Package ‘SigCheck’

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Type Package

Title Check a gene signature’s prognostic performance against random signatures, known signatures, and permuted data/metadata

Version 2.7.0

Author Rory Stark <rory.stark@cruk.cam.ac.uk> and Justin Norden

Maintainer Rory Stark <rory.stark@cruk.cam.ac.uk>

Description While gene signatures are frequently used to predict phenotypes (e.g. predict prognosis of cancer patients), it it not always clear how optimal or meaningful they are (cf David Venet, Jacques E. Dumont, and Vincent Detours’ paper “Most Random Gene Expression Signatures Are Significantly Associated with Breast Cancer Outcome”). Based on suggestions in that paper, SigCheck accepts a data set (as an ExpressionSet) and a gene signature, and compares its performance on survival and/or classification tasks against
a) random gene signatures of the same length;
b) known, related and unrelated gene signatures;
and c) permuted data and/or metadata.

License Artistic-2.0

LazyLoad yes

Depends R (>= 3.2.0), MLInterfaces, Biobase, e1071, BiocParallel, survival

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NeedsCompilation no

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SigCheck-package

Check a gene signature's survival and/or classification performance against random signatures, known signatures, and permuted data/metadata.

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Description

While gene signatures are frequently used to predict phenotypes (e.g. predict prognosis of cancer patients), it is not always clear how optimal or meaningful they are (cf. David Venet, Jacques E. Dumont, and Vincent Detours' paper "Most Random Gene Expression Signatures Are Significantly Associated with Breast Cancer Outcome"). Based on suggestions in that paper, SigCheck accepts a data set (as an ExpressionSet) and a gene signature, and compares its performance on survival and/or classification tasks against a) random gene signatures of the same length; b) known, related and unrelated gene signatures; and c) permuted data and/or metadata.

Details

Package: SigCheck
Type: Package
Version: 2.0
Date: 2015-05-18
License: Artistic-2.0

To use SigCheck, first create a new SigCheck object using the function `sigCheck`. This will establish the baseline performance of the signature. Next, either run specific checks, or use the high level function `sigCheckAll` to run all the core functions in turn. The three core functions enable 1) comparison of baseline performance against signatures composed of random genes (`sigCheckRandom`); 2) comparison of baseline performance against known, and mostly unrelated, gene signatures (`sigCheckKnown`); and 3) comparison of baseline performance against randomly permuted data and/or metadata (`sigCheckPermuted`).

At a minimum, SigCheck requires a data set (as an ExpressionSet), metadata indicating the membership of each sample in one of two classes, and a signature (a subset of features in the ExpressionSet). If survival data are available, survival analyses are carried out. Validation samples can be divided into two classes using one of the simple default methods (based on overall expression value or their first principal component). Alternatively, more sophisticated classification algorithms can be deployed, using the `MLearn` function from the MLInterfaces package to build a classifier (using `link{smvI}` by default). If no validation samples are specified, leave-one-out (LOO) cross-validation is utilized to build multiple classifiers, each predicting one sample. If no survival data are provided, signatures are evaluated based on classification performance.

Output of each check includes the distribution of random performance scores (either survival p-value or classification performance) and the ranking of the passed signature within this distribution. An empirical p-value calculation based on this rank is also returned indicating confidence that the performance of the signature being checked has unique power.
classifyResults

Author(s)
First version written by Justin Norden with Rory Stark at the University of Cambridge, Cancer Research UK Cambridge Institute.
Second version, including all survival analysis, written by Rory Stark at CRUK-CI.
Maintainer: Rory Stark <rory.stark@cruk.cam.ac.uk>

References

classifyResults
Precomputed list of results for a calls to sigCheckRandom and sigCheckKnown using the breastCancerNKI dataset.

Description
This object represents the results lists returned by calls to sigCheckRandom and sigCheckKnown. It is used by the vignette accompanying the SigCheck package as an example result. It was derived by running the code in the example below. It loads to object, classifyRandom and classifyKnown.

Usage
data(classifyResults)

Examples
## Not run:
# This is how classifyResults is built
library(breastCancerNKI)
data(nki)
nki = nki[,!is.na(nki$e.dmfs)]
data(knownSignatures)
check <- sigCheck(nki, classes="e.dmfs",
signature=knownSignatures$cancer$VANTVEER,
annotation="HUGO.gene.symbol",
validationSamples=101:ncol(nki),
scoreMethod="classifier")

classifyRandom <- sigCheckRandom(check, iterations=1000)
classifyKnown <- sigCheckKnown(check)

## End(Not run)
# Example usage of classifyResults
data(classifyResults)
par(mfrow=c(1,2))
sigCheckPlot(classifyRandom, classifier=TRUE)
sigCheckPlot(classifyKnown, classifier=TRUE)
Description

Previously identified gene signature sets. These include three signature sets from Venet et. al.

Usage

data(knownSignatures)

Format

The data object knownSignatures is a list of sets of gene signatures. Each set is a list of gene signatures. Each signature is a vector of gene names.

Gene signature sets include:

- "cancer": 48 gene signatures derived from cancer samples, from Venet et. al.
- "proliferation": 5 gene signatures comprising genes associated with cell proliferation, including a "super signature", from Venet et. al.
- "non.cancer": 3 gene signatures derived from non-cancer sources, from Venet et. al.

Details

These data are taken directly from the supplemental material for Venet et. al "Most random gene expression signatures are significantly associated with breast cancer outcome".

Note

Other signatures of interest can be downloaded at http://www.broad.mit.edu/gsea/downloads.jsp#msigdb and read in using the read.gmt function in the qusage package.

Source


References


Examples

data(knownSignatures)
names(knownSignatures)
names(knownSignatures$cancer)
knownSignatures$cancer$VANTVEER
nkiResults

Precomputed list of results for a call to `sigCheckAll` using the breastCancerNKI dataset.

Description

This object represents the results lists returned by a call to `sigCheckAll`. It is used by the vignette accompanying the SigCheck package as an example result. It was derived by running the code in the example below.

Usage

data(nkiResults)

Examples

```r
## Not run:
# This is how nkiResults is built
library(breastCancerNKI)
data(nki)
nki = nki[,!is.na(nki$e.dmfs)]
data(knownSignatures)
check <- sigCheck(nki, classes="e.dmfs", survival="t.dmfs",
  signature=knownSignatures$cancer$VANTVEER,
  annotation="HUGO.gene.symbol",
  validationSamples=which(nki$series=="NKI2"))
nkiResults <- sigCheckAll(check, iterations=1000)

## End(Not run)

# Example usage of nkiResults
data(nkiResults)
sigCheckPlot(nkiResults)
```

sigCheck

Create a SigCheckObject and establish baseline performance.

Description

Main constructor for a SigCheckObject. Also establishes baseline survival analysis and/or classification performance.

Usage

```r
sigCheck(expressionSet, classes, survival, signature,
  annotation, validationSamples,
  scoreMethod="PCA1", threshold=median,
  classifierMethod=svmI, modeVal,
  survivalLabel, timeLabel,
  plotTrainingKM=TRUE, plotValidationKM=TRUE,
  impute=TRUE)
```
Arguments

expressionSet  An ExpressionSet object containing the data to be checked, including an expression matrix, feature labels, and samples. expressionSet can also be an existing SigCheckObject, in which case everything will be inherited from the passed object except the values for any specified parameters.

classes  Specifies which label is to be used to determine the prognostic categories (must be one of varLabels(expressionSet)). There should be only two unique values in expressionSet$classes.

survival  Specifies which label is to be used to determine survival times. (must be one of varLabels(expressionSet)). This may be missing if only classification is being checked.

signature  A vector of feature labels specifying which features comprise the signature to be checked. These feature labels should match values as specified in the annotation parameter. Alternatively, this can be an integer vector of feature indexes.

annotation  Character string specifying which fvarLabels field should be used as the annotation. If missing, the row names of the expressionSet are used as the feature names.

validationSamples  Optional specification, as a vector of sample indices, of what samples in the expressionSet should be considered validation samples. If present, the main checks will be performed using only these samples. If a the scoreMethod parameter is equal to "classifier", the remaining samples will be used as a training set to construct a classifier that will be used to separate the training samples. If a classifier is used, and validationSamples is not specified, a leave-one-out (LOO) validation method will be used, where a separate classifier will be trained to classify each sample using the all the remaining samples.

scoreMethod  specification of how the samples should be split into groups for survival analysis. If a character sting, one of the following values:
- "PCA1": default scoring method for separating validation samples into groups by taking the value of the first principal component of the expression values in the signature for each sample.
- "High": score used for separating validation samples into groups for each sample is the mean value over all the expression values in the signature for each sample.
- "classifier": score used for separating validation samples into groups is determined by a classifier specified in the classifierMethod parameter. If the survival parameter is specified, the classifier method must return a real-valued score for each predicted sample.

scoreMethod can also be a user-defined function that computes a score. The function should take a single parameter, an ExpressionSet, and return a vector of score, one for each row.

if the survival parameter is missing, scoreMethod value must be "classifier".

threshold  specifies the threshold used for separating the validation samples into classes based on the score derived using scoreMethod. Can be either a function, (with default median) or a number between zero and one indicating a percentile. Validation samples will be divided into a group whose percentile scores are less than this value, and another group with percentile scores greater than or equal to this value.
value. threshold may also be a vector of two percentiles, in which case samples will be divided into High, Low, and Mid groups. The survival p-value will be computed using only the high and low groups, with the mid group samples excluded.

classifierMethod

if the scoreMethod is equal to "classifier", this specifies what classifier to use. It is a MLInterfaces learnerSchema object indicating the machine learning method to use for classification. Default is svmI for linear Support Vector Machine classification. See MLearn for available methods.

modeVal

specifies which of the two category values (one of the values implied by the classes parameter) should be considered as the default value when computing the performance of a "mode" classifier. Is missing, the actual mode (most commonly occurring) value of the training set will be used.

survivalLabel

String to use in the Y-axis of any Kaplan-Meier plots generated, this indicates what aspect of survival is being predicted, such as time to recurrence or death.

timeLabel

String to use in the X-axis of an Kaplan-Meier plots generated, this indicates the units of time, such as days or months to outcome event.

plotTrainingKM

if the survival and validationSamples parameters are provided, a Kaplan-Meier plot can be plotted automatically for the training set samples if this is TRUE. A value of FALSE will suppress the plot being automatically generated.

plotValidationKM

if the survival parameter is provided, a Kaplan-Meier plot can be plotted automatically for the validation set samples if this is TRUE. A value of FALSE will suppress the plot being automatically generated. Note that if the validationSamples parameter is missing, the resulting plot will be over all samples.

impute

if TRUE, missing data values in the expressionSet will be imputed. If FALSE, any features with any missing values will be removed from the dataset.

Details

This function constructs a new SigCheckObject and carried out a baseline analysis, which will vary depending on which parameters are specified.

If the survival parameter is specified, a survival analysis is carried out. If the validationSamples parameter is specified, this will be done separately on the validation samples and the remaining (training/discovery) samples. The main result is a p-value indicating the confidence that the samples are separable into groups with distinct survival outcomes. This value is obtained using the survdiff function in the survival package (and applying pchisq to the $chisq component of the result). The samples are separated into groups using the scoreMethod and threshold parameters (and possibly the classifierMethod parameter).

If the survival parameter is not specified, then the scoreMethod parameter must be equal to "classifier", and a pure classification analysis is completed (as was done in SigCheck 1.0). If the validationSamples parameter is specified, the remaining samples are used as a training set to construct a classifier that is used to classify the validation samples. If validationSamples is not specified, leave-one-out cross-validation is used whereby a separate classifier is trained to predict each sample using all of the others.

Value

If the baseline analysis can be completed, a SigCheckObject is returned.
Author(s)
Rory Stark with Justin Norden

See Also
sigCheckAll, sigCheckRandom, sigCheckKnown, sigCheckPermuted.

Examples

library(breastCancerNKI)
data(nki)
nki <- nki[,!is.na(nki$e.dmfs)]
data(knownSignatures)

## survival analysis
check <- sigCheck(nki, classes="e.dmfs", survival="t.dmfs",
                  signature=knownSignatures$cancer$VANTVEER,
                  annotation="HUGO.gene.symbol")
check@survivalPval

check <- sigCheck(check, classes="e.dmfs", survival="t.dmfs",
                  signature=knownSignatures$cancer$VANTVEER,
                  annotation="HUGO.gene.symbol",
                  scoreMethod="High", threshold=.33)
check@survivalPval

## survival analysis with separate training and validation using SVM
check <- sigCheck(nki, classes="e.dmfs", survival="t.dmfs",
                  signature=knownSignatures$cancer$VANTVEER,
                  annotation="HUGO.gene.symbol", validationSamples=150:319,
                  scoreMethod="classifier")
check

---

sigCheckAll  
Run a default set of checks on a gene signature.

Description

High-level function for package SigCheck that runs a default set of checks against a predictive signature.

Usage

sigCheckAll(check,
            iterations=10, known="cancer",
            plotResults=TRUE, ...)

Arguments

check  
A SigCheckObject, as returned by sigCheck.

iterations  
Number of iterations to run to generate background distributions. This is how many random signatures the primary signature will be compared to, as well as how many of each type of permuted dataset will be generated for comparison.
**sigCheckAll**

known Specification of a set of known (previously identified) signatures to compare to. See `sigCheckKnown` for more details.

plotResults By default, plots of the results will be generated unless this is set or FALSE.

... Extra parameters to pass through `sigCheckPlot`.

**Details**

This high-level function will run four checks, plot the results, and return a consolidated result set. First, it calls `sigCheckRandom` to compare the performance of interactions randomly selected signatures. Next, it calls `sigCheckKnown` to check the performance of the signature against a database of signatures previously identified to discriminate in other domains.

Finally, two calls are made to `sigCheckPermuted` to check the performance of randomly permuted metadata and expression data. The first call permutes the survival data if they are available (toPermute="survival"); otherwise it permutes the category assignments (toPermute="categories") The second call permuted the expression value for each gene (permuting each row in the ExpressionSet, equivalent to toPermute="features").

If `plotResults` is TRUE, the results are plotted. If a classifier is involved, a set of four classification results are plotted in a 2x2 grid, showing how the classification performance of the main signature compares to that of a mode classifier and to the distribution of performance values observed for the random and known signature sets, as well as how it performs using the two type of permuted dataset. If survival data is available, another 2x2 grid is plotted showing how the baseline survival p-value compares to a p-value of 0.05 and to the distribution of p-values observed for the random and known signatures, as well as for the permuted data.

**Value**

A list containing four elements, each containing the result of a check.

- `$checkRandom` is the result list returned by `sigCheckRandom`.
- `$checkKnown` is the result list returned by `sigCheckKnown`.
  The third element of the result list will be one of the following:
  - `$checkPermutedSurvival` is the result list returned by `sigCheckPermuted` with toPermute="survival".
  - `$checkPermutedCategories` is the result list returned by `sigCheckPermuted` with toPermute="categories".
    The fourth element of the list will be:
    - `$checkPermutedFeatures` is the result list returned by `sigCheckPermuted` with toPermute="features".

**Author(s)**

Rory Stark

**References**


**See Also**

`sigCheck, sigCheckRandom, sigCheckPermuted, sigCheckKnown, sigCheckPlot`
Examples

```r
# Disable parallel so Bioconductor build won't hang
library(BiocParallel)
register(SerialParam())

library(breastCancerNKI)
data(nki)
nki <- nki[,!is.na(nki$e.dmfs)]
data(knownSignatures)
ITERATIONS <- 5 # should be at least 20, 1000 for real checks

## survival analysis
check <- sigCheck(nki, classes="e.dmfs", survival="t.dmfs",
                  signature=knownSignatures$cancer$VANTVEER,
                  annotation="HUGO.gene.symbol",
                  validationSamples=150:319)
results <- sigCheckAll(check, iterations=ITERATIONS,
                        known=knownSignatures$cancer[1:20])

## classification analysis
check <- sigCheck(nki, classes="e.dmfs",
                  signature=knownSignatures$cancer$VANTVEER,
                  annotation="HUGO.gene.symbol",
                  validationSamples=275:319,
                  scoreMethod="classifier")
results <- sigCheckAll(check, iterations=ITERATIONS,
                        known=knownSignatures$cancer[1:20])
```

---

**sigCheckKnown**

`Check signature performance against a panel of known signatures.`

**Description**

Performance of a signature is compared to performance of a panel of known (previously identified) signature.

**Usage**

```r
sigCheckKnown(check, known="cancer")
```

**Arguments**

- `check` A `SigCheckObject`, as returned by `sigCheck`.
- `known` Either a character string specifying which set of signatures to use from the included sets in `knownSignatures`, or a list of previously identified signatures to compare performance against. Each element in the list should be a vector of feature labels. Default is to use the "cancer" signatures from the included k `knownSignatures` data set, taken from Venet et. al.
Details

Each specified known signature will be evaluated in the same manner as the primary signature. If survival data were supplied, a survival analysis will be carried out on the validation samples, and a p-value computed as a performance measure. If no survival data are available, the training samples will be used to train a classifier, and the performance score will be percentage of validation samples correctly classified. (If no validation samples are provided, leave-one-out cross validation will be used to calculate the classification performance for each known signature).

An empirical p-value will be computed based on the percentile rank of the performance of the primary signature compared to a null distribution of the performance of the known signatures.

Value

A result list with the following elements:

- $checkType$ is equal to "Known".
- $knownSigs$ is the number of tests run (equal to the number of known signatures indicated where at least one gene matches a feature).
- $rank$ is the performance rank of the primary signature within the performance of the known signatures.
- $checkPval$ is the empirical p-value computed using the scores of the known signature as a null distribution. A value of zero indicates that no known signatures performed as good or better than the primary signature.
- $survivalPval$ represents the performance of the primary signature, if survival data were provided.
- $survivalPvalsKnown$ is a vector of performance scores (p-values) for each known signature on the validation samples, if survival data were provided.
- $trainingPvalsKnown$ is a vector of performance scores (p-values) for each known signature on the training samples, if survival data and separate validation samples were provided.
- $sigPerformance$ is the proportion of validation samples correctly classified by the primary signature if a classifier was used.
- $modePerformance$ is the proportion of validation samples correctly classified using a mode classifier.
- $performanceKnown$ is a vector of classification performance scores for each known signature, each indicating the proportion of validation samples correctly classified is a classifier was used.

Author(s)

Rory Stark

References


See Also

knownSignatures, sigCheck, sigCheckAll, sigCheckRandom, sigCheckPermuted, sigCheckPlot
Examples

```r
# Disable parallel so Bioconductor build won't hang
library(BiocParallel)
register(SerialParam())

library(breastCancerNKI)
data(nki)
nki <- nki[, !is.na(nki$e.dmfs)]
data(knownSignatures)

## survival analysis
check <- sigCheck(nki, classes="e.dmfs", survival="t.dmfs",
                  signature=knownSignatures$cancer$VANTVEER,
                  annotation="HUGO.gene.symbol",
                  validationSamples=150:319)

knownResult <- sigCheckKnown(check)
knownResult$checkPval
knownResult$survivalPvalsKnown[knownResult$survivalPvalsKnown <
                                 knownResult$checkPval]

sigCheckPlot(knownResult)
```

---

**SigCheckObject-class  Class "SigCheckObject"**

Description

The main object containing everything associated with an expression dataset and a gene signatures. Used for subsequent checks of the unique prognostic and/or classification performance of the signature. Based on an ExpressionSet object.

Objects from the Class

The preferred way to create a SigCheckObject is to use the sigCheck function.

Slots

- `checkType`: Object of class "character"
- `classes`: Object of class "character"
- `annotation`: Object of class "character"
- `survival`: Object of class "character"
- `signature`: Object of class "vector"
- `signatureLabels`: Object of class "vector"
- `validationSamples`: Object of class "vector"
- `survivalMethod`: Object of class "character"
- `threshold`: Object of class "ANY"
- `survivalScores`: Object of class "numeric"
- `survivalConfusionMatrix`: Object of class "matrix"
- `survivalClassificationScore`: Object of class "numeric"
survivalPval: Object of class "numeric", representing performance of the signature in dividing the samples into sets with distinct survival prognosis.

survivalTrainingScores: Object of class "numeric"~~
survivalTrainingConfusionMatrix: Object of class "matrix"~~
survivalTrainingClassificationScore: Object of class "numeric"~~
survivalTrainingPval: Object of class "numeric"~~
survivalLabel: Object of class "character"~~
timeLabel: Object of class "character"~~
classifierMethod: Object of class "learnerSchema"~~
sigPerformance: Object of class "numeric"~~
confusion: Object of class "matrix"~~
modeVal: Object of class "character"~~
modePerformance: Object of class "numeric"~~
classifier: Object of class "classifierOutput"~~
experimentData: Object of class "MIAME"~~
assayData: Object of class "AssayData"~~
phenoData: Object of class "AnnotatedDataFrame"~~
featureData: Object of class "AnnotatedDataFrame"~~
protocolData: Object of class "AnnotatedDataFrame"~~
.__classVersion__: Object of class "Versions"~~

**Extends**

Class "ExpressionSet", directly. Class "eSet", by class "ExpressionSet", distance 2. Class "VersionedBiobase", by class "ExpressionSet", distance 3. Class "Versioned", by class "ExpressionSet", distance 4.

**Methods**

No public methods, access slots directly if required.

**Note**

More methods and documentation coming soon...

**Author(s)**

Rory Stark

**See Also**

`sigCheck`

**Examples**

`showClass("SigCheckObject")`
sigCheckPermuted

Description
Performance of a signature on intact data is compared to performance on permuted data and/or metadata. Data may be permuted by by feature (expression values of each feature permuted across samples), samples (expression values of all features permuted within each sample). Metadata may be permuted by categories (permuted assignment of samples to classification categories) or survival (permuted assignment of survival times to samples).

Usage
sigCheckPermuted(check, toPermute="categories", iterations=10)

Arguments
check A SigCheckObject, as returned by sigCheck.
toPermute Character string or vector of strings indicating what should be permuted. Allowable values:
  • "features": the expression values for each feature will be permuted (permutation by row).
  • "samples": the expression values for each sample will be permuted (permutation by column).
  • "survival": the values in survival will be permuted.
  • "categories": the values in classes will be permuted.
iterations The number of permuted dataset the primary signature will be compared to. This should be at least 1,000 to compute a meaningful empirical p-value for comparative performance.

Details
The primary signature will be evaluated against each permuted dataset in the same manner as for the intact dataset.

If survival data were supplied, a survival analysis will be carried out on the validation samples, and a p-value computed as a performance measure. If no survival data are available, the training samples will be used to train a classifier, and the performance score will be percentage of validation samples correctly classified. (If no validation samples are provided, leave-one-out cross validation will be used to calculate the classification performance for each permuted dataset).

An empirical p-value will be computed based on the percentile rank of the performance of the signature on the intact dataset compared to a null distribution of the performance of the signature on all the permuted datasets.

Value
A result list with the following elements:
  • $checkType is equal to "Permuted".
• $permute$ is equal to the passed value of $toPermute$.
• $tests$ is the number of tests run (equal to $iterations$.)
• $rank$ is the performance rank of the signature on the intact dataset compared to its perform-
  ance in the permuted datasets.
• $checkPval$ is the empirical p-value computed using the performance scores of the signature
  on permuted datasets as a null distribution. A value of zero indicates that the signature did not
  perform better on any permuted datasets than it does using the intact data.
• $survivalPval$ represents the performance of the primary signature on the original dataset if
  survival data were provided.
• $survivalPvalsPermuted$ is a vector of performance scores (p-values) for each permuted
  dataset, if survival data were provided.
• $trainingPvalsPermuted$ is a vector of performance scores (p-values) for each permuted
  dataset, if survival data and separate validation samples were provided.
• $sigPerformance$ is the proportion of validation samples correctly classified using the intact
  dataset if a classifier was used.
• $modePerformance$ is the proportion of validation samples correctly classified in the intact
  dataset using a mode classifier.
• $performancePermuted$ is a vector of classification performance scores for each permuted
  dataset, each indicating the proportion of validation samples correctly classified if a classifier
  was used.

Author(s)

Rory Stark

See Also

$\text{sigCheck, sigCheckAll, sigCheckRandom, sigCheckKnown}$

Examples

# Disable parallel so Bioconductor build won't hang
library(BiocParallel)
register(SerialParam())

library(breastCancerNKI)
data(nki)
nki <- nki[,!is.na(nki$e.dmfs)]
data(knownSignatures)
ITERATIONS <- 5  # should be at least 20, 1000 for real checks

## survival analysis
check <- sigCheck(nki, classes="e.dmfs", survival="t.dmfs",
signature=knownSignatures$cancer$VANTVEER,
annotation="HUGO.gene.symbol",
validationSamples=150:319)

par(mfrow=c(1,2))
permutedCategories <- sigCheckPermuted(check, toPermute="categories",
            iterations=ITERATIONS)

permutedCategories$checkPval
sigCheckPlot(permutedCategories)
permutedSurvival <- sigCheckPermuted(check, toPermute="survival", iterations=ITERATIONS)
permutedSurvival$checkPval
sigCheckPlot(permutedSurvival)

---

**sigCheckPlot**  
*Plot results of a signature check or set of checks*

**Description**

Plots results of a signature check, as returned by *sigCheckRandom, sigCheckKnown, sigCheckPermuted,* or *sigCheckAll.*

**Usage**

```r
sigCheckPlot(checkResults, classifier=FALSE, title, nolegend=FALSE, ...)
```

**Arguments**

- **checkResults** The list returned by *sigCheckRandom, sigCheckKnown, sigCheckPermuted,* or *sigCheck.*
- **classifier** If a classifier was used in the original call to *sigCheck,* setting this to TRUE will result in a plot showing how the primary signature compares based on classification performance (rather than survival).
- **title** Title string for plot. If missing, a default plot title will be generated.
- **nolegend** IF TRUE, no legend will be included with the plot(s).
- **...** Additional arguments to be passed to the plot function.

**Details**

For results based on survival analysis, the background distribution of p-values (in 1-log10() format) derived from the check (either random signatures, known signatures, or performance using permuted data) is plotted. Up to two vertical red lines are also plotted: a solid red line representing the performance of the primary signature/data, and a dotted red line representing a p-value of 0.05. One or both of these may be missing if their performance falls outside the range of the background distributions.

For results based on classification performance, the x-axis represents the range of classification performance scores computed in the check, and the y-axis representing how many times that score was obtained. In addition, vertical lines are plotted representing the classification performance of the originally specified signature (solid red line) and the performance of a classifier that always predicts the mode value of the training samples (dotted red line).

If the results of *sigCheckAll* is passed in, all four results plots are generated in a 2x2 grid.

**Value**

none
Note

Better formance of the signature being checked results in the solid red line being to the right of the background distribution. For survival results, this indicates a lower-value. For classification results, this indicates superior classification performance.

Author(s)

Rory Stark with Justin Norden

See Also

`sigCheck, sigCheckAll, sigCheckRandom, sigCheckKnown, sigCheckPermuted`

Examples

```r
# Disable parallel so Bioconductor build won't hang
library(BiocParallel)
register(SerialParam())

library(breastCancerNKI)
data(nki)
nki <- nki[, !is.na(nki$e.dmfs)]
data(knownSignatures)
ITERATIONS <- 5 # should be at least 1000 for real checks

## survival analysis with separate training and validation using SVM
check <- sigCheck(nki, classes="e.dmfs", survival="t.dmfs",
                  signature=knownSignatures$cancer$VANTVEER,
                  annotation="HUGO.gene.symbol",
                  validationSamples=250:319,
                  scoreMethod="classifier", threshold=.33)

results <- sigCheckRandom(check, iterations=ITERATIONS)
par(mfrow=c(1,2))
sigCheckPlot(results)
sigCheckPlot(results, classifier=TRUE)
```

---

**sigCheckRandom**

Check signature performance against signatures composed of randomly selected features

**Description**

Performance of a signature is compared to performance of signatures composed of the same number of randomly-selected features.

**Usage**

```
sigCheckRandom(check, iterations=10)
```
Arguments

check    A SigCheckObject, as returned by sigCheck.
iterations    The number of random signatures the primary signature will be compared to. This should be at least 1,000 to compute a meaningful empirical p-value for comparative performance.

Details

sigCheckRandom will select iterations signatures, each consisting of the same number of features as are in the primary signature provided in the call to sigCheck that created the SigCheckObject sampled at random from all available features.

Each random signature will be evaluated in the same manner as the primary signature. If survival data were supplied, a survival analysis will be carried out on the validation samples, and a p-value computed as a performance measure. If no survival data are available, the training samples will be used to train a classifier, and the performance score will be percentage of validation samples correctly classified. (If no validation samples are provided, leave-one-out cross validation will be used to calculate the classification performance for each random signature).

An empirical p-value will be computed based on the percentile rank of the performance of the primary signature compared to a null distribution of the performance of the random signatures.

Value

A result list with the following elements:

- $checkType is equal to "Random".
- $tests is the number of tests run (equal to iterations.)
- $rank is the performance rank of the primary signature within the performance of the random signatures.
- $checkPval is the empirical p-value computed using the scores of the random signature as a null distribution. A value of zero indicates that no random signatures performed as good or better than the primary signature.
- $survivalPval represents the performance of the primary, if survival data were provided.
- $survivalPvalsRandom is a vector of performance scores (p-values) for each random signature on the validation samples, if survival data were provided.
- $trainingPvalsRandom is a vector of performance scores (p-values) for each random signature on the training samples, if survival data and separate validation samples were provided.
- $sigPerformance is the proportion of validation samples correctly classified by the primary signature if a classifier was used.
- $modePerformance is the proportion of validation samples correctly classified using a mode classifier.
- $performanceRandom is a vector of classification performance scores for each random signature, each indicating the proportion of validation samples correctly classified if a classifier was used.

Author(s)

Rory Stark
sigCheckRandom

See Also

sigCheck, sigCheckAll, sigCheckPermuted, sigCheckKnown, sigCheckPlot

Examples

# Disable parallel so Bioconductor build won't hang
library(BiocParallel)
register(SerialParam())

library(breastCancerNKI)
data(nki)
nki <- nki[,!is.na(nki$e.dmfs)]
data(knownSignatures)
ITERATIONS <- 5  # should be at least 20, 1000 for real checks

## survival analysis
check <- sigCheck(nki, classes="e.dmfs", survival="t.dmfs",
signature=knownSignatures$cancer$VANTVEER,
annotation="HUGO.gene.symbol",
validationSamples=150:319)

randomResult <- sigCheckRandom(check, iterations=ITERATIONS)
randomResult$checkPval
sigCheckPlot(randomResult)
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