

Package ‘DataVisualizations’

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Type Package

Title Visualizations of High-Dimensional Data

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Description Gives access to data visualisation methods that are relevant from the data scientist's point of view. The flagship idea of 'DataVisualizations' is the mirrored density plot (MD-plot) for either classified or non-classified multivariate data published in Thrun, M.C. et al.: ``Analyzing the Fine Structure of Distributions" (2020), PLoS ONE, <[DOI:10.1371/journal.pone.0238835](https://doi.org/10.1371/journal.pone.0238835)>. The MD-plot outperforms the box-and-whisker diagram (box plot), violin plot and bean plot and geom_violin plot of ggplot2. Furthermore, a collection of various visualization methods for univariate data is provided. In the case of exploratory data analysis, 'DataVisualizations' makes it possible to inspect the distribution of each feature of a dataset visually through a combination of four methods. One of these methods is the Pareto density estimation (PDE) of the probability density function (pdf). Additionally, visualizations of the distribution of distances using PDE, the scatter-density plot using PDE for two variables as well as the Shepard density plot and the Bland-Altman plot are presented here. Pertaining to classified high-dimensional data, a number of visualizations are described, such as f.ex. the heat map and silhouette plot. A political map of the world or Germany can be visualized with the additional information defined by a classification of countries or regions. By extending the political map further, an uncomplicated function for a Choropleth map can be used which is useful for measurements across a geographic area. For categorical features, the Pie charts, slope charts and fan plots, improved by the ABC analysis, become usable. More detailed explanations are found in the book by Thrun, M.C.: ``Projection-Based Clustering through Self-Organization and Swarm Intelligence" (2018) <[DOI:10.1007/978-3-658-20540-9](https://doi.org/10.1007/978-3-658-20540-9)>.

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Imports Rcpp (>= 0.12.12), RcppParallel (>= 5.1.4), ggplot2, sp, pracma, reshape2

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DataVisualizations-package

Visualizations of High-Dimensional Data

Description

Gives access to data visualisation methods that are relevant from the data scientist's point of view. The flagship idea of 'DataVisualizations' is the mirrored density plot (MD-plot) for either classified or non-classified multivariate data published in Thrun, M.C. et al.: "Analyzing the Fine Structure of Distributions" (2020), PLoS ONE, <DOI:10.1371/journal.pone.0238835>. The MD-plot outperforms the box-and-whisker diagram (box plot), violin plot and bean plot and geom_violin plot of ggplot2. Furthermore, a collection of various visualization methods for univariate data is provided. In the case of exploratory data analysis, 'DataVisualizations' makes it possible to inspect the distribution of each feature of a dataset visually through a combination of four methods. One of these methods is the Pareto density estimation (PDE) of the probability density function (pdf). Additionally, visualizations of the distribution of distances using PDE, the scatter-density plot using PDE for two variables as well as the Shepard density plot and the Bland-Altman plot are presented here. Pertaining to classified high-dimensional data, a number of visualizations are described, such as f.ex. the heat map and silhouette plot. A political map of the world or Germany can be visualized with the additional information defined by a classification of countries or regions. By extending the political map further, an uncomplicated function for a Choropleth map can be used which is useful for measurements across a geographic area. For categorical features, the Pie charts, slope charts and fan plots, improved by the ABC analysis, become usable. More detailed explanations are found in the book by Thrun, M.C.: "Projection-Based Clustering through Self-Organization and Swarm Intelligence" (2018) <DOI:10.1007/978-3-658-20540-9>.

Details

For a brief introduction to **DataVisualizations** please see the vignette [A Quick Tour in Data Visualizations](#).

Please see <https://www.deepbionics.org/>. Depending on the context please cite either [Thrun, 2018] regarding visualizations in the context of clustering or [Thrun/Ultsch, 2018] for other visualizations.

For the Mirrored Density Plot (MD plot) please cite [Thrun et al., 2020] and see the extensive vignette in <https://md-plot.readthedocs.io/en/latest/index.html>. The MD plot is also available in Python <https://pypi.org/project/md-plot/>

Index of help topics:

ABCbarplot	Barplot with Sorted Data Colored by ABCanalysis
AccountingInformation_PrimeStandard_Q3_2019	Accounting Information in the Prime Standard in Q3 in 2019 (AI_PS_Q3_2019)
BimodalityAmplitude	Bimodality Amplitude
CCDFplot	plot Complementary Cumulative Distribution Function (CCDF) in Log/Log uses ecdf, $CCDF(x) = 1 - cdf(x)$
ClassBarPlot	ClassBarPlot
ClassBoxplot	Creates Boxplot plot for all classes
ClassErrorbar	ClassErrorbar
ClassMDplot	Class MDplot for Data w.r.t. all classes
ClassPDEplot	PDE Plot for all classes
ClassPDEplotMaxLikeli	Create PDE plot for all classes with maximum likelihood
Classplot	Classplot
CombineCols	Combine vectors of various lengths
CombineRows	Combine matrices of various lengths
Crosstable	Crosstable plot
DataVisualizations-package	Visualizations of High-Dimensional Data
DefaultColorSequence	Default color sequence for plots
DensityContour	Contour plot of densities
DensityScatter	Scatter plot with densities
DrawWorldWithCls	Plot a classified world map
DualaxisClassplot	Dualaxis Classplot
DualaxisLinechart	DualaxisLinechart
Fanplot	The fan plot
FundamentalData_Q1_2018	Fundamental Data of the 1st Quarter in 2018
GoogleMapsCoordinates	Google Maps with marked coordinates
Heatmap	Heatmap for Clustering
HeatmapColors	Default color sequence for plots
ITS	Income Tax Share
InspectBoxplots	Inspect Boxplots
InspectCorrelation	Inspect the Correlation
InspectDistances	Inspection of Distance-Distribution
InspectScatterplots	Pairwise scatterplots and optimal histograms
InspectStandardization	QQplot of Data versus Normalized Data
InspectVariable	Visualization of Distribution of one variable
JitterUniqueValues	Jitters Unique Values
Lsun3D	Lsun3D inspired by FCPS [Thrun/Ultsch, 2020] introduced in [Thrun, 2018]

MAplot	Minus versus Add plot
MDplot	Mirrored Density plot (MD-plot)
MDplot4multiplevectors	Mirrored Density plot (MD-plot)for Multiple Vectors
MDstrips	High-dimensional Density Strips based on Pareto Density Estimation
MTY	Municipal Income Tax Yield
Meanrobust	Robust Empirical Mean Estimation
Multiplot	Plot multiple ggplots objects in one panel
OpposingViolinBiclassPlot	OpposingViolinBiclassPlot
OptimalNoBins	Optimal Number Of Bins
PDEnormrobust	PDEnormrobust
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ParetoDensityEstimation	Pareto Density Estimation V3
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ParetoRadius_fast	Fast ParetoRadius for distributions
Piechart	The pie chart
Pixelmatrix	Plot of a Pixel Matrix
Plot3D	3D plot of points
PlotGraph2D	PlotGraph2D
PlotMissingvalues	Plot of the Amount Of Missing Values
PlotProductratio	Product-Ratio Plot
PmatrixColormap	P-Matrix colors
QQplot	QQplot with a Linear Fit
ROC	ROC plot
RobustNorm_BackTrafo	Transforms the Robust Normalization back
RobustNormalization	RobustNormalization
ShepardDensityScatter	Shepard PDE scatter
Sheparddiagram	Draws a Shepard Diagram
SignedLog	Signed Log
Silhouetteplot	Silhouette plot of classified data.
Slopechart	Slope Chart
StatPDEdensity	Pareto Density Estimation
Stdrobust	Standard Deviation Robust
Worldmap	plots a world map by country codes
categoricalVariable	A categorical Feature.
estimateDensity2D	estimateDensity2D
stat_pde_density	Calculate Pareto density estimation for ggplot2 plots
world_country_polygons	world_country_polygons
zplot	Plotting for 3 dimensional data

Author(s)

Michael Thrun, Felix Pape, Onno Hansen-Goos, Alfred Ultsch

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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.

[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., 2020] Thrun, M. C., Gehlert, T. & Ultsch, A.: Analyzing the Fine Structure of Distributions, PLoS ONE, Vol. 15(10), pp. 1-66, DOI 10.1371/journal.pone.0238835, 2020.

Examples

```
data("Lsun3D")
Data=Lsun3D$Data
```

```
Pixelmatrix(Data)
```

```
InspectDistances(as.matrix(dist(Data)))
```

```
MAList=MAplot(ITS,MTY)
```

```
data("Lsun3D")
Cls=Lsun3D$Cls
Data=Lsun3D$Data
#clear cluster structure
plot(Data[,1:2],col=Cls)
#However, the silhouette plot does not indicate a very good clustering in cluster 1 and 2
```

```
Silhouetteplot(Data,Cls = Cls)
```

```
Heatmap(as.matrix(dist(Data)),Cls = Cls)
```

ABCbarplot

*Barplot with Sorted Data Colored by ABCanalysis***Description**

This plot can be read like a scree plot for PCA. It allowed to select the most important values visually.

Usage

```
ABCbarplot(Data,
           Colors=DataVisualizations::DefaultColorSequence[1:3],
           main,xlab,ylab="Value")
```

Arguments

Data	[1:n] vector of Data, e.g. eigenvalues of PCA
Colors	three colors for A, B and C
main	title of plot
xlab	xlabel
ylab	ylabel

Details

ABC analysis is explained in **ABCanalysis**. The visualization is based on **ggplot2**.

Value

List V of	
ABCanalysis	output of ABCanalysis
ggobject	object of ggplot2 plotted
DF	Data frame if another plot should be done manually

Author(s)

Michael Thrun

References

Ultsch. A ., Lotsch J.: Computed ABC Analysis for Rational Selection of Most Informative Variables in Multivariate Data, PloS one, Vol. 10(6), pp. e0129767. doi 10.1371/journal.pone.0129767, 2015.

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

```
data('FundamentalData_Q1_2018')
Data=as.matrix(FundamentalData_Q1_2018$Data)
Data[!is.finite(Data)]=0
results=prcomp(Data)
main="Scree plot with Class A of the Most-Important Eigenvalues"
plotlist = ABCbarplot(results$sdev,ylab='Eigenvalues',main=main)
plotlist$ggobject
```

AccountingInformation_PrimeStandard_Q3_2019

*Accounting Information in the Prime Standard in Q3 in 2019
(AI_PS_Q3_2019)*

Description

Accounting Information of 261 companies traded in the Frankfurt stock exchange in the German Prime standard.

Usage

```
data("AccountingInformation_PrimeStandard_Q3_2019")
```

Format

A list with of three objects

Key [1:n] Key of the 261 observations

Data [1:n,1:d] numeric matrix of 261 observations on the 45 variables describing the accounting information

Cls [1:n] a numeric vector of k clusters of the clustering performed in [Thrun/Ultsch, 2019]

Details

Detailed data description can be found in [Thrun/Ultsch, 2019].

Source

Yahoo Finance

References

[Thrun/Ultsch, 2019] Thrun, M. C., & Ultsch, A.: Stock Selection via Knowledge Discovery using Swarm Intelligence with Emergence, IEEE Intelligent Systems, Vol. under review, pp., 2019.

Examples

```
data(AccountingInformation_PrimeStandard_Q3_2019)

str(AI_PS_Q3_2019)
dim(AI_PS_Q3_2019$Data)
```

BimodalityAmplitude *Bimodality Amplitude*

Description

Computes the Bimodality Amplitude of [Zhang et al., 2003]

Usage

```
BimodalityAmplitude(x, PlotIt=FALSE)
```

Arguments

x	Data vector.
PlotIt	FALSE, TRUE if a figure with the antimodes and peaks is plotted

Details

This function calculates the Bimodality Amplitude of a data vector. This is a measure of the proportion of bimodality and the existence of bimodality. The value lies between zero and one (that is: [0,1]) where the value of zero implies that the data is unimodal and the value of one implies the data is two point masses.

Note

function was rewritten after the flow of a function of Sathish Deevi because the original function was incorrect.

Author(s)

Michael Thrun

References

Zhang, C., Mapes, B., & Soden, B.: Bimodality in tropical water vapour, Quarterly Journal of the Royal Meteorological Society, Vol. 129(594), pp. 2847-2866, 2003.

Examples

```
#Example 1
data<-c(rnorm(299,0,1),rnorm(299,5,1))
BimodalityAmplitude(data,TRUE)
```

```
#Example 2
dist1<-rnorm(2100,5,2)
dist2<-dist1+11
data<-c(dist1,dist2)
```

```
BimodalityAmplitude(data,TRUE)
```

```
#Example 3
dist1<-rnorm(210,-15,1)
dist2<-rep(dist1,3)+30
data<-c(dist1,dist2)
```

```
BimodalityAmplitude(data,TRUE)
```

```
#Example 4
data<-runif(1000,-15,1)
```

```
BimodalityAmplitude(data,TRUE)
```

categoricalVariable *A categorical Feature.*

Description

Character vector of length 391029 with five different labels.

Usage

```
data("categoricalVariable")
```

Examples

```
data(categoricalVariable)
unique(categoricalVariable)
```

CCDFplot	<i>plot Complementary Cumulative Distribution Function (CCDF) in Log/Log uses ecdf, $CCDF(x) = 1-cdf(x)$</i>
----------	---

Description

plot Complementary Cumulative Distribution Function (CCDF) in Log/Log uses ecdf, $CCDF(x) = 1-cdf(x)$

Arguments

Feature	Vector of data to be plotted, or a matrix with given probability density function in column 2 and/or a cumulative density function in column 3
pch	Optional, default: pch=0 for Line, other numbers see documentation about pch of plot
PlotIt	Optional, if PlotIt==T (default) do a plot, otherwise return only values
LogLogPlot	Optional, if LogLogPlot==T (default) do a log/log plot
xlab	Optional, xlab of plot
ylab	Optional, ylab of plot
main	Optional, main of plot
...	Optional, further arguments for plot

Value

V\$CCDFFuniqX, V\$CCDFFuniqY $CCDFFuniqY = 1-cdf(CCDFFuniqX)$, such that `plot(CCDFFuniqX, CCDFFuniqY)...`

Author(s)

Michael Thrun

ClassBarPlot	<i>ClassBarPlot</i>
--------------	---------------------

Description

Represent values for each class and instance as bar plot with optional error deviation, e.g., mean values of features depending on class with standard deviation.

Usage

```
ClassBarPlot(Values, Cls, Deviation, Names, ClassColors,
             ylab = "Values", xlab = "Instances", PlotIt = TRUE)
```

Arguments

Values	[1:n] Numeric vector with values (y-axis) in matching order to Cls, Deviation and Names.
Cls	[1:n] Numeric vector of classes in matching order to Values and Deviation and Names.
Deviation	[1:n] Numeric vector with deviation in matching order to Values and Cls and Names.
Names	[1:n] Character or numeric vector of instances (x-axis) in matching order to Values and Cls and Deviation.
ClassColors	Character vector of color names stating either the colors for each class or defining colors matching the class vector cls.
ylab	Character stating y label.
xlab	Character stating x label.
PlotIt	Logical value indicating visual output TRUE => create visual output FALSE => do not create visual output (Default: Boolean=TRUE).

Value

ggplot2 object

Author(s)

Quirin Stier

Examples

```
# Compute means and counts
tmpVar1 <- aggregate(Sepal.Length ~ Species, data = iris,
FUN = function(x) c(mean = mean(x), n = length(x)))
tmpVar2 <- aggregate(Sepal.Width ~ Species, data = iris,
FUN = function(x) c(mean = mean(x), n = length(x)))
tmpVar3 <- aggregate(Petal.Length ~ Species, data = iris,
FUN = function(x) c(mean = mean(x), n = length(x)))
tmpVar4 <- aggregate(Petal.Width ~ Species, data = iris,
FUN = function(x) c(mean = mean(x), n = length(x)))

# Extract mean and count
tmpVar1_mean <- tmpVar1$Sepal.Length[, "mean"]
tmpVar2_mean <- tmpVar2$Sepal.Width[, "mean"]
tmpVar3_mean <- tmpVar3$Petal.Length[, "mean"]
tmpVar4_mean <- tmpVar4$Petal.Width[, "mean"]

# Compute standard deviations
tmpVar5 <- aggregate(Sepal.Length ~ Species, data = iris, FUN = sd)
tmpVar6 <- aggregate(Sepal.Width ~ Species, data = iris, FUN = sd)
tmpVar7 <- aggregate(Petal.Length ~ Species, data = iris, FUN = sd)
tmpVar8 <- aggregate(Petal.Width ~ Species, data = iris, FUN = sd)
```

```
# Combine results
Values <- c(tmpVar1_mean, tmpVar2_mean, tmpVar3_mean, tmpVar4_mean)
Class <- rep(1:3, 4)
Deviation <- c(tmpVar5$Sepal.Length, tmpVar6$Sepal.Width, tmpVar7$Petal.Length,
tmpVar8$Petal.Width)

  if(length(Values) == length(Class)){
    ClassBarPlot(Values = Values, Cls = Class, Deviation = Deviation)
  }
```

ClassBoxplot

Creates Boxplot plot for all classes

Description

Boxplot the data for all classes

Usage

```
ClassBoxplot(Data, Cls, ColorSequence = DataVisualizations::DefaultColorSequence,
  ClassNames = NULL, All=FALSE, PlotLegend = TRUE,
  main = 'Boxplot per Class', xlab = 'Classes', ylab = 'Range of Data')
```

Arguments

Data	Vector of the data to be plotted
Cls	Vector of class identifiers.
ColorSequence	Optional: The sequence of colors used, Default: DefaultColorSequence()
ClassNames	Optional: The names of the classes. Default: C1 - C(Number of Classes)
All	Optional: adds full data vector for comparison against classes
PlotLegend	Optional: Add a legend to plot. Default: TRUE)
main	Optional: Title of the plot. Default: "ClassBoxPlot"
xlab	Optional: Title of the x axis. Default: "Classes"
ylab	Optional: Title of the y axis. Default: "Data"

Value

A List of

ClassData	The DataFrame used to plot
ggobject	The ggplot2 plot object

in mode invisible

Author(s)

Michael Thrun, Felix Pape

Examples

```
data(ITS)
#please download package from cran
#model=AdaptGauss::AdaptGauss(ITS)
#Classification=AdaptGauss::ClassifyByDecisionBoundaries(ITS,

#DecisionBoundaries = AdaptGauss::BayesDecisionBoundaries(model$Means,model$SDs,model$Weights))

DataVisualizations::ClassBoxplot(ITS,Classification)$gobject
```

ClassErrorbar

ClassErrorbar

Description

Plots ClassErrorbars at Xvalue positions for one or more than one classes with user means and defined whiskers

Usage

```
ClassErrorbar(Xvalues, Ymatrix, Cls, ClassNames, ClassCols, ClassShape,

MeanFun = median, SDFun, JitterPosition = 0.5,

main = "Error bar plot", xlab, ylab, WhiskerWidth = 7, Whisker_lwd = 1, BW = TRUE)
```

Arguments

Xvalues	[1:m] Numerical or character vector, positions of error bars (see details) in on x-axis for the m variables
Ymatrix	[1:n,1:d] of n cases and d=m*k variables with for which the error-bar statistics defined by MeanFun and SDFun should be computed
Cls	Optional, [1:d] numerical vector of k classes for the d variables. Each class is one method that will be shown as distinctive set of error bars in the plot
ClassNames	Optional, [1:k] character vector of k methods
ClassCols	Optional, [1:k] character vector of k colors
ClassShape	Optional, [1:k] numerical vector of k shapes, see pch in Classplot for details
MeanFun	Optional, error bar statistic of mean points, default=median

Sdfun	Optional, error bar statistic for the length of whiskers, default is the robust estimation of standard deviation
JitterPosition	Optional, how much in values of Xvalues should the error bars jitter around Xvalues to not overlap
main	Optional, title of plot
xlab	Optional, x-axis label
ylab	Optional, y-axis label
WhiskerWidth	Optional, scalar above zero defining the width of the end of the whiskers
Whisker_lwd	Optional, scalar above zero defining the thickness of the whisker lines
BW	Optional, FALSE: usual ggplot2 background and style which is good for screen visualizations. Default: TRUE: theme_bw() is used which is more appropriate for publications

Details

If $k=1$, e.g., one method is used, $d=m$ and $Cls=\text{rep}(1,m)$. All vector $[1:k]$ assume the occurrence of the classes in Cls as ordered with increasing value.

Statistics are provided in long table format with the column names $Xvalues$, $Mean$, SD and $Method$. The method column specifies the names of the k classes.

If $Xvalues$ is a character vector (see example), ggplot2 automatically sets the position on the x-axis. Otherwise specific numeric positions can be set. This allows also for plotting a smooth line over the average (see example).

Value

List with

ggobj	The ggplot object of the ClassErrorbar
Statistics	$[1:(d*k)1:4]$ data frame of statistics per class used for plotting

Author(s)

Michael Thrun

Examples

```
data('FundamentalData_Q1_2018')
Data=as.matrix(FundamentalData_Q1_2018$Data)
Cls = FundamentalData_Q1_2018$Cls
Class1Data = matrix(NA, nrow = nrow(Data), ncol = 2)
Class2Data = matrix(NA, nrow = nrow(Data), ncol = 2)
Class1Data[which(Cls==1), ] = Data[which(Cls==1), c("TotalAssets", "TotalLiabilities")]
Class2Data[which(Cls==2), ] = Data[which(Cls==2), c("TotalAssets", "TotalLiabilities")]
YMatrix = cbind(Class1Data,
                 Class2Data)

#Option 1: character vector
ClassErrorbar(c("TotalRevenue", "GrossProfit"),
```

```

        YMatrix, c
(1,1,2,2),
    ClassNames=c("Class 1", "Class 2"),
    main="ClassErrorbar of Q1 2018 for total revenue and gross profit",
    xlab="GrossProfit/TotalRevenue",
    ylab="Median +- std",
    WhiskerWidth = 1)

#Option 2: numerical vector
ClassErrorbar(c(1,2),
    YMatrix,
    c(1,1,2,2),
    ClassNames=c("Class 1", "Class 2"),
    main="ClassErrorbar of Q1 2018 for total revenue and gross profit",
    xlab="GrossProfit/TotalRevenue",
    ylab="Median +- std",
    WhiskerWidth = 1)

#Option 3: numerical vector + line
## Not run:
#arbitrary data
Y_someOtherData=cbind(YMatrix,YMatrix,
    YMatrix,YMatrix)
some_values=c(2,3,4,5,6,8,9,10)
ClassErrorbar(some_values,
    Y_someOtherData,
    c(1,1,2,2),
    ClassNames=c("Class 1", "Class 2"),
    main="ClassErrorbar of Q1 2018 for total revenue and gross profit",
    xlab="GrossProfit/TotalRevenue",
    ylab="Median +- std",
    WhiskerWidth = 1)$ggobj+
geom_smooth(method="auto", se=F, fullrange=F, level=0.95)

## End(Not run)

```

ClassMDplot

Class MDplot for Data w.r.t. all classes

Description

Creates a Mirrored-Density plot w.r.t. to each class of a numerical vector of data.

Usage

```

ClassMDplot(Data, Cls, ColorSequence = DataVisualizations::DefaultColorSequence,
            ClassNames = NULL, PlotLegend = TRUE, Ordering = "Columnwise",
            main = 'MDplot for each Class',

```

```
xlab = 'Classes', ylab = 'PDE of Data per Class',
Fill = 'darkblue', MinimalAmoutOfData=40,
MinimalAmoutOfUniqueData=12, SampleSize=1e+05, ...)
```

Arguments

Data	[1:n] Vector of the data to be plotted
Cls	[1:n] Vector of class identifiers of k clusters one number is the label of one cluster
ColorSequence	Optional: [1:k] vector, The sequence of colors used, Default: DataVisualizations::DefaultColorSequence
ClassNames	Optional: [1:k] named numerical vector, The names of the classes. Default: Class 1 - Class k with k beeing the number of classes
PlotLegend	Optional: Add a legent to plot. Default: TRUE)
Ordering	Optional: Ordering of Classes, please see MDplot for details)
main	Optional: Title of the plot. Default: MDplot for each Class
Fill	Optional: [1:k] Vector with the colors, the MD's are to be colored with. If only one value is given, all MD's are colored in the same color.
xlab	Optional: Title of the x axis. Default: "Classes"
ylab	Optional: Title of the y axis. Default: "Data"
MinimalAmoutOfData	Optional: numeric value defining a threshold. Below this threshold no density estimation is performed and a Jitter plot with a median line is drawn. Please see MDplot for details.
MinimalAmoutOfUniqueData	Optional: numeric value defining a threshold. Below this threshold no density estimation and statistical testing is performed and a Jitter plot is drawn. Only Data Science experts should change this value after they understand how the density is estimated (see [Utsch, 2005]).
SampleSize	Optional: numeric value defining a threshold. Above this thresholdclass-wise uniform sampling of finite cases is performed in order to shorten computation time. If required, SampleSize=n can be set to omit this procedure.
...	Further arguments that are documented in MDplot except for OnlyPlotOutput which is always true.

Details

Further examples for the ClassMDplot can be found in https://md-plot.readthedocs.io/en/latest/application/example_application.html.

The CIs vector is reordered from lowest to highest number. The ClassNames vector and ColorSequence vectors are matched by this ordering of CIs, i.e. the lowest number gets the first color or class name.

Value

A List of

`ClassData` The matrix [1:m,1:NoOfClasses] used to plot with the reordered Cls, rows are filled partly with NaN, m is the length of the number of data in largest class.

`ggobject` The ggplot2 plot object

in mode invisible

Note

Function is still experimental because ColorSequence does not work yet, because we are unable to specify the colors in ggplot2. If someone knows a solution, please mail the maintainer of the package. Similar issue for PlotLegend.

Author(s)

Michael Thrun, Felix Pape

References

Thrun, M. C., Breuer, L., & Ultsch, A. : Knowledge discovery from low-frequency stream nitrate concentrations: hydrology and biology contributions, Proc. European Conference on Data Analysis (ECDA), Paderborn, Germany, 2018.

See Also

https://md-plot.readthedocs.io/en/latest/application/example_application.html

`MDplot` <https://pypi.org/project/md-plot/>

Examples

```
data(ITS)

#shortcut for example if AdaptGauss not installed
Classification = kmeans(ITS, centers = 2)$cluster

#better approach
#please download package from cran
#model=AdaptGauss::AdaptGauss(ITS)
#Classification=AdaptGauss::ClassifyByDecisionBoundaries(ITS,

#DecisionBoundaries = AdaptGauss::BayesDecisionBoundaries(model$Means,model$SDs,model$Weights))
ClassNames=c(1,2)
names(ClassNames)=c("Insert name \n of Class 1","Insert name \n of Class 2")
ClassMDplot(ITS,Classification,ClassNames = ClassNames)
```

ClassPDEplot *PDE Plot for all classes*

Description

PDEplot the data for all classes, weights the pdf with priors

Usage

```
ClassPDEplot(Data, Cls, ColorSequence,
             ColorSymbSequence, PlotLegend = 1,
             SameKernelsAndRadius = 0, xlim, ylim, ...)
```

Arguments

Data	The Data to be plotted
Cls	Vector of class identifiers. Can be integers or NaN's, need not be consecutive nor positive
ColorSequence	Optional: the sequence of colors used, Default: DefaultColorSequence
ColorSymbSequence	Optional: the plot symbols used (theoretisch nicht notwendig, da erst wichtig, wenn mehr als 562 Cluster)
PlotLegend	Optional: add a legend to plot (default == 1)
SameKernelsAndRadius	Optional: Use the same PDE kernels and radii for all distributions (default == 0)
xlim	Optional: range of the x axis
ylim	Optional: range of the y axis
...	further arguments passed to plot

Value

Kernels of the Pareto density estimation in mode invisible

Author(s)

Michael Thrun

Examples

```

data(ITS)
#please download package from cran
#model=AdaptGauss::AdaptGauss(ITS)
#Classification=AdaptGauss::ClassifyByDecisionBoundaries(ITS,

#DecisionBoundaries = AdaptGauss::BayesDecisionBoundaries(model$Means,model$SDs,model$Weights))

DataVisualizations::ClassPDEplot(ITS,Classification)$gobject

```

ClassPDEplotMaxLikeli *Create PDE plot for all classes with maximum likelihood*

Description

PDEplot the data for allclasses, weight the Plot with 1 (= maximum likelihood)

Usage

```

ClassPDEplotMaxLikeli(Data, Cls, ColorSequence = DataVisualizations::DefaultColorSequence,
  ClassNames, PlotLegend = TRUE, MinAnzKernels = 0,PlotNorm,
  main = "Pareto Density Estimation (PDE)",
  xlab = "Data", ylab = "ParetoDensity", xlim, ylim, lwd=1, ...)

```

Arguments

Data	The Data to be plotted
Cls	Vector of class identifiers. Can be integers or NaN's, need not be consecutive nor positive
ColorSequence	Optional: the sequence of colors used, Default: DefaultColorSequence
ClassNames	Optional: the names of the classes to be displayed in the legend
PlotLegend	Optional: add a legent to plot (default == 1)
MinAnzKernels	Optional: Minimum number of kernels
PlotNorm	Optional: ==1 => plot Normal distribuion on top , ==2 = plot robust normal distribution,; default: PlotNorm= 0
main	Optional: Title of the plot
xlab	Optional: title of the x axis
ylab	Optional: title of the y axis

xlim Optional: area of the x-axis to be plotted
 lwd Optional: area of the y-axis to be plotted
 ylim numerical scalar defining the width of the lines
 ... further arguments passed to plot

Value

Kernels Kernels of the distributions
 ClassParetoDensities
 Pareto densities for classes
 ggobject ggplot2 plot object. This should be used to further modify the plot

Author(s)

Felix Pape

References

Aubert, A. H., Thrun, M. C., Breuer, L., & Ultsch, A. : Knowledge discovery from high-frequency stream nitrate concentrations: hydrology and biology contributions, Scientific reports, Nature, Vol. 6(31536), pp. doi 10.1038/srep31536, 2016.

Examples

```
data(ITS)
#model=AdaptGauss::AdaptGauss(ITS)
##please download package from cran
#Classification=AdaptGauss::ClassifyByDecisionBoundaries(ITS,
#DecisionBoundaries = AdaptGauss::BayesDecisionBoundaries(model$Means,model$SDs,model$Weights))
DataVisualizations::ClassPDEplotMaxLikeli(ITS,Classification)$ggobject
```

Classplot

Classplot

Description

Allows to plot one time series or feature with a classification as a labeled scatter plot with a line. The colors are the labels defined by the classification.

Usage

```
Classplot(X, Y, Cls, Plotter, Names = NULL, Subsample=TRUE, na.rm = FALSE,
xlab = "X", ylab = "Y", main = "Class Plot", Colors = NULL,
Size = 8, PointBorderCol="black",
LineColor = NULL, LineWidth = 1, LineType = NULL,
Showgrid = TRUE, pch, AnnotateIt = FALSE, SaveIt = FALSE,
Nudge_x_Names = 0, Nudge_y_Names = 0, Legend = "", SmallClassesOnTop = TRUE,
...)
```

Arguments

X	[1:n] numeric vector or time
Y	[1:n] numeric vector of feature
Cls	[1:n] numeric vector of k classes, if not set per default every point is in first class
Names	Either [1:n] character vector of k classes, or [1:k] character vector defining the k names, one per class, vector has to be named by class labels. If not set, per default Cls is used, if set, names the legend and the points.
Subsample	Boolean, default TRUE, if TRUE and n>5000 takes optimal subsample for the visualization so that not too much points overlap
na.rm	Function may not work with non finite values. If these cases should be automatically removed, set parameter TRUE
xlab	Optional, string for xlabel
ylab	Optional, string for ylabel
main	Optional, string for title of plot
Colors	Optional, [1:k] string defining the k colors, one per class, Vector can be named by class labels than colors are matched to specific labels instead of 1:k ordering
AnnotateIt	Optional, in case of Plotter==ggplot and given Names annotates each point if TRUE
Size	Optional, size of points, beware: default is appropriate for "plotly", or "native" but should smaller for "ggplot"
PointBorderCol	Optional, string, color of the dot outline for "plotly" for "ggplot". If FALSE and Plotter="ggplot" or Plotter="plotly", no borders for points which is useful if many points overlap.
LineColor	Optional, name of color, in plotly then all points are connected by a curve, in ggplot2 all points of one class are connected by a curve of the color the class
LineWidth	Optional, number defining the width of the curve (plotly only)
LineType	Optional, string defining the type of the curve in plotly only, "dot", "dash", "-" for ggplot2: just set =1 here and then the curve is plotted

Showgrid	Optional, boolean (plotly only)
Plotter	Optional, either "ggplot" (default if Names given), "plotly" (default if no Names given), or "native"
pch	[1:n] numeric vector of length n of the cases of CIs for the k classes. It defines the symbols to use, for native Plotter or ggplot, usually k can be in a range from zero to 25
SaveIt	Optional, boolean, if true saves plot as html (plotly) or png (ggplot2)
Nudge_x_Names	Optional, numerical scalar, for Plotter "ggplot" only, if Names are set, moves them consistently respective to x-axis within units of x-axis
Nudge_y_Names	Optional, numerical scalar, for Plotter "ggplot" only, if Names are set, moves them consistently respective to y-axis within units of y-axis
SmallClassesOnTop	Optional, boolean, decide if small classes should be plotted on top for visibility (default setting) or not.
Legend	Optional, if argument is not missing, character string defining the title of the legend which automatically enables the legend
...	Further arguments for <code>ggplot2::ggplot</code> , or <code>plotly::plot_ly</code> , or <code>plot</code> (except "pch" and "type") depending on Plotter

Details

The mapping of colors to the labels of CIs is consecutive, i.e., the label with the smallest value in CIs gets the first color in Colors. The Colors are plotted in order from label with the highest number of points to the label with the lowest number of points being on top.

Default is "plotly" if Names are NULL. However, ggplot2 is preferable in case that Names parameter is used because overlapping text labels are avoided. In that case the default is "ggplot". Note that ggplot2 options are currently slightly restricted.

For example, the function is useful to see if temporal clustering has time dependent variations and for Hidden Markov Models (see Mthrun/RHmm on GitHub).

Value

plotly object or ggplot2 object depending on Plotter

Author(s)

Michael Thrun

See Also

[DualaxisClassplot](#)

Examples

```

data(Lsun3D)
Classplot(Lsun3D$Data[,1],Lsun3D$Data[,2],Lsun3D$Cls)

#ggplot 2 with different symbols
Classplot(
  Lsun3D$Data[, 1],
  Lsun3D$Data[, 2],
  Lsun3D$Cls,
  Plotter = "ggplot2",
  Size = 3,
  pch = Lsun3D$Cls + 5
)

#plotly with line
data(Lsun3D)
Classplot(Lsun3D$Data[,1],Lsun3D$Data[,2],Lsun3D$Cls,
LineType="-",LineColor = "green")

#ggplot2 with annotations
data(Lsun3D)
ind=sample(1:nrow(Lsun3D$Data),20)
Classplot(Lsun3D$Data[ind,1],Lsun3D$Data[ind,2],Lsun3D$Cls[ind],
Names = rownames(Lsun3D$Data)[ind],Size =1,
Plotter = "ggplot2",AnnotateIt = TRUE)

#non 1:k ordered sequence
#of user specific colors
Colors=c("blue","green","red")
names(Colors)=c(3,2,1) #non 1:k ordering

Classplot(Lsun3D$Data[ind,1],Lsun3D$Data[ind,2],Lsun3D$Cls[ind],
Names = rownames(Lsun3D$Data)[ind],Size =1,
Plotter = "ggplot2",AnnotateIt = TRUE,Colors=Colors)

#if named vector is used, user is
#allowed to define more colors than labels
#given for current plot in case of
#multiple plots with standardized labels
Colors=c("blue","green","red","yellow")
names(Colors)=c(1,2,3,4) #1:(k+1) ordering

Classplot(Lsun3D$Data[ind,1],Lsun3D$Data[ind,2],Lsun3D$Cls[ind],
Names = rownames(Lsun3D$Data)[ind],Size =1,
Plotter = "ggplot2",AnnotateIt = TRUE,Colors=Colors)

#ggplot2 with labels and legend per class
data(Lsun3D)
Classplot(Lsun3D$Data[, 1],Lsun3D$Data[, 2],Lsun3D$Cls,
Names = paste0("C",Lsun3D$Cls),Size =2,Legend ="Classes")

```

`CombineCols`*Combine vectors of various lengths*

Description

Combine arbitrary vectors of data, filling in missing rows with NaN

Usage

```
CombineCols(..., na.rm=FALSE)
```

Arguments

`...` `d` vectors of arbitrary lengths, see example
`na.rm` boolean: FALSE: fills with NaN TRUE: fills with zeros

Details

Robust alternative to `cbind` that fills missing values with `nan` instead of extending length of vector by duplicating elements

Value

matrix of dimensionality of `n x d` with `n` being the length of the longest vector and `d` the number of vectors given as input

Note

special application by MCT of `rowr::cbind.fill` which is now not on CRAN anymore

Author(s)

Craig Varrichio

See Also

`CombineRows`

Examples

```
CombineCols(c(1,2,3),c(1),c(2,3))
```

`CombineRows`*Combine matrices of various lengths*

Description

Combine arbitrary matrices of data, filling in missing columns with NaN

Usage

```
CombineRows(...,na.rm=FALSE)
```

Arguments

`...` First argument is a matrix usually with `d` named columns, thereafter either matrices or `d` vectors of arbitrary lengths, see example

`na.rm` boolean: FALSE: fills with NaN TRUE: fills with zeros

Details

Robust alternative to `rbind` that fills missing values with #NaN, tries to match given column names if matrices are inserted otherwise fills up the missing columns at the end.

The first argument has to be a `[1:n,1:d]` matrix. It is assumed that this matrix has to be filled up and other arguments are not of greater size than `d` columns.

Otherwise, the further elements stored in columns `>d` are ignored.

Value

matrix of dimensionality of `n x d` with `n` being the number of rows of the first argument and `d` the number columns of the first argument given as input

Author(s)

Michael Thrun

See Also

`CombineCols`

Examples

```
matrix_pattern=cbind(c(1,2,3),c(4,5,6),c(7,8,9))
```

```
CombineRows(matrix_pattern,c(1),c(2,3))
```

```
CombineRows(matrix_pattern,cbind(c(1,2,3),c(4,5,6)))
```

Crosstable

*Crosstable plot***Description**

Presents a heatmap with values and a cross table of given Data matrix of two features and a bin width or percentualized values. In this approach the bin width is fixes. A more general way to approach this is the kernel density estimation plot of [PDEscatter](#).

Usage

```
Crosstable(Data, xbins = seq(0, 100, 5), ybins = xbins,
NormalizationFactor = 1, PlotIt = TRUE, main='Cross Table',
PlotText=TRUE, TextDigits=0, TextProbs=c(0.05,0.95))
```

Arguments

Data	[1:n,1:2] matrix of two features from which the cross table should be generated from
xbins	[1:k] start of k bins as a vector generated with seq of the first feature of data. Default setting assumes percentiled values between zero and 100.
ybins	[1:k] start of k bins as a vector generated with seq of the second feature of data. Normally the same for both features, other settings are only possible if the length k is equal.
NormalizationFactor	Optional, Data feautres can be seen as regular time series, e.g. 1 measurement for a minute, in this case it is useful to normalize the output, e.g. to hours, then NormalizationFactor=60
PlotIt	Optional, Plots the heatmap if TRUE. The first feature is on the x-axis (left to right) and the second on y-axis (bottom to top).
main	In case of for PlotIt=TRUE: title of plot, see title
PlotText	In case of for PlotIt=TRUE: Default TRUE: plots text in heatmap with the values of the crosstable
TextDigits	In case of for TextDigits=TRUE: integer indicating the number of decimal places to use in round .
TextProbs	In case of for TextDigits=TRUE: [1:2] numeric vector of two probabilities defining the thresholds for white text to grey text and grey text to black text, e.g. below the first threshold (Default 0.05) all values (5% of values) will be printed in white because the lowest values of the heatmap are blue. The second value of 0.95 works well if cross table has many zeros; uses quantile internally.

Details

The interval in each bin is closed to the left and opened to the right. The cross table can be seen as a two-dimensional histogram. The idea to add histograms to the table is taken from [Charpentier, 2014].

Value

The cross table in invisible mode which depicts the number of values (frequency) in an specific range with regard to two features.

The first feature is on the x-axis (left to right), and the second on y-axis (top to bottom) contrary to the plot where it is bottom to top.

Note

For non percentiled values the PlotText part does not seem always to work, but I currently dont know why the text does not always overlap with the heatmap.

Author(s)

Michael Thrun

References

[Charpentier. 2014] Charpentier, Arthur, ed. Computational actuarial science with R. CRC Press, 2014.

See Also

[table](#), [image](#), [PDEscatter](#)

Examples

```
data(ITS)
data(MTY)
#simple but not a good transformation
Data=(cbind(ITS/max(ITS),MTY/max(MTY)))*100
#choice for bins could be better
Crosstable(Data)
```

DefaultColorSequence *Default color sequence for plots*

Description

Defines the default color sequence for plots made within the Projections package.

Usage

```
data("DefaultColorSequence")
```

Format

A vector with 562 different strings describing colors for plots.

DensityContour	<i>Contour plot of densities</i>
----------------	----------------------------------

Description

Density estimation (PDE) [Ultsch, 2005] or "SDH" [Eilers/Goeman, 2004] used for a density contour plot.

Usage

```
DensityContour(X,Y, DensityEstimation="SDH",
SampleSize, na.rm=FALSE,PlotIt=TRUE,
NrOfContourLines=20,Plotter='ggplot', DrawTopView = TRUE,
xlab, ylab, main="DensityContour",
xlim, ylim, Legendlab_ggplot="value",
AddString2lab="",NoBinsOrPareto=NULL,...)
```

Arguments

X	Numeric vector [1:n], first feature (for x axis values)
Y	Numeric vector [1:n], second feature (for y axis values)
DensityEstimation	"SDH" is very fast but maybe not correct, "PDE" is slow but probably more correct, third alternative is the typical R density estimation with "kde2d" which is sensitive to parameters
SampleSize	Numeric, positive scalar, maximum size of the sample used for calculation. High values increase runtime significantly. The default is that no sample is drawn
na.rm	Function may not work with non finite values. If these cases should be automatically removed, set parameter TRUE
PlotIt	TRUE: plots with function call FALSE: Does not plot, plotting can be done using the list element Handle
NrOfContourLines	Numeric, number of contour lines to be drawn. 20 by default.

Plotter	String, name of the plotting backend to use. Possible values are: "ggplot", "plotly". Default: ggplot
DrawTopView	Boolean, True means contour is drawn, otherwise a 3D plot is drawn. Default: TRUE
xlab	String, title of the x axis. Default: "X", see plot() function
ylab	String, title of the y axis. Default: "Y", see plot() function
main	string, the same as "main" in plot() function
xlim	see plot() function
ylim	see plot() function
Legendlab_ggplot	String, in case of Plotter="ggplot" label for the legend. Default: "value"
AddString2lab	adds the same string of information to x and y axis label, e.g. usefull for adding SI units
NoBinsOrPareto	Density specific parameters, for PDEscatter(ParetoRadius) or SDH (nbins) or kde2d(bins)
...	further plot arguments

Details

The DensityContour function generates the density of the xy data as a z coordinate. Afterwards xyz will be plotted either as a contour plot or a 3d plot. It assumes that the cases of x and y are mapped to each other meaning that a cbind(x,y) operation is allowed. This function plots the Density on top of a scatterplot. Variances of x and y should not differ by extreme numbers, otherwise calculate the percentiles on both first. If DrawTopView=FALSE only the plotly option is currently available. If another option is chosen, the method switches automatically there.

PlotIt=FALSE is usefull if one likes to perform adjustments like axis scaling prior to plotting with **ggplot2** or **plotly**.

Value

List of:

X	Numeric vector [1:m], $m \leq n$, first feature used in the plot or the kernels used
Y	Numeric vector [1:m], $m \leq n$, second feature used in the plot or the kernels used
Densities	Number of points within the ParetoRadius of each point, i.e. density information
Handle	Handle of the plot object

Note

MT contributed with several adjustments

Author(s)

Felix Pape

References

[Thrun, 2018] Thrun, M. C.: Projection Based Clustering through Self-Organization and Swarm Intelligence, (Ultsch, A. & Huellermeier, E. Eds., 10.1007/978-3-658-20540-9), Doctoral dissertation, Heidelberg, Springer, ISBN: 978-3658205393, 2018.

[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.

[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.

[Eilers/Goeman, 2004] Eilers, P. H., & Goeman, J. J.: Enhancing scatterplots with smoothed densities, Bioinformatics, Vol. 20(5), pp. 623-628. 2004.

Examples

```
#taken from [Thrun/Ultsch, 2018]
data("ITS")
data("MTY")
Inds=which(ITS<900&MTY<8000)
plot(ITS[Inds],MTY[Inds],main='Bimodality is not visible in normal scatter plot')

DensityContour(ITS[Inds],MTY[Inds],DensityEstimation="SDH",xlab = 'ITS in EUR',
ylab = 'MTY in EUR' ,main='Smoothed Densities histogram indicates Bimodality' )

DensityContour(ITS[Inds],MTY[Inds],DensityEstimation="PDE",xlab = 'ITS in EUR',
ylab = 'MTY in EUR' ,main='PDE indicates Bimodality' )
```

DensityScatter

Scatter plot with densities

Description

Density estimation is performed by (PDE) [Ultsch, 2005] or "SDH" [Eilers/Goeman, 2004] and visualized in a density scatter plot [Brinkmann et al., 2023] in which the points are colored by their density.

Usage

```
DensityScatter(X,Y,DensityEstimation="SDH",
Type="DDCAL", Plotter = "native",Marginals = FALSE,
```

```

SampleSize,na.rm=FALSE, xlab, ylab,
main="DensityScatter", AddString2lab="",
xlim, ylim,NoBinsOrPareto=NULL,...)

```

Arguments

X	Numeric vector [1:n], first feature (for x axis values)
Y	Numeric vector [1:n], second feature (for y axis values)
DensityEstimation	(Optional), "SDH" is very fast but maybe not correct, "PDE" is slow but probably more correct, third alternative is the typical R density estimation with "kde2d" which is sensitive to parameters
Type	(Optional), "DDCAL" uses a new density to point color matching by DDCAL algorithm [Lux/Rinderle-Ma, 2023], "native" uses a simple density to point color matching
Plotter	in case of Type="DDCAL", (Optional) String, name of the plotting backend to use. Possible values are: "native","plotly", or "ggplot2"
Marginals	(Optional) Boolean, if TRUE the marginal distributions of X and Y will be plotted together with the 2D density of X and Y. Default is FALSE
SampleSize	(Optional), Numeric, positive scalar, maximum size of the sample used for calculation. High values increase runtime significantly. The default is that no sample is drawn
na.rm	(Optional), Function may not work with non finite values. If these cases should be automatically removed, set parameter TRUE
xlab	(Optional), String, title of the x axis. Default: "X", see plot() function
ylab	(Optional), String, title of the y axis. Default: "Y", see plot() function
main	(Optional), string, the same as "main" in plot() function
AddString2lab	(Optional), adds the same string of information to x and y axis label, e.g. useful for adding SI units
xlim	(Optional), in case of Type="native", see plot() function
ylim	in case of Type="native", see plot() function
NoBinsOrPareto	(Optional), in case of Type="native", Density specific parameters, for PDEscatter (ParetoRadius) or SDH (nbins) or kde2d(bins)
...	(Optional), further arguments either to ScatterDensity::DensityScatter.DDCAL or to plot()

Details

The `DensityScatter` function generates the density of the xy data as a z coordinate. Afterwards xy points will be plotted as a scatter plot, where the z values define the coloring of the xy points. It assumes that the cases of x and y are mapped to each other meaning that a `cbind(x,y)` operation is allowed. This function plots the Density on top of a scatterplot. Variances of x and y should not differ by extreme numbers, otherwise calculate the percentiles on both first.

Value

List of:

X	Numeric vector [1:m], $m \leq n$, first feature used in the plot or the kernels used
Y	Numeric vector [1:m], $m \leq n$, second feature used in the plot or the kernels used
Densities	Number of points within the ParetoRadius of each point, i.e. density information

Note

MT contributed with several adjustments

Author(s)

Felix Pape

References

[Thrun, 2018] Thrun, M. C.: Projection Based Clustering through Self-Organization and Swarm Intelligence, (Ultsch, A. & Huellermeier, E. Eds., 10.1007/978-3-658-20540-9), Doctoral dissertation, Heidelberg, Springer, ISBN: 978-3658205393, 2018.

[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.

[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.

[Eilers/Goeman, 2004] Eilers, P. H., & Goeman, J. J.: Enhancing scatterplots with smoothed densities, Bioinformatics, Vol. 20(5), pp. 623-628. 2004

[Lux/Rinderle-Ma, 2023] Lux, M. & Rinderle-Ma, S.: DDCAL: Evenly Distributing Data into Low Variance Clusters Based on Iterative Feature Scaling, Journal of Classification vol. 40, pp. 106-144, 2023.

[Brinkmann et al., 2023] Brinkmann, L., Stier, Q., & Thrun, M. C.: Computing Sensitive Color Transitions for the Identification of Two-Dimensional Structures, Proc. Data Science, Statistics & Visualisation (DSSV) and the European Conference on Data Analysis (ECDA), p.109, Antwerp, Belgium, July 5-7, 2023.

Examples

```
#taken from [Thrun/Ultsch, 2018]
data("ITS")
data("MTY")
Inds=which(ITS<900&MTY<8000)
plot(ITS[Inds],MTY[Inds],main='Bimodality is not visible in normal scatter plot')

DensityScatter(ITS[Inds],MTY[Inds],DensityEstimation="SDH",xlab = 'ITS in EUR',
ylab = 'MTY in EUR' ,main='Smoothed Densities histogram indicates Bimodality' )
```

```
DensityScatter(ITS[Inds],MTY[Inds],DensityEstimation="PDE",xlab = 'ITS in EUR',
ylab = 'MTY in EUR' ,main='PDE indicates Bimodality' )
```

DrawWorldWithCls *Plot a classificated world map*

Description

This function plots a world map where the single countries get colored differently by using a classification

Arguments

CountryCode	Vector of Countrys belonging to the Cls
Cls	Classes belonging to the Countries from CountryCode
JoinCode	System that is used for the CountryCodes. Possible are: "ISO3", "UN"
Title	Title that will be written above the map
Colors	Vector that colors for classes will be selected from

Value

a plot

Author(s)

Florian Lerch

DualaxisClassplot *Dualaxis Classplot*

Description

Allows to plot two time series or features with one or two classification(a) as labeled scatter plots. The colors are the labels defined by the classification. Usefull to see if temporal clustering has time dependent variations and for Hidden Markov Models (see Mthrun/RHmm on GitHub).

Usage

```
DualaxisClassplot(X, Y1, Y2, Cls1,
Cls2, xlab = "X", y1lab = "Y1", y2lab = "Y2",
main = "Dual Axis Class Plot", Colors, Showgrid = TRUE, SaveIt = FALSE)
```

Arguments

X	[1:n] numeric vector or time
Y1	[1:n] numeric vector of feature
Y2	[1:n] numeric vector of feature
Cls1	[1:n] numeric vector defining a classification of k1 classes
Cls2	Optional, [1:n] numeric vector defining a classification of k2 classes for Y2
xlab	Optional, string
y1lab	Optional, string
y2lab	Optional, string
main	Optional, string
Colors	[1:(k1+k2)] Colornames
Showgrid	Optional, boolean
SaveIt	Optional, boolean

Value

plotly object

Author(s)

Michael Thrun

See Also

[Classplot](#)

Examples

```
##ToDo
```

DualaxisLinechart *DualaxisLinechart*

Description

A line chart with dual axisSS

Usage

```
DualaxisLinechart(X, Y1, Y2, xlab = "X",  
y1lab = "Y1", y2lab = "Y2", main = "Dual Axis Line Chart",  
cols = c("black", "blue"),Overlaying="y", SaveIt = FALSE)
```

Arguments

X	[1:n] vector, both lines require the same xvalues, e.g. the time of the time series, POSIXlt or POSIXct are accepted
Y1	[1:n] vector of first line
Y2	[1:n] vector of second line
xlab	Optional, string for xlabel
y1lab	Optional, string for first ylabel
y2lab	Optional, string for second ylabel
main	Optional, title of plot
cols	Optional, color of two lines
Overlying	Change only default in case of using subplot
SaveIt	Optional, default FALSE; TRUE if you want to save plot as html in getwd() directory

Details

enables to visualize to lines in one plot overlaying them using plotly (e.g. two time series with two ranges of values)

Value

plotly object

Author(s)

Michael Thrun

Examples

```
#subplot renames the numbering of subsequent plots
y1=runif(100,0,1)
y2=rnorm(100,m=5,s=1)
DualaxisLinechart(1:100, y1, y2,main="Random Time series")
```

```
y1=runif(100,0,1)
y2=(1:100*3+4)*runif(100,0,1)
p1=DualaxisLinechart(1:100, y1, y2,main="Random Time series",Overlying="y2")
```

```
y3=1:100*(-2)+4
y4=rnorm(100,m=0,s=2)
p2=DualaxisLinechart(1:100, y3, y4,main="Random Time series",Overlying="y4")
plotly::subplot(p1,p2)
```

estimateDensity2D *estimateDensity2D*

Description

Estimates densities for two-dimensional data with the given estimation type

Usage

```
estimateDensity2D(X, Y, DensityEstimation = "SDH",
  SampleSize, na.rm = FALSE, NoBinsOrPareto = NULL)
```

Arguments

X	[1:n] numerical vector of first feature
Y	[1:n] numerical vector of second feature
DensityEstimation	Either "PDE","SDH" or "kde2d"
SampleSize	Sample Size in case of big data
na.rm	Function may not work with non finite values. If these cases should be automatically removed, set parameter TRUE
NoBinsOrPareto	Density specific parameters, for PDEscatter(ParetoRadius) or SDH (nbins)) or kde2d(bins)

Details

Each two-dimensional data point is defined by its corresponding X and Y value.

Value

List V with	
X	[1:m] numerical vector of first feature, $m \leq n$ depending if all values are finite an na.rm parameter
Y	[1:m] numerical vector of second feature, $m \leq n$ depending if all values are finite an na.rm parameter
Densities	the density of each two-dimensional data point

Author(s)

Luca Brinkman and Michael Thrun

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, (Vol. 27, pp. 91-100), Berlin, Germany, Springer, 2005.

[Eilers/Goeman, 2004] Eilers, P. H., & Goeman, J. J.: Enhancing scatterplots with smoothed densities, Bioinformatics, Vol. 20(5), pp. 623-628. 2004

Examples

```
X=runif(100)
Y=rnorm(100)
#V=estimateDensity2D(X,Y)
```

Fanplot

The fan plot

Description

The better alternative to the pie chart represents amount of values given in data.

Usage

```
Fanplot(Datavector,Names,Labels,MaxNumberOfSlices,main='',col,
MaxPercentage=FALSE,ShrinkPies=0.05,Rline=1.1, lwd=2,LabelCols="black",...)
```

Arguments

Datavector	[1:n] a vector of n non unique values
Names	Optional, [1:k] names to search for in Datavector, if not set unique of Datavector is calculated.
Labels	Optional, [1:k] Labels if they are specially named, if not Names are used.
MaxNumberOfSlices	Default is k, integer value defining how many labels will be shown. Everything else will be summed up to Other.
main	Optional, title below the fan pie, see plot
col	Optional, the default are the first [1:k] colors of the default color sequence used in this package, otherwise a character vector of [1:k] specifying the colors analog to plot
MaxPercentage	default FALSE; if true the biggest slice is 100 percent instead of the biggest procentual count
ShrinkPies	Optional, distance between biggest and smallest slice of the pie
Rline	Optional, the distance between text and pie is defined here as the length of the line in numerical numbers
lwd	Optional, The line width, a positive number, default is 2

LabelCols	Color of labels
...	Further arguments to <code>fan.plot</code> like circumferential positions for the labels <code>labelpos</code> or additional arguments passed to <code>polygon</code>

Details

A normal pie plot is difficult to interpret for a human observer, because humans are not trained well to observe angles [Gohil, 2015, p. 102]. Therefore, the fan plot is used. As proposed in [Gohil 2015] the `fan.plot()` of the `plotrix` package is used to solve this problem. If Number of Slices is higher than `MaxNumberOfSlices` then `ABCanalysis` is applied (see [Ultsch/Lotsch, 2015]) and group A chosen. If Number of Slices in group A is higher than `MaxNumberOfSlices`, then the most important ones out of group A are chosen. If `MaxNumberOfSlices` is higher than Slices in group A, additional slices are shown depending on the percentage (from high to low).

Color sequence is automatically shortened to the `MaxNumberOfSlices` used in the fan plot.

Value

silent output by calling `invisible` of a list with

Percentages	[1:k] percent values visualized in fanplot
Labels	[1:k] see input <code>Labels</code> , only relevant ones

Author(s)

Michael Thrun

References

[Gohil, 2015] Gohil, Atmajitsinh. R data Visualization cookbook. Packt Publishing Ltd, 2015.

[Ultsch/Lotsch, 2015] Ultsch. A ., Lotsch J.: Computed ABC Analysis for Rational Selection of Most Informative Variables in Multivariate Data, PloS one, Vol. 10(6), pp. e0129767. doi 10.1371/journal.pone.0129767, 2015.

See Also

[fan.plot Piechart](#)

Examples

```
data(categoricalVariable)
Fanplot(categoricalVariable)
```

FundamentalData_Q1_2018

Fundamental Data of the 1st Quarter in 2018

Description

This dataset was extracted out of Yahoo finance and was investigated in [Thrun et al., 2019] and clustered in [Thrun, 2019].

Usage

```
data("FundamentalData_Q1_2018")
```

Format

The format is: List of 3 \$ Data :'data.frame': 269 obs. of 45 variables: ..\$ TotalRevenue : num [1:269] 3779000 78225 48220 63726 3084\$ CostofRevenue : num [1:269] 2348000 60835 26174 35203 882\$ GrossProfit : num [1:269] 1431000 17390 22046 28523 2202\$ SellingGeneralandAdministrative : num [1:269] 459000 NaN 15162 17072 2005\$ Others : num [1:269] -3000 10272 -52 3131 1784\$ TotalOperatingExpenses : num [1:269] 2872000 73833 41284 56787 5081\$ OperatingIncomeeorLoss : num [1:269] 907000 4392 6936 6939 -1997\$ TotalOtherIncomeDIVxpensesNet : num [1:269] -28000 -344 1 -210 -240\$ EarningsBeforeInterestandTaxes : num [1:269] 907000 4392 6936 6939 -1997\$ InterestExpense : num [1:269] -20000 -415 NaN -243 -238\$ IncomeBeforeTax : num [1:269] 879000 4048 6937 6729 -2237\$ IncomeTaxExpense : num [1:269] 233000 1365 2188 1896 7\$ NetIncomeFromContinuingOps : num [1:269] 646000 2683 4749 4833 -2244\$ NetIncome_x : num [1:269] 644000 2817 4645 4833 -2244\$ NetIncome : num [1:269] 644000 2817 4645 4833 -2244\$ CashAndCashEquivalents : num [1:269] 926000 29047 45911 94859 11217\$ NetReceivables : num [1:269] 2527000 46171 20774 151952 2774\$ Inventory : num [1:269] 2011000 471 NaN 10572 8924\$ TotalCurrentAssets : num [1:269] 5674000 80224 68061 267187 25989\$ LongTermInvestments : num [1:269] 234000 450 NaN 4155 872\$ PropertyPlantandEquipment : num [1:269] 4216000 14561 3093 32247 7073\$ IntangibleAssets : num [1:269] 78000 40706 3975 6169 125\$ OtherAssets : num [1:269] 810000 8224 1091 2978 13310\$ DeferredLongTermAssetCharges : num [1:269] 759000 684 1091 784 1405\$ TotalAssets : num [1:269] 11262000 167807 83155 351220 47369\$ AccountsPayable : num [1:269] 1442000 10567 1698 17316 1386\$ ShortDIVurrentLongTermDebt : num [1:269] 1275000 30192 NaN 26668 917\$ OtherCurrentLiabilities : num [1:269] 1064000 36942 22781 92297 2659\$ TotalCurrentLiabilities : num [1:269] 2577000 54430 24479 114210 4299\$ OtherLiabilities : num [1:269] 1795000 19435 6876 29347 2018\$ TotalLiabilities : num [1:269] 5576000 97136 31355 165628 6980\$ CommonStock : num [1:269] 198000 14946 5198 15250 28644\$ RetainedEarnings : num [1:269] NaN 44030 34767 40374 -8965\$ TreasuryStock : num [1:269] 5455000 11686 NaN 129968 20710\$ OtherStockholderEquity : num [1:269] 5455000 11686 NaN 129968 20710\$ TotalStockholderEquity : num [1:269] 5653000 70662 51212 185592 40389\$ NetTangibleAssets : num [1:269] 5325000 6314 40302 140939 40264\$ Depreciation : num [1:269] 156000 2728 331 1381 410\$ AdjustmentsToNetIncome : num [1:269] 216000 1911 116 2912 39\$ ChangesInOtherOperatingActivities : num [1:269] -20000 -2174 -829 NaN 428\$ TotalCashFlowFromOperatingActivities : num [1:269]

```
452000 7349 4274 -8241 -1367 ... ..$ CapitalExpenditures : num [1:269] -88000 -966 -1778 -2067
-155 ... ..$ TotalCashFlowsFromInvestingActivities: num [1:269] 30000 -879 -1766 -2746 -484 ...
..$ TotalCashFlowsFromFinancingActivities: num [1:269] -789000 -6660 -21867 -961 -204 ... ..$
ChangeInCashandCashEquivalents : num [1:269] -306000 -215 2508 -11842 -2062 ... $ Names:
chr [1:269, 1:6] "ICOV" "A1OS" "AAD" "AAG" ... ..- attr(*, "dimnames")=List of 2 .. ..$ : NULL
.. ..$: chr [1:6] "Key" "ISIN" "Company" "Sector" ... $ Cls : num [1:269] 1 1 1 1 2 1 1 1 3 1 ...
```

Details

Stocks are selected by the German Prime standard accordingly to the "Names" data frame. Fundamental Data with missing values is stored in "Data". The rownames of "Data" have the same Key as the first row of "Names" which is the trading symbol. "Cls" provides the clustering as a numerical vector of 1:k classes performed by Databionic Swarm in [Thrun, 2019].

Source

Yahoo finance

References

Thrun, M. C., : Knowledge Discovery in Quarterly Financial Data of Stocks Based on the Prime Standard using a Hybrid of a Swarm with SOM, in Verleysen, M. (Ed.), European Symposium on Artificial Neural Networks, Computational Intelligence and Machine Learning (ESANN), Vol. 27, pp. 397-402, Ciaco, ISBN: 978-287-587-065-0, Bruges, Belgium, 2019.

[Thrun et al., 2019] Thrun, M. C., Gehlert, Tino, & Ultsch, A. : Analyzing the Fine Structure of Distributions, arXiv:1908.06081, 2019.

Examples

```
data(FundamentalData_Q1_2018)
## maybe str(FundamentalData_Q1_2018) ; plot(FundamentalData_Q1_2018) ...
```

GoogleMapsCoordinates *Google Maps with marked coordinates*

Description

Google Maps with marked coordinates.

Usage

```
GoogleMapsCoordinates(Longitude, Latitude, Cls=rep(1, length(Longitude)),
zoom=3, location= c(mean(Longitude), mean(Latitude)), stroke=1.7, size=6, sequence)
```

Arguments

Longitude	sphaerischer winkel der Kugeloberflaeche, coord 1
Latitude	sphaerischer winkel der Kugeloberflaeche, coord 2
Cls	Vorklassification/Clusterung
zoom	map zoom, an integer from 3 (continent) to 21 (building), default value 10 (city). openstreetmaps limits a zoom of 18, and the limit on stamen maps depends on the matype. "auto" automatically determines the zoom for bounding box specifications, and is defaulted to 10 with center/zoom specifications. maps of the whole world currently not supported
location	Optional, default: c(mean(Longitude),mean(Latitude)); an address, longitude/latitude pair (in that order), or left/bottom/right/top bounding box
stroke	Optional, plotting parameter, dicke der linien der coordiantensymbole
size	Optional, plotting parameter, gresse der koordinatensymbole
sequence	Optional, vector of length of number of clusers with numbers indicating the plotting symbols and colors to use

Details

This plot was used in [Thrun, 2018, p. 135].

Value

ggobject()

Note

requires an Internet connection, requires an API key of Google. See ?ggmap::register_google for details.

Author(s)

Michael Thrun

References

[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.

Heatmap

*Heatmap for Clustering***Description**

Heatmap of Distances of Data sorted by Cls. Clustering algorithms provide a Classification of data, where the labels are defined as a numeric vector Cls. Then, a typical cluster-respectively group structure is displayed by the Heatmap function. At the margin of the heatmap a dendrogram can be shown, if hierarchical cluster algorithms are used [Wilkinson,2009]. Here the dendrogram has to be shown separately and only the heatmap itself is displayed

Usage

```
Heatmap(DataOrDistances,Cls,method='euclidean',
        LowLim=0,HiLim,LineWidth=0.5,Clabel="Cluster No.")
```

Arguments

DataOrDistances	if not symmetric, then the function assumes a [1:n,1:d] numeric matrix of n data cases in rows and d variables in columns. In this case, the distance metric specified in method will be used. Otherwise, [1:n,1:n] distance matrix that is symmetric
Cls	[1:n] numerical vector of numbers defining the classification as the main output of the clustering algorithm. It has k unique numbers for k clusters that represent the arbitrary labels of the clustering, assuming a descending order of 1 to k. If not ordered please use ClusterRenameDescendingSize . Otherwise x and y label will be incorrect.
method	Optional, if DataOrDistances is a [1:n,1:d] not symmetric numerical matrix, please see parDist for accessible distance methods, default is Euclidean
LowLim	Optional: limits for the color axis
HiLim	Optional: limits for the color axis
LineWidth	Width of lines separating the clusters in the heatmap
Clabel	Default "Cluster No.", for large number of clusters abbreviations can be used like "Cls No." or "C" in order to fit as the x and y axis labels

Details

"Cluster heatmaps are commonly used in biology and related fields to reveal hierarchical clusters in data matrices. Heatmaps visualize a data matrix by drawing a rectangular grid corresponding to rows and columns in the matrix and coloring the cells by their values in the data matrix. In their most basic form, heatmaps have been used for over a century [Wilkinson, 2012]. In addition to coloring cells, cluster heatmaps reorder the rows and/or columns of the matrix based on the results

of hierarchical clustering. (...) . Cluster heatmaps have high data density, allowing them to compact large amounts of information into a small space [Weinstein, 2008]", [Engle, 2017].

The procedure can be adapted to distance matrices [Thrun, 2018]. Then, the color scale is chosen such that pixels of low distances have blue and teal colors, pixels of middle distances yellow colors, and pixels of high distances have orange and red colors [Thrun, 2018]. The distances are ordered by the clustering and the clusters are divided by black lines. A clustering is valid if the intra-cluster distances are distinctively smaller than inter-cluster distances in the heatmap [Thrun, 2018]. For another example, please see [Thrun, 2018] (Fig. 3.7, p. 31).

Value

object of ggplot2

Author(s)

Michael Thrun

References

[Wilkinson,2009] Wilkinson, L., & Friendly, M.: The history of the cluster heat map, *The American Statistician*, Vol. 63(2), pp. 179-184. 2009.

[Engle et al., 2017] Engle, S., Whalen, S., Joshi, A., & Pollard, K. S.: Unboxing cluster heatmaps, *BMC bioinformatics*, Vol. 18(2), pp. 63. 2017.

[Weinstein, 2008] Weinstein, J. N.: A postgenomic visual icon, *Science*, Vol. 319(5871), pp. 1772-1773. 2008.

[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.

See Also

[Pixelmatrix](#)

Examples

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

#Data
Heatmap(Data,Cls = Cls)

#Distances
Heatmap(as.matrix(dist(Data)),Cls = Cls)
```

HeatmapColors	<i>Default color sequence for plots</i>
---------------	---

Description

Defines the default color sequence for plots made with PixelMatrixPlot

Usage

```
data("HeatmapColors")
```

Format

A vector with different strings describing colors for this plot.

InspectBoxplots	<i>Inspect Boxplots</i>
-----------------	-------------------------

Description

Enables to inspect the boxplots for multiple variables in ggplot2 syntax. Each boxplot also has a point for the mean of the variable.

Usage

```
InspectBoxplots(Data, Names, Means=TRUE)
```

Arguments

Data	Matrix containing the data. Each column is one variable.
Names	Optional: Names of the variables. If missing the columnnames of data are used.
Means	Optional: TRUE: with mean, FALSE: Only median.

Value

The ggplot object of the boxplots

Author(s)

Felix Pape

Examples

```
x <- cbind(A = rnorm(200, 1, 3), B = rnorm(100, -2, 5))
InspectBoxplots(x)
```

 InspectCorrelation *Inspect the Correlation*

Description

Inspects the correlation between two given features using density scatter plots.

Usage

```
InspectCorrelation(X, Y, DensityEstimation = "SDH",
  CorMethod = "spearman", na.rm = TRUE,
  SampleSize = round(sqrt(5e+08), -3),
  NrOfContourLines = 20, Plotter = "native",
  DrawTopView = T, xlab, ylab,
  main = "Spearman correlation coef.:", xlim, ylim,
  Legendlab_ggplot = "value", ...)
```

Arguments

X	Numeric vector [1:n], first feature (for x axis values)
Y	Numeric vector [1:n], second feature (for y axis values)
DensityEstimation	"SDH" is very fast but maybe not correct, "PDE" is slow but proably more correct.
CorMethod	method of correlation of the cor function, One of "pearson" (default), "kendall", or "spearman"
SampleSize	Numeric, positiv scalar, maximum size of the sample used for calculation. High values increase runtime significantly. The default is that no sample is drawn
na.rm	Function may not work with non finite values. If these cases should be automatically removed, set parameter TRUE
NrOfContourLines	Numeric, number of contour lines to be drawn. 20 by default.
Plotter	String, name of the plotting backend to use. Possible values are: "native", "ggplot", "plotly"
DrawTopView	Boolean, True means contur is drawn, otherwise a 3D plot is drawn. Default: TRUE
xlab	String, title of the x axis. Default: "X", see plot() function
ylab	String, title of the y axis. Default: "Y", see plot() function

<code>main</code>	string, the same as "main" in <code>plot()</code> function
<code>xlim</code>	see <code>plot()</code> function
<code>ylim</code>	see <code>plot()</code> function
<code>Legendlab_ggplot</code>	String, in case of <code>Plotter="ggplot"</code> label for the legend. Default: "value"
<code>...</code>	Density specific parameters, for <code>PDEscatter()</code> or <code>SDH(nbins,lambda,Xkernel,Ykernel)</code>

Details

Example shows that features with high correlation coefficient do not correlate because of bimodality.

Value

plotting handler

Author(s)

Michael Thrun

References

[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.

See Also

[DensityScatter](#)

Examples

```
data(ITS)
data(MTY)
Inds=which(ITS<9000&MTY<8000)

InspectCorrelation(ITS[Inds],MTY[Inds])
```

InspectDistances	<i>Inspection of Distance-Distribution</i>
------------------	--

Description

Visualizes the distances between objects in the data matrix

Usage

```
InspectDistances(DataOrDistances,method= "euclidean",sampleSize = 50000,...)
```

Arguments

DataOrDistances	[1:n,1:d] data cases in rows, variables in columns, if not symmetric or [1:n,1:n] distance matrix, if symmetric
method	Optional, if Data[1:n,1:d] see <code>parallelDist::parDist</code> for distance method
sampleSize	double value defining the size of the sample for large distance matrices, see <code>InspectVariable</code>
...	further arguments passed on to <code>InspectVariable</code>

Details

For an interpretation of the distribution analysis of the distance please read [Thrun, 2018, p. 27, 185].

Note

uses `InspectVariable`

Author(s)

Michael Thrun

References

[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.

Examples

```
data("Lsun3D")
Data=Lsun3D$Data

InspectDistances(as.matrix(dist(Data)))
```

InspectScatterplots *Pairwise scatterplots and optimal histograms*

Description

Pairwise scatterplots and optimal histograms of all features stored as columns of data are plotted

Usage

```
InspectScatterplots(Data, Names=colnames(Data))
```

Arguments

Data	[1:n,1:d] Data cases in rows (n), variables in columns (d)
Names	Optional: Names of the variables. If missing the columnnames of data are used.

Details

For two features, PDEscatter function should be used to inspect modalities [Thrun/Ultsch, 2018]. For many features the function takes too long. In such a case this function can be used. See [Thrun/Ultsch, 2018] for optimal histogram description.

Author(s)

Michael Thrun

References

[Thrun/Ultsch, 2018] Thrun, M. C., & Ultsch, A.: Effects of the payout system of income taxes to municipalities in Germany, 12th Professor Aleksander Zelias International Conference on Modelling and Forecasting of Socio-Economic Phenomena, Vol. accepted, Foundation of the Cracow University of Economics, Zakopane, Poland, 2018.

Examples

```
Data=cbind(rnorm(100, mean = 2, sd = 3 ), rnorm(100, mean = 0, sd = 1), rnorm(100, mean = 6, sd = 0.5))  
#InspectScatterplots(Data)
```

InspectStandardization

QQplot of Data versus Normalized Data

Description

Allows to inspect if standardization of data makes sense

Usage

```
InspectStandardization(Data, TransData, xug = -3, xog = 3, xlab = "Normal", yDataLab =  
"Data", yTransDataLab = "Trasformed Data", Symbol4Gerade = "red", main = "", ...)
```

Arguments

Data	...
TransData	...
xug	...
xog	...
xlab	...
yDataLab	...
yTransDataLab	...
Symbol4Gerade	...
main	...
...	...

Details

...

Value

plot

Author(s)

Michael Thrun

References

Michael, J. R.: The stabilized probability plot, *Biometrika*, Vol. 70(1), pp. 11-17, 1983.

InspectVariable *Visualization of Distribution of one variable*

Description

Enables distribution inspection by visualization as described in [Thrun, 2018] and for example used in

Usage

```
InspectVariable(Feature, Name, i = 1, xlim, ylim,
               sampleSize =1e+05, main)
```

Arguments

Feature	[1:n] Variable/Vector of Data to be plotted
Name	Optional, string, for x label
i	Optional, No. of variable/feature, an integer of the for lope
xlim	[2] Optional, range of x-axis for PDEplot and histogram
ylim	[2] Optional, range of y-axis, only for PDEplot
sampleSize	Optional, default(100000), sample size, if datavector is to big
main	string for the title if other than what is described in N

Author(s)

Michael Thrun

References

[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.

[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.

Examples

```
data("ITS")
InspectVariable(ITS,Name='Income in EUR',main='ITS')
```

ITS *Income Tax Share*

Description

Numerical vector of length 11194. details in [Ultsch/Behnisch, 2017; Thrun/Ultsch, 2018].

Usage

```
data("ITS")
```

References

[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.

[Ultsch/Behnisch, 2017] Ultsch, A., Behnisch, M.: Effects of the payout system of income taxes to municipalities in Germany, Applied Geography, Vol. 81, pp. 21-31, 2017.

Examples

```
data(ITS)
str(ITS)
```

JitterUniqueValues *Jitters Unique Values*

Description

Jitters Unique Values for Visualizations

Usage

```
JitterUniqueValues(Data, Npoints = 20,
min = 0.99999, max = 1.00001)
```

Arguments

Data	[1:n] vector of data
Npoints	number of jittered points generated from the m unique values of the datavector Data
min	minimum value of jittering
max	maximum value of jittering

Details

min and max are either multiplied or added to data depending on the range of values. If Npoints==2, then only two values per unique of Data is jittered otherwise additional values are generated. Npoints==1 does not jitter the values but gives the unique values back.

Value

vector of DataJitter[1:(m+Npoints-1)] jittered values

Author(s)

Michael Thrun

See Also

used for example in [MDplot](#)

Examples

```
data=c(rep(1,10),rep(0,10),rep(100,10))  
  
JitterUniqueValues(data,Npoints=1)  
  
JitterUniqueValues(data,Npoints=2)  
  
DataJitter=JitterUniqueValues(data,Npoints=20)
```

Lsun3D

Lsun3D inspired by FCPS [Thrun/Ultsch, 2020] 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
```

MAplot

Minus versus Add plot

Description

Bland-Altman plot [Altman/Bland, 1983].

Usage

```
MAplot(X,Y,islog=TRUE,LoA=FALSE,CI=FALSE,
densityplot=FALSE,main,xlab,ylab,
Cls,lwd=2,ylim=NULL,...)
```

Arguments

X	[1:n] numerical vector of a feature/variable
Y	[1:n] another numerical vector of a feature/variable
islog	Optional, TRUE: MAplot, FALSE: M=x-y versus a=0.5(x+y)
LoA	Optional, if TRUE: limits of agreement are plottet as lines if densityplot=FALSE
CI	Optional, if TRUE: confidence intervals for LoA, see [Stockl et al., 2004], if densityplot=FALSE
densityplot	Optional, FALSE: Scatterplot using Classplot , TRUE: density scatter plot with DensityScatter
main	Optional, see plot
xlab	Optional, see plot
ylab	Optional, see plot
Cls	Optional, prior Classification as a numeric vector.

lwd	Optional, if LoA=TRUE or CI=TRUE the width of the lines, otherwise input argument is ignored
ylim	Optional, default =NULL sets this parameter automatically, otherwise see Classplot.
...	for example, ylim, Please see either Classplot in the mode Plotter="native", or DensityScatter for further arguments depending on densityplot, see also details

Details

Bland-Altman plot [Altman/Bland, 1983] for visual representation of genomic data or in order to decorrelate data.

"The limits of agreement (LoA) are defined as the mean difference \pm 1.96 SD of differences. If these limits do not exceed the maximum allowed difference between methods (the differences within mean \pm 1.96 SD are not clinically important), the two methods are considered to be in agreement and may be used interchangeably." cited as in URL. Please note, that the underlying assumption is the normal distribution of the differences. Input argument LoA=TRUE shows the mean of the difference in blue and \pm 1.96 SD in green. Input argument CI=TRUE shows the mean of the difference in blue and the confidence intervall as red dashed lines similar to the cited URL.

In case of densityplot=FALSE, the function [Classplot](#) is always called with Plotter="native". Then, the input argument "Colors" of points can only be set in [Classplot](#) if "Cls" is given in this function, otherwise the points are always black. The input argument "Size" sets the size of points in [Classplot](#).

Value

MA	[1:n,2] Matrix of Minus component of two features and Add component of two features
Handle	see DensityScatter for output options, if densityplot=TRUE, otherwise NULL
Statistics	Named list of four element, each consisting of one value depending on input parameters LoA and CI, of this function. If not specifically set each list element is NULL. The elements are Mean_value - mean allowed difference, SD_value - standard deviation of difference, LoA_value - Limits of agreement=1.96*SD, CI_value - confidence intervall, i.e., maximum allowed difference

Author(s)

Michael Thrun

References

[Altman/Bland, 1983] Altman D.G., Bland J.M.: Measurement in medicine: the analysis of method comparison studies, *The Statistician*, Vol. 32, p. 307-317, doi:10.2307/2987937, 1983.

<https://www.medcalc.org/en/manual/bland-altman-plot.php>

[Stockl et al., 2004] Stockl, D., Rodriguez Cabaleiro, D., Van Uytfanghe, K., & Thienpont, L. M.: Interpreting method comparison studies by use of the Bland-Altman plot: reflecting the importance of sample size by incorporating confidence limits and predefined error limits in the graphic, *Clinical chemistry*, Vol. 50(11), pp. 2216-2218. 2004.

Examples

```
data("ITS")
data("MTY")
MAList=MAplot(ITS,MTY)
```

MDplot

Mirrored Density plot (MD-plot)

Description

This function creates a MD-plot for each variable of the data matrix. The MD-plot is a visualization for a boxplot-like shape of the PDF published in [Thrun et al., 2020] with the default ordering by shape. It is an improvement of violin or so-called bean plots and posses advantages in comparison to the conventional well-known box plot [Thrun et al., 2020].

A complete guide about the MDplot can be found in <https://md-plot.readthedocs.io/en/latest/index.html>.

Usage

```
MDplot(Data, Names, Ordering='Default', Scaling="None",
Fill='darkblue', RobustGaussian=TRUE, GaussianColor='magenta',
Gaussian_lwd=1.5, BoxPlot=FALSE,BoxColor='darkred',
MDscaling='width', LineColor='black', LineSize=0.01,
QuantityThreshold=50, UniqueValuesThreshold=12,
SampleSize=5e+05,SizeOfJitteredPoints=1,OnlyPlotOutput=TRUE,
main="MD-plot",ylab="Range of values in which PDE is estimated",
BW=FALSE,ForceNames=FALSE)
```

Arguments

Data	[1:n,1:d] Numerical Matrix containing the n cases of d variables. Each column is one variable. A data.frame is automatically transformed to a numerical matrix.
Names	Optional: [1:d] Names of the variables. If missing, the columnnames of data are used. If not missing, than the names can be cleaned or not (see ForceNames).
Ordering	Optional: string, either Default, Columnwise or AsIs, Alphabetical, Average, Bimodal, Variance or Statistics. Please see details for explanation.
Scaling	Optional, Default is None, Percentalize, CompleteRobust, Robust or Log, Please see details for explanation.

Fill	Optional: String or Vector, which gives the color(s) with which MDs are to be filled with.
RobustGaussian	Optional: If TRUE: each MDplot of a variable is overlaid with a robustly estimated unimodal Gaussian distribution in the range of this variable, if statistical testing does not yield a significant p.value. In this case the packages moments , diptest and signal are required. Beware, that internally the 'R's quantile function is used, which is slow for big data or many variables.
GaussianColor	Optional: string, color of robustly estimated gaussian, only for RobustGaussian=TRUE.
Gaussian_lwd	Optional: numerical, line width of robustly estimated gaussian, only for RobustGaussian=TRUE.
BoxPlot	Optional: If TRUE: each MDplot is overlaid with a Box-Whisker Diagram.
BoxColor	Optional: string, color of Boxplot, only for BoxPlot=TRUE.
MDscaling	Optional: if "area", all violins have the same area (before trimming the tails). If "count", areas are scaled proportionally to the number of observations. If "width" (default), all MDs have the same maximum width.
LineColor	Optional: string, color of line around the mirrored densities. NA disables this features which is useful if ones wants to avoid vertical lines leading to outliers.
LineSize	Optional: numerical, linewidth of line around the mirrored densities.
QuantityThreshold	Optional: numeric value defining the threshold of the minimal amount of values in data. Below this threshold no density estimation is performed and a 1D scatter plot with jittered points is drawn. Only Data Science experts should change this value after they understand how the density is estimated (see [Ultsch, 2005]).
UniqueValuesThreshold	Optional: numeric value defining the threshold of the minimal amount of unique values in data. Below this threshold no density estimation and statistical testing is performed and a 1D scatter plot with jittered points drawn. Only Data Science experts should change this value after they understand how the density is estimated (see [Ultsch, 2005]).
SampleSize	Optional: numeric value defining a threshold. Above this threshold uniform sampling of finite cases is performed in order to shorten computation time. If rowr is not installed, uniform sampling of all cases is performed. If required, SampleSize=n can be set to omit this procedure.
SizeOfJitteredPoints	Optional: scalar. If not enough unique values for density estimation are given, data points are jittered. This parameter defines the size of the points.
OnlyPlotOutput	Optional: Default TRUE only a ggplot object is given back, if FALSE: Additionally, scaled data and ordering are the output of this function in a list.
main	string defining the (centered) title of the plot
ylab	string defining the y label, PDE= pareto density estimation (see [Ultsch, 2005])
BW	FALSE: usual ggplot2 background and style which is good for screen visualizations TRUE: theme_bw() is used which is more appropriate for publications
ForceNames	FALSE: Per Default column names are cleaned for proper plotting TRUE: forces to set the column names as given. Beware, this can result in plotting errors.

Details

In short, the MD-plot can be described as a PDE optimized violin plot. The Pareto Density Estimation (PDE) is an approach to estimate the probability density function (pdf) [Ultsch, 2005].

The MD-plot is in the process of being peer-reviewed [Thrun/Ultsch, 2019].

Statistical testing is performed with [dip.test](#) and [agostino.test](#).

For the parameter `Ordering` the following options are possible:

`Default` Ordering of plots by convex/concav/unimodal/nonunimodal shapes using statistical criteria. In this case the **signal** is required.

`Columnwise` Ordering of plots by the order of columns of Data.

`AsIs` Synonym of `Columnwise`: Ordering of plots by the order of columns of Data.

`Alphabetical` Ordering of plots by the order of columns of Data sorted in alphabetical order by column names.

`Average` Ordering of plots by the order of columns of Data sorted in order of increasing column-wise average

`Bimodal` Ordering of plots by the order of columns of Data sorted in order of decreasing bimodality amplitude[Zhang et al., 2003]

`Variance` Ordering of plots by the order of columns of Data sorted in order of increasing inter-quartile range

`Statistics` Ordering of plots depending on the logarithm of the p-values of statistical testing. In this case the packages **moments**, **dipTest** and **signal** are required. Beware, that internally the R's quantile function is used, which is slow for big data or many variables.

For the parameter `Scaling` the following options are possible:

`None` No Scaling of data is done.

`Percentalize` Data is scaled between zero and 100.

`CompleteRobust` Data is first robustly scaled between zero and 1, then centered to zero and outliers are capped by a robustly formula described in [RobustNormalization](#).

`Robust` Data is robustly scaled between zero and 1 by a formula described in the [RobustNormalization](#).

`Log` Data is transformed with a signed log allowing for negative values to be transformed with a logarithm of base 10, please see [SignedLog](#) for details.

Value

In the default case of `OnlyPlotOutput==TRUE`: The ggplot object of the MD-plot.

Otherwise for `OnlyPlotOutput==FALSE`: A list of

`ggplotObj` The ggplot object of the MD-plot.

`Ordering` The ordering of columns of data defined by `Ordering`.

`DataOrdered` [1:n,1:d] matrix of ordered and scaled data defined by `Ordering` and `Scaling`.

Note that the package **ggExtra** is not necessarily required but if given the feature names are automatically rotated.

Note

1.) One would assume that in the first of the two following cases `ggplot2` only adjusts the plotting region but:

`MDplot(MTY)+ylim(c(0,7000))` is equal to `MDplot(MTY[MTY<7000])`.

This means in both cases the data is clipped and AFTERWARDS the density estimation is performed.

2.) Because of a (sometimes) strange behavior of either `ggplot2` or `reshape2`, numerical column names are changed to character by adding 'C_' which can be disabled using `ForceNames=TRUE`.

3.) Columnnames will be automatically deblanked and cleaned. To force specific columnnames the input Names can be used in combination with `ForceNames=TRUE`. However, this can result in plotting errors or other strange behavior.

4.) Overlaying MD-plots with robustly estimated gaussians seldomly will yield magenta (or other `GaussianColor`) lines overlaying more than the violin plot they should overlay, because the width of the two plots is not the same (but I am unable to set it strictly in `ggplot`). In such a case just call the function again.

Author(s)

Michael Thrun, Felix Pape contributed with the idea to use `ggplot2` as the basic framework.

References

[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 10.1371/journal.pone.0238835, 2020.

[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*, Proc Gfkl 2003, pp 91-100, Springer, Berlin, 2005.

[Zhang et al., 2003] Zhang, C., Mapes, B., & Soden, B.: Bimodality in tropical water vapour, *Quarterly Journal of the Royal Meteorological Society*, 129(594), 2847-2866, 2003.

See Also

<https://md-plot.readthedocs.io/en/latest/index.html>

[ClassMDplot](#)

<https://pypi.org/project/md-plot/>

Examples

```
x = cbind(
  A = runif(2000, 1, 5),
  B = c(rnorm(1000, 0, 1), rnorm(1000, 2.6, 1)),
  C = c(rnorm(2000, 2.5, 1)),
  D = rpois(2000, 5)
)
MDplot(x)
```

 MDplot4multiplevectors

Mirrored Density plot (MD-plot)for Multiple Vectors

Description

This function creates a MD-plot for multiple numerical vectors of various lengths. The MD-plot is a visualization for a boxplot-like Shape of the PDF published in [Thrun et al., 2020]. It is an improvement of violin or so-called bean plots and posses advantages in comparison to the conventional well-known box plot [Thrun et al., 2020].

Usage

```
MDplot4multiplevectors(..., Names, Ordering = 'Columnwise',
  Scaling = "None", Fill = 'darkblue', RobustGaussian = TRUE,
  GaussianColor = 'magenta', Gaussian_lwd = 1.5, BoxPlot = FALSE,
  BoxColor = 'darkred', MDscaling = 'width', LineSize = 0.01,
  LineColor = 'black', QuantityThreshold = 40, UniqueValuesThreshold = 12,
  SampleSize = 5e+05, SizeOfJitteredPoints = 1, OnlyPlotOutput = TRUE)
```

Arguments

...	Either d numerical vectors of different lengths or a list of length d where each element of the list is an vector of arbitrary length
Names	Optional: [1:d] Names of the variables. If missing, the columnnames of data are used.
Ordering	Optional: string, either Default, Columnwise, Alphabetical or Statistics. Please see details for explanation.
Scaling	Optional, Default is None, Percentalize, CompleteRobust, Robust or Log, Please see details for explanation.
Fill	Optional: string, color with which MDs are to be filled with.
RobustGaussian	Optional: If TRUE: each MDplot of a variable is overlaid with a roubstly estimated unimodal Gaussian distribution in the range of this variable, if statistical testing does not yield a significant p.value. In this case the packages moments , diptest and signal are required.
GaussianColor	Optional: string, color of robustly estimated gaussian, only for RobustGaussian=TRUE.
Gaussian_lwd	Optional: numerical, line width of robustly estimated gaussian, only for RobustGaussian=TRUE.
BoxPlot	Optional: If TRUE: each MDplot is overlaid with a Box-Whisker Diagram.

BoxColor	Optional: string, color of Boxplot, only for BoxPlot=TRUE.
MDscaling	Optional: if "area", all violins have the same area (before trimming the tails). If "count", areas are scaled proportionally to the number of observations. If "width" (default), all MDs have the same maximum width.
LineSize	Optional: numerical, linewidth of line around the mirrored densities.
LineColor	Optional: string, color of line around the mirrored densities. NA disables this features which is usefull if ones wants to avoid vertical lines leading to outliers.
QuantityThreshold	Optional: numeric value defining a threshold. Below this threshold no density estimation is performed and a jitter plot with a median line is drawn. Only Data Science experts should change this value after they understand how the density is estimated (see [Ultsch, 2005]).
UniqueValuesThreshold	Optional: numeric value defining a threshold. Below this threshold no density estimation and statistical testing is performed and a Jitter plot is drawn. Only Data Science experts should change this value after they understand how the density is estimated (see [Ultsch, 2005]).
SampleSize	Optional: numeric value defining a threshold. Above this threshold uniform sampling of finite cases is performed in order to shorten computation time. If rowr is not installed, uniform sampling of all cases is performed. If required, SampleSize=n can be set to omit this procedure.
SizeOfJitteredPoints	Optional: scalar. If Not enough unique values for density estimation are given, data points are jittered. This parameter defines the size of the points.
OnlyPlotOutput	Optional: Default TRUE only a ggplot object is given back, if FALSE: Additionally Scaled Data and ordering are the output of this function in a list.

Details

Please see [MDplot](#) for details.

Value

In the default case of OnlyPlotOutput==TRUE: The ggplot object of the MD-plot.

Otherwise for OnlyPlotOutput==FALSE: A list of

ggplotObj	The ggplot object of the MD-plot.
Ordering	The ordering of columns of data defined by Ordering.
DataOrdered	[1:n,1:d] matrix of ordered and scaled data defined by Ordering and Scaling.

Note that the package **ggExtra** is not necessarily required but if given the feautre names are automatically rotated.

Note

cbind.fill is internally used from the depriated R package rowr of Craig Varrichio.

Author(s)

Michael Thrun.

References

[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, Proc Gfkl 2003, pp 91-100, Springer, Berlin, 2005.

[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 10.1371/journal.pone.0238835, 2020.

See Also

`ClassMDplot` `MDplot` <https://pypi.org/project/md-plot/>

Examples

```
MDplot4multiplevectors(runif(20000, 1, 5),c(rnorm(20000,0,1),
rnorm(20000,2.6,1)),c(rnorm(2000,2.5,1)),rpois(25000,5),
Names=c('A','B','C','D'))
V=list(runif(20000, 1, 5),c(rnorm(20000,0,1),
rnorm(20000,2.6,1)),c(rnorm(2000,2.5,1)),rpois(25000,5))
MDplot4multiplevectors(V,Names=c('A','B','C','D'))
```

MDstrips

High-dimensional Density Strips based on Pareto Density Estimation

Description

MDstrips visualizes the distribution of each variable in a dataset as a vertical strip of colored tiles. Density is estimated by Pareto Density Estimation (PDE). Low-density regions are shown in blue/green, mid-density regions in yellow, and high-density regions in orange/red. This is a strip-based alternative to MDplot for the high-dimensional case of $d > 100$ in which violins are easy visible due to restricted width of screen.

Usage

```
MDstrips(Data, Ordering = "Default", Scaling = "None",
         QuantityThreshold = 50, UniqueValuesThreshold = 12, SampleSize = 5e+05,
         LabelThreshold = 100, LabelMax = 40, LabelEvery = NULL, LabelVariables = NULL,
         SizeOfJitteredPoints=1,
         palette = c("blue", "green", "yellow", "orange", "red"), ylab, main, BW = TRUE)
```

Arguments

Data	Numeric matrix containing the data. Each column is one variable.
Ordering	Optional: String specifying ordering of variables on the axis. Options are "Default", "Columnwise", "AsIs", "Alphabetical", "Average", "Bimodal", "Variance", "Statistics".
Scaling	Optional, Data scaling method. Options: "None", "Percentalize", "CompleteRobust", "Robust", "Log".
QuantityThreshold	Optional: Minimum number of finite values required to estimate a distribution.
UniqueValuesThreshold	Optional: Minimum number of unique values required to estimate a distribution.
SampleSize	Optional: Maximum sample size. Larger datasets are subsampled for faster computation.
LabelThreshold	Optional: If number of variables exceeds this threshold, not all x-axis labels are shown.
LabelMax	Optional: Maximum number of x-axis labels shown when many variables are present.
LabelEvery	Optional: Integer. Show every k th variable label (overrides LabelMax).
LabelVariables	Optional: Character vector of variables to label explicitly (overrides other options).
SizeOfJitteredPoints	Optional: scalar. If not enough unique values for density estimation are given, data points are jittered. This parameter defines the size of the points.
palette	Optional: Vector of colors for density scale, from low to high density.
ylab	Optional: Label for the y-axis (range of values in which PDE is estimated).
main	Optional: Title of the plot.
BW	Optional: Logical. If TRUE, use black-and-white theme and remove grid lines.

Details

This function is intended for high-dimensional but univariate distribution visualization where MD-plot, violin plots or boxplots become unreadable. By using density-colored strips, a large number of variables can be compared side-by-side.

Pareto Density Estimation (PDE) is used for robustness of univariate density estimation.

If too few values are present for PDE estimation (less than `QuantityThreshold` or less than `UniqueValuesThreshold` unique values), jittered points are drawn instead.

Value

Returns a ggplot object visualizing the density strips.

Author(s)

Michael Thrun

See Also

[MDplot](#) for Mirrored-density plot and the explanation of Ordering and Scaling in Detail.

Examples

```
# Example with toy data
set.seed(123)
X <- matrix(rnorm(1000), ncol = 10)
colnames(X) <- paste0("V", 1:10)

# Default plot
MDstrips(X)

# With statistical ordering and black-and-white theme
MDstrips(X, Ordering = "Statistics", BW = TRUE)

# Show only every 2nd variable label
MDstrips(X, LabelEvery = 2)

# Show only specific variables
MDstrips(X, LabelVariables = c("V1", "V5", "V10"))
```

Meanrobust

Robust Empirical Mean Estimation

Description

If the input is a matrix the mean value will be compute for every column.

Usage

```
Meanrobust(x, p=10, na.rm=TRUE)
```

Arguments

x	vetor or matrix
p	default=10; percent of the top- and bottomcut from x
na.rm	a boolean evaluating to TRUE or FALSE indicating whether all non finite values should be stripped before the computation proceeds.

Author(s)

Zornitsa Manolova

See Also[mean](#)

MTY*Municipal Income Tax Yield*

Description

Numerical vector of length 11194. details in [Ultsch/Behnisch, 2017; Thrun/Ultsch, 2018].

Usage`data("MTY")`**References**

[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.

[Ultsch/Behnisch, 2017] Ultsch, A., Behnisch, M.: Effects of the payout system of income taxes to municipalities in Germany, Applied Geography, Vol. 81, pp. 21-31, 2017.

Examples

```
data(MTY)
str(MTY)
```

Multiplot*Plot multiple ggplots objects in one panel*

Description

ggplot objects can be passed in ..., or to plotlist (as a list of ggplot objects)

For example, if the layout is specified as the matrix(c(1,2,3,3), nrow=2, byrow=TRUE), then plot 1 will go in the upper left, 2 will go in the upper right, and 3 will go all the way across the bottom.

Usage

```
Multiplot(..., Plotlist=NULL, ColNo=1, LayoutMat, Plotter =
  "native", main, main_fontsize=16)
```

Arguments

...	multiple ggplot objects to be plotted
Plotlist	Optional: list filled with ggplot objects to be plotted
ColNo	Number of columns in layout
LayoutMat	A matrix specifying the layout. If present, 'ColNo' is ignored.
Plotter	Optional, either "ggplot", or "native"
main	Optional, string specifying the title of the overall figure
main_fontsize	Optional, scalar defining the font size of the title

Value

List with Plotlist

Author(s)

Michael Thrun based on an idea by Winston Chang

Examples

```
data(Lsun3D)
Data=Lsun3D$Data
Cls=Lsun3D$Cls
obj1=Classplot(Data[,1],Data[,2],Cls=Cls,Plotter="ggplot",Size=3,main="Top plot")
obj2=Classplot(Data[,2],Data[,3],Cls=Cls,Plotter="ggplot",Size=3,main="Middle plot")
obj3=Classplot(Data[,1],Data[,3],Cls=Cls,Plotter="ggplot",Size=3,main="Bottom plot")
V=Multiplot(obj1,obj2,obj3,main="Three Classplots")
```

OpposingViolinBiclassPlot

OpposingViolinBiclassPlot

Description

Creates a set of two violin plots opposing each other

Usage

```
OpposingViolinBiclassPlot(ListData, Names, BoxPlots = FALSE,
  Subtitle = c("AttributeA", "AttributeB"),
  Title = "Opposing Violin Biclass Plot")
```

Arguments

ListData	List of k matrices as elements where each element has shape [1:n, 1:2]
Names	Vector of character names for each element of ListData
BoxPlots	Optional: Boolean variable BoxPlots = TRUE shows a box plot drawn into the violin plot. BoxPlots = FALSE shows no box plot. Default: BoxPlots = FALSE
Subtitle	Optional: Vector of character names for two classes. The classes are described as features contained in the matrix [1:n, 1:2]
Title	Optional: Character containing the title of the plot.

Value

Plotly object.

Author(s)

Quirin Stier

OptimalNoBins

Optimal Number Of Bins

Description

Optimal Number Of Bins is a kernel density estimation for fixed intervals.
Calculation of the optimal number of bins for a histogram.

Usage

OptimalNoBins(Data)

Arguments

Data Data

Details

The bin width ist defined with $bw=3.49*\text{stdrobust}(1/(n)^{1/3})$

Value

optNrOfBins The best possible number of bins. Not less than 10 though

Note

This the second version of the function prior available in **AdaptGauss**

Author(s)

Alfred Ultsch, Michael Thrun

References

David W. Scott Jerome P. Keating: A Primer on Density Estimation for the Great Home Run Race of 98, *STATS* 25, 1999, pp 16-22.

See Also

ParetoRadius

Examples

```
Data = c(rnorm(1000),rnorm(2000)+2,rnorm(1000)*2-1)

optNrOfBins = OptimalNoBins(Data)

minData = min(Data,na.rm = TRUE)

maxData = max(Data,na.rm = TRUE)

i = maxData-minData

optBreaks = seq(minData, maxData, i/optNrOfBins) # bins in fixed intervals

hist(Data, breaks=optBreaks)
```

ParetoDensityEstimation

Pareto Density Estimation V3

Description

This function estimates the Pareto Density for the distribution of one variable. In the default setting the functions estimates internally the appropriate number and position of kernels to estimate the density properly. However, the user can set the kernels manually. In this case density will only be estimated only around these values even if data exists outside the range of kernels or the internally estimated paretoRadius does not contain all datapoints between each kernel. See example for details.

Usage

```
ParetoDensityEstimation(Data, paretoRadius, kernels = NULL,
  MinAnzKernels = 100,
  PlotIt=FALSE,Compute="Cpp",Silent=FALSE)
```

Arguments

Data	[1:n] numeric vector of data.
paretoRadius	Optional scalar, numeric value, see ParetoRadius . If not given it is estimated internally. Please do not set manually
kernels	Optional, [1:m] numeric vector data values where pareto density is measured at. If 0 (by default) kernels will be computed.
MinAnzKernels	Optional, minimal number of kernels in given data range, default MinAnzKernels==100, can be violated by KernelRange
PlotIt	Optional, if TRUE: raw basic r plot of density estimation of debugging purposes. Usually please use ggplot2 interface via PDEplot or MDplot
Compute	Either R, Cpp or Cpp_exp, Compute defines which subalgorithms are used to compute density estimation. Cpp_exp is not verified yet although Cpp_exp is faster than Cpp
Silent	Optional, if TRUE: disables all warnings

Details

Pareto Density Estimation (PDE) is a method for the estimation of probability density functions using hyperspheres. The Pareto-radius of the hyperspheres is derived from the optimization of information for minimal set size. It is shown, that Pareto Density is the best estimate for clusters of Gaussian structure. The method is shown to be robust when cluster overlap and when the variances differ across clusters. This is the best density estimation to judge Gaussian Mixtures of the data see [Ultsch 2003].

If input argument `kernels` is set manually the output arguments `paretoDensity_internal` and `kernels_internal` provide the internally estimated density and kernels. Otherwise these arguments are NULL. The function provides a message if range of kernels and range of data does not overlap completely.

Typically it is not advisable to set `paretoRadius` manually. However in specific cases, the function [ParetoRadius](#) is used prior to calling this function. In such cases the input argument can use a priorly estimated `paretoRadius`.

Value

List With

kernels [1:m] numeric vector. data values at with Pareto Density is measured.

paretoDensity [1:m] numeric vector containing the determined density by `paretoRadius`.

paretoRadius numeric value of defining the radius

kernels_internal Either NULL or internally estimated [1:p] numeric vector of kernels if input argument `kernels` was set by the user

paretoDensity_internal Either NULL or internally estimated density if input argument `kernels` was set by the user

Note

This the second version of the function prior available in **AdaptGauss**

Author(s)

Michael Thrun

References

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, Proc Gfkl 2003, pp 91-100, Springer, Berlin, 2005.

See Also

[ParetoRadius](#)

[PDEplot](#)

[MDplot](#)

Examples

```
#kernels are estimated internally
data = c(rnorm(1000),rnorm(2000)+2,rnorm(1000)*2-1)
pdeVal      <- ParetoDensityEstimation(data)
plot(pdeVal$kernels,pdeVal$paretoDensity,type='l',xaxs='i',
yaxs='i',xlab='Data',ylab='PDE')

##data exist outside of the range kernels
kernels=seq(from=-3,to=3,by=0.01)
pdeVal      <- ParetoDensityEstimation(data, kernels=kernels)
plot(pdeVal$kernels,pdeVal$paretoDensity,type='l',xaxs='i',
yaxs='i',xlab='Data',ylab='PDE')

#data exists in-between kernels that is not measured
pdeVal$paretoRadius#0.42
kernels=seq(from=-8,to=8,by=1)
pdeVal      <- ParetoDensityEstimation(data, kernels=kernels)
plot(pdeVal$kernels,pdeVal$paretoDensity,type='l',xaxs='i',
yaxs='i',xlab='Data',ylab='PDE')
```

ParetoRadius

ParetoRadius for distributions

Description

Calculation of the ParetoRadius i.e. the 18 percentiles of all mutual Euclidian distances in data.

Usage

```
ParetoRadius(Data, maximumNrSamples = 10000,
plotDistancePercentiles = FALSE,Compute="Cpp")
```

Arguments

Data	numeric data vector
maximumNrSamples	Optional, numeric. Maximum number for which the distance calculation can be done. 1000 by default.
plotDistancePercentiles	Optional, logical. If TRUE, a plot of the percentiles of distances is produced. FALSE by default.
Compute	Either Cpp or Cpp_exp defines which subalgorithms are used to compute pareto radus. Cpp_exp is faster but not verified yet.

Details

The Pareto-radius of the hyperspheres is derived from the optimization of information for minimal set size. ParetoRadius() is a kernel density estimation for variable intervals. It works only on Data without missing values (NA) or NaN. In other cases, please use ParetoDensityEstimation directly.

Value

numeric value, the Pareto radius.

Note

This the second version of the function prior available in **AdaptGauss**.

For larger datasets the quantile_c() function is used instead of quantile in R which was programmed by Dirk Eddelbuettel on Jun 6 and taken by the author from <https://github.com/RcppCore/Rcpp/issues/967>.

Author(s)

Michael Thrun

References

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, Proc Gfkl 2003, pp 91-100, Springer, Berlin, 2005.

See Also

ParetoDensityEstimation, OptimalNoBins

ParetoRadius_fast *Fast ParetoRadius for distributions*

Description

Calculation of the ParetoRadius i.e. the 18 percentiles of all mutual Euclidian distances in data.

Usage

```
ParetoRadius_fast(Data, maximumNrSamples = 10000, na.rm=TRUE)
```

Arguments

Data	numeric data vector
maximumNrSamples	Optional, numeric. Maximum number for which the distance calculation can be done. 1000 by default.
na.rm	(Optional: Default=TRUE). Remove na.

Details

The Pareto-radius of the hyperspheres is derived from the optimization of information for minimal set size. ParetoRadius() is a kernel density estimation for variable intervals. It works only on Data without missing values (NA) or NaN. In other cases, please use ParetoDensityEstimation directly.

Value

numeric value, the Pareto radius.

Author(s)

Michael Thrun

References

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, Proc Gfkl 2003, pp 91-100, Springer, Berlin, 2005.

PDEnormrobust	<i>PDEnormrobust</i>
---------------	----------------------

Description

This functions plots ParetoDensityEstimation (PDE) and robustly estimated Gaussian with empirical Mean and Variance

Usage

```
PDEnormrobust(Data,xlab='PDE',ylab,main='PDEnormrobust',
               PlotSymbolPDE='blue',
               PlotSymbolGauss='magenta',PlotIt=TRUE,
               Mark2Sigma=FALSE,Mark3Sigma=FALSE,
               p_mean=10,p_sd=25,...)
```

Arguments

Data	numeric vector, data to be plotted.
xlab	Optional,see plot
ylab	Optional,see plot
main	Optional,see plot
PlotSymbolPDE	line color pdf
PlotSymbolGauss	line color robust gauss
PlotIt	TRUE: shows plot
Mark2Sigma	TRUE: sets to vertical lines marking data outside $M \pm 1.96SD$
Mark3Sigma	TRUE: sets to vertical lines marking data outside $M \pm 2.576SD$
p_mean	scalar between 1-99, percent of the top- and bottomcut from x
p_sd	scalar between 1-99, lowInnerPercentile for robustly estimated standard deviation
...	Further arguments for plot

Details

Within Mark2Sigma 95 percent of data should be contained if distribution is Gaussian

Within Mark3Sigma 99 percent of data should be contained if distribution is Gaussian

The 3sigma rule is usually defined as $M \pm 3SD$ containing 99.7 percent of data but to simplify, the input parameter name is called Mark3Sigma instead Mark2comma576Sigma, the same reason applies to the output parameter Sigma3.

Value

Kernels	numeric vector. The x points of the PDE function.
ParetoDensity	estimated pdf of data, numeric vector, the PDE(x).
ParetoRadius	numeric value, the Pareto Radius used for the plot.
Normaldist	pdf based on robustly estimated parameters
Pars	Named vector of robustly estimated Mean, standard deviation SD, Sigma2=1.96*SD and Sigma3=2.576*SD, EstPercData_Sigma2, EstPercData_Sigma3

Author(s)

Michael Thrun

Examples

```
data(MTY)
PDEnormrobust(unname(MTY))
```

PDEplot

PDE plot

Description

This function plots the Pareto probability density estimation (PDE), uses PDEstimationForGauss and ParetoRadius.

Usage

```
PDEplot(Data, paretoRadius = 0, weight = 1, kernels = NULL,
         LogPlot = F, PlotIt = TRUE, title =
         "ParetoDensityEstimation(PDE)", color = "blue",
         xpoints = FALSE, xlim, ylim, xlab, ylab =
         "PDE", ggPlot = ggplot(), sampleSize = 2e+05, lwd = 2)
```

Arguments

Data	[1:n] numeric vector of data to be plotted.
paretoRadius	numeric, the Pareto Radius. If omitted, calculate by paretoRad.
weight	numeric, Weight*ParetoDensity is plotted. 1 by default.
kernels	numeric vector of kernels. Optional
LogPlot	LogLog PDEplot if TRUE, xpoints has to be FALSE. Optional

PlotIt	logical, if plot. TRUE by default.
title	character vector, title of plot.
color	character vector, color of plot.
xpoints	logical, if TRUE only points are plotted. FALSE by default.
xlim	Arguments to be passed to the plot method.
ylim	Arguments to be passed to the plot method.
xlab	Arguments to be passed to the plot method.
ylab	Arguments to be passed to the plot method.
ggPlot	ggplot2 object to be plotted upon. Insert an existing plot to add a new PDEPlot to it. Default: empty plot
sampleSize	default(200000), sample size, if datavector is too big
lwd	linewidth, see plot

Value

kernels	numeric vector. The x points of the PDE function.
paretoDensity	numeric vector, the PDE(x).
paretoRadius	numeric value, the Pareto Radius used for the plot.
ggPlot	ggplot2 object. Can be used to further modify the plot or add other plots.

Author(s)

Michael Thrun

References

Ultsch, A.: Pareto Density Estimation: A Density Estimation for Knowledge Discovery, Baier D., Wernecke K.D. (Eds), In Innovations in Classification, Data Science, and Information Systems - Proceedings 27th Annual Conference of the German Classification Society (GfKL) 2003, Berlin, Heidelberg, Springer, pp, 91-100, 2005.

Examples

```
x <- rnorm(1000, mean = 0.5, sd = 0.5)
y <- rnorm(750, mean = -0.5, sd = 0.75)
plt <- PDEplot(x, color = "red")$ggPlot
plt <- PDEplot(y, color = "blue", ggPlot = plt)$ggPlot

# Second Example
# ggplotObj=ggplot()
# for(i in 1:length(Variables))
#   ggplotObj=PDEplot(Data[,i],ggPlot = ggplotObj)$ggPlot
```

PDEstrip

1D Density Strip based on Pareto Density Estimation (PDE)

Description

This function renders a single variable's probability density as a horizontal "heat strip", where color encodes local density values. Low-density regions are shown in blue/green, medium-density regions in yellow, and high-density regions in orange/red. It provides a compact alternative to violin or box plots for visualizing the distribution of a single variable.

Usage

```
PDEstrip(Feature, palette = c("blue", "green", "yellow", "orange", "red"))
```

Arguments

Feature	Numeric vector. Finite values are used for Pareto Density Estimation (PDE). Non-finite values are ignored.
palette	Character vector of colors defining the low-to-high density gradient, passed to <code>ggplot2::scale_fill_gradientn()</code> . Default is a five-color palette ranging from blue (low density) to red (high density).

Details

Density is estimated via Pareto Density Estimation (PDE), a robust and adaptive approach to probability density estimation [Utsch, 2005]. The returned density values are min-max normalized to [0,1] and mapped to the user-specified color gradient. The strip is drawn with `geom_tile()` at a fixed `y=1`, so that each feature is visualized as a single horizontal band. The feature name is automatically captured from the input expression and used as the x-axis label.

Value

A `ggplot` object showing a 1D density strip for the given feature.

Note

To match multi-variable strip plots visually, the theme and palette can be customized for consistency. If the feature contains very few unique values, the strip may appear coarse due to sparse kernel locations from PDE.

Author(s)

Michael Thrun

References

Ultsch, A.: Pareto Density Estimation: A Density Estimation for Knowledge Discovery, Baier D., Wernecke K.D. (Eds), In Innovations in Classification, Data Science, and Information Systems - Proceedings 27th Annual Conference of the German Classification Society (GfKL) 2003, Berlin, Heidelberg, Springer, pp, 91-100, 2005.

Examples

```
set.seed(1)
x <- c(rnorm(800, 0, 1), rnorm(200, 3, 0.7))
PDEstrip(x)

# Alternative palette
PDEstrip(x, palette = c("navy", "skyblue", "yellow", "orange", "darkred"))
```

Piechart

The pie chart

Description

the pie chart represents amount of values given in data.

Usage

```
Piechart(Datavector, Names, Labels, MaxNumberOfSlices,
main='', col, Rline=1, ...)
```

Arguments

Datavector	[1:n] a vector of n non unique values
Names	Optional, [1:k] names to search for in Datavector, if not set unique of Datavector is calculated.
Labels	Optional, [1:k] Labels if they are specially named, if not Names are used.
MaxNumberOfSlices	Default is k, integer value defining how many labels will be shown. Everything else will be summed up to Other.
main	Optional, title below the fan pie, see plot
col	Optional, the default are the first [1:k] colors of the default color sequence used in this package, otherwise a character vector of [1:k] specifying the colors analog to plot
Rline	Optional, the radius of the pie in numerical numbers
...	Optional, further arguments passed on to plot

Details

If Number of Slices is higher than MaxNumberOfSlices then ABCanalysis is applied (see [Ultsch/Lotsch, 2015]) and group A chosen. If Number of Slices in group A is higher than MaxNumberOfSlices, then the most important ones out of group A are chosen. If MaxNumberOfSlices is higher than Slices in group A, additional slices are shown depending on the percentage (from high to low). Parameters of visualization a set as in [Schwabish, 2014] defined.

Color sequence is automatically shortened to the MaxNumberOfSlices used in the pie chart.

Value

silent output by calling invisible of a list with

Percentages [1:k] percent values visualized in fanplot

Labels [1:k] see input Labels, only relevant ones

Note

You see in the example below that a pie chart does not visualize such data well contrary to the fanPlot.

Author(s)

Michael Thrun

References

[Schwabish, 2014] Schwabish, Jonathan A. An Economist's Guide to Visualizing Data. Journal of Economic Perspectives, 28 (1): 209-34. DOI: 10.1257/jep.28.1.209, 2014.

[Ultsch/Lotsch, 2015] Ultsch. A., Lotsch J.: Computed ABC Analysis for Rational Selection of Most Informative Variables in Multivariate Data, PloS one, Vol. 10(6), pp. e0129767. doi 10.1371/journal.pone.0129767, 2015.

Examples

```
data(categoricalVariable)
Piechart(categoricalVariable)
```

Pixelmatrix

Plot of a Pixel Matrix

Description

Plots Data matrix as a pixel colour image.

Usage

```
Pixelmatrix(Data, XNames, LowLim, HiLim,
            YNames, main, FillNotFiniteWithHighestValue=FALSE)
```

Arguments

Data	[1:n,1:d] Data cases in rows (n), variables in columns (d)
LowLim	Optional: limits for the color axis
HiLim	Optional: limits for the color axis
XNames	Optional: Vector - names for the X-ticks, NULL: no ticks at all
YNames	Optional: Vector - names for the Y-ticks, NULL: no ticks at all
main	Optional: String - Title of the plot
FillNotFiniteWithHighestValue	Optional: TRUE: fills not finite values with same color as the highest value

Details

Low values are shown in blue and green, middle values in yellow and high values in orange and red.

Author(s)

Michael Thrun, Felix Pape

Examples

```
data("Lsun3D")
Data=Lsun3D$Data

Pixelmatrix(Data)
```

 Plot3D

3D plot of points

Description

A wrapper for Data with systematic clustering colors for either a 2D (x,y) or 3D (x,y,z) plot combined with a classification

Usage

```
Plot3D(Data, Cls, UniqueColors,
       size=2, na.rm=FALSE, Plotter3D="rgl", ...)
```

Arguments

Data	[1:n,1:d] matrix with either d=2 or d=3, if d>3 only the first 3 dimensions are taken
Cls	[1:n] numeric vector of the classification of data with k classes
UniqueColors	[1:k] character vector of colors, if not given DataVisualizations::DefaultColorSequence is used
size	size of points, for plotly additional a vector [1:n] of a mapping of sizes to Cls has to be given in the (...) argument with sizes=
na.rm	if na.rm=TRUE, then missing values are removed
Plotter3D	in case of 3 dimensions, choose either "plotly" or "rgl", if one of this packages is not given, the other one is selected as a fallback method
...	further arguments to be processed by <code>plot3d</code> or <code>geom_point</code> or <code>plot_ly</code> of type "scatter3d"

Details

For `geom_point` only size and na.rm is available as further arguments.

Note

Uses either `geom_point` for 2D or `plot3d` for 3D or `plot_ly`

Author(s)

Michael Thrun

References

RGL vignette in <https://cran.r-project.org/package=rgl>

Examples

```
#Spin3D similar output

data(Lsun3D)
Plot3D(Lsun3D$Data,Lsun3D$Cls,type='s',radius=0.1,box=FALSE,aspect=TRUE)
rgl::grid3d(c("x", "y", "z"))

#Projected Points with Classification
Data=cbind(runif(500,min=-3,max=3),rnorm(500))

# Classification
Cls=ifelse(Data[,1]>0,1,2)
Plot3D(Data,Cls,UniqueColors = DataVisualizations::DefaultColorSequence[c(1,3)],size=2)

## Not run:
#Points with Non-Overlapping Labels
```

```
#require(ggrepel)
Data=cbind(runif(30,min=-1,max=1),rnorm(30,0,0.5))
Names=paste0('VeryLongName',1:30)
ggobj=Plot3D(Data)
ggobj + geom_text_repel(aes(label=Names), size=3)

## End(Not run)
```

PlotGraph2D

PlotGraph2D

Description

plots a neighborhood graph in two dimensions given the 2D coordinates of the points

Usage

```
PlotGraph2D(AdjacencyMatrix, Points, Cls, Colors, xlab = "X", ylab = "Y", xlim,
ylim, Plotter = "native", LineColor = "grey", pch, lwd, main = "",
mainSize, SampleSize=NULL)
```

Arguments

AdjacencyMatrix	[1:n,1:n] numerical matrix consting of binary values. 1 indicates that two points have an edge, zero that they do not
Points	[1:n,1:2] numeric matrix of two feature
Cls	[1:n] numeric vector of k classes, if not set per default every point is in first class
Colors	Optional, string defining the k colors, one per class
xlab	Optional, string for xlabel
ylab	Optional, string for ylabel
xlim	Optional, [1:2] vector of x-axis limits
ylim	Optional, [1:2] vector of y-axis limits
Plotter	Optional, either "native" or "plotly"
LineColor	Optional, color of edges
pch	Optional, for Plotter="native" shape of point, usally can be in a range from zero to 25, see pch of plot for details; for Plotter="Plotly" the size of point
lwd	width of the lines
main	Optional, string for the title of plot
mainSize	Optional, scalar for the size of the title of plot
SampleSize	Optional, scalar for the size of sample of vertices that will be plotted

Details

The points are the vertices of the graph. the adjacency matrix defines the edges. Via adjacency matrix various graphs, like from deldir package, can be used.

Sometimes the amount of vertices is high in which take plotting take very long. For such a case use SampleSize.

Value

native plot or plotly object depending on input argument Plotter

Author(s)

Michael Thrun

References

Lecture of Knowledge Discovery II

See Also

[pch](#)

Examples

```
N=10
x=runif(N)
y=runif(N)
Euklid=as.matrix(dist(cbind(x,y)))
Radius=quantile(as.vector(Euklid),0.5)
RKugelGraphAdjMatrix = matrix(0, ncol = N, nrow = N)
for (i in 1:N) {
  RInd = which(Euklid[i, ] <= Radius, arr.ind = TRUE)
  RKugelGraphAdjMatrix[i, RInd] = 1
}
PlotGraph2D(RKugelGraphAdjMatrix,cbind(x,y))
```

PlotMissingvalues

Plot of the Amount Of Missing Values

Description

Percentage of missing values per feature are visualized as a bar plot.

Usage

```
PlotMissingvalues(Data,Names,
  WhichDefineMissing=c('NA','NaN','DUMMY','.',' '),
  PlotIt=TRUE,
  xlab='Amount Of Missing Values in Percent',
  xlim=c(0,100),...)
```

Arguments

Data	[1:n,1:d] data cases in rows, variables/features in columns
Names	[1:d] optional vector of string describing the names of the features
WhichDefineMissing	[1:d] optional vector of string describing missing values, usefull for character features. Currently up to five different options are possible.
PlotIt	If FALES: Does not plot
xlab	x label of bar plot
xlim	x axis limits in percent
...	Further arguments passed on to barplot, such as main for title

Value

plots not finite and missing values as a bar plot for each feature d and returns with invisible the amount of missing values as a vector. Works even with character variables, but WhichDefineMissing cannot be changed at the current version. Please make a suggestion on GitHub how to improve this.

Note

Does not work with the tibble format, in such a case please call `as.data.frame(as.matrix(Data))`

Author(s)

Michael Thrun

Examples

```
data("ITS")
data("MTY")

PlotMissingvalues(cbind(ITS,MTY),Names=c('ITS','MTY'))
```

PlotProductratio *Product-Ratio Plot*

Description

The product-ratio plot as defined in [Tukey, 1977, p. 594].

Usage

```
PlotProductratio(X, Y, na.rm = FALSE,
  main='Product Ratio Analysis', xlab = "Log of Ratio", ylab = "Root of Product", ...)
```

Arguments

X	[1:n] positive numerical vector, negativ values are removed automatically
Y	[1:n] positive numerical vector, negativ values are removed automatically
na.rm	Function may not work with non finite values. If these cases should be automatically removed, set parameter TRUE
main	see plot
ylab	see plot
xlab	see plot
...	further arguments passed on to plot

Details

In the case where there are many instances of very small values, but a small number of very large ones, this plot is usefull [Tukey, 1977, p. 615].

Value

matrix[1:n,2] with $\sqrt{x*y}$ and $\log(x/y)$ as the two columns

Author(s)

Michael Thrun

References

[Tukey, 1977] Tukey, J. W.: Exploratory data analysis, United States Addison-Wesley Publishing Company, ISBN: 0-201-07616-0, 1977.

Examples

```
#Beware: The data does no fit ne requirements for this approach
data('ITS')
data(MTY)
PlotProductratio(ITS,MTY)
```

PmatrixColormap	<i>P-Matrix colors</i>
-----------------	------------------------

Description

Defines the default color sequence for plots made with PDEscatter

Usage

```
data("PmatrixColormap")
```

Format

Returns the vectors for a (heat) colormap.

QQplot	<i>QQplot with a Linear Fit</i>
--------	---------------------------------

Description

Quantile-quantile plot with a linear fit

Usage

```
QQplot(X,Y,Type=8,NoQuantiles=10000,xlab, ylab,col="red",main='',
lwd=3,pch=20,subplot=FALSE,...)
```

Arguments

X	[1:n] numerical vector, First Feature
Y	1:n] numerical vector, Second Feature to compare first feature with
Type	an integer between 1 and 9 selecting one of the nine quantile algorithms detailed in quantile
NoQuantiles	number of quantiles used in QQ-plot, if number is low and the data has outliers, there may be empty space visible in the plot
xlab	x label, see plot ...
ylab	y label, see plot
col	color of line, see plot
main	title of plot, see plot
lwd	line width of plot, see plot
pch	type of point, see plot
subplot	FALSE: par is set specifically, TRUE: assumption is the usage as a subfigure, par has to be set by the user, no checks are performed, labels have to be set by the user
...	other parameters for qqplot

Details

Output is the evaluation of a linear (regression) fit of `lm` called 'line' and a quantile quantile plot (QQplot). Per default 10.000 quantiles are chosen, but in the case of very large data vectors one can reduce the quantiles for faster computation. The 100 percentiles used for the regression line are of darker blue than the quantiles chosen by the user.

Value

List with	
Quantiles	[1:NoQuantiles,1:2] quantiles in y and y
Residuals	Output of the Regression with residuals.lm(line)
Summary	Output of the Regression with summaryline)
Anova	Output of the Regression with anova(line)

Author(s)

Michael Thrun

References

Michael, J. R.: The stabilized probability plot, *Biometrika*, Vol. 70(1), pp. 11-17, 1983.

Examples

```
data(MTY)
NormalDistribution=rnorm(50000)
QQplot(NormalDistribution,MTY)
```

RobustNormalization *RobustNormalization*

Description

RobustNormalization as described in [Milligan/Cooper, 1988].

Usage

```
RobustNormalization(Data,Centered=FALSE,Capped=FALSE,
na.rm=TRUE,WithBackTransformation=FALSE,
pmin=0.01,pmax=0.99)
```

Arguments

Data	[1:n,1:d] data matrix of n cases and d features
Centered	centered data around zero by median if TRUE
Capped	TRUE: outliers are capped above 1 or below -1 and set to 1 or -1.
na.rm	If TRUE, infinite vlaues are disregarded
WithBackTransformation	If in the case for forecasting with neural networks a backtransformation is required, this parameter can be set to 'TRUE'.
pmin	defines outliers on the lower end of scale
pmax	defines outliers on the higher end of scale

Details

Normalizes features either between -1 to 1 (Centered=TRUE) or 0-1 (Centered=FALSE) without changing the distribution of a feature itself. For a more precise description please read [Thrun, 2018, p.17].

"[The] scaling of the inputs determines the effective scaling of the weights in the last layer of a MLP with BP neural netowrk, it can have a large effect on the quality of the final solution. At the outset it is best to standardize all inputs to have mean zero and standard deviation 1 [(or at least the range under 1)]. This ensures all inputs are treated equally in the regularization prozess, and allows to choose a meaningful range for the random starting weights." [Friedman et al., 2012]

Value

if WithBackTransformation=FALSE: TransformedData[1:n,1:d] i.e., normalized data matrix of n cases and d features

if WithBackTransformation=TRUE: List with

TransformedData	[1:n,1:d] normalized data matrix of n cases and d features
MinX	[1:d] numerical vector used for manual back-transformation of each feature
MaxX	[1:d] numerical vector used for manual back-transformation of each feature
Denom	[1:d] numerical vector used for manual back-transformation of each feature
Center	[1:d] numerical vector used for manual back-transformation of each feature

Author(s)

Michael Thrun

References

[Milligan/Cooper, 1988] Milligan, G. W., & Cooper, M. C.: A study of standardization of variables in cluster analysis, *Journal of Classification*, Vol. 5(2), pp. 181-204. 1988.

[Friedman et al., 2012] Friedman, J., Hastie, T., & Tibshirani, R.: *The Elements of Statistical Learning*, (Second ed. Vol. 1), Springer series in statistics New York, NY, USA., ISBN, 2012.

[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.

See Also

[RobustNorm_BackTrafo](#)

Examples

```
Scaled = RobustNormalization(rnorm(1000, 2, 100), Capped = TRUE)
hist(Scaled)

m = cbind(c(1, 2, 3), c(2, 6, 4))
List = RobustNormalization(m, FALSE, FALSE, FALSE, TRUE)
TransformedData = List$TransformedData

mback = RobustNorm_BackTrafo(TransformedData, List$MinX, List$Denom, List$Center)

sum(m - mback)
```

RobustNorm_BackTrafo *Transforms the Robust Normalization back*

Description

Transforms the Robust Normalization back if Capped=FALSE

Usage

```
RobustNorm_BackTrafo(TransformedData,
MinX, Denom, Center=0)
```

Arguments

TransformedData	[1:n,1:d] matrix
MinX	scalar
Denom	scalar
Center	scalar

Details

For details see [RobustNormalization](#)

Value

[1:n,1:d] Data matrix

Author(s)

Michael Thrun

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

```

data(Lsun3D)
Data = Lsun3D$Data
TransList = RobustNormalization(Data, Centered = TRUE, WithBackTransformation = TRUE)

Lsun3DData = RobustNorm_BackTrafo(TransList$TransformedData,
                                  TransList$MinX,
                                  TransList$Denom,
                                  TransList$Center)

sum(Lsun3DData - Data) #<e-15

```

ROC

*ROC plot***Description**

Receiver operating characteristic curve

Usage

ROC(Data, Cls, Names, Colors)

Arguments

Data	[1:n, 1:d] numeric vector or matrix of scores to be evaluated with ROC.
Cls	[1:n] numeric vector with true classes.
Names	[1:d] character vector with names for scores.
Colors	[1:d] character vector with colores for scores.

Value

ROCit	List of ROCit results for each score column in Data.
Plot	Plotly object.

Author(s)

Quirin Stier

Examples

```
Data = runif(1000,0,1)
Cls = sample(c(0,1), 1000, replace = TRUE)
ROC(Data, Cls)
```

ShepardDensityscatter *Shepard PDE scatter*

Description

Draws ein Shepard Diagram (scatterplot of distances) with an two-dimensional PDE density estimation .

Usage

```
ShepardDensityScatter(InputDists, OutputDists, Plotter= "native", Type = "DDCAL",
DensityEstimation="SDH", Marginals = FALSE, xlab='Input Distances',
ylab='Output Distances',main='ProjectionMethod', sampleSize=500000)
```

Arguments

InputDists	[1:n,1:n] with n cases of data in d variables/features: Matrix containing the distances of the inputspace.
OutputDists	[1:n,1:n] with n cases of data in d dimensionalites of the projection method variables/features: Matrix containing the distances of the outputspace.
Plotter	Optional, either "native" or "plotly"
Type	Optional, either "DDCAL" which creates a special hard color transition sensitive to density-based structures or "Standard" which creates a standard continuous color transition which is proven to be not very sensitive for complex density-based structures.
DensityEstimation	Optional, use either "SDH" or "PDE" for data density estimation.
Marginals	Optional, either TRUE (draw Marginals) or FALSE (do not draw Marginals)
xlab	Label of the x axis in the resulting Plot.
ylab	Label of the y axis in the resulting Plot.
main	Title of the Shepard diagram
sampleSize	Optional, default(500000), reduces a.ount of data for density estimation, if too many distances given

Details

Introduced and described in [Thrun, 2018, p. 63] with examples in [Thrun, 2018, p. 71-72]

Author(s)

Michael Thrun

References

[Thrun, 2018] Thrun, M. C.: Projection Based Clustering through Self-Organization and Swarm Intelligence, doctoral dissertation 2017, Springer, ISBN: 978-3-658-20540-9, Heidelberg, 2018.

Examples

```
data("Lsun3D")
Cls=Lsun3D$Cls
Data=Lsun3D$Data
InputDist=as.matrix(dist(Data))
res = stats::cmdscale(d = InputDist, k = 2, eig = TRUE,
                    add = FALSE, x.ret = FALSE)

ProjectedPoints = as.matrix(res$points)
ShepardDensityScatter(InputDist,as.matrix(dist(ProjectedPoints)),main = 'MDS')
ShepardDensityScatter(InputDist[1:100,1:100],

as.matrix(dist(ProjectedPoints))[1:100,1:100],main = 'MDS')
```

Sheparddiagram	<i>Draws a Shepard Diagram</i>
----------------	--------------------------------

Description

This function plots a Shepard diagram which is a scatter plot of InputDist and OutputDist

Usage

```
Sheparddiagram(InputDists, OutputDists, xlab = "Input Distances",
              ylab= "Output Distances", fancy = F,
              main = "ProjectionMethod", gPlot = ggplot())
```

Arguments

InputDists	[1:n,1:n] with n cases of data in d variables/features: Matrix containing the distances of the inputspace.
OutputDists	[1:n,1:n] with n cases of data in d dimensionalites of the projection method variables/features: Matrix containing the distances of the outputspace.
xlab	Label of the x axis in the resulting Plot.
ylab	Label of the y axis in the resulting Plot.

fancy	Set FALSE for PC and TRUE for publication
main	Title of the Shepard diagram
gPlot	ggplot2 object to plot upon.

Value

ggplot2 object containing the plot.

Author(s)

Michael Thrun

Examples

```
data("Lsun3D")
Cls=Lsun3D$Cls
Data=Lsun3D$Data
InputDist=as.matrix(dist(Data))
res = stats::cmdscale(d = InputDist, k = 2, eig = TRUE,
  add = FALSE, x.ret = FALSE)
ProjectedPoints = as.matrix(res$points)
```

```
Sheparddiagram(InputDist,as.matrix(dist(ProjectedPoints)),main = 'MDS')
```

SignedLog

Signed Log

Description

Computes the Signed Log if Data

Usage

```
SignedLog(Data,Base="Ten")
```

Arguments

Data	[1:n,1:d] Data matrix with n cases and d variables
Base	Either "Ten", "Two", "Zero", or any number.

Details

A neat transformation for data, it it has a better representation on the log scale.

Value

Transformed Data

Note

Number Selections for Base for 2,10, "Two" or "Ten" add 1 to every datapoint as defined in the lectures.

Author(s)

Michael Thrun

References

Prof. Dr. habil. A. Ultsch, Lectures in Knowledge Discovery, 2014.

See Also

[log](#)

Examples

```
# sampling is done
# because otherwise the example takes too long
# in the CRAN check
data('ITS')
ind=sample(length(ITS),1000)

MDplot(SignedLog(cbind(ITS[ind],MTY[ind])*(-1),Base = "Ten"))
```

Silhouetteplot

Silhouette plot of classified data.

Description

Silhouette plot of cluster silhouettes for the n-by-d data matrix Data or distance matrix where the clusters are defined in the vector Cls.

Usage

```
Silhouetteplot(DataOrDistances, Cls, method='euclidean',
PlotIt=TRUE,...)
```

Arguments

DataOrDistances	[1:n,1:d] data cases in rows, variables in columns, if not symmetric or [1:n,1:n] distance matrix, if symmetric
Cls	numeric vector, [1:n,1] classified data
method	Optional if Datamatrix is used, one of "euclidean", "maximum", "manhattan", "canberra", "binary" or "minkowski". Any unambiguous substring can be given, see dist
PlotIt	Optional, Default:TRUE, FALSE to suppress the plot
...	If PlotIt=TRUE: Further arguments to barplot

Details

"The Silhouette plot is a common unsupervised index for visual evaluation of a clustering [L. R. Kaufman/Rousseeuw, 2005] [introduced in [Rousseeuw, 1987]]. A reasonable clustering is characterized by a silhouette width of greater than 0.5, and an average width below 0.2 should be interpreted as indicating a lack of any substantial cluster structure [Everitt et al., 2001, p. 105]. However, it is evident that silhouette scores assume clusters that are spherical or Gaussian in shape [Herrmann, 2011, pp. 91-92]" [Thrun, 2018, p. 29].

Value

silh Silhouette values in a N-by-1 vector

Author(s)

Onno Hansen-Goos, Michael Thrun

References

[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.

[Rousseeuw, 1987] Rousseeuw, Peter J.: Silhouettes: a Graphical Aid to the Interpretation and Validation of Cluster Analysis, Computational and Applied Mathematics, 20, p.53-65, 1987.

Examples

```
data("Lsun3D")
Cls=Lsun3D$Cls
Data=Lsun3D$Data
#clear cluster structure
plot(Data[,1:2],col=Cls)
#However, the silhouette plot does not indicate a very good clustering in cluster 1 and 2
Silhouetteplot(Data,Cls = Cls,main='Silhouetteplot')
```

 Slopechart

Slope Chart

Description

ABC analysis improved slope chart

Usage

```
Slopechart(FirstDatavector,
           SecondDatavector,
           Names,
           Labels,
           MaxNumberOfSlices,
           TopLabels=c('FirstDatavector', 'SecondDatavector'),
           main='Comparison of Descending Frequency')
```

Arguments

FirstDatavector	[1:n] a vector of n non unique values - a features
SecondDatavector	[1:m] a vector of n non unique values - a second feature
Labels	Optional, [1:k] Labels if they are specially named, if not Names are used.
Names	[1:k] names to search for in Datavector, if not set unique of Datavector is calculated.
MaxNumberOfSlices	Default is k, integer value defining how many labels will be shown. Everything else will be summed up to Other.
TopLabels	Labels of of feature names
main	title of the plot

Details

still experimental.

Value

silent output by calling invisible of a list with

Percentages	[1:k] percent values visualized in fanplot
Labels	[1:k] see input Labels, only relevant ones

Author(s)

Michael Thrun

References

[Gohil, 2015] Gohil, Atmajitsinh. R data Visualization cookbook. Packt Publishing Ltd, 2015.

See Also

[Piechart](#), [Fanplot](#)

Examples

```
## will follow
```

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.; Werrnecke, 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.

<code>stat_pde_density</code>	<i>Calculate Pareto density estimation for ggplot2 plots</i>
-------------------------------	--

Description

This function enables to replace the default density estimation for ggplot2 plots with the Pareto density estimation [Utsch, 2005]. It is used for the PDE-Optimized violin plot published in [Thrun et al, 2018].

Usage

```
stat_pde_density(mapping = NULL, data = NULL,
  geom = "violin",
  position = "dodge", ...,
  trim = TRUE, scale =
    "area", na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE)
```

Arguments

<code>mapping</code>	Set of aesthetic mappings created by <code>aes()</code> or <code>aes_()</code> . If specified and <code>inherit.aes = TRUE</code> (the default), it is combined with the default mapping at the top level of the plot. You must supply <code>mapping</code> if there is no plot mapping.
<code>data</code>	The data to be displayed in this layer. There are three options: If <code>NULL</code> , the default, the data is inherited from the plot data as specified in the call to <code>ggplot()</code> . A <code>data.frame</code> , or other object, will override the plot data. All objects will be fortified to produce a data frame. See <code>fortify()</code> for which variables will be created. A function will be called with a single argument, the plot data. The return value must be a <code>data.frame</code> , and will be used as the layer data.
<code>geom</code>	The geometric object to use display the data
<code>position</code>	Position adjustment, either as a string, or the result of a call to a position adjustment function.
<code>...</code>	Other arguments passed on to <code>layer()</code> . These are often aesthetics, used to set an aesthetic to a fixed value, like <code>color = "red"</code> or <code>size = 3</code> . They may also be parameters to the paired <code>geom/stat</code> .
<code>trim</code>	This parameter only matters if you are displaying multiple densities in one plot. If <code>FALSE</code> , the default, each density is computed on the full range of the data. If <code>TRUE</code> , each density is computed over the range of that group: this typically means the estimated <code>x</code> values will not line up, and hence you won't be able to stack density values.

scale	When used with <code>geom_violin</code> : if "area" (default), all violins have the same area (before trimming the tails). If "count", areas are scaled proportionally to the number of observations. If "width", all violins have the same maximum width.
na.rm	If FALSE (the default), removes missing values with a warning. If TRUE, silently removes missing values.
show.legend	logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.
inherit.aes	If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn't inherit behaviour from the default plot specification, e.g. <code>borders()</code> .

Details

Pareto Density Estimation (PDE) is a method for the estimation of probability density functions using hyperspheres. The Pareto-radius of the hyperspheres is derived from the optimization of information for minimal set size. It is shown, that Pareto Density is the best estimate for clusters of Gaussian structure. The method is shown to be robust when cluster overlap and when the variances differ across clusters.

Author(s)

Felix Pape

References

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, Proc Gfkl 2003, pp 91-100, Springer, Berlin, 2005.

[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.

See Also

[stat_density](#)

Examples

```
miris <- reshape2::melt(iris)

ggplot2::ggplot(miris,

mapping = ggplot2::aes(y = .data$value, x = .data$variable)) +

ggplot2::geom_violin(stat = "PDEdensity")
```

Stdrobust	<i>Standard Deviation Robust</i>
-----------	----------------------------------

Description

Robust empirical estimation for standard deviation. NaNs are ignored.

Usage

```
Stdrobust(x, lowInnerPercentile=25, na.rm=TRUE)
```

Arguments

x	a numerical matrix
lowInnerPercentile	optional; default=25; standard deviation approximated by percentilinterval.
na.rm	a boolean evaluating to TRUE or FALSE indicating whether all non finite values should be stripped before the computation proceeds.

Value

out	a vector with the calculated standard deviation for the column
-----	--

Author(s)

Zornitsa Manolova

See Also

[sd quantile](#)

Worldmap	<i>plots a world map by country codes</i>
----------	---

Description

The Worldmap function is used in [Thrun, 2018].

Usage

```
Worldmap(CountryCodes, Cls, Colors,
MissingCountryColor = grDevices::gray(0.8), ...)
```

Arguments

CountryCodes [1:n] vector of characters identifying countries by ISO 3166 codes (2 or 3 letters)
 Cls [1:n] numerical vector of classification
 Colors optional, vector of characters specifying the used colors
 MissingCountryColor if not all countries are specified in CountryCodes then the color of non relevant countries can be changed here
 ... Further arguments passed on to plot, see also `sp::SpatialPolygons`-class

Value

List of
 Colors [1:m] colors used in map, $m \leq n$
 CountryCodeList [1:m] countries found, $m \leq n$
 world_country_polygons `SpatialPolygonsDataFrame`

Author(s)

Michae Thrun

References

Used in
 [Thrun, 2018] Thrun, M. C. : Cluster Analysis of the World Gross-Domestic Product Based on Emergent Self-Organization of a Swarm, 12th Professor Aleksander Zelias International Conference on Modelling and Forecasting of Socio-Economic Phenomena, Foundation of the Cracow University of Economics, Zakopane, Poland, accepted, 2018.
 Source for shapefile: - package `maptoops` and
 Originally 'mappinghacks.com/data/TM_WORLD_BORDERS_SIMPL-0.2.zip', now available from <https://github.com/nasa/World-Wind-Java/tree/master/WorldWind/testData/shapefiles>

Examples

```
# data from [Thrun, 2018]
Cls=c(1L, 1L, 2L, 2L, 2L, 2L, 2L, 1L, 2L, 1L, 1L, 1L, 2L, 2L, 2L,
2L, 2L, 1L, 2L, 2L, 2L, 1L, 2L, 1L, 2L, 1L, 2L, 2L, 1L, 1L, 1L,
1L, 2L, 1L, 1L, 2L, 2L, 2L, 1L, 2L, 2L, 2L, 2L, 2L, 1L, 2L, 1L,
2L, 2L, 2L, 1L, 2L, 2L, 2L, 1L, 1L, 1L, 1L, 3L, 2L, 2L, 2L, 1L,
2L, 1L, 1L, 2L, 1L, 1L, 2L, 2L, 2L, 2L, 2L, 2L, 2L, 2L, 2L, 1L,
1L, 2L, 2L, 2L, 1L, 2L, 1L, 2L, 1L, 1L, 2L, 2L, 1L, 1L, 1L, 2L,
2L, 1L, 2L, 1L, 1L, 1L, 2L, 1L, 2L, 2L, 1L, 1L, 1L, 2L, 2L, 1L,
2L, 2L, 1L, 2L, 2L, 1L, 2L, 1L, 2L, 2L, 2L, 1L, 2L, 1L, 1L, 1L,
2L, 1L, 1L, 2L, 1L, 1L, 2L, 2L, 1L, 2L, 1L, 1L, 2L, 2L, 2L,
2L, 2L, 2L, 1L, 1L, 2L, 2L, 2L, 2L, 1L, 2L, 2L, 2L, 1L, 1L, 1L
)
```

```

Codes=c("AFG", "AGO", "ALB", "ARG", "ATG", "AUS", "AUT", "BDI", "BEL",
"BEN", "BFA", "BGD", "BGR", "BHR", "BHS", "BLZ", "BMU", "BOL",
"BRA", "BRB", "BRN", "BTN", "BWA", "CAF", "CAN", "CH2", "CHE",
"CHL", "CHN", "CIV", "CMR", "COG", "COL", "COM", "CPV", "CRI",
"CUB", "CYP", "DJI", "DMA", "DNK", "DOM", "DZA", "ECU", "EGY",
"ESP", "ETH", "FIN", "FJI", "FRA", "FSM", "GAB", "GBR", "GER",
"GHA", "GIN", "GMB", "GNB", "GNQ", "GRC", "GRD", "GTM", "GUY",
"HKG", "HND", "HTI", "HUN", "IDN", "IND", "IRL", "IRN", "IRQ",
"ISL", "ISR", "ITA", "JAM", "JOR", "JPN", "KEN", "KHM", "KIR",
"KNA", "KOR", "LAO", "LBN", "LBR", "LCA", "LKA", "LSO", "LUX",
"MAC", "MAR", "MDG", "MDV", "MEX", "MHL", "MLI", "MLT", "MNG",
"MOZ", "MRT", "MUS", "MWI", "MYS", "NAM", "NER", "NGA", "NIC",
"NLD", "NOR", "NPL", "NZL", "OMN", "PAK", "PAN", "PER", "PHL",
"PLW", "PNG", "POL", "PRI", "PRT", "PRY", "ROM", "RWA", "SDN",
"SEN", "SGP", "SLB", "SLE", "SLV", "SOM", "STP", "SUR", "SWE",
"SWZ", "SYC", "SYR", "TCD", "TGO", "THA", "TON", "TTO", "TUN",
"TUR", "TWN", "TZA", "UGA", "URY", "USA", "VCT", "VEN", "VNM",
"VUT", "WSM", "ZAF", "ZAR", "ZMB", "ZWE")
Worldmap(Codes,C1s)

```

world_country_polygons

world_country_polygons

Description

world_country_polygons shapefile

Usage

```
data("world_country_polygons")
```

Format

world_country_polygons stores data objects using classes defined in the sp package or inheriting from those classes updated to sp Y= 1.4 and rgdal >= 1.5.

Since DataVisualization Version 1.2.1 it stores now a CRS objects with a comment containing an WKT2 CRS representation, thanks to a suggestion of Roger Bivand.

Details

Note that the rebuilt CRS object contains a revised version of the input Proj4 string as well as the WKT2 string, and may be used with both older and newer versions of sp. See mapproj package for further details. Also note that since sp >= 2.0 mapproj and rgdal were deprecated without change to the workflow. See terra for an alternative to mapproj.

Author(s)

Hamza Tayyab, Michael Thrun

Source

maptools package

References

maptools package

Examples

```
data(world_country_polygons)
str(world_country_polygons)
```

zplot

Plotting for 3 dimensional data

Description

Plots z above xy plane as 3D mountain or 2D contourlines

Usage

```
zplot(x, y, z, DrawTopView = TRUE, NrOfContourLines = 20,
      TwoDplotter = "native", xlim, ylim)
```

Arguments

x	Vector of x-coordinates of the data. If y and z are missing: Matrix containing 3 rows, one for each coordinate
y	Vector of y-coordinates of the data.
z	Vector of z-coordinates of the data.
DrawTopView	Optional: Boolean, if true plot contours otherwise a 3D plot. Default: True
NrOfContourLines	Optional: Numeric. Only used when DrawTopView == True. Number of lines to be drawn in 2D contour plots. Default: 20
TwoDplotter	Optional: String indicating which backend to use for plotting. Possible Values: 'ggplot', 'native', 'plotly'
xlim	[1:2] scalar vector setting the limits of x-axis
ylim	[1:2] scalar vector setting the limits of y-axis

Value

If the plotting backend does support it, this will return a handle for the generated plot.

Author(s)

Felix pape

Examples

```
## Not run:  
data("Lsun3D")  
Data=Lsun3D$Data  
if(exists("zplot", where = asNamespace("DataVisualizations")))  
  DataVisualizations::zplot(Data[,1],Data[,2],Data[,3])  
  
## End(Not run)
```

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