

# Package ‘macat’

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**Title** MicroArray Chromosome Analysis Tool

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**Suggests** hgu95av2.db, stjudem

**Description** This library contains functions to investigate links between differential gene expression and the chromosomal localization of the genes. MACAT is motivated by the common observation of phenomena involving large chromosomal regions in tumor cells. MACAT is the implementation of a statistical approach for identifying significantly differentially expressed chromosome regions. The functions have been tested on a publicly available data set about acute lymphoblastic leukemia (Yeoh et al.Cancer Cell 2002), which is provided in the library 'stjudem'.

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**License** Artistic-2.0

**biocViews** Microarray, DifferentialExpression, Visualization

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Auxiliary Computation Functions . . . . .	2
buildMACAT . . . . .	3
compute.sliding . . . . .	4
discreteKernelize . . . . .	5
discretize . . . . .	6
discretize.tscores . . . . .	7
discretizeAll . . . . .	8
evalScoring . . . . .	9
evaluateParameters . . . . .	11
getResults . . . . .	13
html . . . . .	14
kernelize . . . . .	15
kernelizeAll . . . . .	16
kernelizeToPython . . . . .	17
Kernels . . . . .	18
loaddatapkg . . . . .	19
plot.MACATevalScoring . . . . .	20
preprocessedLoader . . . . .	21
Python data format . . . . .	22
scoring . . . . .	23
stjd . . . . .	24
<b>Index</b>	<b>26</b>

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Auxiliary Computation Functions

*Auxiliary Functions for Computations in MACAT*

---

**Description**

Auxiliary functions for internal usage by other MACAT functions. Normally not called by user.

**Details**

Internal auxiliary functions. Not called by user.

**Author(s)**

MACAT development team

**See Also**

[evalScoring](#)

---

buildMACAT	<i>Create MACAT list from objects in workspace</i>
------------	--

---

### Description

This is a wrapper around the `preprocessedLoader` function. Use it, when you want to build a MACAT-list structure from objects already in your workspace.

### Usage

```
buildMACAT(matrix, chip, labels = NULL, chromLocObj = NULL)
```

### Arguments

<code>matrix</code>	expression matrix with rows=genes and columns=samples; Rownames have to match chip; Columnnames are not mandatory.
<code>chip</code>	Identifier for used microarray
<code>labels</code>	Classlabels for samples, has to have length=number of columns in matrix
<code>chromLocObj</code>	Object of class <code>chromLocation</code> specifying the genomic position, each probe on the array is mapped to. If not provided, it is build in the function using <code>annotate</code> 's function <code>buildChromLocation</code> .

### Details

This is only a convenience wrapper around the function [preprocessedLoader](#) for the case, that you want to build a MACAT-list from objects in your workspace.

### Value

A MACAT-list structure. For an example and a description of the format see `data st jude` in package `'stjudem'`.

### Author(s)

MACAT development team

### See Also

[preprocessedLoader](#), `st jude` in package `'stjudem'`

### Examples

```
X <- matrix(rnorm(200),nrow=20,ncol=10)
rownames(X) <- c('34916_s_at', '34917_at', '34462_at', '163_at', '35219_at',
'31641_s_at', '33300_at', '33301_g_at', '38950_r_at', '41249_at',
'294_s_at', '32004_s_at', '33299_at', '41243_at', '33341_at', '362_at',
'1918_at', '41499_at', '41500_at', '41282_s_at')
colnames(X) <- paste("Sample", 1:10, sep="")
```

```

y <- rep(c("A","B"),c(5,5))
toy <- buildMACAT(X,"hgu95av2.db",y)
summary(toy)

```

---

compute.sliding	<i>Compute and plot smoothing of expression values or scores along the chromosome</i>
-----------------	---

---

### Description

'compute.sliding' computes a smoothing of the expression data or scores along the chromosome using the specified kernel function. This function is also used within the 'evalScoring' function. 'plotSliding' creates a plot of the smoothed expression values / scores.

### Usage

```

compute.sliding(data, chromosome, sample, kernel, kernelparams=NULL, step.width = 1e+06)
plotSliding(data, chromosome, sample, kernel, kernelparams=NULL,
step.width=1000000, ...)

```

### Arguments

data	A MACATData list holding the Expression values and gene locations
chromosome	the chromosome to be smoothed
sample	the sample (patient) whose expression values are smoothed
kernel	a kernel function (one of rbf, kNN, basePairDistance or your own)
kernelparams	a list of named parameters for the kernel (by default estimated from the data)
step.width	the smoothing is computed stepwise every step.width basepairs (default is 100000)
...	further graphical parameters passed on to <a href="#">plot.default</a>

### Value

for compute.sliding: a matrix of dimension (steps x 2) with in the first column the locations in basepairs where an interpolation is computed, and in the second column the smoothed values. plotSliding does not return anything and is merely called for its side-effect producing the plot.

### Author(s)

MACAT development team

### See Also

[kernelize](#), [evalScoring](#)

## Examples

```
data(stjd)
# just compute smoothed values:
smooth = compute.sliding(stjd, chromosome=3, sample=6, rbf,
                        kernelparams=list(gamma=1/10^13))
# compute and plot smoothed values:
plotSliding(stjd, chromosome=3, sample=6, rbf,
            kernelparams=list(gamma=1/10^13), pch=20,
            main="Chromosome 3")
```

---

discreteKernelize      *Discretize and smooth expression values*

---

## Description

returns discretized kernelized expression values and saves them to a file if argument 'saveToFile' is TRUE. For details on discretization see [discretize](#).

## Usage

```
discreteKernelize(data, chrom, margin = 10, step.width = 1e+05, kernel = rbf,
                 kernelparams = list(gamma = 1/10^13), saveToFile = FALSE)
```

## Arguments

data	MACATData Object
chrom	chromosome to kernelize
margin	symmetric quantile in percent
step.width	size of the interpolation steps
kernel	kernel function one of rbf, kNN, basePairDistance or your own
kernelparams	list of named kernel parameters
saveToFile	logicval indicating whether to write a flatfile or not; default is FALSE

## Details

Filename of the flatfile is: discrete\_kernelized\_seq\_margin\_<margin>\_chrom\_<chrom>.py where <margin> is the discretization parameter and <chrom> the name of the chromosome.

## Value

discretized and kernelized expression matrix

## Author(s)

The MACAT Development team

**See Also**[pydata](#), [kernelizeAll](#)**Examples**

```
#loaddatapkg("stjudem")
#data(stjude)
data(stjd)
discretizedKernelized = discreteKernelize(stjd, 13)
```

---

**discretize***Discretize expression values*

---

**Description**

'discretize' returns the discretized expression data for all chromosomes in `chrom` and all samples that have a label listed in `label`. Discretization is performed by comparing the value gene-wise (location-wise) with the symmetric upper and lower quantile given by `margin` (in percent `margin/2` lower and upper quantile).

**Usage**

```
discretize(data, chrom, label, margin = 10)
discretizeChromosome(data, chrom, margin=10)
discretizeOne(data, chrom, sample, margin=10)
```

**Arguments**

<code>data</code>	MACATData object
<code>chrom</code>	list of chromosomes
<code>label</code>	list of labels
<code>margin</code>	symmetric quantile in percent
<code>sample</code>	the sample for which you want discretized expression data

**Value**

returns a discretized expression matrix for all genes on the chromosomes in `'chrom'` and all samples that have a label in `'label'`.

**Author(s)**

MACAT development team

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

---

discretize.tscores      *Discretize regularized t-scores*

---

### Description

discretize.tscores returns a discretized version of the scores in the MACATevalScoring object. Discretization is performed by comparing the value gene-wise (location-wise) with the symmetric upper and lower quantile given by margin (in percent margin/2 lower and upper quantile). discretizeAllClasses produces a flatfile readable by PYTHON.

### Usage

```
discretize.tscores(scores)
discretizeAllClasses.tscores(data, chrom, nperms=10, kernel=rbf, kernelparams=NULL, step.width=100000)
```

### Arguments

scores	a MACATevalScoring object obtained from evalScoring
data	a MACATData Object containing all expression values, geneLocations and labels (obtained from preprocessedLoader)
chrom	chromosome that is discretized
nperms	number of permutations for the computation of empirical p values (evalScoring)
kernel	kernel function used for smoothing one of rbf, kNN, basePairDistance or your own
kernelparams	list of parameters for the kernels
step.width	size of a interpolation step in basepairs

### Details

The filename for the python flat files are discrete\_chrom\_<chrom>\_class\_<label>.py where <chrom> and <label> are the names of the chromosome and class label.

### Value

discretize.tscores  
   a vector of discretized tscores  
 discretizeAllClasses.tscores  
   creates python flatfiles (see details)

### Author(s)

The MACAT development team

### See Also

[evalScoring](#), [kernels](#), [pythondata](#)

## Examples

```
#loaddatapkg("stjudem")
#data(stjude)
data(stjd)
# simple scoring with short running time
scores = evalScoring(stjd, "T", 1, nperms=100, cross.validate=FALSE)
discrete = discretize.tscores(scores)
```

---

discretizeAll

*Discretize complete expression matrix*

---

## Description

perform discretization on all chromosomes and write python flat files

## Usage

```
discretizeAll(data, margin = 10)
```

## Arguments

data	MACATData Object
margin	symmetric quantile in percent

## Details

The filename for the python flat files are `discrete_seqs_margin_<margin>_chrom_<chrom>.py` where `<chrom>` and `<margin>` are the names of the chromosome and the margin used for discretization. For details on the discretization see [discretize](#).

## Value

produces python flat file

## Author(s)

The MACAT Development team

## See Also

[discretize](#)



**Examples**

```
# !!! takes some time !!!
## Not run:
#loaddatapkg("stjudem")
#data(stjude)
data(stjd)
discretizeAll(stjd, margin=10)

## End(Not run)
```

---

evalScoring	<i>Score differential expression, assess significance, and smooth scores along the chromosome</i>
-------------	---

---

**Description**

This function computes for all genes on one chromosome the regularized t-statistic to score differential gene expression for two given groups of samples. Additionally these scores are computed for a number of permutations to assess significance. Afterwards these scores are smoothed with a given kernel along the chromosome to give scores for chromosomal regions.

**Usage**

```
evalScoring(data, class, chromosome, nperms=1000, permute="labels",
            pcompute="empirical", subset=NULL,
            newlabels=NULL, kernel=rbf, kernelparams=NULL, cross.validate=TRUE,
            paramMultipliers=2^(-4:4), ncross=10, step.width=100000,
            memory.limit=TRUE, verbose=TRUE)
```

**Arguments**

data	Gene expression data in the MACAT list format. See data(stjude) for an example.
class	Which of the given class labels is to be analyzed
chromosome	Chromosome to be analyzed
nperms	Number of permutations
permute	Method to do permutations. Default 'labels' does permutations of the class labels, which is the common and faster way to assess significance of differential expression. The alternative 'locations' does permutations of gene locations, is much slower and right now should be considered preliminary at best.
pcompute	Method to determine the p-value for differential expression of each gene. Is only evaluated if the argument permute='labels' and in that case passed on to the function scoring
subset	If a subset of samples is to be used, give vector of column- indices of these samples in the original matrix here.

<code>newlabels</code>	If other labels than the ones in the MACAT-list-structure are to be used, give them as character vector/factor here. Make sure argument 'class' is one of them.
<code>kernel</code>	Choose kernel to smooth scores along the chromosome. Available are 'kNN' for k-Nearest-Neighbors, 'rbf' for radial-basis-function (Gaussian), 'basePairDistance' for a kernel, which averages over all genes within a given range of base pairs around a position.
<code>kernelparams</code>	Additional parameters for the kernel as list, e.g., <code>kernelparams=list(k=5)</code> for taking the 5 nearest neighbours in the kNN-kernel. If NULL some defaults are set within the function.
<code>cross.validate</code>	Logical. Should the parameter settings for the kernel function be optimized by a cross-validation?
<code>paramMultipliers</code>	Numeric vector. If you do cross-validation of the kernel parameters, specify the multipliers of the given (standard) parameters to search over for the optimal one.
<code>ncross</code>	Integer. If you do cross-validation, specify how many folds.
<code>step.width</code>	Defines the resolution of smoothed scores on the chromosome, is in fact the distance in base pairs between 2 positions, for which smoothed scores are to be calculated.
<code>memory.limit</code>	If you have a computer with lots of RAM, setting this to FALSE will increase speed of computations.
<code>verbose</code>	logical; should function's progress be reported to STDOUT ?; default: TRUE.

## Details

Please see the package vignette for more details on this function.

## Value

List of class 'MACATEvalScoring' with 11 components:

<code>original.geneid</code>	Gene IDs of the genes on the chosen chromosome, sorted according to their position on the chromosome
<code>original.loc</code>	Location of genes on chromosome in base pairs from 5' end
<code>original.score</code>	Regularized t-score of genes on chromosome
<code>original.pvalue</code>	Empirical p-value of genes on chromosome. How often was a higher score observed than this one with random permutations? In other words, how significant seems this score to be?
<code>steps</code>	Positions on the chromosome in bp from 5', for which smoothed scores have been computed.
<code>sliding.value</code>	Smoothed regularized t-scores at step-positions.
<code>lower.permuted.border</code>	Smoothed scores from permutations, lower significance border, currently 2.5%-quantile of permutation scores.

```

upper.permuted.border      Smoothed scores from permutations, upper significance border, currently 97.5%-
                           quantile of permutation scores.
chromosome                 Chromosome, which has been analyzed
class                     Class, which has been analyzed
chip                       Identifier for used microarray

```

**Author(s)**

MACAT development team

**See Also**

[scoring](#), [plot.MACATevalScoring](#), [getResults](#)

**Examples**

```

data(stjd) # load example data

# if you have the data package 'stjudem' installed,
# you should work on the full data therein, of which
# the provided example data, is just a piece
#loaddatapkg("stjudem")
#data(stjude)

# T-lymphocyte versus B-lymphocyte on chromosome 1,
# smoothed with k-Nearest-Neighbours kernel(k=15),
# few permutations for higher speed
chrom1Tknn <- evalScoring(stjd,"T",chromosome="1",permute="labels",
nperms=100,kernel=kNN,kernelparams=list(k=15),step.width=100000)

# plotting on x11:
if (interactive())
  plot(chrom1Tknn)

# plotting on HTML:
if (interactive())
  plot(chrom1Tknn,"html")

```

---

evaluateParameters      *Evaluate Performance of Kernel Parameters by Cross-validation*

---

**Description**

For a given data set, chromosome, class, and kernel function, this function helps in determining optimal settings for the kernel parameter(s). The performance of individual parameter setting is assessed by cross- validation.

**Usage**

```
evaluateParameters(data, class, chromosome, kernel, kernelparams = NULL,
                  paramMultipliers = 2^(-4:4), subset = NULL,
                  newlabels = NULL, ncross = 10, verbose = TRUE)
```

**Arguments**

data	Gene expression data in the MACAT list format. See data(stjude) for an example.
class	Sample class to be analyzed
chromosome	Chromosome to be analyzed
kernel	Choose kernel to smooth scores along the chromosome. Available are 'kNN' for k-Nearest-Neighbors, 'rbf' for radial-basis-function (Gaussian), 'basePairDistance' for a kernel, which averages over all genes within a given range of base pairs around a position.
kernelparams	Additional parameters for the kernel as list, e.g., kernelparams=list(k=5) for taking the 5 nearest neighbours in the kNN-kernel. If NULL some defaults are set within the function.
paramMultipliers	Numeric vector. If you do cross-validation of the kernel parameters, specify these as multipliers of the given (standard) kernel parameter, depending on your kernel choice (see page 5 of the vignette). The multiplication results are the kernel argument settings, among which you want to search for the optimal one using cross-validation.
subset	If a subset of samples is to be used, give vector of column- indices of these samples in the original matrix here.
newlabels	If other labels than the ones in the MACAT-list-structure are to be used, give them as character vector/factor here. Make sure argument 'class' is one of them.
ncross	Integer. Specify how many folds in cross-validation.
verbose	Logical. Should progress be reported to STDOUT?

**Value**

A list of class 'MACATevP' with 4 components:

[parameterName]	List of assessed settings for the parameter [parameterName].
avgResid	Average Residual Sum of Squares for the parameter settings in the same order as the first component.
multiplier	Multiplier of the original parameters in the same order as the first components.
best	List of parameter settings considered optimal by cross- validation. Can be directly inserted under the argument 'kernelparams' of the 'evalScoring' function.

**Author(s)**

MACAT development team

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

```

data(stjd)
evalkNN6 <- evaluateParameters(stjd, class="T", chromosome=6, kernel=kNN,
                             paramMultipliers=c(0.01, seq(0.2, 2.0, 0.2), 2.5))
if (interactive() && capabilities("X11"))
  plot(evalkNN6)

```

---

<code>getResults</code>	<i>Access results of 'evalScoring'</i>
-------------------------	--

---

**Description**

This function processes the result of the `evalScoring` function and returns a list of probe sets within chromosome regions deemed significant by MACAT. Additional annotation for these probe sets is provided along with their identifiers.

**Usage**

```
getResults(MACATevalScoringOBJ)
```

**Arguments**

MACATevalScoringOBJ  
Object of class `MACATevalScoring`, usually the result from `evalScoring`

**Details**

The p-values have been computed individually for probe sets (genes), not for whole chromosome regions. Thus, regions deemed significant by sliding window approach do not have to consist only of probe sets with low p-values. These probe-set p-values are not used to determine whether a region is considered significant or not. Instead the comparison between actual and interpolated scores to actual and interpolated boundaries determines whether a region is considered significant.

This function is called within the `plot` function for the results of `evalScoring`, when HTML output is desired.

**Value**

A list with the following components, describing probe sets within chromosome regions deemed significant:

probeID	IDs of probe sets within these chromosome regions
cytoband	chromosomal bands these probe sets have been annotated to
geneSYM	gene symbols these probe sets have been annotated to

pvalue	p-values for probe sets; see details
locusid	EntrezGene-(formerly LocusLink) IDs of these probe sets
genedescription	Description of genes the probe sets have been annotated to
probeScore	the differential expression scores for the probe sets
chromosome	chromosome, the analysis has been done for
class	sample class, the analysis has been done for

**Author(s)**

MACAT development team

**See Also**

[evalScoring](#)

**Examples**

```
data(stjd)
myevalres <- evalScoring(stjd, class="T", chromosome=6, nperms=10,
                        cross.validate=FALSE)
results <- getResults(myevalres)
summary(results)
results$probeID[1:20]
```

---

html

*HTML functions for MACAT.*

---

**Description**

HTML functions for internal usage by other MACAT functions. Normally not called by user.

**Details**

Internal HTML functions. Not called by user.

**Author(s)**

MACAT development team

**See Also**

[plot.MACATevalScoring](#)

---

kernelize	<i>Smooth expression values or scores</i>
-----------	---

---

### Description

'kernelize' uses a kernel to smooth the data given in geneLocations by computing a weighted sum of the values vector. The weights for each position are given in the kernelweights matrix. A kernelweights matrix can be obtained by using the kernelmatrix function.

### Usage

```
getsteps(geneLocations, step.width)
kernelmatrix(steps, geneLocations, kernel, kernelparams)
kernelize(values, kernelweights)
```

### Arguments

geneLocations	a list of gene locations (length n)
step.width	the width of steps in basepairs
steps	a list of locations where the kernelization shall be computed
kernel	kernel function one of rbf, kNN or basePairDistance (or your own)
kernelparams	a list of named parameters for the kernel (default is fitted to the data)
values	vector of length n or matrix (m x n) of values that are to be smoothed
kernelweights	a matrix of (n x steps) where n is the length of the values vector and steps is the number of points where you wish to interpolate

### Value

getsteps	a list of locations starting at min(geneLocations) going to max(geneLocations) with steps of size step.width
kernelmatrix	a matrix of (n x steps) containing the kernel weights for each location in steps
kernelize	a vector of length steps or a matrix (m x steps) containing the smoothed values

### Author(s)

MACAT Development team

### See Also

[compute.sliding](#), [evalScoring](#)

## Examples

```
data(stjd)
genes = seq(100)
geneLocations = abs(stjd$geneLocation[genes])
geneExpression = stjd$expr[genes,]
step.width = 100000
steps = getsteps(geneLocations, step.width)
weights = kernelmatrix(steps, geneLocations, rbf, list(gamma=1/10^13))
kernelized = kernelize(geneExpression, weights)
plot(steps, kernelized[1,])
```

---

kernelizeAll

*Smooth expression data for all chromosomes*

---

## Description

'kernelizeAll' smoothes complete expression matrix and writes the result into one text file for each chromosome. These text files can be read into Python.

## Usage

```
kernelizeAll(data, step.width = 1e+05, kernel = rbf,
             kernelparams = list(gamma = 1/10^13))
```

## Arguments

data	MACATData Object
step.width	size of steps for kernelization
kernel	kernel function one of rbf, kNN, basePairDistance or your own
kernelparams	list of named kernel parameters

## Details

filename of the python flatfiles: kernelized\_seq\_chrom\_<chrom>.py where <chrom> is the name of the chromosome.

## Value

does not return anything; called for its side-effect that is to produce Python-readable text files

## Author(s)

The MACAT Development Team

## See Also

[pydata](#), [kernelizeToPython](#)



**Examples**

```

## Not run:
# !!! takes quite some time !!!
loadDatapkg("stjudem")
data(stjude)
kernelizeAll(stjude)

## End(Not run)

```

---

kernelizeToPython      *Smooth expression values and write to file*

---

**Description**

Smooths expression data for one chromosome and writes the result into a text file, which can be read into PYTHON, or returns it without writing. 'kernelizeToPython' is the one-chromosome version of [kernelizeAll](#).

**Usage**

```

kernelizeToPython(data, chrom, step.width = 1e+05, kernel = rbf,
                  kernelparams = list(gamma = 1/10^13), saveToFile = TRUE)

```

**Arguments**

data	MACATData Object
chrom	kernelize all genes that are on this chromosome
step.width	width of interpolation steps
kernel	kernel function one of rbf, kNN, basePairDistance or your own
kernelparams	list of named kernel parameters
saveToFile	logical indicating whether to save as flat file or not

**Details**

filename of the flatfile: kernelized\_seq\_chrom\_<chrom>.py where <chrom> is the name of the chromosome.

**Value**

returns kernelized expression matrix

**Author(s)**

The MACAT Development team

**See Also**

[pydata](#), [kernelizeAll](#)

**Examples**

```
## Not run:
data(stjd)
kernelized = kernelizeToPython(stjd, 3)

## End(Not run)
```

---

Kernels

*various kernel functions for computations in MACAT*

---

**Description**

Various Kernel functions for computations in MACAT. Normally not called by user. All kernel functions have the same arguments in the same order!!!

**Usage**

```
kNN(geneLocations, position, params)
rbf(geneLocations, position, params = list(gamma=1/10^13))
basePairDistance(geneLocations, position, params = list(distance = 1e+06))
```

**Arguments**

geneLocations	Location of genes
position	Position on chromosome
params	special kernel parameters

**kNN:** k = number of nearest genes  
**rbf:** gamma = kernel width  
**basePairDistance:** distance = distance within which all genes are averaged

**Details**

For internal use by other MACAT-functions. Not called by user.

**Value**

returns kernel weight for position, computed from the geneLocations

**Author(s)**

MACAT development team

**See Also**

[evalScoring](#), [compute.sliding](#), [kernelize](#)

**Examples**

```
data(stjd)
genes = seq(100)
geneLocations = abs(stjd$geneLocation[genes])
position = c(1000) # location for which you want the kernelweights
kernelweights = rbf(as.matrix(geneLocations), as.matrix(position),
  list(gamma=1/10e13))
hist(kernelweights)
```

---

loaddatapkg

*Load data package*

---

**Description**

This function loads the data package, you need for seeing the demo and the examples. If you have already installed the data package, it will simply attach it via `library`. Otherwise it will try to download and install the package using functions from the package

**Usage**

```
loaddatapkg(mydatapkg, installDir=.libPaths()[1])
```

**Arguments**

<code>mydatapkg</code>	Name of the data package to load as String
<code>installDir</code>	Directory, into which the new package will be installed, if is not already installed. Defaults to the first entry of the standard installation paths.

**Note**

The package `stjudem` by now is a Bioconductor example data package, too. Thus, you can also install with the following command: `BiocManager::install('stjudem')`

**Author(s)**

Joern Toedling

**See Also**

[install.packages](#)

**Examples**

```
## Not run: loaddatapkg("stjudem") # to load the data package "stjudem"
```

---

plot.MACATevalScoring *Plot function for MACATevalScoring objects.*

---

### Description

Function plots scores, 0.025 and 0.975 quantiles of the permuted scores (grey lines), and sliding average score (red line) along the chromosome. Yellow dots highlight regions, in which the smoothed absolute scores exceed the permutation-derived quantile boundaries.

### Usage

```
## S3 method for class 'MACATevalScoring'  
plot(x, output = "x11",  
      HTMLfilename = NULL, mytitle = NULL, new.device = TRUE, ...)
```

### Arguments

x	MACATevalScoring object.
output	plot "x11" or create a "html" -file with further information. HTML-page will open automatically.
HTMLfilename	HTML-filename, default:Results<CHOMOSOME>_<CLASS>.html
mytitle	Title of HTML-page, default: "Results of class <CLASS> on chromosome <CHROMOSOME>"
new.device	if FALSE: Possibility to plot several plots in one device
...	further arguments passed on to generic function plot

### Details

One can create a HTML-page on-the-fly if argument output='html'. The HTML-page provides informations about highlighted regions in the plot. Furthermore there are click-able Entrezgene-IDs for further analysis.

### Author(s)

MACAT development team

### See Also

[evalScoring](#), [getResults](#)

### Examples

```
# see function 'evalScoring' for an example
```

---

```
preprocessedLoader      Read in data and produce MACAT list
```

---

### Description

This function reads expression data either from a saved R-file (.RData,.rda), or from a tab-separated text-file (.xls). For building a MACAT-list structure from objects in your workspace, you can either use this function or the convenience wrapper 'buildMACAT'.

### Usage

```
preprocessedLoader(rdatafile, chip, labels = NULL, chromLocObj = NULL,
  rdatafile = TRUE, tabfile = FALSE, labelfile = FALSE)
```

### Arguments

rdatafile	Complete name of the expression data file, or the expression matrix
chip	Identifier of the used microarray. To date only commercial Affymetrix microarrays are supported by MACAT
labels	Classlabels of the samples, vector of same length as number of columns in expression matrix; alternatively complete name of textfile with one label per line
chromLocObj	Object of class chromLocation specifying the genomic position, each probe on the array is mapped to. If not provided, it is build in the function using annotate's function buildChromLocation.
rdatafile	Logical; is first argument a saved R-file?
tabfile	Logical; is first argument a tab-separated text file?
labelfile	Logical; is third argument a file with one label per line?

### Value

List of class 'MACATData' with 6 components:

geneName	Identifiers of genes/probe sets in expression data
geneLocation	Location of genes on their chromosome as distance from 5'end in base pairs Negative numbers denote genes on the antisense strand.
chromosome	Chromosome of the respective gene. Components 'geneName', 'geneLocation', and 'chromosome' are in the same order.
expr	expression matrix with rows = genes and columns = samples/patients
labels	(disease) subtype of each sample, has length = number of columns of expression matrix
chip	Identifier for Microarray used for the experiments

**Note**

At present, `macat` can only work with Affymetrix microarrays, for which an annotation package is installed on your system. Such annotation packages can either be obtained from the Bioconductor annotation packages repository or be constructed using the Bioconductor package `AnnBuilder`. For an example, see the common annotation package `hgu95av2`.

**Author(s)**

MACAT development team

**See Also**

`buildMACAT`, `read.table`, `stjd`, `stjude` in package `'stjudem'`

**Examples**

```
## Not run:
# assume you have your HG-U95Av2 expression values in a
# tab-separated text file, called 'foo.txt'
mydata <- preprocessedLoader("foo.txt", "hgu95av2", rdafile=FALSE, tabfile=TRUE)

## End(Not run)
```

---

Python data format      *Flat file format*

---

**Description**

This is a description of the text files, usually written by MACAT functions such as `kernelizeToPython`. These text files can be read into PYTHON. Each flat files contains a list of matrices. The outer list has one entry for each class in the data set, the inner matrices consist of all the sequences from the specified chromosome belonging to that class. Each row represents one sample, each column a gene from the respective chromosome.

The lists are delimited by '[' and ']' brackets. The matrices are written as lists of lists (e.g. `[[[],[],...,[]]`).

**Examples**

```
# The files look like this:
# [ [[1.11, 1.32, 0.92, ...],[...],[...]],
#   [[0.45, 0.91, 1.84, ...],[...],[...]],
#   [[1.06, 1.59, 0.73, ...],[...],[...]],
# ]
```

---

scoring	<i>Compute (regularized) t-scores for gene expression data</i>
---------	--

---

### Description

This function computes for all genes in an expression matrix the (regularized) t-scores (statistics) with the given class labels and a number of permutations of these labels. Each gene is also assigned a p-value either empirically from the permutation scores or from a t-distribution.

### Usage

```
scoring(data, labels, method = "SAM", pcompute = "tdist",
        nperms = 1000, memory.limit = TRUE, verbose = TRUE)
```

### Arguments

data	Expression matrix with rows = genes and columns = samples
labels	Vector or factor of class labels; Scoring works only with two classes!
method	Either "SAM" to compute regularized t-scores, or "t.test" to compute Student's t-statistic
pcompute	Method to compute p-values for each genes, either "empirical" to do permutations and compute p-values from them, or "tdist" to compute p-values based on respective t-distribution
nperms	Number of permutations of the labels to be investigated, if argument 'pcompute="empirical"'
memory.limit	Logical, if you have a really good computer (>2GB RAM), setting this FALSE will increase speed of computations
verbose	Logical, if progress should be reported to STDOUT

### Details

If 'pcompute="empirical"', the statistic is computed based on the given class labels, afterwards for 'nperms' permutations of the labels. The p-value for each gene is then the proportion of permutation statistics that are higher or equal than the statistic from the real labels. For each gene the 2.5%- and the 97.5%-quantile of the permutation statistics are also returned as lower and upper 'significance threshold'.

If 'pcompute="tdist"', the statistic is computed only based on the given class labels, and the p-value is computed from the t-distribution with (Number of samples - 2) degrees of freedom.

### Value

A list, with four components:

observed	(Regularized) t-scores for all genes based on the given labels
pvalues	P-values for all genes, either from permutations or t-distribution

`expected.lower` 2.5%-quantile of permutation test-statistics, supposed to be a lower 'significance border' for the gene; or NULL if p-values were computed from t-distribution

`expected.upper` 97.5%-quantile of permutation test-statistics, supposed to be an upper 'significance border' for the gene; or NULL if p-values were computed from t-distribution

### Note

In package `macat`, this function is only called internally by the function `evalScoring`

### Author(s)

MACAT development team

### References

Regarding the regularized t-score please see the `macat` vignette.

### See Also

`evalScoring`

### Examples

```
data(stjd)
# compute gene-wise regularized t-statistics for
# T- vs. B-lymphocyte ALL:
isT <- as.numeric(stjd$labels=="T")
TvsB <- scoring(stjd$expr,isT,method="SAM",pcompute="none")
summary(TvsB$observed)
```

---

<code>stjd</code>	<i>Subset Microarray Data from St.Jude Children Research Hospital (USA)</i>
-------------------	---

---

### Description

Example for list-structure used by many functions in `MACAT`. It's based on the gene expression data published by Yeoh et al. (2002) The data has been preprocessed using `'vsn'` on probe level and the probe values have been summed up to probe set values using the `'median polish'` procedure. This is a subset of the data, containing only the data for the 5000 probe sets with the highest variance across the samples and for 10 exemplary samples, 5 from T-lymphocytic Acute Lymphocytic Leukemia (ALL) and 5 from B-lymphocytic ALL.

### Usage

```
data(stjd)
```



**Format**

List of class 'MACATData' with 6 components:

**geneName:** Identifiers of genes/probe sets in expression data

**geneLocation:** Location of genes on their chromosome as distance from 5' end in base pairs Negative numbers denote genes on the antisense strand.

**chromosome:** Chromosome of the respective gene. Components 'geneName', 'geneLocation', and 'chromosome' are in the same order.

**expr:** expression matrix with rows = genes and columns = samples/patients

**labels:** (disease) subtype of each sample, has length = number of columns of expression matrix

**chip:** Identifier for Microarray used for the experiments (here for the Affymetrix HG-U95av2 Oligonucleotide GeneChip)

**Note**

For the full data package see the Bioconductor data package `stjudem`. If it is not already installed on your system, try `if (!requireNamespace("BiocManager", quietly=TRUE)); install.packages("BiocManager"); BiocManager::install("stjudem")`

**References**

Yeoh et al. Classification, subtype discovery, and prediction of outcome in pediatric acute lymphoblastic leukemia by gene expression profiling. *Cancer Cell*. March 2002. 1: 133-143.

**See Also**

[buildMACAT](#), `stjude` in package 'stjudem' for the complete expression data

**Examples**

```
data(stjd)
summary(stjd)
```

# Index

- \* **datasets**
  - stjd, [24](#)
- \* **file**
  - preprocessedLoader, [21](#)
- \* **hplot**
  - plot.MACATevalScoring, [20](#)
- \* **internal**
  - Auxiliary Computation Functions, [2](#)
  - discretizeAll, [8](#)
  - html, [14](#)
  - kernelizeAll, [16](#)
  - kernelizeToPython, [17](#)
  - Kernels, [18](#)
  - loaddatapkg, [19](#)
  - Python data format, [22](#)
- \* **manip**
  - buildMACAT, [3](#)
  - compute.sliding, [4](#)
  - discreteKernelize, [5](#)
  - discretize, [6](#)
  - discretize.tscores, [7](#)
  - evalScoring, [9](#)
  - evaluateParameters, [11](#)
  - getResults, [13](#)
  - kernelize, [15](#)
  - scoring, [23](#)
- Auxiliary Computation Functions, [2](#)
- basePairDistance (Kernels), [18](#)
- buildMACAT, [3](#), [22](#), [25](#)
- compare.gammas (Auxiliary Computation Functions), [2](#)
- compute.sliding, [4](#), [15](#), [19](#)
- crossvalParam (Auxiliary Computation Functions), [2](#)
- demo.part (Auxiliary Computation Functions), [2](#)
- discreteKernelize, [5](#)
- discretize, [5](#), [6](#), [8](#)
- discretize.tscores, [7](#)
- discretizeAll, [6](#), [8](#)
- discretizeAllClasses.tscores (discretize.tscores), [7](#)
- discretizeChromosome (discretize), [6](#)
- discretizeOne (discretize), [6](#)
- evalParams (Auxiliary Computation Functions), [2](#)
- evalScoring, [2](#), [4](#), [7](#), [9](#), [13–15](#), [19](#), [20](#), [24](#)
- evaluateParameters, [11](#)
- fitkernelparams (Kernels), [18](#)
- getExpression.MACATData (Auxiliary Computation Functions), [2](#)
- getExpressionByChromosome.MACATData (Auxiliary Computation Functions), [2](#)
- getExpressionByClass.MACATData (Auxiliary Computation Functions), [2](#)
- getExpressionByProbeset.MACATData (Auxiliary Computation Functions), [2](#)
- getFromDb (Auxiliary Computation Functions), [2](#)
- getHtml (html), [14](#)
- getResults, [11](#), [13](#), [20](#)
- getsteps (kernelize), [15](#)
- html, [14](#)
- install.packages, [19](#)
- kernelize, [4](#), [15](#), [19](#)
- kernelizeAll, [6](#), [16](#), [17](#), [18](#)
- kernelizeToPython, [16](#), [17](#), [22](#)
- kernelmatrix (kernelize), [15](#)

Kernels, [18](#)  
kernels, [7](#)  
kernels (Kernels), [18](#)  
kNN (Kernels), [18](#)

loaddatapkg, [19](#)  
Loader (preprocessedLoader), [21](#)

MACATData (preprocessedLoader), [21](#)  
MACATinput (preprocessedLoader), [21](#)  
maxDistances (Auxiliary Computation Functions), [2](#)  
myhtml (html), [14](#)

pair.distances (Auxiliary Computation Functions), [2](#)  
plot.default, [4](#)  
plot.MACATevalScoring, [11](#), [14](#), [20](#)  
plot.MACATevP (evaluateParameters), [11](#)  
plotSliding (compute.sliding), [4](#)  
preprocessedLoader, [3](#), [21](#)  
pydata, [6](#), [16](#), [18](#)  
pydata (Python data format), [22](#)  
Python data format, [22](#)  
pythondata, [7](#)  
pythondata (Python data format), [22](#)

rawDataToPython (Auxiliary Computation Functions), [2](#)  
rbf (Kernels), [18](#)  
read.table, [22](#)

saveForPython (Auxiliary Computation Functions), [2](#)  
scoring, [11](#), [23](#)  
slidingAverageAt (Auxiliary Computation Functions), [2](#)  
squaredDist (Auxiliary Computation Functions), [2](#)  
stjd, [22](#), [24](#)

toPython (Auxiliary Computation Functions), [2](#)