

Package: AdaptGauss (via r-universe)

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Type Package

Title Gaussian Mixture Models (GMM)

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Description Multimodal distributions can be modelled as a mixture of components. The model is derived using the Pareto Density Estimation (PDE) for an estimation of the pdf. PDE has been designed in particular to identify groups/classes in a dataset. Precise limits for the classes can be calculated using the theorem of Bayes. Verification of the model is possible by QQ plot, Chi-squared test and Kolmogorov-Smirnov test. The package is based on the publication of Ultsch, A., Thrun, M.C., Hansen-Goos, O., Lotsch, J. (2015) <[DOI:10.3390/ijms161025897](https://doi.org/10.3390/ijms161025897)>.

Imports Rcpp, shiny, pracma, methods, DataVisualizations

Suggests mclust, grid, foreach, dqrng, parallelDist, knitr (>= 1.12), rmarkdown (>= 0.9), reshape2, ggplot2, plotly

LinkingTo Rcpp

Depends R (>= 2.10)

License GPL-3

LazyLoad yes

URL <https://www.uni-marburg.de/fb12/datenbionik/software-en>

Encoding UTF-8

NeedsCompilation yes

VignetteBuilder knitr

BugReports <https://github.com/Mthrun/AdaptGauss/issuesConfig/pak/sysreqs>:
make libicu-dev zlib1g-dev

Repository <https://mthrun.r-universe.dev>

RemoteUrl <https://github.com/mthrun/adaptgauss>

RemoteRef HEAD

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AdaptGauss-package	<i>Gaussian Mixture Models (GMM)</i>
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Description

Multimodal distributions can be modelled as a mixture of components. The model is derived using the Pareto Density Estimation (PDE) for an estimation of the pdf. PDE has been designed in particular to identify groups/classes in a dataset. Precise limits for the classes can be calculated using the theorem of Bayes. Verification of the model is possible by QQ plot, Chi-squared test and Kolmogorov-Smirnov test. The package is based on the publication of Ultsch, A., Thrun, M.C., Hansen-Goos, O., Lotsch, J. (2015) <DOI:10.3390/ijms161025897>.

Details

Multimodal distributions can be modelled as a mixture of components. The model is derived using the Pareto Density Estimation (PDE) for an estimation of the pdf [Ultsch 2005]. PDE has been designed in particular to identify groups/classes in a dataset. The expectation maximization algorithm estimates a Gaussian mixture model of density states [Bishop 2006] and the limits between the different states are defined by Bayes decision boundaries [Duda 2001]. The model can be verified with Chi-squared test, Kolmogorov-Smirnov test and QQ plot.

The correct number of modes may be found with AIC or BIC.

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

Author(s)

Michael Thrun, Onno Hansen-Goos, Rabea Griese, Catharina Lippmann, Florian Lerch, Jorn Lotsch, Alfred Ultsch Maintainer: Michael Thrun <m.thrun@gmx.net>

References

Ultsch, A., Thrun, M.C., Hansen-Goos, O., Loetsch, J.: Identification of Molecular Fingerprints in Human Heat Pain Thresholds by Use of an Interactive Mixture Model R Toolbox(AdaptGauss), International Journal of Molecular Sciences, doi:10.3390/ijms161025897, 2015.

Duda, R.O., P.E. Hart, and D.G. Stork, Pattern classification. 2nd. Edition. New York, 2001, p 512 ff

Bishop, Christopher M. Pattern recognition and machine learning. springer, 2006, p 435 ff

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 M.C., Ultsch, A.: Models of Income Distributions for Knowledge Discovery, European Conference on Data Analysis, DOI 10.13140/RG.2.1.4463.0244, Colchester 2015.

Examples

```
## Statistically significant GMM

data=c(rnorm(3000,2,1),rnorm(3000,7,3),rnorm(3000,-2,0.5))

gmm=AdaptGauss::AdaptGauss(data,

Means = c(-2, 2, 7),

SDs = c(0.5, 1, 4),

Weights = c(0.3333, 0.3333, 0.3333))

AdaptGauss::Chi2testMixtures(data,

gmm$Means,gmm$SDs,gmm$Weights,PlotIt=T)

AdaptGauss::QQplotGMM(data,gmm$Means,gmm$SDs,gmm$Weights)

## Statistically non significant GMM

data('LKWFahrzeitSeehafen2010')

gmm=AdaptGauss::AdaptGauss(LKWFahrzeitSeehafen2010,
```

```

Means = c(52.74, 385.38, 619.46, 162.08),
SDs = c(38.22, 93.21, 57.72, 48.36),
Weights = c(0.2434, 0.5589, 0.1484, 0.0749))

AdaptGauss::Chi2testMixtures(LKWFahrzeitSeehafen2010,
gmm$Means,gmm$SDs,gmm$Weights,PlotIt=T)

AdaptGauss::QqplotGMM(LKWFahrzeitSeehafen2010,gmm$Means,gmm$SDs,gmm$Weights)

```

AdaptGauss

Adapt Gaussian Mixture Model (GMM)

Description

Adapt interactively a Gaussians Mixture Model GMM to the empirical PDF of the data (generated by DataVisualizations::ParetoDensityEstimation) such that $N(\text{Means}, \text{SDs}) * \text{Weights}$ is a model for Data

Usage

```

AdaptGauss(Data, Means = NaN, SDs = NaN, Weights = NaN,
           ParetoRadius = NaN, LB = NaN, HB = NaN,
           ListOfAdaptGauss, fast = T)

```

Arguments

Data	Data for empirical PDF. Has to be an Array of values. NaNs and NULLs will be deleted
Means	Optional: Means of gaussians of GMM.
SDs	Optional: StandardDeviations of gaussians of GMM. (Has to be the same length as Means)
Weights	Optional: Weights of gaussians of GMM. (Has to be the same length as Means)
ParetoRadius	Optional: Pareto Radius of Pareto Desity Estimation (PDE).
LB	Optional: Low boundary of estimation. All values below LB will be deleted. Default: min(Data)
HB	Optional: High boundary of estimation. All values above HB will be deleted. Default: max(Data)

ListOfAdaptGauss

Optional: If editing of an existing Model is the goal, enables to give the Output of AdaptGaus as the Input of AdaptGauss() instead of setting Means, SDs and Weights separately

fast

Default=TRUE; FALSE: Using mclust's EM see function densityMclust of that package, TRUE: Naive but faster EM implementation, which may be numerical unstable, because log(gauss) is not used

Details

Data: maximum length is 10000. If larger, Data will be randomly reduced to 10000 Elements.
 MeansIn/DeviationsIn/WeightsIN: If empty, either one or three Gaussian's are generated by kmeans algorithm. Pareto Radius: If empty: will be generated by DataVisualizations::ParetoDensityEstimation
 RMS: Root Mean Square error is normalized by RMS of Gaussian's with Mean=mean(data) and SD=sd(data), see [Ultsch et.al., 2015] for further details.

Value

List with

Means Means of Gaussian's.

SDs Standard SDs of Gaussian's.

Weights Weights of Gaussian's.

ParetoRadius Pareto Radius: Either ParetoRadiusIn, the pareto radius enerated by PretoDensityEstimation(if no Pareto Radius in Input).

RMS Root Mean Square of Deviation between Gaussian Mixture Model GMM to the empirical PDF. Normalized by RMS of one Gaussian with mean=meanrobust(data) and sdev=stdrobust(data). Further Details in [Ultsch et al 2015]

BayesBoundaries

vector[1:L-1], Bayes decision boundaries

Author(s)

Onno Hansen-Goos, Michael Thrun

References

Ultsch, A., Thrun, M.C., Hansen-Goos, O., Loetsch, J.: Identification of Molecular Fingerprints in Human Heat Pain Thresholds by Use of an Interactive Mixture Model R Toolbox(AdaptGauss), International Journal of Molecular Sciences, doi:10.3390/ijms161025897, 2015.

Thrun M.C., Ultsch, A.: Models of Income Distributions for Knowledge Discovery, European Conference on Data Analysis, DOI 10.13140/RG.2.1.4463.0244, Colchester 2015.

Examples

```
data1=c(rnorm(1000))
## Not run: Vals1=AdaptGauss(data1)
```

```
data2=c(rnorm(1000),rnorm(2000)+2,rnorm(1000)*2-1)
## Not run: Vals2=AdaptGauss(data2,c(-1,0,2),c(2,1,1),c(0.25,0.25,0.5),0.3,-6,6)
```

 Bayes4Mixtures

Posterioris of Bayes Theorem

Description

Calculates the posterioris of Bayes theorem

Usage

```
Bayes4Mixtures(Data, Means, SDs, Weights, IsLogDistribution,
  PlotIt, CorrectBorders, Color, xlab, lwd)
```

Arguments

Data	vector (1:N) of data points
Means	vector[1:L] of Means of Gaussians (of GMM), L == Number of Gaussians
SDs	vector of standard deviations, estimated Gaussian Kernels, has to be the same length as Means
Weights	vector of relative number of points in Gaussians (prior probabilities), has to be the same length as Means
IsLogDistribution	Optional, ==1 if distribution(i) is a LogNormal, default vector of zeros of length L
PlotIt	Optional, Default: FALSE; TRUE do a Plot
CorrectBorders	Optional, ==TRUE data at right borders of GMM distribution will be assigned to last gaussian, left border vice versa. (default ==FALSE) normal Bayes Theorem
Color	Optional, character vector of colors, default rainbow()
xlab	Optional, label of x-axis, default 'Data', see intern R documentation
lwd	Width of Line, see intern R documentation

Details

See conference presentation for further explanation.

Value

List with

Posterioris (1:N,1:L) of Posterioris corresponding to Data

NormalizationFactor

(1:N) denominator of Bayes theorem corresponding to Data

Author(s)

Catharina Lippmann, Onno Hansen-Goos, Michael Thrun

References

Thrun M.C.,Ultsch, A.: Models of Income Distributions for Knowledge Discovery, European Conference on Data Analysis, DOI 10.13140/RG.2.1.4463.0244, Colchester 2015.

See Also

[BayesDecisionBoundaries](#),[AdaptGauss](#)

BayesClassification *BayesClassification*

Description

Bayes Klassifikation den Daten zuordnen

Usage

```
BayesClassification(Data, Means, SDs, Weights, IsLogDistribution = Means
* 0, ClassLabels = c(1:length(Means)))
```

Arguments

Data	vector of Data
Means	vector[1:L] of Means of Gaussians (of GMM)
SDs	vector of standard deviations, estimated Gaussian Kernels, has to be the same length as Means
Weights	vector of relative number of points in Gaussians (prior probabilities), has to be the same length as Means
IsLogDistribution	Optional, ==1 if distribution(i) is a LogNormal, default vector of zeros of length 1:L
ClassLabels	Optional numbered class labels that are assigned to the classes. default (1:L), L number of different components of gaussian mixture model

Value

Cls(1:n,1:d) classification of Data, such that 1= first component of gaussian mixture model, 2= second component of gaussian mixture model and so on. For Every datapoint a number is returned.

Author(s)

Michael Thrun

 BayesDecisionBoundaries

Decision Boundaries calculated through Bayes Theorem

Description

Function finds the intersections of Gaussians or LogNormals

Usage

BayesDecisionBoundaries(Means,SDs,Weights,IsLogDistribution,MinData,MaxData,Ycoor)

Arguments

Means	vector[1:L] of Means of Gaussians (of GMM)
SDs	vector of standard deviations, estimated Gaussian Kernels, has to be the same length as Means
Weights	vector of relative number of points in Gaussians (prior probabilities), has to be the same length as Means
IsLogDistribution	Optional, ==1 if distribution(i) is a LogNormal, default vector of zeros of length 1:L
MinData	Optional, Beginning of range, where the Boundaries are searched for, default min(M)
MaxData	Optional, End of range, where the Boundaries are searched for, default max(M)
Ycoor	Optional, Bool, if TRUE instead of vector of DecisionBoundaries list of DecisionBoundaries and DBY is returned

Value

DecisionBoundaries	vector[1:L-1], Bayes decision boundaries
DBY	if (Ycoor==TRUE), y values at the cross points of the Gaussians is also returned, that the return is a list of DecisionBoundaries and DBY

Author(s)

Michael Thrun, Rabea Griese

References

Duda, R. O., Hart, P. E., & Stork, D. G. (2001). Pattern classification. 2nd. Edition. New York, p. 512ff

See Also

[AdaptGauss](#),[Intersect2Mixtures](#),[Bayes4Mixtures](#)

 BayesFor2GMM

Posterioris of Bayes Theorem for a two group GMM

Description

Calculates the posterioris of Bayes theorem, splits the GMM in two groups beforehand.

Usage

```
BayesFor2GMM(Data, Means, SDs, Weights, IsLogDistribution = Means * 0,
  Ind1 = c(1:floor(length(Means)/2)), Ind2 = c((floor(length(Means)/2)
  + 1):length(Means)), PlotIt = 0, CorrectBorders = 0)
```

Arguments

Data	vector (1:N) of data points
Means	vector[1:L] of Means of Gaussians (of GMM), L == Number of Gaussians
SDs	vector of standard deviations, estimated Gaussian Kernels, has to be the same length as Means
Weights	vector of relative number of points in Gaussians (prior probabilities), has to be the same length as Means
IsLogDistribution	Optional, ==1 if distribution(i) is a LogNormal, default vector of zeros of length L
Ind1	indices from (1:C) such that [M(Ind1),S(Ind1),W(Ind1)] is one mixture, [M(Ind2),S(Ind2),W(Ind2)] the second mixture default Ind1= 1:C/2, Ind2= C/2+1:C
Ind2	indices from (1:C) such that [M(Ind1),S(Ind1),W(Ind1)] is one mixture, [M(Ind2),S(Ind2),W(Ind2)] the second mixture default Ind1= 1:C/2, Ind2= C/2+1:C
PlotIt	Optional, Default: FALSE; TRUE do a Plot
CorrectBorders	Optional, ==TRUE data at right borders of GMM distribution will be assigned to last gaussian, left border vice versa. (default ==FALSE) normal Bayes Theorem

Details

See conference presentation for further explanation.

Value

List With

Posterioris: (1:N,1:L) of Posterioris corresponding to Data

NormalizationFactor: (1:N) denominator of Bayes theorem corresponding to Data

Author(s)

Alfred Ultsch, Michael Thrun

References

Thrun M.C.,Ultsch, A.: Models of Income Distributions for Knowledge Discovery, European Conference on Data Analysis, DOI 10.13140/RG.2.1.4463.0244, Colchester 2015.

See Also

BayesDecisionBoundaries,AdaptGauss

CDFMixtures

cumulative distribution of mixture model

Description

returns the cdf (cumulative distribution function) of a mixture model of gaussian or log gaussians

Usage

CDFMixtures(Kernels,Means,SDs,Weights,IsLogDistribution)

Arguments

Kernels	at these locations $N(\text{Means}, \text{Sdevs}) * \text{Weights}$ is used for cdf calculation, NOTE: Kernels are usually (but not necessarily) sorted and unique
Means	vector(1:L), Means of Gaussians, $L == \text{Number of Gaussians}$
SDs	estimated Gaussian Kernels = standard deviations
Weights	optional, relative number of points in Gaussians (prior probabilities): $\text{sum}(\text{Weights}) == 1$, default weight is $1/L$
IsLogDistribution	Optional, if $\text{IsLogDistribution}(i) == 1$, then mixture is lognormal default $== 0*(1:L)$

Value

List with

- CDFGaussMixture
(1:N,1), cdf of Sum of SingleGaussians at Kernels
- CDFSingleGaussian
(1:N,1:L), cdf of mixtures at Kernels

Author(s)

Rabea Griese

See Also

[Chi2testMixtures](#)

Chi2testMixtures *Pearson's chi-squared goodness of fit test*

Description

Chi2testMixtures is goodness of fit test which establishes whether an observed distribution (data) differs from a Gauss Mixture Model (GMM). Returns a P value of a special case of a chi-square test and visualizes data versus a given GMM.

Usage

```
Chi2testMixtures(Data, Means, SDs, Weights,
                 IsLogDistribution, PlotIt, UpperLimit, VarName, NoRepetitionst)
```

Arguments

Data	vector of data points (1:n)
Means	vector of Means of Gaussians (1:c)
SDs	vector of standard deviations, estimated Gaussian Kernels (1:c)
Weights	vector of relative number of points in Gaussians (prior probabilities) (1:c)
IsLogDistribution	Optional, if IsLogDistribution(i)==1, then mixture is lognormal, default vector of zeros of length 1:L
PlotIt	Optional, Default: FALSE, do a Plot of the compared cdfs and the KS-test distribution (Diff)
UpperLimit	Optional. test only for Data <= UpperLimit, Default = max(Data) i.e all Data.
VarName	If PlotIt=TRUE, the name of the inspected variable, default 'Data'
NoRepetitions	Optional, scalar, default =1000, Number of Repetitions for monte carlo sampling

Details

The null hypothesis is that the estimated data distribution does not differ significantly from the GMM. Let O_i be the observed features and E_i be the expected number E , then the test statistic is defined with the minimum chi-square estimate $T = \sum((O_i - E_i)^2 / E_i) * 1/m$, where m the number of data points. The expected number E_i may be derived for each bin. If there is a significant difference between the O_i and the E_i , the Pvalue is small and the null hypothesis can be rejected.

Further details, see [Thrun & Ultsch, 2015].

Value

List with	
Pvalue	Pvalue of a suiting chi-square , Pvalue ==0 if Pvalue <0.001
BinCenters	bin centers
ObsNrInBin	No. of data in bin
ExpectedNrInBin	No. of data that should be in bin according to GMM
Chi2Value	the TestStatistic T i.e.: $\sum((\text{ObsNrInBin}(\text{Ind})-\text{ExpectedNrInBin}(\text{Ind}))^2/\text{ExpectedNrInBin}(\text{Ind}))$ with $\text{Ind} = \text{find}(\text{ExpectedNrInBin} \geq 10)$ The value of Chi2Value is compared to a chi-squared distribution.

Note

The statistic assumption is that the the test statistic follows a chi square distribution. The number of degrees of freedom is equal to the number of datapoints $n-1-3*c$

Author(s)

Rabea Griese, Michael Thrun

References

- Hartung, J., Elpelt, B., and Kloesener, K.H.: Statistik, 8. Aufl. Verlag Oldenburg (1991).
- Thrun, M. C., Ultsch, A.: Models of Income Distributions for Knowledge Discovery, European Conference on Data Analysis, DOI 10.13140/RG.2.1.4463.0244, pp. 28-29, Colchester 2015.

ClassifyByDecisionBoundaries

Classify Data according to decision Boundaries

Description

The Decision Boundaries calculated through Bayes Theorem.

Usage

ClassifyByDecisionBoundaries(Data,DecisionBoundaries,ClassLabels)

Arguments

Data	vector of Data
DecisionBoundaries	decision boundaries, BayesDecisionBoundaries
ClassLabels	Optional numbered class labels that are assigned to the classes. default (1:L), L number of different components of gaussian mixture model

Value

Cls(1:n,1:d) classification of Data, such that 1= first component of gaussian mixture model, 2= second component of gaussian mixture model and so on. For Every datapoint a number is returned.

Author(s)

Michael Thrun

References

Duda, R. O., Hart, P. E., & Stork, D. G. (2001). Pattern classification. 2nd. Edition. New York, p. 512ff

See Also

[BayesDecisionBoundaries](#), [Bayes4Mixtures](#)

EMGauss

EM Algorithm for GMM

Description

Expectation-Maximization algorithm to calculate optimal Gaussian Mixture Model for given data in one Dimension.

Usage

EMGauss(Data, K, Means, SDs,Weights, MaxNumberOfIterations,fast)

Arguments

Data	vector of data points
K	estimated amount of Gaussian Kernels
Means	vector(1:L), Means of Gaussians, L == Number of Gaussians
SDs	estimated Gaussian Kernels = standard deviations
Weights	optional, relative number of points in Gaussians (prior probabilities): sum(Weights) ==1, default weight is 1/L
MaxNumberOfIterations	Optional, Number of Iterations; default=10
fast	Default: FALSE: Using mclust's EM see function densityMclust of that package, TRUE: Naive but faster EM implementation, which may be numerical unstable, because log(gauss) is not used

Details

No adding or removing of Gaussian kernels. Number of Gaussian has to be set by the length of the vector of Means, SDs and Weights. This EM is only for univariate data. For multivariate data see package `mclust`

Value

List with

Means	means of GMM generated by EM algorithm
SDs	standard deviations of GMM generated by EM algorithm
Weights	prior probabilities of Gaussians

Author(s)

Onno Hansen-Goos, Michael Thrun, Florian Lerch

References

Bishop, Christopher M. Pattern recognition and machine learning. springer, 2006, p 435 ff

See Also

[AdaptGauss](#)

GMMplot_ggplot2

Plots the Gaussian Mixture Model (GMM) withing ggplot2

Description

PlotMixtures and PlotMixturesAndBoundaries for ggplot2

Usage

```
GMMplot_ggplot2(Data, Means, SDs, Weights,
  BayesBoundaries, SingleGausses = TRUE, Hist = FALSE)
```

Arguments

Data	vector (1:N) of data points
Means	vector[1:L] of Means of Gaussians (of GMM), L == Number of Gaussians
SDs	vector of standard deviations, estimated Gaussian Kernels, has to be the same length as Means
Weights	vector of relative number of points in Gaussians (prior probabilities), has to be the same length as Means

BayesBoundaries	Optional, x values for baye boundaries, if missing 'BayesDecisionBoundaries' is called
SingleGausses	Optional, SingleGausses=T than components of the mixture in blue will be shown.
Hist	Optional, geom_histogram overlaid

Value

ggplot2 object

Note

MT standardized code for CRAN and added dec boundaries and doku

Author(s)

Joern Loetsch, Michael Thrun (ctb)

See Also

[PlotMixturesAndBoundaries](#), [PlotMixtures](#), [BayesDecisionBoundaries](#)

Examples

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

```
GMMplot_ggplot2(data,c(-1,0,2),c(2,1,1),c(0.25,0.25,0.5),SingleGausses=TRUE)
```

InformationCriteria4GMM

Information Criteria For GMM

Description

Calculates the AIC and BIC criteria

Usage

```
InformationCriteria4GMM(Data, Means, SDs, Weights, IsLogDistribution)
```

Arguments

Data	vector (1:N) of data points
Means	vector[1:L] of Means of Gaussians (of GMM), L == Number of Gaussians
SDs	vector of standard deviations, estimated Gaussian Kernels, has to be the same length as Means
Weights	vector of relative number of points in Gaussians (prior probabilities), has to be the same length as Means
IsLogDistribution	Optional, ==1 if distribution(i) is a LogNormal, default vector of zeros of length L, LogNormal Modes are at this point only experimental

Details

AIC = $2*k - 2*\text{LogLikelihood}$, $k = \text{nr. of model parameter} = 3*\text{Nr. of Gaussians}$ One Gaussian: $K=2$ (Weight is then not an parameter!) SMALL SAMPLE CORRECTION: for $n = \text{nr of Data}$ and $n < 40 * k$, AIC is adjusted to $\text{AIC} = \text{AIC} + (2*k*(k+1))/(n-k-1)$

BIC = $k * \log(n) - 2*\text{LogLikelihood}$

Only for a Gaussian Mixture Model (GMM) verified, for the Log Gaussian, Gaussian, Log Gaussian (LGL) Model only experimental

Value

List with

K	Number of gaussian mixtures
AIC	Akaike Informations criterium
BIC	Bayes Information criterium
LogLikelihood	LogLikelihood of GMM, see LogLikelihood4Mixtures
PDFmixture	probability density function of GMM, see Pdf4Mixtures
LogPDFdata	$\log(\text{PDFmixture})$

Author(s)

Michael Thrun

References

- Aubert, A. H., Thrun, M. C., Breuer, L., & Ultsch, A.: Knowledge discovery from data structure: hydrology versus biology controlled in-stream nitrate concentration, Scientific reports, Vol. (in revision), pp., 2016.
- Aho, K., Derryberry, D., & Peterson, T.: Model selection for ecologists: the worldviews of AIC and BIC. Ecology, 95(3), pp. 631-636, 2014.

Intersect2Mixtures *Intersect of two Gaussians*

Description

Finds the intersect of two gaussians or log gaussians

Usage

Intersect2Mixtures(Mean1,SD1,Weight1,Mean2,SD2,Weight2,IsLogDistribution,MinData,MaxData)

Arguments

Mean1	mean of 1.gaussian
SD1	standard deviations of 1.gaussian
Weight1	weight of 1. gaussian
Mean2	mean of 2.gaussian
SD2	standard deviations of 2.gaussian
Weight2	weight of 2. gaussian
IsLogDistribution	Optional, ==1 if distribution(i) is a LogNormal, default vector of zeros of length 2
MinData	Optional, Beginning of range, where the intersect is searched for, default min(Mean1,Mean2)
MaxData	Optional, End of range, where the intersect is searched for, default max(Mean1,Mean2)

Value

CutX	x value, where gaussian 1=gaussian2
CutY	y value, where gaussian 1=gaussian2

Author(s)

Michael Thrun, Rabea Griese

See Also

[BayesDecisionBoundaries](#)

KStestMixtures	<i>Kolmogorov-Smirnov test</i>
----------------	--------------------------------

Description

Returns a P value and visualizes for Kolmogorov-Smirnov test of Data versus a given Gauss Mixture Model

Usage

```
KStestMixtures(Data, Means, SDs, Weights, IsLogDistribution,
PlotIt, UpperLimit, NoRepetitions, Silent)
```

Arguments

Data	vector of data points
Means	vector of Means of Gaussians
SDs	vector of standard deviations, estimated Gaussian Kernels
Weights	vector of relative number of points in Gaussians (prior probabilities)
IsLogDistribution	Optional, if IsLogDistribution(i)==1, then mixture is lognormal, default vector of zeros of length 1:L
PlotIt	Optional, Default: FALSE, do a Plot of the compared cdfs and the KS-test distribution (Diff)
UpperLimit	Optional. test only for Data <= UpperLimit, Default = max(Data) i.e all Data.
NoRepetitions	Optional, default =1000, scalar, Number of Repetitions for monte carlo sampling
Silent	Optional, default=TRUE, If FALSE, shows progress of computation by points (On windows systems a progress bar)

Details

The null hypothesis is that the estimated data distribution does not differ significantly from the GMM. If there is a significant difference, then the Pvalue is small and the null hypothesis is rejected.

Value

List with

Pvalue	Pvalue of a suiting Kolmogorov-Smirnov test, Pvalue ==0 if Pvalue <0.001
DataKernels	such that plot(DataKernels,DataCDF) gives the cdf(Data)
DataCDF	such that plot(DataKernels,DataCDF) gives the cdf(Data)
CDFGaussMixture	No. of data that should be in bin according to GMM

Author(s)

Michael Thrun, Alfred Ultsch

References

Smirnov, N., Table for Estimating the Goodness of Fit of Empirical Distributions. 1948, (2), 279-281.

LikelihoodRatio4Mixtures

Likelihood Ratio for Gaussian Mixtures

Description

Computes the likelihood ratio for two Gaussian Mixture Models.

Usage

LikelihoodRatio4Mixtures(Data,NullMixture,OneMixture,PlotIt,LowerLimit,UpperLimit)

Arguments

Data	Data points.
NullMixture	A Matrix: cbind(Means0,SDs0,Weights0) or cbind(Means0,SDs0,Weights0,IsLog0). The null model; usually with less Gaussians than the OneMixture
OneMixture	A Matrix: cbind(Means1,SDs1,Weights1) or cbind(Means1,SDs1,Weights1,IsLog1). The alternative model usually with more Gaussians than the OneMixture.
PlotIt	Optional: zero or one. o a Plot of the compared cdf's and the KS-test distribution (Diff)
LowerLimit	Optional: test only for Data \geq LowerLimit, Default = min(Data) i.e all Data.
UpperLimit	Optional: test only for Data \leq UpperLimit, Default = max(Data) i.e all Data.

Value

List with	
Pvalue	the error that we make, if we accept OneMixture as the better Model over the NullMixture
NullLogLikelihood	log likelihood of GMM Null
OneLogLikelihood	log likelihood of GMM One

Author(s)

Alfred Ultsch, Michael Thrun, Catharina Lippmann

Examples

```

data2=c(rnorm(1000),rnorm(2000)+2,rnorm(1000)*2-1)
## Not run: Vals=AdaptGauss(data2,c(-1,0,2),c(2,1,1),c(0.25,0.25,0.5),0.3,-6,6)
NullMixture=cbind(Vals$Means,Vals$SDs,Vals$Weights)

## End(Not run)
## Not run: Vals2=AdaptGauss(data2,c(-1,0,2,3),c(2,1,1,1),c(0.25,0.25,0.25,0.25),0.3,-6,6)
OneMixture=cbind(Vals2$Means,Vals2$SDs,Vals2$Weights)

## End(Not run)
## Not run:
res=LikelihoodRatio4Mixtures(Data,NullMixture,OneMixture,T)

## End(Not run)

```

LKWFahrzeitSeehafen2010

Truck driving time seaport 2010

Description

Truck driving time to seaports measured in 2010.

Usage

```
data("LKWFahrzeitSeehafen2010")
```

Format

The format is: num [1:11441] 84.7 13.2 11.5 41.4 52.9 ...

References

Behnisch, M., Ultsch, A.: Knowledge Discovery in Spatial Planning Data - A Concept for Cluster Understanding, in: Helbich, M., Arsanjani, J. J., Leitner, M. (eds.): Computational Approaches for Urban Environments, in: Gatrell, J.D., Jensen, R.R.: Geotechnologies and the Environment Series, Vol, 13, Springer, Berlin, pp. 49-75, 2015.

Examples

```

data(LKWFahrzeitSeehafen2010)
## maybe str(LKWFahrzeitSeehafen2010) ; plot(LKWFahrzeitSeehafen2010) ...

```

 LogLikelihood4Mixtures

LogLikelihood for Gaussian Mixture Models

Description

Computes the LogLikelihood for Gaussian Mixture Models.

Usage

```
LogLikelihood4Mixtures(Data, Means, SDs, Weights, IsLogDistribution)
```

Arguments

Data	Data for empirical PDF. Has to be an Array of values. NaNs and NULLs will be deleted
Means	Optional: Means of gaussians of GMM.
SDs	Optional: StandardDeviations of gaussians of GMM. (Has to be the same length as Means)
Weights	Optional: Weights of gaussians of GMM. (Has to be the same length as Means)
IsLogDistribution	Optional, ==1 if distribution(i) is a LogNormal, default vector of zeros of length 1:L

Value

List with	
LogLikelihood	LogLikelihood = = sum(log(PDFmixture))
LogPDF	=log(PDFmixture)
PDFmixture	die Probability density function for each point

Author(s)

Alfred Ultsch, Catharina Lippmann

References

Pattern Recognition and Machine Learning, C.M. Bishop, 2006, isbn: ISBN-13: 978-0387-31073-2, p. 433 (9.14)

 Pdf4Mixtures

Calculates pdf for GMM

Description

Calculate Gaussianthe probability density function for a Mixture Model

Usage

```
Pdf4Mixtures(Data, Means, SDs, Weights,IsLogDistribution,PlotIt)
```

Arguments

Data	vector (1:N) of data points
Means	vector[1:L] of Means of Gaussians (of GMM),L == Number of Gaussians
SDs	vector of standard deviations, estimated Gaussian Kernels, has to be the same length as Means
Weights	vector of relative number of points in Gaussians (prior probabilities), has to be the same length as Means
IsLogDistribution	Optional, ==1 if distribution(i) is a LogNormal, default vector of zeros of length 1:L
PlotIt	Optional: =TRUE plot of pdf

Value

List with	
PDF4modes	matrix, where the columns are the gaussians
PDF	matrix, where the columns are the gaussians weighted by Weights
PDFmixture	linear superpositions of PDF - prior probabilities of Gaussians

Author(s)

Michael Thrun

See Also

[PlotMixtures](#)

Examples

```
data=c(rnorm(1000),rnorm(2000)+2,rnorm(1000)*2-1)
Pdf4Mixtures(data,c(-1,0,2),c(2,1,1),c(0.25,0.25,0.5), PlotIt=TRUE)
```

PlotMixtures	<i>Shows GMM</i>
--------------	------------------

Description

Plots Gaussian Mixture Model without Bayes decision boundaries, such that:

Black is the PDE of Data

Red is color of the GMM

Blue is the color of components of the mixture

Arguments

Data	vector (1:N) of data points
Means	vector[1:L] of Means of Gaussians (of GMM), L == Number of Gaussians
SDs	vector of standard deviations, estimated Gaussian Kernels, has to be the same length as Means
Weights	vector of relative number of points in Gaussians (prior probabilities), has to be the same length as Means
IsLogDistribution	Optional, ==1 if distribution(i) is a LogNormal, default vector of zeros of length 1:L
Plotter	Optional, plotting package, either native or plotly
SingleColor	Optional, Color for line plot of all the single gaussians, default magenta
MixtureColor	Optional, Color of line lot for the mixture default red
DataColor	Optional, Color of line plot for the data, default black
SingleGausses	Optional, If TRUE, single gaussians are shown, default FALSE
axes	Optional, Default: TRUE with axis, see argument axis of plot
xlab	Optional, see plot
ylab	Optional, see plot
xlim	Optional, see plot
ylim	Optional, see plot
ParetoRad	Optional: Precalculated Pareto Radius to use
...	other plot arguments like xlim = c(1,10)

Details

Example shows that overlapping variances of gaussians will result in inappropriate decision boundaries.

Author(s)

Michael Thrun, Quirin Stier

See Also

[PlotMixturesAndBoundaries](#)

Examples

```
data=c(rnorm(1000),rnorm(2000)+2,rnorm(1000)*2-1)
PlotMixtures(data,c(-1,0,2),c(2,1,1),c(0.25,0.25,0.5),SingleColor='blue',SingleGausses=TRUE)
```

PlotMixturesAndBoundaries

Shows GMM with Boundaries

Description

Plots Gaussian Mixture Model with Bayes decision boundaries, such that:

Black is the PDE of Data

Red is color of the GMM

Magenta are the Bayes boundaries

Usage

```
PlotMixturesAndBoundaries(Data, Means, SDs, Weights,
IsLogDistribution = rep(FALSE, length(Means)), Plotter="native",
SingleColor = "blue", MixtureColor = "red", DataColor = "black",
BoundaryColor = "magenta", xlab, ylab,
SingleGausses =TRUE, ...)
```

Arguments

Data	vector (1:N) of data points
Means	vector[1:L] of Means of Gaussians (of GMM),L == Number of Gaussians
SDs	vector of standard deviations, estimated Gaussian Kernels, has to be the same length as Means
Weights	vector of relative number of points in Gaussians (prior probabilities), has to be the same length as Means
IsLogDistribution	Optional, ==1 if distribution(i) is a LogNormal, default vector of zeros of length 1:L
Plotter	Optional, plotting package, either native or plotly

SingleColor	Optional, Color for line plot of all the single gaussians, default magenta
MixtureColor	Optional, Color of line plot for the mixture, default red
DataColor	Optional, Color of line plot for the data, default black
BoundaryColor	Optional, Color of bayesian boundaries
xlab	Optional, x label, see plot
ylab	Optional, y label, ee plot
SingleGausses	Optional, SingleGausses=T than components of the mixture in blue will be shown.
...	Optional, see plot for plot properties and for SingleGausses PlotMixtures

Author(s)

Michael Thrun

See Also

[BayesDecisionBoundaries,PlotMixtures](#)

QQplotGMM

Quantile Quantile Plot of Data

Description

Quantile Quantile plot of data against gaussian distribution mixture model with optional best-fit-line

Usage

QQplotGMM(Data, Means, SDs, Weights, IsLogDistribution, Line, PlotSymbol, xug, xog, LineWidth, PointWidth, ylab, main, ...)

Arguments

Data	vector (1:N) of data points
Means	vector[1:L] of Means of Gaussians (of GMM),L == Number of Gaussians
SDs	vector of standard deviations, estimated Gaussian Kernels, has to be the same length as Means
Weights	vector of relative number of points in Gaussians (prior probabilities), has to be the same length as Means
IsLogDistribution	Optional, ==1 if distribution(i) is a LogNormal, default Zeros of Length L
Line	Optional, Default: TRUE=Regression Line is drawn
xug	Optional, lower limit of the interval [xug, xog], in which a line will be interpolated

xog	Optional, upper limit of the interval [xug, xog], in which a line will be interpolated
PlotSymbol	Optional, plot symbol. Default is 20.
LineWidth	Optional, width of regression line, if Line==TRUE
PointWidth	Optional, width of points
ylab	Optional, see plot
main	Optional, see plot
...	Note: xlab cannot be changed, other parameters see qqplot

Details

Only verified for a Gaussian Mixture Model, usage of IsLogDistribution for LogNormal Modes is experimental!

Value

List with

x	The x coordinates of the points that were plotted
y	The original data vector, i.e., the corresponding y coordinates

Author(s)

Michael Thrun

References

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

See Also

[qqplot](#)

Examples

```
data=c(rnorm(1000),rnorm(2000)+2,rnorm(1000)*2-1)
QQplotGMM(data,c(-1,0,2),c(2,1,1),c(0.25,0.25,0.5))
```

RandomLogGMM

Random Number Generator for Log or Gaussian Mixture Model

Description

Function finds the intersections of Gaussians or LogNormals

Usage

RandomLogGMM(Means,SDs,Weights,IsLogDistribution,TotalNoPoints)

Arguments

Means	vector[1:L] of Means of Gaussians (of GMM)
SDs	vector of standard deviations, estimated Gaussian Kernels, has to be the same length as Means
Weights	vector of relative number of points in Gaussians (prior probabilities), has to be the same length as Means
IsLogDistribution	Optional, ==1 if distribution(i) is a LogNormal, default vector of Zeros of Length L
TotalNoPoints	Optional, number of point for log or GMM generated

Value

Returns vector of [1:TotalNoPoints] of genrated points for log oder gaussian mixture model

Author(s)

Alfred Ultsch,Michael Thrun, Rabea Griese

See Also

[QQplotGMM](#),[Chi2testMixtures](#)

Symlognpdf

computes a special case of log normal distribution density

Description

Symlognpdf is an internal function for **AdaptLGL**.

Usage

Symlognpdf(Data, Mean, SD)

Arguments

Data	vector of data points used for sampling
Mean	Mean of log Gaussian
SD	Standard deviation of log Gaussian

Value

M>0 Log normal distribution density

M<0 Log normal distribution density mirrored at y axis

Note

not for external usage.

See Also

[AdaptLGL](#)

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