

# Package ‘pamr’

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**Title** Pam: prediction analysis for microarrays

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**Author** T. Hastie, R. Tibshirani, Balasubramanian Narasimhan, Gil Chu

**Description** Some functions for sample classification in microarrays

**Maintainer** Rob Tibshirani <tibs@stat.stanford.edu>

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khan *Khan microarray data*

---

### Description

The khan data frame has 2309 rows and 65 columns. These are one of the datasets data used in the Tibshirani et al paper in PNAS on nearest shrunken centroids.

### Details

The first row contains the sample labels. The first two columns of gene ids and names. The remaining values of the matrix are gene expression values.

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pamr.adaptthresh *A function to adaptive choose threshold scales, for use in pamr.train*

---

### Description

A function to adaptive choose threshold scales, for use in pamr.train

### Usage

```
pamr.adaptthresh(object, ntries = 10, reduction.factor = 0.9, full.out = FALSE)
```

### Arguments

object	The result of a call to pamr.train
ntries	Number of iterations to use in algorithm
reduction.factor	Amount by which a scaling is reduced in one step of the algorithm
full.out	Should full output be returned? Default FALSE

## Details

`pamr.adaptthresh` Adaptively searches for set of good threshold scales. The baseline (default) scale is 1 for each class. The idea is that for easy to classify classes, the threshold scale can be increased without increasing the error rate for that class, and resulting in fewer genes needed for the classification rule. The scalings from `pamr.adaptthresh` are then used in `pamr.train`, and `pamr.cv`. The results may be better than those obtained with the default values of `threshold.scale`.

## Author(s)

Trevor Hastie, Robert Tibshirani, Balasubramanian Narasimhan, and Gilbert Chu

## References

Robert Tibshirani, Trevor Hastie, Balasubramanian Narasimhan, and Gilbert Chu. "Diagnosis of multiple cancer types by shrunken centroids of gene expression" PNAS 2002 99:6567-6572 (May 14).

Robert Tibshirani, Trevor Hastie, Balasubramanian Narasimhan, and Gilbert Chu (2002). Class prediction by nearest shrunken centroids, with applications to DNA microarrays. Stanford tech report.

## Examples

```
set.seed(120)
x <- matrix(rnorm(1000*20), ncol=20)
y <- sample(c(1:4), size=20, replace=TRUE)
mydata <- list(x=x, y=y)
mytrain <- pamr.train(mydata)
new.scales <- pamr.adaptthresh(mytrain)

mytrain2 <- pamr.train(mydata, threshold.scale=new.scales)

myresults2 <- pamr.cv(mytrain2, mydata)
```

---

`pamr.batchadjust` *A function to mean-adjust microarray data by batches*

---

## Description

A function to mean-adjust microarray data by batches

## Usage

```
pamr.batchadjust(data)
```

**Arguments**

`data` The input data. A list with components: `x`- an expression genes in the rows, samples in the columns, and `y`- a vector of the class labels for each sample, and `batchlabels`- a vector of batch labels for each sample. This object if the same form as that produced by `pamr.from.excel`.

**Details**

`pamr.batchadjust` does a genewise one-way ANOVA adjustment for expression values. Let  $x(i,j)$  be the expression for gene  $i$  in sample  $j$ . Suppose sample  $j$  in in batch  $b$ , and let  $B$  be the set of all samples in batch  $b$ . Then `pamr.batchadjust` adjusts  $x(i,j)$  to  $x(i,j) - \text{mean}[x(i,j)]$  where the mean is taken over all samples  $j$  in  $B$

**Value**

A data object of the same form as the input data, with `x` replaced by the adjusted `x`

**Author(s)**

Trevor Hastie, Robert Tibshirani, Balasubramanian Narasimhan, and Gilbert Chu

**Examples**

```
set.seed(120)
#generate some data
x <- matrix(rnorm(1000*20), ncol=20)
y <- sample(c(1:4), size=20, replace=TRUE)
batchlabels <- sample(c(1:5), size=20, replace=TRUE)
mydata <- list(x=x, y=factor(y), batchlabels=factor(batchlabels))

mydata2 <- pamr.batchadjust(mydata)
```

---

`pamr.confusion` *A function giving a table of true versus predicted values, from a nearest shrunken centroid fit.*

---

**Description**

A function giving a table of true versus predicted values, from a nearest shrunken centroid fit.

**Usage**

```
pamr.confusion(fit, threshold, extra=TRUE)
```

**Arguments**

`fit` The result of a call to `pamr.train` or `pamr.cv`  
`threshold` The desired threshold value  
`extra` Should the classwise and overall error rates be returned? Default TRUE

**Details**

`pamr.confusion` Gives a cross-tabulation of true versus predicted classes for the fit returned by `pamr.train` or `pamr.cv`, at the specified threshold.

**Author(s)**

Trevor Hastie, Robert Tibshirani, Balasubramanian Narasimhan, and Gilbert Chu

**Examples**

```
set.seed(120)
x <- matrix(rnorm(1000*20), ncol=20)
y <- sample(c(1:4), size=20, replace=TRUE)
mydata <- list(x=x, y=y)
mytrain <- pamr.train(mydata)
mycv <- pamr.cv(mytrain, mydata)
pamr.confusion(mytrain, threshold=2)
pamr.confusion(mycv, threshold=2)
```

---

```
pamr.confusion.survival
```

*Compute confusion matrix from pamr survival fit*

---

**Description**

computes confusion matrix for (survival.time,censoring) outcome based on fit object "fit" and class predictions "yhat" soft response probabilities for (survival.time,censoring) are first estimated using Kaplan-Meier method applied to training data

**Usage**

```
pamr.confusion.survival(fit, survival.time, censoring.status, yhat)
```

**Arguments**

<code>fit</code>	The result of a call to <code>pamr.train</code> or <code>pamr.cv</code>
<code>survival.time</code>	Survival time
<code>censoring.status</code>	censoring status
<code>yhat</code>	class predictions

**Author(s)**

Trevor Hastie, Robert Tibshirani, Balasubramanian Narasimhan, and Gilbert Chu

pamr.cv

*A function to cross-validate the nearest shrunken centroid classifier***Description**

A function to cross-validate the nearest shrunken centroid classifier produced by pamr.train

**Usage**

```
pamr.cv(fit, data, nfold = NULL, folds = NULL, ...)
```

**Arguments**

fit	The result of a call to pamr.train
data	A list with at least two components: x- an expression genes in the rows, samples in the columns), and y- a vector of the class labels for each sample. Same form as data object used by pamr.train.
nfold	Number of cross-validation folds. Default is the smallest class size
folds	A list with nfold components, each component a vector of indices of the samples in that fold. By default a (random) balanced cross-validation is used.
...	Any additional arguments that are to be passed to pamr.train

**Details**

pamr.cv carries out cross-validation for a nearest shrunken centroid classifier.

**Value**

A list with components

threshold	A vector of the thresholds tried in the shrinkage
errors	The number of cross-validation errors for each threshold value
loglik	The cross-validated multinomial log-likelihood value for each threshold value
size	A vector of the number of genes that survived the thresholding, for each threshold value tried.
.	
yhat	A matrix of size n by nthreshold, containing the cross-validated class predictions for each threshold value, in each column
prob	A matrix of size n by nthreshold, containing the cross-validated class probabilities for each threshold value, in each column
folds	The cross-validation folds used
cv.objects	Train objects (output of pamr.train), from each of the CV folds
call	The calling sequence used

**Author(s)**

Trevor Hastie, Robert Tibshirani, Balasubramanian Narasimhan, and Gilbert Chu

**Examples**

```
set.seed(120)
x <- matrix(rnorm(1000*20), ncol=20)
y <- sample(c(1:4), size=20, replace=TRUE)

mydata <- list(x=x, y=factor(y), geneid=as.character(1:nrow(x)),
              genenames=paste("g", as.character(1:nrow(x)), sep=""))

mytrain <- pamr.train(mydata)
mycv <- pamr.cv(mytrain, mydata)
```

---

`pamr.decorrelate` *A function to decorrelate (adjust) the feature matrix with respect to some additional predictors*

---

**Description**

A function to decorrelate (adjust) the feature matrix with respect to some additional predictors

**Usage**

```
pamr.decorrelate(x, adjusting.predictors, xtest=NULL, adjusting.predictors.test=NULL)
```

**Arguments**

<code>x</code>	Matrix of training set feature values, with genes in the rows, samples in the columns
<code>adjusting.predictors</code>	List of training set predictors to be used for adjustment
<code>xtest</code>	Optional matrix of test set feature values, to be adjusted in the same way as the training set
<code>adjusting.predictors.test</code>	Optional list of test set predictors to be used for adjustment

**Details**

`pamr.decorrelate` Does a least squares regression of each row of `x` on the adjusting predictors, and returns the residuals. If `xtest` is provided, it also returns the adjusted version of `xtest`, using the training set least squares regression model for adjustment

**Value**

A list with components

`x.adj`                Adjusted x matrix  
`xtest.adj`          Adjusted xtest matrix, if xtest we provided

**Author(s)**

Trevor Hastie, Robert Tibshirani, Balasubramanian Narasimhan, and Gilbert Chu

**References**

Robert Tibshirani, Trevor Hastie, Balasubramanian Narasimhan, and Gilbert Chu Diagnosis of multiple cancer types by shrunken centroids of gene expression PNAS 99: 6567-6572. Available at [www.pnas.org](http://www.pnas.org)

**Examples**

```
#generate some data
set.seed(120)

x<-matrix(rnorm(1000*20),ncol=20)
y<-c(rep(1,10),rep(2,10))
adjusting.predictors=list(pred1=rnorm(20), pred2=as.factor(sample(c(1,2),replace
=TRUE,size=20)))
xtest=matrix(rnorm(1000*10),ncol=10)
adjusting.predictors.test=list(pred1=rnorm(10), pred2=as.factor(sample(c(1,2),replace
=TRUE,size=10)))

# decorrelate training x wrt adjusting predictors

x.adj=pamr.decorrelate(x,adjusting.predictors)$x.adj
# train classifier with adjusted x

d=list(x=x.adj,y=y)
a<-pamr.train(d)

# decorrelate training and test x wrt adjusting predictors, then make
#predictions for test set

temp<-pamr.decorrelate(x,adjusting.predictors, xtest=xtest, adjusting.predictors.test=adjusting.predictors.test)

d=list(x=temp$x.adj,y=y)
a<-pamr.train(d)
aa<-pamr.predict(a,temp$xtest.adj, threshold=.5)
```

---

pamr.fdr	<i>A function to estimate false discovery rates for the nearest shrunken centroid classifier</i>
----------	--

---

**Description**

A function to estimate false discovery rates for the nearest shrunken centroid classifier

**Usage**

```
pamr.fdr(trained.obj, data, nperms=100,
         xl.mode=c("regular", "firsttime", "onetime", "lasttime"), xl.time=NULL, xl.prevfit=NU
```

**Arguments**

trained.obj	The result of a call to pamr.train
data	Data object; same as the one passed to pamr.train
nperms	Number of permutations for estimation of FDRs. Default is 100
xl.mode	Used by Excel interface
xl.time	Used by Excel interface
xl.prevfit	Used by Excel interface

**Details**

pamr.fdr estimates false discovery rates for a nearest shrunken centroid classifier

**Value**

A list with components:

results	Matrix of estimates FDRs for various various threshold values. Reported are both the median and 90th percentile of the FDR over permutations
pi0	The estimated proportion of genes that are null, i.e. not significantly different

**Author(s)**

Trevor Hastie, Robert Tibshirani, Balasubramanian Narasimhan, and Gilbert Chu

**Examples**

```
set.seed(120)
x <- matrix(rnorm(1000*20), ncol=20)
y <- sample(c(1:4), size=20, replace=TRUE)

mydata <- list(x=x, y=factor(y), geneid=as.character(1:nrow(x)),
              genenames=paste("g", as.character(1:nrow(x)), sep=""))
```

```
mytrain <- pamr.train(mydata)
myfdr <- pamr.fdr(mytrain, mydata)
```

---

`pamr.from.excel`      *A function to read in a text file saved from Excel*

---

### Description

A function to read in a text file saved from Excel. The spreadsheet is assumed to be of the format used by the SAM program.

### Usage

```
pamr.from.excel(file, ncols, sample.labels = FALSE, batch.labels = FALSE)
```

### Arguments

<code>file</code>	Character name of a text file. This is assumed to be a tab-delimited text file saved from an excel spreadsheet from "SAM". The spreadsheet has one row of expression values per gene. In addition there is one information row and two information columns. The first row has class labels for each of the samples. The first column had gene identifiers, and the second column has gene names. In the SAM program, for the multiclass option, the samples must be labelled 1,2,3 etc. Here we allow general labels, like "lymphoma", "colon cancer" etc
<code>ncols</code>	Number of columns in file
<code>sample.labels</code>	Optional argument. If true, "file" is assumed to have an additional row at the top, consisting of two blank cells followed by a sample labels for each of the columns. If available, these sample labels are used by various plotting routines.
<code>batch.labels</code>	Optional argument. If true, "file" is assumed to have an additional row at the top, consisting of two blank cells followed by a batch labels for each of the columns. If <code>sample.labels=T</code> as well, the row of batch labels are assumed to come after the row of sample labels. The batch labels are used by the function <code>pamr.batchadjust</code> .

### Details

`pamr.from.excel` Reads in the text file "file", and creates an object with components `x` (the matrix of expression values), `y`- a vector of class labels for each sample, `geneid`- a vector of gene identifiers and `genenames`- a vector of gene names

**Value**

A list with components

x	the matrix of expression values
y	a vector of class labels for each sample,
geneid	a vector of gene identifiers
genenames	a vector of gene names
samplelabels	a vector of sample labels, if provided in "file"
batchlabels	a vector of batch labels, if provided in "file"

**Author(s)**

Trevor Hastie, Robert Tibshirani, Balasubramanian Narasimhan, and Gilbert Chu

---

pamr.geneplot	<i>A function to plot the genes that survive the thresholding from the nearest shrunken centroid classifier</i>
---------------	---

---

**Description**

A function to plot the genes that survive the thresholding, from the nearest shrunken centroid classifier produced by pamr.train

**Usage**

```
pamr.geneplot(fit, data, threshold)
```

**Arguments**

fit	The result of a call to pamr.train
data	The input data. In the same format as the input data for pamr.train
threshold	The desired threshold value

**Details**

pamr.geneplot Plots the raw gene expression for genes that survive the specified threshold. Plot is stratified by class. Plot is set up to display only up to about 20 or 25 genes, otherwise it gets too crowded. Hence threshold should be chosen to yield at most about 20 or 25 genes.

**Author(s)**

Trevor Hastie, Robert Tibshirani, Balasubramanian Narasimhan, and Gilbert Chu

### Examples

```
set.seed(120)
x <- matrix(rnorm(1000*20), ncol=20)
y <- sample(c(1:4), size=20, replace=TRUE)
mydata <- list(x=x, y=y)
mytrain <- pamr.train(mydata)
pamr.genepplot(mytrain, mydata, threshold=1.6)
```

---

`pamr.indeterminate` *A function that takes estimate class probabilities and produces a class prediction or indeterminate prediction*

---

### Description

A function that takes estimate class probabilities and produces a class prediction or indeterminate prediction

### Usage

```
pamr.indeterminate(prob, mingap=0)
```

### Arguments

<code>prob</code>	Estimated class probabilities, from <code>pamr.predict</code> with <code>type="posterior"</code> )
<code>mingap</code>	Minimum difference between highest and second highest probability. If difference is < <code>mingap</code> , prediction is set to indeterminate (NA)

### Author(s)

Trevor Hastie, Robert Tibshirani, Balasubramanian Narasimhan, and Gilbert Chu

### Examples

```
set.seed(120)
x <- matrix(rnorm(1000*20), ncol=20)
y <- sample(c(1:4), size=20, replace=TRUE)
mydata <- list(x=x, y=y)
mytrain <- pamr.train(mydata)
prob<- pamr.predict(mytrain, mydata$x , threshold=1, type="posterior")
pamr.indeterminate(prob, mingap=.75)
```

---

pamr.knnimpute      *A function to impute missing expression data*

---

### Description

A function to impute missing expression data, using nearest neighbor averaging.

### Usage

```
pamr.knnimpute(data ,k = 10, rowmax = 0.5, colmax = 0.8, maxp = 1500)
```

### Arguments

data	The PAM input data. A list with components: $x$ , an expression matrix with genes in the rows, samples in the columns, and $y$ , a vector of the class labels for each sample. Same form as used by <code>pamr.train</code> , and same as that produced by <code>pamr.from.excel</code>
k	Number of neighbors to be used in the imputation (default=10)
rowmax	The maximum percent missing data allowed in any row (default 50%). For any rows with more than <code>rowmax%</code> missing are imputed using the overall mean per sample.
colmax	The maximum percent missing data allowed in any column (default 80%). If any column has more than <code>colmax%</code> missing data, the program halts and reports an error.
maxp	The largest block of genes imputed using the knn algorithm inside <code>pamr.knnimpute</code> (default 1500); larger blocks are divided by two-means clustering (recursively) prior to imputation. If <code>maxp=p</code> , only knn imputation is done.

### Details

`pamr.knnimpute` uses  $k$ -nearest neighbors in the space of genes to impute missing expression values.

For each gene with missing values, we find the  $k$  nearest neighbors using a Euclidean metric, confined to the columns for which that gene is NOT missing. Each candidate neighbor might be missing some of the coordinates used to calculate the distance. In this case we average the distance from the non-missing coordinates. Having found the  $k$  nearest neighbors for a gene, we impute the missing elements by averaging those (non-missing) elements of its neighbors. This can fail if ALL the neighbors are missing in a particular element. In this case we use the overall column mean for that block of genes.

Since nearest neighbor imputation costs  $O(p \log(p))$  operations per gene, where  $p$  is the number of rows, the computational time can be excessive for large  $p$  and a large number of missing rows. Our strategy is to break blocks with more than `maxp` genes into two smaller blocks using two-mean clustering. This is done recursively till all blocks have less than `maxp` genes. For each block, knn imputation is done separately. We have set the default value of `maxp` to 1500. Depending on the speed of the machine, and number of samples, this number might be increased. Making it too small is counter-productive, because the number of two-mean clustering algorithms will increase.

**Value**

data                    The input data list, with x replaced by the imputed version of x

**Author(s)**

Trevor Hastie, Robert Tibshirani, Balasubramanian Narasimhan, and Gilbert Chu

**References**

Hastie, T., Tibshirani, R., Sherlock, G., Eisen, M., Brown, P. and Botstein, D., Imputing Missing Data for Gene Expression Arrays, Stanford University Statistics Department Technical report (1999), <http://www-stat.stanford.edu/~hastie/Papers/missing.pdf>

Olga Troyanskaya, Michael Cantor, Gavin Sherlock, Pat Brown, Trevor Hastie, Robert Tibshirani, David Botstein and Russ B. Altman, Missing value estimation methods for DNA microarrays BIOINFORMATICS Vol. 17 no. 6, 2001 Pages 520-525

---

pamr.listgenes	<i>A function to list the genes that survive the thresholding, from the nearest shrunken centroid classifier</i>
----------------	--

---

**Description**

A function to list the genes that survive the thresholding, from the nearest shrunken centroid classifier produced by pamr.train.

**Usage**

```
pamr.listgenes(fit, data, threshold, fitcv=NULL, genenames=FALSE)
```

**Arguments**

fit	The result of a call to pamr.train
data	The input data. In the same format as the input data for pamr.train
threshold	The desired threshold value
fitcv	Optional object, result of a call to pamr.cv
genenames	Include genenames in the list? If yes, they are taken from "data". Default is false (geneid is always included in the list).

**Details**

pamr.listgenes List the geneids, and standardized centroids for each class, for genes surviving at the given threshold. If fitcv is provided, the function also reports the average rank of the gene in the cross-validation folds, and the proportion of times that the gene is chosen (at the given threshold) in the cross-validation folds.

**Author(s)**

Trevor Hastie, Robert Tibshirani, Balasubramanian Narasimhan, and Gilbert Chu

**Examples**

```
#generate some data
set.seed(120)
x <- matrix(rnorm(1000*20),ncol=20)
y <- sample(c(1:4),size=20,replace=TRUE)

mydata <- list(x=x,y=factor(y), geneid=as.character(1:nrow(x)),
              genenames=paste("g", as.character(1:nrow(x)), sep=""))

#train classifier
mytrain<- pamr.train(mydata)

pamr.listgenes(mytrain, mydata, threshold=1.6)
```

---

pamr.makeclasses    *A function to interactively define classes from a clustering tree*

---

**Description**

function to interactively define classes from a clustering tree

**Usage**

```
pamr.makeclasses(data, sort.by.class=FALSE, ...)
```

**Arguments**

data	The input data. A list with components: x- an expression genes in the rows, samples in the columns, and y- a vector of the class labels for each sample, and batchlabels- a vector of batch labels for each sample. This object is the same form as that produced by pamr.from.excel.
sort.by.class	Optional argument. If true, the clustering tree is forced to put all samples in the same class (as defined by the class labels y in 'data') together in the tree. This is useful if a regrouping of classes is desired. Eg: given classes 1,2,3,4 you want to define new classes (1,3) vs (2,4) or 2 vs (1,3)
...	Any additional arguments to be passed to hclust

## Details

`pamr.makeclasses` Using this function the user interactively defines a new set of classes, to be used in `pamr.train`, `pamr.cv` etc. After invoking `pamr.makeclasses`, a clustering tree is drawn. This calls the R function `hclust`, and any arguments for `hclust` can be passed to it. Using the left button, the user clicks at the junction point defining the subgroup 1. More groups can be added to class 1 by clicking on further junction points. The user ends the definition of class 1 by clicking on the rightmost button [in Windows, an additional menu appears and he chooses Stop] . This process is continued for classes 2,3 etc. Note that some sample may be left out of the new classes. Two consecutive clicks of the right button ends the definition for all classes.

At the end, the clustering is redrawn, with the new class labels shown.

Note: this function is "fragile". The user must click close to the junction point, to avoid confusion with other junction points. Classes 1,2,3.. cannot have samples in common (if they do, an Error message will appear). If the function is confused about the desired choices, it will complain and ask the user to rerun `pamr.makeclasses`. The user should also check that the labels on the final redrawn cluster tree agrees with the desired classes.

## Value

A vector of class labels 1,2,3... If a component is NA (missing), then the sample is not assigned to any class. This vector should be assigned to the newy component of data, for use in `pamr.train` etc. Note that `pamr.train` uses the class labels in the component "newy" if it is present. Otherwise it uses the data labels "y".

## Author(s)

Trevor Hastie, Robert Tibshirani, Balasubramanian Narasimhan, and Gilbert Chu

## Examples

```
set.seed(120)
#generate some data
x <- matrix(rnorm(1000*40),ncol=40)
y <- sample(c(1:4),size=40,replace=TRUE)
batchlabels <- sample(c(1:5),size=40,replace=TRUE)

mydata <- list(x=x,y=factor(y),batchlabels=factor(batchlabels),
              geneid=as.character(1:nrow(x)),
              genenames=paste("g",as.character(1:nrow(x)),sep=""))

# mydata$newy <- pamr.makeclasses(mydata)    Run this and define some new classes

train <- pamr.train(mydata)
```

---

pamr.menu	<i>A function that interactively leads the user through a PAM analysis</i>
-----------	--

---

**Description**

A function that interactively leads the user through a PAM analysis

**Usage**

```
pamr.menu(data)
```

**Arguments**

data	A list with at least two components: x- an expression genes in the rows, samples in the columns), and y- a vector of the class labels for each sample. Same form as data object used by pamr.train.
------	---

**Details**

pamr.menu provides a menu for training, cross-validating and plotting a nearest shrunken centroid analysis.

**Author(s)**

Trevor Hastie, Robert Tibshirani, Balasubramanian Narasimhan, and Gilbert Chu

**Examples**

```
set.seed(120)
x <- matrix(rnorm(1000*20), ncol=20)
y <- sample(c(1:4), size=20, replace=TRUE)
mydata <- list(x=x, y=y)
# pamr.menu(mydata)
```

---

pamr.plotcen	<i>A function to plot the shrunken class centroids, from the nearest shrunken centroid classifier</i>
--------------	---

---

**Description**

A function to plot the shrunken class centroids, from the nearest shrunken centroid classifier produced by pamr.train.

**Usage**

```
pamr.plotcen(fit, data, threshold)
```

**Arguments**

fit	The result of a call to pamr.train
data	The input data, in the same form as that used by pamr.train,
threshold	The desired threshold value

**Details**

pamr.plotcen plots the shrunken class centroids for each class, for genes surviving the threshold for at least once class. If genenames are included in "data", they are added to the plot. Note: for many classes and long gene names, this plot may need some manual prettying.

**Author(s)**

Trevor Hastie, Robert Tibshirani, Balasubramanian Narasimhan, and Gilbert Chu

**Examples**

```
set.seed(120)
x <- matrix(rnorm(1000*20), ncol=20)
y <- sample(c(1:4), size=20, replace=TRUE)
mydata <- list(x=x, y=y, genenames=as.character(1:1000))
mytrain <- pamr.train(mydata)
mycv <- pamr.cv(mytrain, mydata)
pamr.plotcen(mytrain, mydata, threshold=1.6)
```

---

pamr.plotcv	<i>A function to plot the cross-validated error curves from the nearest shrunken centroid classifier</i>
-------------	--

---

**Description**

A function to plot the cross-validated error curves the nearest shrunken centroid classifier

**Usage**

```
pamr.plotcv(fit)
```

**Arguments**

fit	The result of a call to pamr.cv
-----	---------------------------------

**Details**

pamr.plotcv plots the cross-validated misclassification error curves, from nearest shrunken centroid classifier. An overall plot, and a plot by class, are produced.

**Author(s)**

Trevor Hastie, Robert Tibshirani, Balasubramanian Narasimhan, and Gilbert Chu

**Examples**

```
set.seed(120)
x <- matrix(rnorm(1000*20), ncol=20)
y <- sample(c(1:4), size=20, replace=TRUE)
mydata <- list(x=x, y=y)
mytrain <- pamr.train(mydata)
mycv <- pamr.cv(mytrain, mydata)
pamr.plotcv(mycv)
```

---

pamr.plotcvprob      *A function to plot the cross-validated sample probabilities from the nearest shrunken centroid classifier*

---

**Description**

A function to plot the cross-validated sample probabilities from the nearest shrunken centroid classifier

**Usage**

```
pamr.plotcvprob(fit, data, threshold)
```

**Arguments**

fit	The result of a call to pamr.cv
data	A list with at least two components: x- an expression genes in the rows, samples in the columns), and y- a vector of the class labels for each sample. Same form as data object used by pamr.train.
threshold	Threshold value to be used

**Details**

pamr.plotcvprob plots the cross-validated sample probabilities the from nearest shrunken centroid classifier, stratified by the true classes.

**Author(s)**

Trevor Hastie, Robert Tibshirani, Balasubramanian Narasimhan, and Gilbert Chu

**Examples**

```

set.seed(120)
x <- matrix(rnorm(1000*20), ncol=20)
y <- sample(c(1:4), size=20, replace=TRUE)
mydata <- list(x=x, y=y)
mytrain <- pamr.train(mydata)
mycv <- pamr.cv(mytrain, mydata)
pamr.plotcvprob(mycv, mydata, threshold=1.6)

```

---

pamr.plotfdr	<i>A function to plot the FDR curve from the nearest shrunken centroid classifier</i>
--------------	---

---

**Description**

A function to plot the FDR curve the nearest shrunken centroid classifier

**Usage**

```
pamr.plotfdr(fdrfit, call.win.metafile = FALSE)
```

**Arguments**

fdrfit	The result of a call to pamr.fdr
call.win.metafile	Used by Excel interface

**Details**

pamr.plotfdr plots the FDR curves from nearest shrunken centroid classifier. The median FDR (solid line) and upper 90 percentile (broken line) are shown

**Author(s)**

Trevor Hastie, Robert Tibshirani, Balasubramanian Narasimhan, and Gilbert Chu

**Examples**

```

set.seed(120)
x <- matrix(rnorm(1000*20), ncol=20)
y <- sample(c(1:2), size=20, replace=TRUE)
x[1:50, y==2] = x[1:50, y==2] + 3
mydata <- list(x=x, y=y)
mytrain <- pamr.train(mydata)
myfdr <- pamr.fdr(mytrain, mydata)
pamr.plotfdr(myfdr)

```

---

pamr.plotstrata     *A function to plot the survival curves in each Kaplan Meier stratum*

---

### Description

A function to plot the survival curves in each Kaplan Meier stratum

### Usage

```
pamr.plotstrata(fit, survival.time, censoring.status)
```

### Arguments

```
fit                    The result of a call to pamr.train
survival.time                Vector of survival times
censoring.status            Vector of censoring status values
```

### Author(s)

Trevor Hastie, Robert Tibshirani, Balasubramanian Narasimhan, and Gilbert Chu

### Examples

```
gendata<-function(n=100, p=2000){
  tim <- 3*abs(rnorm(n))
  u<-runif(n,min(tim),max(tim))
  y<-pmin(tim,u)
  ic<-1*(tim<u)
  m <- median(tim)
  x<-matrix(rnorm(p*n),ncol=n)
  x[1:100, tim>m] <- x[1:100, tim>m]+3
  return(list(x=x,y=y,ic=ic))
}

# generate training data; 2000 genes, 100 samples

junk<-gendata(n=100)
y<-junk$y
ic<-junk$ic
x<-junk$x
d <- list(x=x, survival.time=y, censoring.status=ic,
          geneid=as.character(1:nrow(x)),
          genenames=paste("g", as.character(1:nrow(x)), sep=""))

# train model
a3<- pamr.train(d, ngroup.survival=2)
```

```
pamr.plotstrata(a3, d$survival.time, d$censoring.status)
```

---

```
pamr.plotsurvival A function to plots Kaplan-Meier curves stratified by a group variable
```

---

### Description

A function to plots Kaplan-Meier curves stratified by a group variable

### Usage

```
pamr.plotsurvival(group, survival.time, censoring.status)
```

### Arguments

```
group          A grouping factor
survival.time  Vector of survival times
censoring.status Vector of censoring status values: 1=died, 0=censored
```

### Author(s)

Trevor Hastie, Robert Tibshirani, Balasubramanian Narasimhan, and Gilbert Chu

### Examples

```
gendata<-function(n=100, p=2000){
  tim <- 3*abs(rnorm(n))
  u<-runif(n,min(tim),max(tim))
  y<-pmin(tim,u)
  ic<-1*(tim<u)
  m <- median(tim)
  x<-matrix(rnorm(p*n),ncol=n)
  x[1:100, tim>m] <- x[1:100, tim>m]+3
  return(list(x=x,y=y,ic=ic))
}

# generate training data; 2000 genes, 100 samples

junk<-gendata(n=100)
y<-junk$y
ic<-junk$ic
x<-junk$x
d <- list(x=x,survival.time=y, censoring.status=ic,
          geneid=as.character(1:nrow(x)),
```

```

        genenames=paste("g", as.character(1:nrow(x)), sep="")

# train model
a3<- pamr.train(d, ngroup.survival=2)

#make class predictions

yhat <- pamr.predict(a3,d$x, threshold=1.0)

pamr.plotsurvival(yhat, d$survival.time, d$censoring.status)

```

---

pamr.predict	<i>A function giving prediction information, from a nearest shrunken centroid fit.</i>
--------------	--

---

### Description

A function giving prediction information, from a nearest shrunken centroid fit.

### Usage

```
pamr.predict(fit, newx, threshold, type= c("class", "posterior", "centroid", "nonze
```

### Arguments

fit	The result of a call to pamr.train
newx	Matrix of features at which predictions are to be made
threshold	The desired threshold value
type	Type of prediction desired: class predictions, posterior probabilities, (unshrunken) class centroids, vector of genes surviving the threshold
prior	Prior probabilities for each class. Default is that specified in "fit"
threshold.scale	Additional scaling factors to be applied to the thresholds. Vector of length equal to the number of classes. Default is that specified in "fit".

### Details

pamr.predict Give a cross-tabulation of true versus predicted classes for the fit returned by pamr.train or pamr.cv, at the specified threshold

### Author(s)

Trevor Hastie, Robert Tibshirani, Balasubramanian Narasimhan, and Gilbert Chu

**Examples**

```

set.seed(120)
x <- matrix(rnorm(1000*20), ncol=20)
y <- sample(c(1:4), size=20, replace=TRUE)
mydata <- list(x=x, y=y)
mytrain <- pamr.train(mydata)
mycv <- pamr.cv(mytrain, mydata)
pamr.predict(mytrain, mydata$x, threshold=1)

```

---

`pamr.predictmany` *A function giving prediction information for many threshold values, from a nearest shrunken centroid fit.*

---

**Description**

A function giving prediction information for many threshold values, from a nearest shrunken centroid fit

**Usage**

```

pamr.predictmany(fit, newx, threshold=fit$threshold, prior =fit$prior, threshold.scale, ...)

```

**Arguments**

<code>fit</code>	The result of a call to <code>pamr.train</code>
<code>newx</code>	Matrix of features at which predictions are to be made
<code>threshold</code>	The desired threshold values
<code>prior</code>	Prior probabilities for each class. Default is that specified in "fit"
<code>threshold.scale</code>	Additional scaling factors to be applied to the thresholds. Vector of length equal to the number of classes. Default is that specified in "fit".
<code>...</code>	Additional arguments to be passed to <code>pamr.predict</code>

**Author(s)**

Trevor Hastie, Robert Tibshirani, Balasubramanian Narasimhan, and Gilbert Chu

**Examples**

```

set.seed(120)
x <- matrix(rnorm(1000*20), ncol=20)
y <- sample(c(1:4), size=20, replace=TRUE)
mydata <- list(x=x, y=y)
mytrain <- pamr.train(mydata)

pamr.predictmany(mytrain, mydata$x)

```

---

`pamr.surv.to.class2`*A function to assign observations to categories, based on their survival times.*

---

**Description**

A function to assign observations to categories, based on their survival times.

**Usage**

```
pamr.surv.to.class2(y, icens, cutoffs=NULL, n.class=NULL, class.names=NULL, newy=y
```

**Arguments**

<code>y</code>	vector of survival times
<code>icens</code>	Vector of censorng status values: 1=died, 0=censored
<code>cutoffs</code>	Survival time cutoffs for categories. Default NULL
<code>n.class</code>	Number of classes to create: if cutoffs is NULL, n.class equal classes are created.
<code>class.names</code>	Character names for classes
<code>newy</code>	New set of survival times, for which probabilities are computed (see below). Default is <code>y</code>
<code>newic</code>	New set of censoring statuses, for which probabilities are computed (see below). Default is <code>icens</code>

**Details**

`pamr.pamr.surv.to.class2` splits observations into categories based on their survival times and the Kaplan-Meier estimates. For example if `n.class=2`, it makes two categories, one below the median survival, the other above. For each observation (`newy`, `ic`), it then computes the probability of that observation falling in each category. For an uncensored observation that probability is just 1 or 0 depending on when the death occurred. For a censored observation, the probabilities are based on the Kaplan Meier and are typically between 0 and 1.

**Value**

<code>class</code>	The category labels
<code>prob</code>	The estimates class probabilities
<code>cutoffs</code>	The cutoffs used

**Author(s)**

Trevor Hastie, Robert Tibshirani, Balasubramanian Narasimhan, and Gilbert Chu

**Examples**

```

gendata<-function(n=100, p=2000){
  tim <- 3*abs(rnorm(n))
  u<-runif(n,min(tim),max(tim))
  y<-pmin(tim,u)
  ic<-1*(tim<u)
  m <- median(tim)
  x<-matrix(rnorm(p*n),ncol=n)
  x[1:100, tim>m] <- x[1:100, tim>m]+3
  return(list(x=x,y=y,ic=ic))
}

# generate training data; 2000 genes, 100 samples

junk<-gendata(n=100)
y<-junk$y
ic<-junk$ic
x<-junk$x
d <- list(x=x, survival.time=y, censoring.status=ic,
          geneid=as.character(1:nrow(x)),
          genenames=paste("g", as.character(1:nrow(x)), sep=""))

# train model
a3<- pamr.train(d, ngroup.survival=2)

# generate test data
junkk<- gendata(n=500)

dd <- list(x=junkk$x, survival.time=junkk$y, censoring.status=junkk$ic)

# compute soft labels
proby <- pamr.surv.to.class2(dd$survival.time, dd$censoring.status,
                             n.class=a3$ngroup.survival)$prob

```

---

```
pamr.test.errors.surv.compute
```

*A function giving a table of true versus predicted values, from a nearest shrunken centroid fit from survival data.*

---

**Description**

A function giving a table of true versus predicted values, from a nearest shrunken centroid fit from survival data.

**Usage**

```
pamr.test.errors.surv.compute(proby, yhat)
```

**Arguments**

proby                   Survival class probabilities, from pamr.surv.to.class2  
 yhat                    Estimated class labels, from pamr.predict

**Details**

pamr.test.errors.surv.compute computes the errors between the true 'soft' class labels proby and the estimated ones "yhat"

**Author(s)**

Trevor Hastie, Robert Tibshirani, Balasubramanian Narasimhan, and Gilbert Chu

**Examples**

```
gendata<-function(n=100, p=2000){
  tim <- 3*abs(rnorm(n))
  u<-runif(n,min(tim),max(tim))
  y<-pmin(tim,u)
  ic<-1*(tim<u)
  m <- median(tim)
  x<-matrix(rnorm(p*n),ncol=n)
  x[1:100, tim>m] <- x[1:100, tim>m]+3
  return(list(x=x,y=y,ic=ic))
}

# generate training data; 2000 genes, 100 samples

junk<-gendata(n=100)
y<-junk$y
ic<-junk$ic
x<-junk$x
d <- list(x=x, survival.time=y, censoring.status=ic,
          geneid=as.character(1:nrow(x)),
          genenames=paste("g", as.character(1:nrow(x)), sep=""))

# train model
a3<- pamr.train(d, ngroup.survival=2)

# generate test data
junkk<- gendata(n=500)

dd <- list(x=junkk$x, survival.time=junkk$y, censoring.status=junkk$ic)

# compute soft labels
proby <- pamr.surv.to.class2(dd$survival.time, dd$censoring.status,
                             n.class=a3$ngroup.survival)$prob

# make class predictions for test data
```

```
yhat <- pamr.predict(a3,dd$x, threshold=1.0)

# compute test errors

pamr.test.errors.surv.compute(proby, yhat)
```

---

pamr.to.excel      *A function to write out a data object into a tab-delimited text file*

---

### Description

A function to write out a data object into a tab-delimited text file

### Usage

```
pamr.to.excel(data, file, trace=TRUE)
```

### Arguments

data	A data object, of the same form as is read in by pamr.from.excel. Must have components x (the matrix of expression values), y- a vector of class labels for each sample, geneid- a vector of gene identifiers and genenames- a vector of gene names. Optional components: samplelabels and batchlabels, both character vectors
file	Character name of a text file.
trace	Optional argument. If true, progress in writing out file is reported.

### Details

pamr.to.excel writes out the data object into a tab-delimited text file, of the same form as is read in by pamr.from.excel. Useful for writing out data that has been imputed by pamr.knnimpute or adjusted by pamr.batchadjust. Note- this function writes the file out one line at a time, and hence can take a while for big datasets.

### Author(s)

Trevor Hastie, Robert Tibshirani, Balasubramanian Narasimhan, and Gilbert Chu

---

pamr.train                      *A function to train a nearest shrunken centroid classifier*

---

### Description

A function that computes a nearest shrunken centroid for gene expression (microarray) data

### Usage

```
pamr.train(data, gene.subset=NULL, sample.subset=NULL,
           threshold = NULL, n.threshold = 30,
           scale.sd = TRUE, threshold.scale = NULL, se.scale = NULL, offset.percent =
           hetero=NULL, prior = NULL, remove.zeros = TRUE, sign.contrast="both",
           ngroup.survival = 2)
```

### Arguments

data	The input data. A list with components: x- an expression genes in the rows, samples in the columns), and y- a vector of the class labels for each sample. Optional components- genenames, a vector of gene names, and geneid- a vector of gene identifiers.
gene.subset	Subset of genes to be used. Can be either a logical vector of length total number of genes, or a list of integers of the row numbers of the genes to be used
sample.subset	Subset of samples to be used. Can be either a logical vector of length total number of samples, or a list of integers of the column numbers of the samples to be used.
threshold	A vector of threshold values for the centroid shrinkage. Default is a set of 30 values chosen by the software
n.threshold	Number of threshold values desired (default 30)
scale.sd	Scale each threshold by the within class standard deviations? Default: true
threshold.scale	Additional scaling factors to be applied to the thresholds. Vector of length equal to the number of classes. Default- a vectors of ones.
se.scale	Vector of scaling factors for the within class standard errors. Default is $\sqrt{1/n.class - 1/n}$ , where n is the overall sample size and n.class is the sample sizes in each class. This default adjusts for different class sizes.
offset.percent	Fudge factor added to the denominator of each t-statistic, expressed as a percentile of the gene standard deviation values. This is a small positive quantity to penalize genes with expression values near zero, which can result in very large ratios. This factor is especially important for Affy data. Default is the median of the standard deviations of each gene.
hetero	Should a heterogeneity transformation be done? If yes, hetero must be set to one of the class labels (see Details below). Default is no (hetero=NULL)

prior	Vector of length the number of classes, representing prior probabilities for each of the classes. The prior is used in Bayes rule for making class prediction. Default is NULL, and prior is then taken to be $n.class/n$ , where $n$ is the overall sample size and $n.class$ is the sample sizes in each class.
remove.zeros	Remove threshold values yielding zero genes? Default TRUE
sign.contrast	Directions of allowed deviations of class-wise average gene expression from the overall average gene expression. Default is "both" (positive or negative). Can also be set to "positive" or "negative".
ngroup.survival	Number of groups formed for survival data. Default 2

### Details

`pamr.train` fits a nearest shrunken centroid classifier to gene expression data. Details may be found in the PNAS paper referenced below. One feature not described there is "heterogeneity analysis". Suppose there are two classes labelled "A" and "B". Class "A" is considered a normal class, and "B" an abnormal class. Setting `hetero="A"` transforms expression values  $x[i,j]$  to  $|x[i,j] - \text{mean}(x[i,j])|$  where the mean is taken only over samples in class "A". The transformed feature values are then used in Pam. This is useful when the abnormal class "B" is heterogeneous, i.e. a given gene might have higher expression than normal for some class "B" samples, and lower for others. With more than 2 classes, each class is centered on the class specified by `hetero`.

### Value

A list with components

<code>y</code>	The outcome classes.
<code>yhat</code>	A matrix of predicted classes, each column representing the results from one threshold.
.	
<code>prob</code>	A array of predicted class probabilities. of dimension $n$ by $n.class$ by $n.threshold$ . $n$ is the number samples, $n.class$ is the number of classes, $n.threshold$ is the number of thresholds tried
<code>centroids</code>	A matrix of (unshrunk) class centroids, $n$ by $n.class$
<code>hetero</code>	Value of <code>hetero</code> used in call to <code>pamr.train</code>
<code>norm.cent</code>	Centroid of "normal" group, if <code>hetero</code> was specified
<code>centroid.overall</code>	A vector containing the (unshrunk) overall centroid (all classes together)
<code>sd</code>	A vector of the standard deviations for each gene
<code>threshold</code>	A vector of the threshold tried in the shrinkage
<code>nonzero</code>	A vector of the number of genes that survived the thresholding, for each threshold value tried
<code>threshold.scale</code>	A vector of threshold scale factors that were used

<code>se.scale</code>	A vector of standard error scale factors that were used
<code>call</code>	The calling sequence used
<code>prior</code>	The prior probabilities used
<code>errors</code>	The number of trainin errors for each threshold value

**Author(s)**

Trevor Hastie, Robert Tibshirani, Balasubramanian Narasimhan, and Gilbert Chu

**References**

Robert Tibshirani, Trevor Hastie, Balasubramanian Narasimhan, and Gilbert Chu Diagnosis of multiple cancer types by shrunken centroids of gene expression PNAS 99: 6567-6572. Available at [www.pnas.org](http://www.pnas.org)

**Examples**

```
#generate some data
set.seed(120)
x <- matrix(rnorm(1000*20), ncol=20)
y <- sample(c(1:4), size=20, replace=TRUE)
mydata <- list(x=x, y=factor(y))

#train classifier
results<- pamr.train(mydata)

# train classifier on all data except class 4
results2 <- pamr.train(mydata, sample.subset=(mydata$y!=4))

# train classifier on only the first 500 genes
results3 <- pamr.train(mydata, gene.subset=1:500)
```

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