target")
```



**Details**

Size 770, Dimensions 2, stored in Target\$Data  
Classes 6, stored in Target\$Cls

**References**

[Ultsch, 2005] Ultsch, A.: U\* C: Self-organized Clustering with Emergent Feature Maps, Proc. Lernen, Wissensentdeckung und Adaptivitaet (LWA/FGML), pp. 240-244, Saarbruecken, Germany, 2005.

[Thrun/Ultsch, 2020] Thrun, M. C., & Ultsch, A.: Clustering Benchmark Datasets Exploiting the Fundamental Clustering Problems, Data in Brief, Vol. 30(C), pp. 105501, doi:[10.1016/j.dib.2020.105501](https://doi.org/10.1016/j.dib.2020.105501), 2020.

**Examples**

```
data(Target)  
str(Target)
```

---

Tetra

*Tetra introduced in [Ultsch, 1993]*

---

**Description**

Almost touching clusters. Detailed description of dataset and its clustering challenge is provided in [Thrun/Ultsch, 2020].

**Usage**

```
data("Tetra")
```

**Details**

Size 400, Dimensions 3, stored in Tetra\$Data  
Classes 4, stored in Tetra\$Cls

**References**

[Ultsch, 1993] Ultsch, A.: Self-organizing neural networks for visualisation and classification, Information and classification, (pp. 307-313), Springer, 1993.

[Thrun/Ultsch, 2020] Thrun, M. C., & Ultsch, A.: Clustering Benchmark Datasets Exploiting the Fundamental Clustering Problems, Data in Brief, Vol. 30(C), pp. 105501, doi:[10.1016/j.dib.2020.105501](https://doi.org/10.1016/j.dib.2020.105501), 2020.

**Examples**

```
data(Tetra)  
str(Tetra)
```

---

TwoDiamonds

*TwoDiamonds introduced in [Ultsch, 2003a, 2003b]*

---

### Description

Cluster border defined by density. Detailed description of dataset and its clustering challenge is provided in [Thrun/Ultsch, 2020].

### Usage

```
data("TwoDiamonds")
```

### Details

Size 800, Dimensions 2, stored in `TwoDiamonds$Data`

Classes 2, stored in `TwoDiamonds$Cls`

### References

[Ultsch, 2003a] Ultsch, A. Optimal density estimation in data containing clusters of unknown structure, technical report, Vol. 34, University of Marburg, Department of Mathematics and Computer Science, 2003.

[Ultsch, 2003b] Ultsch, A.: U\*-matrix: a tool to visualize clusters in high dimensional data, Fachbereich Mathematik und Informatik, 2003.

[Thrun/Ultsch, 2020] Thrun, M. C., & Ultsch, A.: Clustering Benchmark Datasets Exploiting the Fundamental Clustering Problems, Data in Brief, Vol. 30(C), pp. 105501, doi:10.1016/j.dib.2020.105501, 2020.

### Examples

```
data(TwoDiamonds)
str(TwoDiamonds)
```

---

WingNut

*WingNut introduced in [Ultsch, 2005]*

---

### Description

Density vs. distance. Detailed description of dataset and its clustering challenge is provided in [Thrun/Ultsch, 2020].

### Usage

```
data("WingNut")
```

**Details**

Size 1016, Dimensions 2, stored in `WingNut$Data`

Classes 2, stored in `WingNut$Cls`

**References**

[Ultsch, 2005] Ultsch, A.: Clustering with SOM: U\* C, Proc. Proceedings of the 5th Workshop on Self-Organizing Maps, Vol. 2, pp. 75-82, 2005.

[Thrun/Ultsch, 2020] Thrun, M. C., & Ultsch, A.: Clustering Benchmark Datasets Exploiting the Fundamental Clustering Problems, Data in Brief, Vol. 30(C), pp. 105501, doi:[10.1016/j.dib.2020.105501](https://doi.org/10.1016/j.dib.2020.105501), 2020.

**Examples**

```
data(WingNut)
str(WingNut)
```

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