Package ‘PDATK’

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Type Package
Title Pancreatic Ductal Adenocarcinoma Tool-Kit
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Description Pancreatic ductal adenocarcinoma (PDA) has a relatively poor prognosis and is one of the most lethal cancers. Molecular classification of gene expression profiles holds the potential to identify meaningful subtypes which can inform therapeutic strategy in the clinical setting. The Pancreatic Cancer Adenocarcinoma Tool-Kit (PDATK) provides an S4 class-based interface for performing unsupervised subtype discovery, cross-cohort meta-clustering, gene-expression-based classification, and subsequent survival analysis to identify prognostically useful subtypes in pancreatic cancer and beyond. Two novel methods, Consensus Subtypes in Pancreatic Cancer (CSPC) and Pancreatic Cancer Overall Survival Predictor (PCOSP) are included for consensus-based meta-clustering and overall-survival prediction, respectively. Additionally, four published subtype classifiers and three published prognostic gene signatures are included to allow users to easily recreate published results, apply existing classifiers to new data, and benchmark the relative performance of new methods. The use of existing Bioconductor classes as input to all PDATK classes and methods enables integration with existing Bioconductor datasets, including the 21 pancreatic cancer patient cohorts available in the MetaGxPancreas data package. PDATK has been used to replicate results from Sandhu et al (2019) [https://doi.org/10.1200/cci.18.00102] and an additional paper is in the works using CSPC to validate subtypes from the included published classifiers, both of which use the data available in MetaGxPancreas. The inclusion of subtype centroids and prognostic gene signatures from these and other publications will enable researchers and clinicians to classify novel patient gene expression data, allowing the direct clinical application of the classifiers included in PDATK. Overall, PDATK provides a rich set of tools to identify and validate useful prognostic and molecular subtypes based on gene-expression data, benchmark new classifiers against existing ones, and apply discovered classifiers on novel patient data to inform clinical decision making.

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.findAllCohortPairs  

Find all non-self pair-wise combinations of cohorts

Description

Find all non-self pair-wise combinations of cohorts

Usage

 findAllCohortPairs(clusterNames)

Arguments

clusterNames  
A character vector of cohort names

Value

A data.frame with the index of all non-self pair-wise cohort combinations. Rownames are the names of the two clusters being compared.
Generate a random sample from each group

**Description**

Returns a list of equally size random samples from two or more sample groupings.

**Usage**

```r
.randomSampleIndex(n, labels, groups)
```

**Arguments**

- `n` The sample size
- `labels` A vector of the group labels for all rows of the groups
- `groups` A vector of group labels for the data to sample from
- `numSamples` The number of samples to take

**Value**

A subset of your object with n random samples from each group in groups. The number of rows returned will equal the number of groups times the sample size.

---

**assignColDataColumn**

**Assign a new column directly to the colData slot of a SummarizedExperiment.**

**Description**

`assignColDataColumn`

Assign a new column directly to the colData slot of a SummarizedExperiment.

**Usage**

```r
assignColDataColumn(SE, colname, values)
```

**Arguments**

- `SE` A SummarizedExperiment object to assign colData columns to
- `colname` The name of the column to assign values to.
- `values` The values to assign to the col

**Value**

The SE object with the new column in the objects colData slot.
assignSubtypes

Assign Sample Subtypes to an S4 Object

Description

Assign Sample Subtypes to an S4 Object

Usage

assignSubtypes(object, subtypes, ...)

Arguments

object An S4 object containing a slot representing samples or patients.
subtypes A mapping to assign subtypes to the samples or patients in the object.
... Allow new parameters to be defined for this generic.

Value

object with subtypes assigned to the sample metadata and the isSubtyped metadata item set to TRUE.

Examples

data(sampleICGCmicro)
data(cohortSubtypeDFs)

cohortList <- assignSubtypes(sampleICGCmicro,
subtypes=cohortSubtypeDFs$ICGCMICRO,
sampleCol='sample_name',
subtypeCol='subtype')
Assign Subtype Annotations to a SurvivalExperiment Object

Description

Assign Subtype Annotations to a SurvivalExperiment Object

Usage

```r
## S4 method for signature 'CohortList,list'
assignSubtypes(
  object,
  subtypes,
  ..., 
  sampleCol = "sample_name",
  subtypeCol = "subtype"
)
```

Arguments

- `object`: A CohortList.
- `subtypes`: A list of data.frame objects, one per cohort, with subtypes to assign to the colData slot of cohorts with a matching name.
- `...`: Catch unnamed parameters. Not used.
- `sampleCol`: A character vector indicating the name of the column with sample identifiers in the subtype column. Must match the name of the sample identifier in colData.
- `subtypeCol`: A character vector indicating the name of the column with the subtype labels in the subtypes data.frame.

Value

The CohortList with the subtypes in the subtypes column of the colData slot and a metadata item, hasSubtypes, set to TRUE for each SurvivalExperiment.

Examples

```r
data(sampleCohortList)
data(cohortSubtypeDFs)

cohortList <- assignSubtypes(sampleCohortList,
                         subtypes=cohortSubtypeDFs[names(sampleCohortList)],
                         sampleCol='sample_name',
                         subtypeCol='subtype')
```
Assign Subtype Annotations to a SurvivalExperiment Object

Description

Assign Subtype Annotations to a SurvivalExperiment Object

Usage

```r
## S4 method for signature 'SurvivalExperiment,data.frame'
assignSubtypes(
  object,
  subtypes,
  ...,
  sampleCol = "sample_name",
  subtypeCol = "subtype"
)
```

Arguments

- `object`: A `SurvivalExperiment` object where the subtype annotations will be added to the `colData` slot as the subtype column.
- `subtypes`: A `data.frame` with ...
  - `...`: Force subsequent arguments to be named. Not used.
- `sampleCol`: A character vector specifying the name of the column containing the sample names. These must match the colnames of the `SurvivalExperiment`. If the sample names are the rownames of the `subtypes` data frame then set this parameter to 'rownames'. Defaults to 'sample_name'.
- `subtypeCol`: A character vector specifying the name of the subtype column in the `subtypes` data frame object. Defaults to 'subtype'.

Value

The `SurvivalExperiment` with the subtypes in the `subtypes` column of the `colData` slot and a metadata item, `hasSubtypes`, set to TRUE.

Examples

```r
data(sampleICGCmicro)
data(cohortSubtypeDFs)

cohortList <- assignSubtypes(sampleICGCmicro,
  subtypes=cohortSubtypeDFs$ICGCMICRO,
  sampleCol='sample_name',
  subtypeCol='subtype')
```
Description

Make A Bar Plot Comparing Performance Between Two S4 Objects Representing Mathematical Models.

Usage

barPlotModelComparison(model1, model2, ...)

Arguments

model1  An S4 object containing results of a mathematical model
model2  An S4 object containing results of a different mathematical model, but with the same or overlapping samples.
...  Allow new parameters to be defined for this generic.

Value

A bar plot comparing some aspect of model1 and model2

Examples

data(sampleCohortList)
data(sampleValPCOSPmodel)
data(sampleICGCmicro)

# Set parallelization settings
BiocParallel::register(BiocParallel::SerialParam())

# Setup the models
set.seed(1987)
clinicalModel <- ClinicalModel(sampleICGCmicro,
   formula='prognosis ~ sex + age + T + N + M + grade',
   randomSeed=1987)

# Train the models
trainedClinicalModel <- trainModel(clinicalModel)

# Make predictions
clinicalPredCohortList <- predictClasses(sampleCohortList[c('PCSI', 'TCGA')],
   model=trainedClinicalModel)

# Validate the models
validatedClinicalModel <- validateModel(trainedClinicalModel, valData=clinicalPredCohortList)

# Plot the comparison
modelCompBarPlot <- barPlotModelComparison(validatedClinicalModel, sampleValPCOSPmodel, stat='AUC')

---

**barPlotModelComparison, ClinicalModel, PCOSP_or_RLS_or_RGA-method**

*Make a Bar Plot Comparison Model Performance Between a ClinicalModel and a PCOSP, RLSModel or RGAModel object.*

### Description

Make a Bar Plot Comparison Model Performance Between a ClinicalModel and a PCOSP, RLSModel or RGAModel object.

### Usage

```r
## S4 method for signature 'ClinicalModel, PCOSP_or_RLS_or_RGA'
barPlotModelComparison(model1, model2, stat, ...)
```

### Arguments

- `model1`: A ClinicalModel object.
- `model2`: A PCOSP or RLSModel or RGAModel object.
- `stat`: A character vector specifying which statistic to compare the models using. Options are 'AUC', 'log_D_index' or 'concordance_index'.
- `...`: Not used.

### Value

A ggplot2 object showing a barplot coloured by the model and comparing the stat between all cohorts that both models were validated with.

### Examples

```r
data(sampleValPCOSPmodel)
data(sampleCohortList)
data(sampleICGCmicro)

# Set parallelization settings
BiocParallel::register(BiocParallel::SerialParam())

# Setup the models
clinicalModel <- ClinicalModel(sampleICGCmicro, formula='prognosis ~ sex + age + T + N + M + grade',
```

```
randomSeed=1987)

# Train the models
trainedClinicalModel <- trainModel(clinicalModel)

# Make predictions
clinicalPredCohortList <- predictClasses(sampleCohortList[c('PCSI', 'TCGA')],
    model=trainedClinicalModel)

# Validate the models
validatedClinicalModel <- validateModel(trainedClinicalModel,
    valData=clinicalPredCohortList)

# Plot the comparison
modelCompBarPlot <- barPlotModelComparison(validatedClinicalModel,
    sampleValPCOSPmodel, stat='AUC')

---

**birnbaum**

*Published classifier gene signature for Birnbaum*

### Description

The genes and coefficients for the gene signature from Birnbaum et al. (2017)

### Examples

```r
# Loads chen, birnbaum and haiderSigScores objects
data(existingClassifierData)
```

---

**chen**

*Published classifier gene signature for Chen*

### Description

The genes and coefficients for the gene signature from Chen et al. (2015)

### Examples

```r
# Loads chen, birnbaum and haiderSigScores objects
data(existingClassifierData)
```
ClinicalModel Constructor for the ClinicalModel Class

Description

Constructor for the ClinicalModel Class

Usage

ClinicalModel(trainData, formula, minDaysSurvived = 365, ..., randomSeed)

Arguments

- `trainData` A SurvivalExperiment or CohortList object to construct a clinical model using
- `formula` A formula object or a character vector coercible to one. All columns specified in the formula must be in the colData slot of the all SurvivalExperiments in trainData.
- `minDaysSurvived` An integer specifying the minimum number of days required to be 'good' prognosis. Default is 365.
- `...` Force all subsequent parameters to be named. Not used.
- `randomSeed` An integer randomSeed that was used to train the model. Users should specify this when initializing a model to ensure reproducibilty.

Value

A ClinicalModel object.

Examples

data(sampleICGCmicro)
set.seed(1987)
clinicalModel <- ClinicalModel(sampleICGCmicro,
    formula='prognosis ~ sex + age + T + N + M + grade', randomSeed=1987)
ClinicalModel-class

ClinicalModel Class Definition

Description
An S4 class with a number of predefined methods for accessing slots relevant to a survival model. More specific model types will inherit from this class for their accessor methods and constructor.

Examples
data(sampleICGCmicro)
set.seed(1987)
survModel <- SurvivalModel(sampleICGCmicro, minDaysSurvived=385, randomSeed=1987)

CohortList
Constructor for the CohortList class, a specialized list for storing SurvivalExperiment objects.

Description
Constructor for the CohortList class, a specialized list for storing SurvivalExperiment objects.

Usage
CohortList(..., mDataTypes)

Arguments

... One or more SurvivalExperiment objects.

mDataTypes A character vector with the same length as ... which indicates the molecular data type in each cohort. This will be assigned to mcols for the CohortList as well as to the metadata of each item in the list as mDataType.

Value
A CohortList object containing one or more SurvivalExperiment objects.

Examples
data(sampleICGCmicro)
set.seed(1987)
cohortList <- CohortList(list(survExp1=sampleICGCmicro, survExp2=sampleICGCmicro), mDataTypes=c('rna_micro', 'rna_micro'))
## CohortList-class

### Description

A list containing only `SurvivalExperiment` objects.

### cohortSubtypeDFs

#### Description

A list of `data.frames` containing clinical subtypes for the data in the `cohortSubtypeDFs` object.

#### Examples

```r
data(cohortSubtypeDFs)
```

## compareModels

### Description

Compare Two Mathematical Models Represented as S4 Objects

### Usage

```r
compareModels(model1, model2, ...)
```

### Arguments

- `model1`: A S4 object representing some kind of mathematical model.
- `model2`: A S4 object representing some kind of mathematical model.
- `...`: Allow new parameters to be defined for this generic.

### Value

A S4 object with statistics about the performance of each model.
Examples

data(sampleValPCOSPmodel)
data(sampleClinicalModel)
data(sampleCohortList)

# Set parallelization settings
BiocParallel::register(BiocParallel::SerialParam())

# Train the model
trainedClinicalModel <- trainModel(sampleClinicalModel)

# Predict risk/risk-class
ClinicalPredPCSI <- predictClasses(sampleCohortList[c('PCSI', 'TCGA')],
                                   model=trainedClinicalModel)

# Validate the models
validatedClinicalModel <- validateModel(trainedClinicalModel,
                                         valData=ClinicalPredPCSI)

# Compare the models
modelComp <- compareModels(sampleValPCOSPmodel, validatedClinicalModel)
head(modelComp)

Description

Compare Two SurvivalModel Objects, Returning A ModelComparison Object With Statistics Comparing the Performance of Each Model.

Usage

## S4 method for signature 'ModelComparison,SurvivalModel'
compareModels(model1, model2, model2Name)

Arguments

model1          An object inheriting from the SurvivalModel class.
model2          Another object inheriting from the SurvivalModel class.
model2Name      A character vector with the name of the second model.

Value

A ModelComparison object with statistics comparing the two models.
Examples

```r
data(sampleValPCOSPmodel)
data(sampleClinicalModel)
data(sampleCohortList)

# Set parallelization settings
BiocParallel::register(BiocParallel::SerialParam())

# Train the models
trainedClinicalModel <- trainModel(sampleClinicalModel)

# Predict risk/risk-class
clinicalPredCohortL <- predictClasses(sampleCohortList[c('PCSI', 'TCGA')],
  model=trainedClinicalModel)

# Validate the models
validatedClinicalModel <- validateModel(trainedClinicalModel,
  valData=clinicalPredCohortL)

# Compare the models
modelComp <- compareModels(sampleValPCOSPmodel, validatedClinicalModel)
head(modelComp)

# Compare model comparison to another model
modelCompComp <- compareModels(modelComp, sampleValPCOSPmodel)
```

---

**compareModels,SurvivalModel,SurvivalModel-method**

*Compare Two SurvivalModel Objects, Returning A ModelComparison Object With Statistics Comparing the Performance of Each Model.*

**Description**

Compare Two SurvivalModel Objects, Returning A ModelComparison Object With Statistics Comparing the Performance of Each Model.

**Usage**

```r
## S4 method for signature 'SurvivalModel,SurvivalModel'
compareModels(model1, model2, modelNames)
```

**Arguments**

- `model1`: An object inheriting from the SurvivalModel class.
- `model2`: Another object inheriting from the SurvivalModel class.
- `modelNames`: Optional character vector with a name for each model. Defaults to the class of the model plus 1 and 2 if missing.
Value

A ModelComparison object with statistics comparing the two models.

Examples

data(sampleValPCOSPmodel)
data(sampleClinicalModel)
data(sampleCohortList)

# Set parallelization settings
BiocParallel::register(BiocParallel::SerialParam())

# Train the model
trainedClinicalModel <- trainModel(sampleClinicalModel)

# Predict risk/risk-class
ClinicalPredPCSI <- predictClasses(sampleCohortList[c('PCSI', 'TCGA')],
model=trainedClinicalModel)

# Validate the models
validatedClinicalModel <- validateModel(trainedClinicalModel,
valData=ClinicalPredPCSI)

# Compare the models
modelComp <- compareModels(sampleValPCOSPmodel, validatedClinicalModel)
head(modelComp)

---

**ConsensusMetaclusteringModel**

*Constructor for a ConsensusClusterModel Object.*

Description

Constructor for a ConsensusClusterModel Object.

Usage

ConsensusMetaclusteringModel(trainData, ..., randomSeed)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>trainData</td>
<td>A MultiAssayExperiment or SummarizedExperiment containing molecular data to be used for consensus clustering with ConsensusClusterPlus::ConsensusClusterPlus</td>
</tr>
<tr>
<td>...</td>
<td>Force subsequent parameters to be named. Not used.</td>
</tr>
<tr>
<td>randomSeed</td>
<td>An integer randomSeed that will be passed to the randomSeed parameter of the ConsensusClusterPlus::ConsensusClusterPlus function when training the model.</td>
</tr>
</tbody>
</table>
Value

A ConsensusMetaclusteringModel object containing the training data and ready to be trained.

See Also

ConsensusClusterPlus::ConsensusClusterPlus

Examples

data(CSPC_MAE)
set.seed(1987)
conMetaclustModel <- ConsensusMetaclusteringModel(CSPC_MAE, randomSeed=1987)

ConsensusMetaclusteringModel-class

An S4Model Containing Molecular Data to be Consensus Clustered

Description

An S4 wrapper class providing an interface to the ConsensusClusterPlus function from the package with the same name.

CoxModel

CoxModel constructor

Description

Build a CoxModel object from a MultiAssayExperiment of SurvivalExperiments. Allows easy application of the survival::coxph function to many SurvivalExperiment at once, assuming they share the survivalPredictor column.

Usage

CoxModel(object, survivalPredictor = "metacluster_labels")

Arguments

object A MultiAssayExperiment containing only SurvivalExperiment objects.
survivalPredictor A character vector indicating the name of the one or more columns in the colData slot of each SurvivalExperiment to use for testing survival differences between different groups. Must be a valid column in the colData of ALL experiments.
Value

A CoxModel object, with object in the trainData slot.

Examples

library(MultiAssayExperiment)
data(CSPC_MAE)

# Create a SurvivalExperiment object
experiments(CSPC_MAE) <- endoapply(experiments(CSPC_MAE), SurvivalExperiment,
  event_occurred='vital_status', survival_time='days_to_death')

# Create a CoxModel object
coxModel <- CoxModel(CSPC_MAE, survivalPredictor='sample_type')
Render A Density Plot of Model Performance for an S4 Object

Usage

densityPlotModelComparison(object, refModel, ...)

Arguments

object An S4 object representing a statistical or ML model.
refModel An S4 object representing a statistical or ML model to compare object against.
... Allow additional parameters to be defined for this generic.

Value

A ggplot object containing the plot.

Render a Density Plot Comparing Model Performance Between Two PCOSP, RLSModel or RGAModel object.

Usage

## S4 method for signature 'PCOSP_or_RLS_or_RGA,PCOSP_or_RLS_or_RGA'
densityPlotModelComparison(
  object,
  refModel,
  ..., title, xlab, ylab, mDataTypeLabels
)
**dropNotCensored**

**Arguments**

- **object**
  A PCOSP, RLSModel or RGAModel object.

- **refModel**
  A PCOSP, RLSModel or RGAModel object to compare performance against.

- **...**
  Catch unnamed parameters. Not used.

- **title**
  Optional character vector with plot title.

- **xlab**
  Optional character vector with x-axis label.

- **ylab**
  Optional character vector with y-axis label.

- **mDataTypeLabels**
  Optional character vector who's names are one or more existing mDataTypes in object and refModel and who's values are the desired mDataType labels in the plot facets.

**Value**

A ggplot object with a density plot of model AUCs for object and a vertical line for the average AUC of refModel, faceted by mDataType.

**Description**

Remove Censored Patient Samples from An S4 Object.

**Usage**

```r
dropNotCensored(object, ...)
```

**Arguments**

- **object**
  An S4 object containing survival data which needs to have patients who were not censored before some criteria.

- **...**
  Allow new parameters to be defined for this generic.

**Value**

S4 The object subset to only those patients which pass the censoring criteria.

**Examples**

```r
data(sampleICGCmicro)
ICGCmicro <- dropNotCensored(sampleICGCmicro)
```
dropNotCensored,CohortList-method

Remove Censored Patients from Each SurvivalExperiment in a CohortList

Description
Remove Censored Patients from Each SurvivalExperiment in a CohortList

Usage

```r
## S4 method for signature 'CohortList'
dropNotCensored(object, minDaysSurvived = 365)
```

Arguments

- `object` A CohortList for which to drop patients who died before each SurvivalExperiment item a specified date.
- `minDaysSurvived` An integer specifying the minimum number of days a patient needs to have survived to be included in the cohort.

Value
The CohortList with censored samples removed.

Examples

```r
data(sampleCohortList)
valCohortList <- dropNotCensored(sampleCohortList)
```

dropNotCensored,SurvivalExperiment-method

Remove Censored Patients from A SurvivalExperiment Object

Description
Remove Censored Patients from A SurvivalExperiment Object

Usage

```r
## S4 method for signature 'SurvivalExperiment'
dropNotCensored(object, minDaysSurvived = 365)
```
existingClassifierData

Arguments

object A SurvivalExperiment to censor.
minDaysSurvived An integer specifying the minimum number of days a patient needs to have survived to be included in the cohort.

Details

Censored means no event before end of measurement. Since we want not censored, we keep patients who had an event before minDaysSurvived. Therefore we keep individuals surviving > minDaysSurvived or who had an event (died) before minDaysSurvived.

Value

The SurvivalExperiment with censored samples removed.

Examples

data(sampleICGCmicro)
ICGCmicro <- dropNotCensored(sampleICGCmicro)

existingClassifierData

data(sampleICGCmicro)
ICGCmicro <- dropNotCensored(sampleICGCmicro)

Description

existingClassifierData

Value

Three objects:

• chen: The genes and coefficients for the gene signature from Chen et al. (2015)
• birnbaum: The genes and coefficients for the gene signature from Birnbaum et al. (2017)
• haiderSigScores: The classifier risk scores from Haider et al. (2014)

Examples

# Loads chen, birnbaum and haiderSigScores objects
data(existingClassifierData)
findCommonGenes  
*Find the common genes in an S4 object.*

**Description**

Find the common genes in an S4 object.

**Usage**

```r
findCommonGenes(object, ...)
```

**Arguments**

- `object`: An S4 object to find common genes for.
- `...`: Allow new parameters to be defined for this generic.

**Value**

A character vector of common gene names.

**Examples**

```r
data(sampleCohortList)
commonGenes <- findCommonGenes(sampleCohortList)
head(commonGenes)
```

---

**findCommonGenes,CohortList-method**

*Intersect Gene Names for All SurvivalExperiments in a CohortList*

**Description**

Intersect Gene Names for All SurvivalExperiments in a CohortList

**Usage**

```r
## S4 method for signature 'CohortList'
findCommonGenes(object)
```

**Arguments**

- `object`: A CohortList of SurvivalExperiments to find common genes between.
findCommonGenes,MultiAssayExperiment-method

Value

A character vector of genes common to all SurvivalExperiments in the CohortList.

Examples

```r
data(sampleCohortList)
commonGenes <- findCommonGenes(sampleCohortList)
head(commonGenes)
```

Description

Intersect Gene Names for All experiments in a MultiAssayExperiment

Usage

```r
## S4 method for signature 'MultiAssayExperiment'
findCommonGenes(object)
```

Arguments

- **object** A MultiAssayExperiment where rownames represent genes.

Value

A character vector of genes common to all experiments in the MultiAssayExperiment.

findCommonSamples  

Find Common Samples in a List-like S4 Object where The Columns of Each Item Represent Samples

Description

Find Common Samples in a List-like S4 Object where The Columns of Each Item Represent Samples

Usage

```r
findCommonSamples(object, ...)
```
Arguments

object  A S4 object, where the columns of each element represent samples.
... Allow new parameters to be defined for this generic.

Value

A character vector of common sample names.

Examples

data(sampleCohortList)
commonSamples <- findCommonSamples(sampleCohortList)
head(commonSamples)

Description

Find Common Samples in a CohortList Object where The Columns of Each Item Represent Samples

Usage

## S4 method for signature 'CohortList'
findCommonSamples(object)

Arguments

object  A CohortList for which we want to find common samples between all SurvivalExperiment objects.

Value

A character vector of common sample names.

Examples

data(sampleCohortList)
commonSamples <- findCommonSamples(sampleCohortList)
head(commonSamples)
Generate a forest plot from an S4 object

Usage

forestPlot(object, ...)

Arguments

object An S4 object to create a forest plot of.
... Allow new parameters to this generic.

Value

None, draws a forest plot.

Examples

data(sampleValPCOSPmodel)

# Plot
dIndexForestPlot <- forestPlot(sampleValPCOSPmodel, stat='log_D_index')

Render a forest plot from the validationStats slot of a PCOSP model object.

Usage

## S4 method for signature 'ModelComparison'
forestPlot(
  object,
  stat,
  groupBy = "cohort",
  colourBy = "model",
  vline,
...,
xlab,
ylab,
transform,
colours,
title
)

Arguments

object  A ModelComparison object to forest plot.
stat    A character vector specifying a statistic to plot.
groupBy A character vector with one or more columns in validationStats to group by. These will be the facets in your forest plot.
colourBy A character vector specifying the columns in validationStats to colour by.
vline   An integer value on the x-axis to place a dotted vertical line.
...     Force subsequent parameters to be named, not used.
xlab    A character vector specifying the desired x label. Automatically guesses based on the stat argument.
ylab    A character vector specifying the desired y label. Defaults to 'Cohort (P-value)'.
transform The name of a numeric function to transform the statistic before making the forest plot.
colours A character vector of colours to pass into ggplot2::scale_fill_manual, which modify the colourBy argument.
title   A character vector with a title to add to the plot.

Value

A ggplot2 object.

Examples

data(sampleValPCOSPmodel)
data(sampleClinicalModel)
data(sampleCohortList)

# Set parallelization settings
BiocParallel::register(BiocParallel::SerialParam())

# Train the models
trainedClinicalModel <- trainModel(sampleClinicalModel)

# Predict risk/risk-class
ClinicalPredCohortL <- predictClasses(sampleCohortList[,'PCSI', 'TCGA'],
    model=trainedClinicalModel)
forestPlot,PCOSP_or_ClinicalModel-method

# Validate the models
validatedClinicalModel <- validateModel(trainedClinicalModel,
valData=ClinicalPredCohortL)

# Compare the models
modelComp <- compareModels(sampleValPCOSPmodel, validatedClinicalModel)

# Make the forest plot
modelComp <- modelComp[modelComp$isSummary == TRUE, ]
modelCindexCompForestPlot <- forestPlot(modelComp, stat='concordance_index')

---

forestPlot,PCOSP_or_ClinicalModel-method

Render a forest plot from the validationStats slot of a PCOSP model object.

Description

Render a forest plot from the validationStats slot of a PCOSP model object.

Usage

## S4 method for signature 'PCOSP_or_ClinicalModel'
forestPlot(
  object,
  stat,
  groupBy = "mDataType",
  colourBy = "isSummary",
  vline,
  ..., 
  xlab,
  ylab,
  transform,
  colours,
  title
)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>object</td>
<td>A PCOSP model which has been validated with validateModel and therefore has data in the validationStats slot.</td>
</tr>
<tr>
<td>stat</td>
<td>A character vector specifying a statistic to plot.</td>
</tr>
<tr>
<td>groupBy</td>
<td>A character vector with one or more columns in validationStats to group by. These will be the facets in your forestplot.</td>
</tr>
<tr>
<td>colourBy</td>
<td>A character vector specifying the columns in validationStats to colour by.</td>
</tr>
<tr>
<td>vline</td>
<td>An integer value on the x-axis to place a dotted vertical line.</td>
</tr>
</tbody>
</table>
... Force subsequent parameters to be named, not used.

xlab A character vector specifying the desired x label. Automatically guesses based on the stat argument.

ylab A character vector specifying the desired y label. Defaults to 'Cohort (P-value)'.

transform The name of a numeric function to transform the statistic before making the forest plot.

colours A character vector of colours to pass into ggplot2::scale_fill_manual, which modify the colourBy argument.

title A character vector with a title to add to the plot.

Value

A ggplot2 object.

Examples

data(sampleValPCOSPmodel)

# Plot
dIndexForestPlot <- forestPlot(sampleValPCOSPmodel, stat='log_D_index')

---

GeneFuModel Constructor Method

Description

GeneFuModel Constructor Method

Usage

GeneFuModel(
  trainCohorts = SurvivalExperiment(),
  minDaysSurvived = 365,
  ...
)

Arguments

trainCohorts A CohortList or SurvivalExperiment containing training data for the genefu model. If you don't have training data, but have a trained model this will default to an empty SurvivalExperiment. You can then assign the model using the models setter method.
minDaysSurvived

An integer specifying the minimum days survived to be considered in the ‘good’ survival prognosis group.

... Fall through parameter to SurvivalModel constructor.

randomSeed

An integer randomSeed that was used to train the model. Users should specify this when initializing a model to ensure reproducibility.

Value

A GeneFuModel object, with model parameters in the

Examples

```r
set.seed(1987)
geneFuModel <- GeneFuModel(randomSeed=1987)
```

GeneFuModel-class

A SurvivalModel Sub-class Designed to Hold A Survival Model Generated Using the genefu R package.

Description

A SurvivalModel Sub-class Designed to Hold A Survival Model Generated Using the genefu R package.

getModelSeed

Generic for retrieving the randomSeed parameter from a SurvivalModel object.

Description

This should be used to set the seed before model training to ensure reproducible results.

Usage

```r
getModelSeed(object)
```

Arguments

object An S4 object to get the seed from.

Value

An integer seed to be used when training the a SurvivalModel.
getTopFeatures

Description
Get the Top Predictive Features from an S4 Object

Usage
getTopFeatures(object, ...)
getTopFeatures, MultiAssayExperiment-method

Arguments

object  An S4 object to get top scoring features from.
...  Allow additional parameters to be defined for this generic.

Value

A character vector of top predictive features.

Examples

data(sampleTrainedPCOSPmodel)

# Get the top features
topFeatures <- getTopFeatures(sampleTrainedPCOSPmodel, numModels=2)

---

getTopFeatures, MultiAssayExperiment-method

Get the Top Ranked Features in a MultiAssayExperiment object

Description

Get the Top Ranked Features in a MultiAssayExperiment object

Usage

## S4 method for signature 'MultiAssayExperiment'
getTopFeatures(object, numFeats, ...)

Arguments

object  A SummarizedExperiment to extract top features from
numFeats  An integer number of top ranked features to extract.
...  Fall through arguments to rankFeatures.

Value

A character vector of top ranked features, with the features in order of rank ascending.

See Also

rankFeatures, MultiAssayExperiment-method
getTopFeatures,PCOSP-method

Get the top features for classification using a PCOSP model object.

Description
Get the top features for classification using a PCOSP model object.

Usage
```
## S4 method for signature 'PCOSP'
getTopFeatures(object, numModels)
```

Arguments
- **object**: A PCOSP model object which has been trained with `trainModel`.
- **numModels**: An integer specifying the number of top models to use features from. Defaults to top 10% of KTSPs models.

Value
A character vector of gene names representing the unique genes from the top `numModels` KTSPs models in the model object.

Examples
```
data(sampleTrainedPCOSPmodel)

# Get the top features
topFeatures <- getTopFeatures(sampleTrainedPCOSPmodel, numModels=5)
```

getTopFeatures,SummarizedExperiment-method

Get the Top Ranked Features in a SummarizedExperiment object

Description
Get the Top Ranked Features in a SummarizedExperiment object.

Usage
```
## S4 method for signature 'SummarizedExperiment'
getTopFeatures(object, numFeats, ..., rankCol = "feature_rank")
```

Arguments
- **object**: A SummarizedExperiment object.
- **numFeats**: An integer specifying the number of top features.
- **rankCol**: A character string specifying the column name to use for ranking.

Value
A character vector of gene names representing the unique genes from the top `numFeats` features in the model object.

Examples
```
data(sampleSummarizedExperiment)

# Get the top features
topFeatures <- getTopFeatures(sampleSummarizedExperiment, numFeats=5)
```
Arguments

- **object**: A `SummarizedExperiment` to extract top features from
- **numFeats**: An integer number of top ranked features to extract.
- **...**: Fall through arguments to `rankFeatures`, which is used to calculate the ranks if `rankCol` is not present the object `rowData`.
- **rankCol**: The name of the column containing the integer feature ranks. Defaults to `feature_rank`, as calculated with `rankFeatures`, but users can alternatively specify their own custom rank column if desired.

Value

A character vector of top ranked features, with the features in order of rank ascending.

Examples

```r
data(sampleICGCmicro)
getTopFeatures(sampleICGCmicro, numFeats=20)
```

---

**haiderSigScores**

*Classifier survival scores for Haider*

Description

The classifier risk scores from Haider et al. (2014)

Examples

```r
# Loads chen, birnbaum and haiderSigScores objects
data(existingClassifierData)
```

---

**hasColDataColumns**

*Check for Column Names in the colData Slot of a SummarizedExperiment*

Description

Check for Column Names in the colData Slot of a `SummarizedExperiment`

Usage

```r
hasColDataColumns(SE, values)
```
merge, SurvivalExperiment, SurvivalExperiment-method

Arguments

- **SE**
  A SummarizedExperiment object to check for the existence of colData columns.

- **values**
  A character vector with one or more column name to check for in the column data.

Value

logical True if all of values are column names in the SummarizedExperiment object, FALSE otherwise.

Examples

```r
SE <- SummarizedExperiment(matrix(rnorm(100), 10, 10),
  colData=data.frame(test=rep(1, 10)))
hasColDataColumns(SE, 'test')
```

---

merge, SurvivalExperiment, SurvivalExperiment-method

*Merge two SurvivalExperiments, subsetting to shared rows and columns*

Description

Merge two SurvivalExperiments, subsetting to shared rows and columns

Usage

```r
## S4 method for signature 'SurvivalExperiment,SurvivalExperiment'
merge(x, y, cohortNames)
```

Arguments

- **x**
  A SurvivalExperiment.

- **y**
  A SurvivalExperiment.

- **cohortNames**
  An optional character vector specifying the a name for each SurvivalExperiment.

Value

A SurvivalExperiment object with merge data from x and y, and the assay from each in the assays slot.
Examples

data(sampleICGCmicro)
survExp2 <- sampleICGCmicro
mergedSurvExp <- merge(survExp2, sampleICGCmicro,
  cohortNames=c('copyICGCmicro', 'ICGCmicro'))
mergedSurvExp

ModelComparison Constructor

Description

ModelComparison Constructor

Usage

ModelComparison(model1, model2, ...)

Arguments

model1 An object with a validationStats method which returns a data.table. Probably this object should inherit from SurvivalModel.

model2 An object with a validationStats method which returns a data.table. Probably this object should inherit from SurvivalModel.

... Not used.

Value

A ModelComparison object, which is a wrapper for DataFrame which is used for method dispatch.

Examples

data(sampleValPCOSPmodel)
data(sampleClinicalModel)
data(sampleCohortList)

# Set parallelization settings
BiocParallel::register(BiocParallel::SerialParam())

# Train the models
trainedClinicalModel <- trainModel(sampleClinicalModel)

# Predict risk/risk-class
clinicalPredCohortL <- predictClasses(sampleCohortList[c('PCSI', 'TCGA')],
  model=trainedClinicalModel)

# Validate the models
validatedClinicalModel <- validateModel(trainedClinicalModel,
    valData=clinicalPredCohortL)

# Compare the models
modelComp <- ModelComparison(sampleValPCOSPmodel, validatedClinicalModel)
head(modelComp)

---

ModelComparison-class  

ModelComparison Class Definition

---

modelParams  

Generic for Accessing the Model Parameters of an S4 Object

---

Description

Generic for Accessing the Model Parameters of an S4 Object

Usage

modelParams(object, ...)

Arguments

  object  
  A S4 Object.

  ...  
  Allow additional arguments to be defined for this generic.

Value

A List- or list-like object containing all the parameters needed to reproduce a specific model training run, including environmental settings like the random seed and RNGkind.

Examples

data(CSPC_MAE)
set.seed(1987)
metaclustModel <- ConMetaclustModel(CSPC_MAE, randomSeed=1987)
modelParams(metaclustModel)
modelParams,S4Model-method

Accessor for the Model Parameters of an S4Model Object

Description

Accessor for the Model Parameters of an S4Model Object

Usage

```R
## S4 method for signature 'S4Model'
modelParams(object)
```

Arguments

- `object` A S4Model Object

Value

A `List`- or list-like object containing all the parameters needed to reproduce a specific model training run, including environmental settings like the random seed and RNGkind.

modelParams<-

Generic for Setting the Model Parameters of An S4 Object

Description

Generic for Setting the Model Parameters of An S4 Object

Usage

`modelParams(object, ...) <- value`

Arguments

- `object` An S4 Object
- `...` Allow additional parameters to be defined for this generic.
- `value` A `List`- or list-like object containing the parameters for the model.

Value

None, modifies the object.
Examples

```r
data(CSPC_MAE)
set.seed(1987)
metaclustModel <- ConMetaclustModel(CSPC_MAE, randomSeed=1987)
modelParams(metaclustModel) <- list(alpha=0.05)
```

---

`modelParams<-`, `S4Model`, `List_or_list_or_NULL-method`

*Setter for the* `modelParams` *of an* `S4Model`

### Description

Setter for the `modelParams` of an `S4Model`

### Usage

```r
## S4 replacement method for signature 'S4Model,List_or_list_or_NULL'
modelParams(object) <- value
```

#### Arguments

- `object`  
  An `S4Model`

- `value`  
  A List- or list-like object containing the parameters for the model.

### Details

This method if not intended for interactive use and will throw an warning when used interactively.

### Value

None, modifies the object.

---

`models`

*Accessor for the models slot of an S4 object*

### Description

Accessor for the models slot of an S4 object

### Usage

```r
models(object, ...)
```
models,S4Model-method

Arguments

object An S4 object to retrieve models from.
...

Value

An S4 object representing a model.

Examples

data(CSPC_MAE)
set.seed(1987)
metaclustModel <- ConMetaclustModel(CSPC_MAE, randomSeed=1987)
models(metaclustModel)
models<-

models, SurvivalModel-method

*Getter for the models slot of a SurvivalModel object*

**Description**

Getter for the models slot of a SurvivalModel object

**Usage**

```r
## S4 method for signature 'SurvivalModel'
models(object)
```

**Arguments**

- `object` A SurvivalModel model object to retrieve the models slot from.

**Value**

A SimpleList of top scoring KTSPmodels

**Examples**

```r
data(samplePCOSPmodel)
models(samplePCOSPmodel)
```

models<-

*Accessor for the models slot of an S4 object*

**Description**

Accessor for the models slot of an S4 object

**Usage**

```r
models(object, ...) <- value
```

**Arguments**

- `object` An S4 object to retrieve models from.
- `...` Allow new parameters to be defined for this generic.
- `value` A List- or list-like object.
Value

None, updates the object.

Examples

data(CSPC_MAE)
set.seed(1987)
metaclustModel <- ConMetaclustModel(CSPC_MAE, randomSeed=1987)
models(metaclustModel) <- list(model1='some_kind_of_model')

Description

Setter for the Models Slot of an S4Model Object

Usage

## S4 replacement method for signature 'S4Model, List_or_list_or_NULL'
models(object) <- value

Arguments

object An S4Model object to retrieve models from.
value A List- or list-like object.

Value

An List- or list-like object representing a model.

Description

Setter for the models slot of a SurvivalModel object

Usage

## S4 replacement method for signature 'SurvivalModel, SimpleList'
models(object) <- value
NetworkCommunitySearchModel

Arguments

  object  A SurvivalModel object to update
  value   A SimpleList of trained KTSP models

Value

  None, updates the object.

Examples

  data(samplePCOSPmodel)
  models(samplePCOSPmodel) <- SimpleList(model=NA)

NCSModel-class  S4Model Class for Metaclustering Using Network Community Search

Description

  S4Model Class for Metaclustering Using Network Community Search

NetworkCommunitySearchModel

  Constructor for a NetworkCommunitySearchModel (NCSModel)

Description

  Use igraph::fastgreedy.community cross-cohort metaclusters for a ConsensusMetaclusteringModel
  which has been validated with validateModel.

Usage

  NetworkCommunitySearchModel(model)

Arguments

  model   A validated ConsensusMetaclusteringModel object.

Value

  An NCSModel object containing the relevant data from the ConsensusMetaclusteringModel.
**normalize, data.frame_or_matrix-method**

*Normalize a data.frame Object*

**Description**

Normalize a data.frame Object

**Usage**

```r
## S4 method for signature 'data.frame_or_matrix'
normalize(object, MARGIN = 2, FUN = "proprocessCaret", ...)
```

**Arguments**

- `object`: A data.frame object to normalize.
- `MARGIN`: An integer indicating if rows (1) or columns (2) should be normalized. Defaults to 2 for columns.
- `FUN`: A function to normalize your data with. Should accept a rectangular object such as a matrix, data.frame, or data.table and return an object of the same class with the data normalized using FUN.
- `...`: Fall through parameters to FUN. For the default FUN, these are passed to caret::preProcess to allow configuration of the normalization method. Omitting any arguments with the default FUN will scale and center the data.

**Value**

The data.frame normalized.

**normalize, DFrame-method**

*Normalize a S4 DFrame Object*

**Description**

Normalize a S4 DFrame Object

**Usage**

```r
## S4 method for signature 'DFrame'
normalize(object, MARGIN = 2, FUN = "preprocessCaret", ...)
```
Arguments

object
A DFrame or DataFrame object to normalize.

MARGIN
An integer indicating if rows (1) or columns (2) should be normalized. Defaults to 2 for columns.

FUN
A function to normalize your data with. Should accept a rectangular object such as a matrix, data.frame, or data.table and return an object of the same class with the data normalized using FUN.

... Fall through parameters to FUN. For the default FUN, these are passed to caret::preProcess to allow configuration of the normalization method. Omitting any arguments with the default FUN will scale and center the data.

Value

A normalized DataFrame object.

Description

For this method to work, there must be a normalize method defined for all classes of experiments in the MultiAssayExperiment

Usage

## S4 method for signature 'MultiAssayExperiment'
normalize(
  object,
  MARGIN = 2,
  FUN = "preprocessCaret",
  ...
)

Arguments

object
A SummarizedExperiment object with assays to normalize.

MARGIN
An integer indicating if rows (1) or columns (2) should be normalized. Defaults to 2 for columns.

FUN
A function to normalize your data with. Should accept a rectangular object such as a matrix, data.frame, or data.table and return an object of the same class with the data normalized using FUN.

... Fall through parameters to FUN. For the default FUN, these are passed to caret::preProcess to allow configuration of the normalization method. Omitting any arguments with the default FUN will scale and center the data.
### Description

Normalize the assays in a `SummarizedExperiment` Object

### Usage

```r
## S4 method for signature 'SummarizedExperiment'
normalize(
  object,
  MARGIN = 2,
  FUN = "preprocessCaret",
  ...
)
```

### Arguments

- **object**: A `SummarizedExperiment` object with assays to normalize.
- **MARGIN**: An integer indicating if rows (1) or columns (2) should be normalized. Defaults to columns. Defaults to 2.
- **FUN**: A function to normalize your data with. The function should accept a matrix, normalize the columns then return a matrix. The data will be transposed before applying FUN if MARGIN=1.
- **...**: Fall through parameters to FUN. When using the default FUN, the data is scaled and centered when no additional arguments are specified.
- **whichAssays**: A numeric or character vector specifying the indices or names of the assays to normalize. Defaults to all assays.

### Details

When using the default FUN, it is also possible to impute missing values. See `?caret::preProcess` for information on available methods.

### Value

The `MultiAssayExperiment` with one or more of the assays normalized and information about the normalization method in the normalization item of the object metadata.

### See Also

`preprocessCaret`, `caret::preProcess`
Details

When using the default FUN, it is also possible to impute missing values. See ?caret::preProcess for information on available methods.

Value

The SummarizedExperiment with one or more of the matrices in assays normalized and the normalization details in the normalization item of the object metadata.

See Also

caret::preProcess

| normalsMAE | A MultiAssayExperiment containing cohorts of normal patients, for package examples. |

Description

A MultiAssayExperiment containing cohorts of normal patients, for package examples.

Examples

data(normalsMAE)

optimalKMinimizeAmbiguity

Predict optimal K values by minimizing the difference between the ECDF of clustering consensus at two points in a subinterval.

Description

Predict optimal K values by minimizing the difference between the ECDF of clustering consensus at two points in a subinterval.

Usage

optimalKMinimizeAmbiguity(assayClusters, subinterval = c(0.1, 0.9))
PCOSP

Arguments

assayClusters  A SimpleList of clustering results from a ConsensusMetaclusteringModel, as returned by `models(object)` where object is a trained ConsensusMetaclusteringModel object.

subinterval  A numeric vector of two float values, the first being the lower and second being the upper limit of the subinterval to compare cluster ambiguity over. Default is c(0.1, 0.9), i.e. comparing the 10th and 90th percentile of cluster consensus to calculate the ambiguity of a given clustering solution. This is the value used to selected the optimal K value from the potential solutions for each assay in the training data.

Value

A numeric vector the same length as assayClusters, with an optimal K prediction for each assay in the rawdata slot of the trained ConsensusMetaclusteringModel object which assayClusters came from.

---

PCOSP  
Pancreatic Cancer Overall Survival Predictor (PCOSP) Constructor

Description

Pancreatic Cancer Overall Survival Predictor (PCOSP) Constructor

Usage

PCOSP(trainCohorts, minDaysSurvived = 365, ..., randomSeed)

Arguments

trainCohorts  A CohortList or SurvivalExperiment containing the training data for the PCOSP model.

minDaysSurvived  An integer indicating the minimum number of day required to be in the 'good' survival group. Any patients below this cut-off will be considered low survival. Default is 365 days.

...  Force subsequent parameters to be named. This parameter is not used.

randomSeed  An integer randomSeed that was used to train the model. Users should specify this when initializing a model to ensure reproducibility.

Details

This function assumes there is only 1 assay per SurvivalExperiment.
PCOSP_or_RLS_or_RGA-class

Value

A PCOSP object with training data in the assays slot, concatenating together the molecular data types and labelling the genes with the data type to ensure the results are easily interpretable.

Examples

data(sampleICGCmicro)
set.seed(1987)
PCOSPmodel <- PCOSP(sampleICGCmicro, minDaysSurvived=365, randomSeed=1987)

PCOSP-class

Pancreatic Cancer Overall Survival Predictor (PCOSP) Class

Description

Pancreatic Cancer Overall Survival Predictor (PCOSP) Class

PCOSP_or_ClinicalModel-class

Class Union for PCOSP and ClinicalModel Types

Description

Class union used for method dispatch without inheritance

PCOSP_or_RLS_or_RGA-class

Class Union for PCOSP, RLSModel and RGAModel Types

Description

Class union used for method dispatch without inheritance
Description
A Generic for Plotting a Network Graph From an S4 Object

Usage
plotNetworkGraph(object, ...)

Arguments
- object: An S4 object with a valid plotNetworkGraph method set.
- ...: Allow additional arguments to be defined for this generic.

Value
A network plot, either as an object or via side effects.

plotNetworkGraph,NCSModel-method
Plot a Network Graph for a Classified NCSModel Object

Description
Visualize metacusters predicted using network community search on the consensus clustering results for a MultiAssayExperiment of patient cohorts.

Usage
## S4 method for signature 'NCSModel'
plotNetworkGraph(object, ..., palette = "Set1", clusterLabels)

Arguments
- object: A classified NCSModel object, as returned by the predictClasses method.
- ...: Not used, force subsequent arguments to be named.
- palette: character A valid pallete for use in RColourBrewer::brewer.pal
- clusterLabels: A character vector of names for the metaclusters. Defaults to the cluster number.

Value
A ggplot object containing the network graph, showing the relative edge distances between each cluster in each cohort along with the predicted metacluster label.
plotROC

Plot ROC curves for an S4 object

Description
Plot ROC curves for an S4 object

Usage
plotROC(object, ...)

Arguments

object An S4 object with a defined plotROC method.
...

Allow new parameters to be added to this generic.

Value
A ggplot object containing the ROC curves.

plotROC,PCOSP-method

Plot ROC curves for a PCOSP model object.

Description
Plot ROC curves for a PCOSP model object.

Usage
## S4 method for signature 'PCOSP'
plotROC(object, alpha = 0.05, ..., xlabel, ylabel, title)

Arguments

object A PCOSP model which has been validated with the validateModel method.
alpha A float specifying the significance level for the plot. Non-significant cohorts will have dotted lines.
...

Catch unnamed parameters. Not used.
xlabel A character vector specifying the x label.
ylabel A character vector specifying the y label.
title A character vector specifying the plot title.

Value
A ggplot object containing the ROC curves.
Examples

```r
data(sampleValPCOSPmodel)

# Plot ROC curves
AUROCplot <- plotROC(sampleValPCOSPmodel)
```

---

### plotSurvivalCurves

Generic for Plotting Survival Curves from an S4 Object

#### Description

Generic for Plotting Survival Curves from an S4 Object

#### Usage

```r
plotSurvivalCurves(object, ...)
```

#### Arguments

- `object`: An S4 object to plot survival curves for.
- `...`: Allow new parameters to be defined on this generic.

#### Value

A plot, either via side-effects or as the return value.

---

### plotSurvivalCurves, CoxModel-method

Plot Survival Curves from a Fit CoxModel Object

#### Description

Plot Survival Curves from a Fit CoxModel Object

#### Usage

```r
## S4 method for signature 'CoxModel'
plotSurvivalCurves(object, byCohort = TRUE, ..., facet.by = "cohort")
```
predictClasses

Arguments

object
A CoxModel object with survival curves fit via the trainModel method.
byCohort
TRUE to return a single plot object faceted by facet.by, FALSE to get a list of individual survival curves per cohort.
... 
Fall through parameters to survminer::ggsurvplot function.
facet.by
What column of the object modelDT to use for faceting the survival plot. Defaults to 'cohorts'. Only used if byCohort is TRUE.

Value

A ggplot or list of ggplot objects containing the survival curves for each cohort in the trainData slot of the CoxModel.

Description

Predict Classes for New Data Based on a Train Classifier Model

Usage

predictClasses(object, model, ...)

Arguments

object
An S4 object containing data to predict classes from.
model
An S4 object containing one or more trained classification models.
... 
Allow further parameters to be defined on this generic.

Value

The S4 object with class predictions added to the metadata.

Examples

data(sampleTrainedPCOSPmodel)
data(samplePCISurvExp)

# Set parallelization settings
BiocParallel::register(BiocParallel::SerialParam())

# Make predictions
PCOSPpredSurvExp <- predictClasses(samplePCISurvExp,
model=sampleTrainedPCOSPmodel)
head(colData(PCOSPpredSurvExp))
predictClasses, CohortList, ClinicalModel-method

Use a Clinical GLM to Predict Classes for a CohortList of SurvivalExperiment Objects.

Description

Use a Clinical GLM to Predict Classes for a CohortList of SurvivalExperiment Objects.

Usage

## S4 method for signature 'CohortList,ClinicalModel'

predictClasses(object, model, ..., na.action = "na.exclude", type = "response")

Arguments

object A CohortList with SurvivalExperiments to predict classes for. The colData slot in ALL SurvivalExperiments must have column names which match the formula in the model object.

model A trained ClinicalModel object, as return by trainModel.

... Fall through parameters to stats::predict.

na.action The na.action parameter passed to stats::predict.glm.

type The type parameter passed to stats::predict.glm.

Value

A CohortList with the model predictions in the colData slot as clinical_prob_good for each SurvivalExperiment, and the model in the metadata as predictionModel.

Examples

data(sampleClinicalModel)
data(sampleCohortList)

# Set parallelization settings
BiocParallel::register(BiocParallel::SerialParam())

# Train Model
trainedClinicalModel <- trainModel(sampleClinicalModel)

# Make predictions
ClinicalPredCohortList <- predictClasses(sampleCohortList[c('PCSI', 'TCGA')], model=trainedClinicalModel)

head(colData(ClinicalPredCohortList[[1]]))
**predictClasses,CohortList,GenFuModel-method**

*Use a Gene Signature Based Prediction Model from the genefu Package to Predict Signature Scores for Each Sample*

---

**Description**

Use a Gene Signature Based Prediction Model from the genefu Package to Predict Signature Scores for Each Sample

**Usage**

```r
## S4 method for signature 'CohortList,GenFuModel'
predictClasses(object, model, ..., annot = NA)
```

**Arguments**

- `object`: A CohortList with SurvivalExperiments to predict classes for.
- `model`: A trained GenFuModel object.
- `...`: Fall through parameters to `genefu::sig.score`.
- `annot`: The `annot` parameter passed to `genefu::sig.score`. Defaults to NA, which assumes your assay rowname match the gene labels in the model.

**Value**

A CohortList with the model predictions in the colData slot as `genefu_score` for each SurvivalExperiment, and the model in the metadata as `predictionModel`.

---

**predictClasses,CohortList,PCOSP_or_RLS_or_RGA-method**

*Predict Survival Prognosis Classes and Risk Scores for A CohortList Using a PCOSP, RLSModel or RGAModel object.*

---

**Description**

Predict Survival Prognosis Classes and Risk Scores for A CohortList Using a PCOSP, RLSModel or RGAModel object.

**Usage**

```r
## S4 method for signature 'CohortList,PCOSP_or_RLS_or_RGA'
predictClasses(object, model, ...)
```
**predictClasses, ConsensusMetaclusteringModel, ANY-method**

**Arguments**

- **object** A CohortList with SurvivalExperiments to predict classes for.
- **model** A trained PCOSP model to use for predicting classes.
- **...** Fall through arguments to BiocParallel::bplapply for configuring parallelization settings.

**Value**

A CohortList with the model predictions attached to each SurvivalExperiment in the metadata slot and the prob_good_survival column added to the colData slot.

**Examples**

```r
data(sampleTrainedPCOSPmodel)
data(sampleCohortList)

# Set parallelization settings
BiocParallel::register(BiocParallel::SerialParam())

# Make predictions
PCOSPpredCohortList <- predictClasses(sampleCohortList[seq_len(2)],
model=sampleTrainedPCOSPmodel)
head(colData(PCOSPpredCohortList[[1]]))
```

**Description**

Compute the optimal clustering solution out of possibilities generated with trainModel. Assigns the cluster labels to the MultiAssayExperiment object.

**Usage**

```r
## S4 method for signature 'ConsensusMetaclusteringModel, ANY'
predictClasses(object, ..., optimal_k_function = optimalKMinimizeAmbiguity)
```

**Arguments**

- **object** A MultiAssayExperiment object
- **...** Fall through arguments to optimal_k_function. For the default optimal_k_function, you can specify subinterval argument which defines the interval of the ECDF to minimize ambiguity over. Defaults to c(0.1, 0.9) if not specified. See ?optimalKMinimizeAmbiguity for more details on the subinterval parameter.
optimal_k_function

A function which accepts as its input models(object) of a trained ConsensusMetaclusteringModel object, and returns a vector of optimal K values, one for each assay in rawdata(object). The default method is optimalKMinimizeAmbiguity, see ?optimalKMinimizeAmbiguity for more details. Please note this argument must be named or it will not work.

Value

A object ConsensusMetaclusteringModel, with class predictions assigned to the colData of trianData

predictClasses,NCSModel,ANY-method

Predict Metacluster Labels for a NetworkCommunitySearchModel

Description

Predict Metacluster Labels for a NetworkCommunitySearchModel

Usage

## S4 method for signature 'NCSModel,ANY'
predictClasses(object)

Arguments

object A NCSModel which has been trained.

Value

The object model with

predictClasses,SurvivalExperiment,ClinicalModel-method

Predict Survival Prognosis Classes and Risk Scores for A SurvivalModel Using a ClinicalModel Object.

Description

Predict Survival Prognosis Classes and Risk Scores for A SurvivalModel Using a ClinicalModel Object.

Usage

## S4 method for signature 'SurvivalExperiment,ClinicalModel'
predictClasses(object, model, ..., na.action = "na.exclude", type = "response")
predictClasses(SurvivalExperiment, GeneFuModel-method)

Arguments

- **object**: A SurvivalExperiment object with the correct columns in colData to match the formula for the ClinicalModel object.
- **model**: A trained ClinicalModel object, as return by trainModel.
- **...**: Fall through parameters to stats::predict.
- **na.action**: The na.action parameter passed to stats::predict.glm.
- **type**: The type parameter passed to stats::predict.glm

Value

A SurvivalExperiment with the model predictions in the colData slot as clinical_prob_good.

Examples

```r
data(sampleClinicalModel)
data(samplePCSIsurvExp)

# Set parallelization settings
BiocParallel::register(BiocParallel::SerialParam())

# Train Model
trainedClinicalModel <- trainModel(sampleClinicalModel)

# Make predictions
ClinicalPredSurvExp <- predictClasses(samplePCSIsurvExp, model=trainedClinicalModel)
head(colData(ClinicalPredSurvExp))
```

Description

Use a Gene Signature Based Prediction Model from the genefu Package to Predict Signature Scores for Each Sample.

Usage

```r
## S4 method for signature 'SurvivalExperiment, GeneFuModel'
predictClasses(object, model, ..., annot = NA)
```
predictClasses, SurvivalExperiment, PCOSP_or_RLS_or_RGA-method

Arguments

- **object**: A SurvivalExperiment to predict classes for.
- **model**: A GeneFuModel object to predict classes with.
- **...**: Fall through parameters to genefu::sig.score.
- **annot**: A named parameter with annotations mapping from the gene identifiers in the genefu model.

Details

A signature score should be interpreted as unit-less continuous risk predictor.

Value

The SurvivalExperiment passed to the object argument with the genefu_score column added to the objects colData slot.

Description

Predict Survival Prognosis Classes and Risk Scores for A CohortList Using a PCOSP, RLSModel or RGAModel object.

Usage

```r
## S4 method for signature 'SurvivalExperiment,PCOSP_or_RLS_or_RGA'
predictClasses(object, model, ...)
```

Arguments

- **object**: A SurvivalExperiment object to predict classes for.
- **model**: A trained PCOSP model to use for predicting classes.
- **...**: Fall through arguments to BiocParallel::bplapply for configuring parallelization settings.

Value

A SurvivalExperiment with the predictions in its metadata and a column in colData, prob_good_survival, which contains the proportion of models which predicted good prognosis for each sample.

See Also

- BiocParallel::bplapply
- switchBox::SWAP.KTSP.Classify
Examples

```r
data(sampleTrainedPCOSPmodel)
data(samplePCSIsurvExp)

# Set parallelization settings
BiocParallel::register(BiocParallel::SerialParam())

# Make predictions
PCOSPpredSurvExp <- predictClasses(samplePCSIsurvExp,
    model=sampleTrainedPCOSPmodel)
head(colData(PCOSPpredSurvExp))
```

---

```r
preprocessCaret(x, ...)
```

**Arguments**

- `x` The data to be normalized with `caret::preProcess` and `caret::predict`.
- `...` Fall through parameters to `caret::preProcess`. This can be used to apply a range of different preprocessing methods from that package.

**Value**

- `x` preprocessed according to the arguments in `...`.

**See Also**

- `caret::preProcess`, `stats::predict`
RandomGeneAssignmentModel

**RandomGeneAssignmentModel Constructor**

**Description**
RandomGeneAssignmentModel Constructor

**Usage**
RandomGeneAssignmentModel(trainCohorts, minDaysSurvived = 365, ..., randomSeed)

**Arguments**
- `trainCohorts`: A `SurvivalExperiment` containing training data for the `SurvivalModel` object.
- `minDaysSurvived`: An integer minimum number of days survived to be classified as a 'good' prognosis.
- `...`: Force subsequent parameters to be named. Not used.
- `randomSeed`: An integer randomSeed that was used to train the model. Users should specify this when initializing a model to ensure reproducibility.

**Value**
A `SurvivalModel` object.

**Examples**
```r
data(sampleICGCmicro)
set.seed(1987)
RGAmodel <- RGAModel(sampleICGCmicro, minDaysSurvived=365, randomSeed=1987)
```

---

RandomLabelShufflingModel

**RandomLabelShufflingModel Constructor**

**Description**
RandomLabelShufflingModel Constructor

**Usage**
RandomLabelShufflingModel(trainCohorts, minDaysSurvived = 365, ..., randomSeed)
**Arguments**

- **trainCohorts**
  A 'SurviveExperiment' containing training data for the SurvivalModel object.

- **minDaysSurvived**
  An integer minimum number of days survived to be classified as a 'good' prognosis.

- **...**
  Force subsequent parameters to be named. Not used.

- **randomSeed**
  An integer randomSeed that was used to train the model. Users should specify this when initializing a model to ensure reproducibility.

**Value**

A SurvivalModel object.

**Examples**

```r
data(sampleICGCmicro)
set.seed(1987)
RLSmodel <- RLSModel(sampleICGCmicro, minDaysSurvived=365, randomSeed=1987)
```

---

**rankFeatures**

*Rank the Features in a S4 Object*

**Description**

Rank the Features in a S4 Object

**Usage**

```r
rankFeatures(object, ...)
```

**Arguments**

- **object**
  An S4 object where rows represent features.

- **...**
  Allow new parameters to be defined for this generic.

**Value**

The object with the features per value and ranking of the features in the `rowData` slow of the object.

**Examples**

```r
data(sampleICGCmicro)
rankFeatures(sampleICGCmicro)
```
Rank the Features in a MultiAssayExperiment Object

## S4 method for signature 'MultiAssayExperiment'

```r
class("MultiAssayExperiment")
```

### Description

Rank the Features in a MultiAssayExperiment Object

### Usage

```r
## S4 method for signature 'MultiAssayExperiment'
rankFeatures(
  object,
  FUN = "mad",
  RANK_FUN = "dense_rank",
  ..., 
  descending = TRUE,
  weights
)
```

### Arguments

- `object`: A MultiAssayExperiment to rank the features in.
- `FUN`: A vectorized feature scoring function, such as `var` or `mad`. Defaults to `mad` from the BiocGenerics package.
- `RANK_FUN`: A ranking function, such as `rank` or `dense_rank`. Defaults to `dense_rank` from dplyr.
- `...`: Fall through arguments to `FUN`, such as `na.rm=TRUE`.
- `descending`: Should your rank function be called with `~` before the values from `FUN`. Defaults to `TRUE`, which should be used if high values returned from `FUN` are good.
- `weights`: A named numeric weighting vector with a weight for each experiment in the MultiAssayExperiment object. Names must match the `names(experiments(object))`. Passed to `matrixStats::weightedMedian` when aggregating feature scores per assay. Defaults to the sample size of an assay relative to the largest sample size when this parameter is missing.

### Value

The MultiAssayExperiment with the item `featureRanks` in the object metadata, which stores a DataFrame containing ranks across all assays for each unique feature and the additional columns `feature_score` and `feature_rank`, as calculated with `FUN` and `RANK_FUN`, respectively. Information about which functions were used for each column can be found in the object `mcols` in the `calculated_with` column.

### See Also

- `BiocGenerics::mad`, `dplyr::dense_rank`, `matrixStats::weightedMedian`
rankFeatures, SummarizedExperiment-method

Rank the Features in a SummarizedExperiment Object

Description

Rank the Features in a SummarizedExperiment Object

Usage

```r
## S4 method for signature 'SummarizedExperiment'
rankFeatures(
  object,
  FUN = "rowMads",
  RANK_FUN = "dense_rank",
  ..., 
  descending = TRUE,
  assay = 1
)
```

Arguments

- `object` A SummarizedExperiment to rank the features in.
- `FUN` A row-wise summary function, such as `rowVars`, `rowMads`, etc. defaults to `MatrixGenerics::rowMads`.
- `RANK_FUN` A ranking function, such as `rank` or `dense_rank`. Defaults to `dplyr::dense_rank`.
- `...` Fall through arguments to `FUN`, such as `na.rm=TRUE`.
- `descending` Should your rank function be called with `-` before the values from `FUN`. Defaults to `TRUE`.
- `assay` integer assay to use for the ranking, as passed to the `SummarizedExperiment::assay` function. Defaults to the first assay.

Value

The SummarizedExperiment with the column `feature_score` and `feature_rank` in the `rowData` slot. Information about which functions were used for each column can be found in the object `mcols` in the `calculated_with` column.

Examples

```r
data(sampleICGCmicro)
rankFeatures(sampleICGCmicro, FUN='rowMads', RANK_FUN='dense_rank')
```
removeColDataFactorColumns

Remove any factor columns from the colData of an S4 object

Description
Remove any factor columns from the colData of an S4 object

Usage
removeColDataFactorColumns(x)

Arguments
x An S4 object with a colData method defined for it.

Value
x with colData factor columns converted to either integer or character, as appropriate.

Examples
data(sampleICGCmicro)
removeColDataFactorColumns(sampleICGCmicro)

removeFactorColumns

Convert factor columns in a rectangular object

Description
Convert factor columns in a rectangular object

Usage
removeFactorColumns(x)

Arguments
x A list-like rectangular object such as a data.frame, data.table, or DataFrame.

Value
x with factor columns converted to either integer or character, as appropriate.
**renameColDataColumns**

*Examples*

```r
x <- data.frame(a=factor(LETTERS[1:5]), b=factor(runif(5, 0, 1)))
removeFactorColumns(x)
```

**Description**

Rename the columns in the `colData` slot, or do nothing if they don’t match.

**Usage**

```r
renameColDataColumns(x, values)
```

**Arguments**

- `x` An S4 object with a `colData` method.
- `values` A character vector where names are the existing column names and values are the new column names.

**Value**

`x` with updated column names, if they match any existing columns.

**Examples**

```r
data(sampleICGCmicro)
renameColDataColumns(sampleICGCmicro, c(event_occurred='days_survived'))
```

---

**renameColumns**

*Rename columns or do nothing if the names don’t match*

**Description**

Rename columns or do nothing if the names don’t match.

**Usage**

```r
renameColumns(x, values)
```
Arguments

x An object for which colnames is defined, probably a data.frame or other similar object.

values A character vector where names are the old column names and values are the new column names. Uses gsub internally to do the renaming.

Value

x with the updated column names if they are present. Does not fail if the column names are missing.

Examples

x <- data.frame(a=factor(LETTERS[1:5]), b=factor(runif(5, 0, 1)))
renameColumns(x, c(a='c'))

---

RGAModel-class  

RGAModel Class Definition

---

Description

RGAModel Class Definition

---

RLSModel-class  

RLSModel Class Definition

---

Description

RLSModel Class Definition

---

runGSEA  

Run Gene Set Enrichment Analysis

---

Description

Run Gene Set Enrichment Analysis

Usage

runGSEA(object, geneSet, ...)

---
Arguments

object An S4 object to conduct Gene Set Enrichment Analysis (GSEA) with.
geneSet An object representing a gene set, such as a data.frame.
... Allow additional parameters to be defined for this generic.

Value

A data.frame containing the significantly enriched gene sets.

Description

Run Gene Set Enrichment Analysis On A PCOSP Model Object.

Usage

## S4 method for signature 'PCOSP,data.frame'
runGSEA(object, geneSet, numModels, ..., adjMethod = "fdr", allResults = FALSE)

Arguments

object A PCOSP model which has been trained with trainModel.
geneSet A data.frame with two columns, the first being the name of the gene and the second the gene set. The gene names must match the rownames of object. Additional columns will be dropped.
numModels The number of models to use when selecting the top features from the PCOSP model in object. If missing will default to the top 10% of models.
... Force subsequent parameters to be named. Not used.
adjMethod An optional parameter specifying the multiple testing correction to use in piano::runGSAhyper. This parameter must be named.
allResults Return the full results from piano::runGSAhyper instead of a data.frame of significant results? Default is FALSE. This parameter must be named.

Value

A data.table containing the significantly enriched gene sets.
S4Model-class

An S4 Virtual Class For the Concept of a Statistical or ML Model

Description

An S4 Virtual Class For the Concept of a Statistical or ML Model

Slots

- trainData: An object inheriting from List or list representing the training data for the model.
- modelParams: An object inheriting from List or list representing the parameters needed to train the model.
- models: An object inheriting from List or list representing the trained models.
- validationStats: An object inheriting from DFrame or data.frame and storing statistics assessing model performance.
- validationData: An object inheriting List or list representing the data used to validate or evaluate the performance of a model.
- elementMetadata: A DataFrame or 'data.frame' of item metadata for the models slot.
- metadata: A List or list of model level metadata.

sampleClinicalModel

Sample ClinicalModel Containing the ICGC micro-array cohort from MetaGxPancreas as training data.

Description

Sample ClinicalModel Containing the ICGC micro-array cohort from MetaGxPancreas as training data.

See Also

MetaGxPancreas::loadPancreasDatasets

Examples

data(sampleClinicalModel)
sampleCohortList

**Description**

A CohortList object containing sample data for the PCOSP vignette. This data is a subset of the Pancreas datasets available in MetaGxPancreas.

**See Also**

MetaGxPancreas::loadPancreasDatasets

**Examples**

data(sampleCohortList)

---

sampleICGCmicro

**Description**

A Sample SurvivalExperiment Containing Data from the ICGC micro-array cohort from MetaGxPancreas

**See Also**

MetaGxPancreas::loadPancreasDatasets

**Examples**

data(sampleICGCmicro)
**samplePCOSPmodel**

A Sample PCOSP Model Containing the ICGC micro-array cohort from MetaGxPancreas as training data.

**Description**

A Sample PCOSP Model Containing the ICGC micro-array cohort from MetaGxPancreas as training data.

**See Also**

MetaGxPancreas::loadPancreasDatasets

**Examples**

```r
data(samplePCOSPmodel)
```

---

**samplePCOSPpredList**

Sample CohortList with PCOSP Risk Predictions

**Description**

Sample CohortList with PCOSP Risk Predictions

**See Also**

MetaGxPancreas::loadPancreasDatasets

**Examples**

```r
data(samplePCOSPpredList)
```
SampleSurvExp

Sample SurvivalExperiment Containing the PCSI rna-sequencing cohort from MetaGxPancreas.

Description

Used as validation data for modelling examples

See Also

MetaGxPancreas::loadPancreasDatasets

Examples

data(samplePCSIsurvExp)

SampleRGAmodel

Sample RGA Model Containing the ICGC micro-array cohort from MetaGxPancreas as training data.

Description

Sample RGA Model Containing the ICGC micro-array cohort from MetaGxPancreas as training data.

See Also

MetaGxPancreas::loadPancreasDatasets

Examples

data(sampleRGAmodel)
sampleRLSmodel

Sample RLS Model Containing the ICGC micro-array cohort from MetaGxPancreas as training data.

Description

Sample RLS Model Containing the ICGC micro-array cohort from MetaGxPancreas as training data.

See Also

MetaGxPancreas::loadPancreasDatasets

Examples

data(sampleRLSmodel)

---

sampleTrainedPCOSPmodel

A Sample Trained PCOSP Model Containing the ICGC micro-array cohort from MetaGxPancreas as training data.

Description

A Sample Trained PCOSP Model Containing the ICGC micro-array cohort from MetaGxPancreas as training data.

See Also

MetaGxPancreas::loadPancreasDatasets

Examples

data(sampleTrainedPCOSPmodel)
Description

Sample Validated PCOSP Model for Plotting Examples

See Also

MetaGxPancreas::loadPancreasDatasets

Examples

data(sampleValPCOSPmodel)

show,S4Model-method

Show method for Classes Inheriting from S4Model

Description

Show method for Classes Inheriting from S4Model

Usage

## S4 method for signature 'S4Model'
show(object)

Arguments

object

A S4Model derivative to show.

Value

None, prints to console.

Examples

data(CSPC_MAE)
set.seed(1987)
metaclustModel <- ConMetaclustModel(CSPC_MAE, randomSeed=1987)
metaclustModel
subset,CohortList-method

Subset method for a CohortList

Description

Works using endoapply of \( \) over the list SurvivalExperiments.

Usage

```r
## S4 method for signature 'CohortList'
subset(x, subset = TRUE, select = TRUE, invert = FALSE)
```

Arguments

- \( x \) 
  A CohortList object
- \( \text{subset} \)
  The row query. Defaults to TRUE, i.e., select all.
- \( \text{select} \)
  The column query. Defaults to TRUE, i.e., select all.
- \( \text{invert} \)
  A logical vector indicating if the matches should be inverted. Default is FALSE.

Value

A CohortList containing only the rows and columns selected in \( i \) and \( j \), respectively.

Examples

```r
data(sampleCohortList)
commonGenes <- findCommonGenes(sampleCohortList)
commonGenesCohortList <- subset(sampleCohortList, subset=commonGenes)
```

SurvivalExperiment

Constructor for SurvivalExperiment Class

Builds a SurvivalExperiment object, which is just a wrapper for a SummarizedExperiment with mandatory survival metadata numeric columns \( \text{survival\_time} \) and \( \text{event\_occurred} \).

Description

Constructor for SurvivalExperiment Class

Builds a SurvivalExperiment object, which is just a wrapper for a SummarizedExperiment with mandatory survival metadata numeric columns \( \text{survival\_time} \) and \( \text{event\_occurred} \).
SurvivalExperiment-class

Usage

SurvivalExperiment(
  ..., 
  survival_time = "survival_time",
  event_occurred = "event_occurred"
)

Arguments

... pairlist Fall through arguments to the SummarizedExperiment constructor. If the first argument to dots is a SummarizedExperiment, that object is used instead.

survival_time A character vector indicating the column name in colData which contains the integer number of days a patient has survived since treatment at the time of data collection. If event_occurred is 1/TRUE, then this is the number of days the patient lived.

event_occurred A character vector indicating the column name in colData which contains logical or integer values where 0/FALSE means a patient is alive and 1/TRUE means a patient is deceased.

Value

A SurvivalExperiment object.

Examples

data(sampleICGCmicro)

# build a SurvivalExperiment from raw data
ICGCmicro <- SurvivalExperiment(assays=assays(sampleICGCmicro),
  rowData=rowData(sampleICGCmicro), colData=colData(sampleICGCmicro),
  metadata=metadata(sampleICGCmicro), survival_time='survival_time',
  event_occurred='event_occurred')

# build a SurvivalExperiment from an existig SummarizedExperment
ICGmicroSumExp <- as(sampleICGCmicro, 'SummarizedExperiment')
ICGmicro <- SurvivalExperiment(ICGmicroSumExp,
  survival_time='survival_time', event_occurred='event_occurred')

Description

A SummarizedExperiment with mandatory numeric survival metadata columns survival_time and event_occurred.
SurvivalModel-class

Constructor for a SurvivalModel Object.

Description

Constructor for a SurvivalModel Object.

Usage

SurvivalModel(trainCohorts, minDaysSurvived = 365, ..., randomSeed)

Arguments

- **trainCohorts**: A 'SurvivalExperiment' containing training data for the SurvivalModel object.
- **minDaysSurvived**: An integer minimum number of days survived to be classified as a 'good' prognosis.
- **...**: Force subsequent parameters to be named. Not used.
- **randomSeed**: An integer randomSeed that was used to train the model. Users should specify this when initializing a model to ensure reproducibility.

Value

A SurvivalModel object.

Examples

```r
data(sampleICGCmicro)
set.seed(1987)
survModel <- SurvivalModel(sampleICGCmicro, minDaysSurvived = 365, randomSeed = 1987)
```

SurvivalModel-class

A Generic Container for Storing Mathematical Models of SurvivalExperiments

Description

An S4 class with a number of predefined methods for accessing slots relevant to a survival model. More specific model types will inherit from this class for their accessor methods and constructor.
Slots

models  A SimpleList containing one or more model object.

validationData  A CohortList containing one or more SurvivalExperiment objects used to validate the model. This slot is populated by the when the validateModel method is called on a SurvivalModel object.

validationStats  A data.frame object containing validation statistics calculated by the validateModel method.

Examples

data(sampleICGCmicro)
set.seed(1987)
survModel <- SurvivalModel(sampleICGCmicro, minDaysSurvived=385, randomSeed=1987)

trainData

Generic for Accessing the Training Data of an S4 Object

Description

Generic for Accessing the Training Data of an S4 Object

Usage

trainData(object, ...)

Arguments

object  An S4 object to retrieve training data from.

...  Allow new parameters to be defined for this generic.

Value

The training data for an S4 object.

Examples

data(CSPC_MAE)
set.seed(1987)
metaclustModel <- ConMetaclustModel(CSPC_MAE, randomSeed=1987)
trainData, S4Model-method

Accessor for the Training Data in a S4Model Object

Description

Accessor for the Training Data in a S4Model Object

Usage

```r
## S4 method for signature 'S4Model'
trainData(object)
```

Arguments

- `object` An S4Model object to retrieve training data from.

Value

The training data for an S4Model Object.

trainData<- Generic for Accessing the Training Data of an S4 Object

Description

Generic for Accessing the Training Data of an S4 Object

Usage

```r
trainData(object, ...) <- value
```

Arguments

- `object` An S4 object to retrieve training data from.
- `...` Allow new parameters to be defined for this generic.
- `value` An object to place in the objects training data slot.

Value

None, updates the object.
trainData<-,S4Model-method

Examples

```r
data(CSPC_MAE)
set.seed(1987)
metaclustModel <- ConMetaclustModel(CSPC_MAE, randomSeed=1987)
trainData(metaclustModel) <- CSPC_MAE
```

**Description**

Accessor for the Training Data in a S4Model Object

**Usage**

```r
## S4 replacement method for signature 'S4Model'
trainData(object) <- value
```

**Arguments**

- **object**
  - An S4Model object to retrieve training data from.
- **value**
  - An object to put into the model training data.

**Value**

The training data for an S4Model Object.

**trainModel**

Train a Model Based on the Data in an S4 Object

**Description**

Train a Model Based on the Data in an S4 Object

**Usage**

```r
trainModel(object, ...)
```

**Arguments**

- **object**
  - An S4 object representing an untrained statistical or machine. learning model.
- **...**
  - Allow new method to be defined for this generic.
Value

The same object with the @model slot populated with the fit model

Examples

data(samplePCOSPmodel)
set.seed(getModelSeed(samplePCOSPmodel))

# Set parallelization settings
BiocParallel::register(BiocParallel::SerialParam())

trainModel(samplePCOSPmodel, numModels=5, minAccuracy=0.6)

trainModel,ClinicalModel-method

Fit a GLM Using Clinical Predictors Specified in a ClinicalModel Object.

Description

Fit a GLM Using Clinical Predictors Specified in a ClinicalModel Object.

Usage

## S4 method for signature 'ClinicalModel'
trainModel(
  object,
  ...
  family = binomial(link = "logit"),
  na.action = na.exclude
)

Arguments

object A ClinicalModel object, with survival data for the model in the colData slot.
...
family Argument to the family parameter of stats::glm. Defaults to binomial(link='logit').
This parameter must be named.
n.a.action Argument to the na.action parameter of stats::glm. Deafults to 'na.omit', dropping rows with NA values in one or more of the formula variables.

Value

A ClinicalModel object with a glm object in the models slot.
Examples

```r
data(sampleClinicalModel)
set.seed(getModelSeed(sampleClinicalModel))

# Set parallelization settings
BiocParallel::register(BiocParallel::SerialParam())

trainedClinicalModel <- trainModel(sampleClinicalModel)
```

Description

Since consensus clustering is an unsupervised learning method, there isn't really a 'training step' per se. Instead this method computes the consensus clusters and stores the results in the models slot.

Usage

```r
## S4 method for signature 'ConsensusMetaclusteringModel'
trainModel(
  object,
  maxK = 5,
  reps = 10,
  distance = "pearson",
  clusterAlg = "hc",
  plot = NULL,
  ...
)
```

Arguments

- **object**: A ConsensusMetaclusteringModel to train.
- **maxK**: The maximum number of clusters to test. Defaults to 5.
- **reps**: How many random samples should clustering be repeated on? Default is 10, but 1000+ is recommended for real world use.
- **distance**: The distance method to use. Defaults to 'pearson'. See ?ConsensusClusterPlus::ConsensusClusterPlus for more options.
- **plot**: An optional path to output the plots generated by each call to ConsensusClusterPlus::ConsensusClusterPlus. Default is NULL, which suppresses all plots, otherwise passed to the clustering function.
- **...**: Fall through parameters to BiocParallel::bplapply. This can be used to customize your parallelization using BPPARAM or to pass additional arguments to ConsensusClusterPlus.
Value

The ConsensusMetaclusteringModel with the clustering results in the models slot.

Description

Computes models with the survival package for \texttt{coxph}, \texttt{survfit}, \texttt{survdiff} as well as computes the fit p-values using \texttt{pchisq} with the \texttt{chisq} values from \texttt{survdiff}. Modelling data is stored in \texttt{modelData}, as well as a \texttt{data.table} with all model data merged in \texttt{modelDT}. These items are all assigned to the models slot.

Usage

```r
## S4 method for signature 'CoxModel'
trainModel(object)
```

Arguments

- `object`: A \texttt{CoxModel} object to fit models for.

Value

A \texttt{CoxModel} object with the results of \texttt{coxph}, \texttt{survfit} and \texttt{survdiff} in the models slot as lists where each item corresponds to the data in \texttt{modelData}. For convenience, all the model data has also been merged into a single \texttt{data.table} in the \texttt{modelDT} item of models.

Description

Train a GeneFuModel Object

Usage

```r
## S4 method for signature 'GeneFuModel'
trainModel(object)
```

Arguments

- `object`: A \texttt{GeneFuModel} object to train.
Value

An error message, since we have not finished implementing this functionality yet.

Description

Train a NetworkCommunitySearchModel

Usage

## S4 method for signature 'NCSModel'
trainModel(object, alpha = 0.05, minRepro = 0.5, minCor = 0)

Arguments

object An NCSModel object, created from a ConsensusMetaclusteringModel.
alpha A float specifying the significance level for cluster reproducibility. Default is 0.05.
minRepro A float specifying the minimum in-group proportion (IGP) for a cluster to be included in the metacluster labels. Default is 0.5.
minCor A float specifying the minimum correlation between a centroid and assay cluster to be included in the metacluster labels. Default is 0.0.

Value

The NCSModel from object with the networkEdges item of the models slot filtered based on the specified criteria. The criteria are also stored in the modelParam slots to ensure reproducibility.

Description

Uses the switchBox SWAP.Train.KTSP function to fit a number of k top scoring pair models to the data, filtering the results to the best models based on the specified parameters.

Usage

## S4 method for signature 'PCOSP'
trainModel(object, numModels = 10, minAccuracy = 0.6, ...)
Arguments

object A PCOSP object to train.
numModels An integer specifying the number of models to train. Defaults to 10. We recommend using 1000+ for good results.
minAccuracy A float specifying the balanced accuracy required to consider a model 'top scoring'. Defaults to 0.6. Must be in the range [0, 1].
...

Details

This function is parallelized with BiocParallel, thus if you wish to change the back-end for parallelization, number of threads, or any other parallelization configuration please pass BPPARAM to bplapply.

Value

A PCOSP object with the trained model in the model slot.

See Also

switchBox::SWAP.KTSP.Train BiocParallel::bplapply

Examples

data(samplePCOSPmodel)

# Set parallelization settings
BiocParallel::register(BiocParallel::SerialParam())

set.seed(getModelSeed(samplePCOSPmodel))
trainModel(samplePCOSPmodel, numModels=2, minAccuracy=0.6)
trainModel,RLSModel-method

Arguments

- **object**: A RGAModel object to train.
- **numModels**: An integer specifying the number of models to train. Defaults to 10. We recommend using 1000+ for good results.
- **minAccuracy**: A float specifying the balanced accuracy required to consider a model 'top scoring'. Defaults to 0. Must be in the range 0 to 1.
- ...Fall through arguments to BiocParallel::bplapply.

Details

This function is parallelized with BiocParallel, thus if you wish to change the back-end for parallelization, number of threads, or any other parallelization configuration please pass BPPARAM to bplapply.

Value

A RGAModel object with the trained model in the model slot.

See Also

switchBox::SWAP.KTSP.Train BiocParallel::bplapply

Examples

data(sampleRGAModel)
set.seed(getModelSeed(sampleRGAModel))

  # Set parallelization settings
  BiocParallel::register(BiocParallel::SerialParam())

  trainedRGAModel <- trainModel(sampleRGAModel, numModels=2, minAccuracy=0)

---

trainModel,RLSModel-method

*Train a PCOSP Model Based on The Data the assay trainMatrix.*

Description

Uses the switchBox SWAP.Train.KTSP function to fit a number of k top scoring pair models to the data, filtering the results to the best models based on the specified parameters.

Usage

```r
  ## S4 method for signature 'RLSModel'
  trainModel(object, numModels = 10, minAccuracy = 0, ...)
```
validateModel

Perform Validation on an S4 Object Representing a Trained Model

Description

Perform Validation on an S4 Object Representing a Trained Model

Usage

validateModel(model, valData, ...)
validateModel, ClinicalModel, CohortList-method

**Arguments**

- **model**
  - An S4 object.
- **valData**
  - Any Data to verify the model with.
- **...**
  - Allow new parameters to be defined for this generic.

**Value**

The S4 object with added model performance metadata.

**Examples**

data(sampleTrainedPCOSPmodel)
data(samplePCOSPpredList)

# Set parallelization settings
BiocParallel::register(BiocParallel::SerialParam())

# Validate model
validatedPCOSPmodel <- validateModel(sampleTrainedPCOSPmodel,
  valData=samplePCOSPpredList[[1]])

validateModel, ClinicalModel, CohortList-method

*Evaluate the Performance of a List of Trained KTSP Models from a PCOSP Model*

**Description**

Evaluate the Performance of a List of Trained KTSP Models from a PCOSP Model

**Usage**

```r
## S4 method for signature 'ClinicalModel,CohortList'
validateModel(model, valData, ...)
```

**Arguments**

- **model**
  - A trained ClinicalModel object, as returned by the `trainModel` method.
- **valData**
  - A CohortList containing one or more `SurvivalExperiment`s. The first assay in each `SurvivalExperiment` will be classified using all top scoring KTSP models in `models(model)`.
- **...**
  - Fallthrough arguments to `BiocParallel::bplapply`, use this to configure the parallelization settings for this function. For example to specify BPARAM.

**Value**

The model object with the validationStats and validationData slots occupied.
validateModel, ClinicalModel, SurvivalExperiment-method

**Description**

Validate a ClinicalModel object with a single SurvivalExperiment object.

**Usage**

```r
## S4 method for signature 'ClinicalModel, SurvivalExperiment'
validateModel(model, valData)
```

**Arguments**

- `model`    A ClinicalModel object which has been trained using trainModel.
- `valData`  A SurvivalExperiment to validate the model with.

**Value**

The ClinicalModel with the validation statistics in the validationStats slot and the validation data in the validationData slot.
Examples

```r
data(sampleClinicalModel)
data(sampleCohortList)

# Set parallelization settings
BiocParallel::register(BiocParallel::SerialParam())

# Train Model
trainedClinicalModel <- trainModel(sampleClinicalModel)

# Make predictions
clinicalPredCohortList <- predictClasses(sampleCohortList[c('PCSI', 'TCGA')],
                                           model=trainedClinicalModel)

# Validate model
validatedClinicalModel <- validateModel(trainedClinicalModel,
                                         valData=clinicalPredCohortList)
```

Description

Compute the Inter-Cohort Cluster Correlation and Clustering Reproducibility of All Clusters in Each Cohort.

Usage

```r
## S4 method for signature
## 'ConsensusMetaclusteringModel,ConsensusMetaclusteringModel-method'
validateModel(model, valData, ...)
```

Arguments

- `model` A ConsensusMetaclusteringModel object with cluster_labels in assigned to
each experiment, as returned by predictClasses.

- `valData` A ConsensusMetaclusteringModel object with cluster_labels assigned to each
  experiment, as returned by predictClasses. This consensus cluster should
  contain outgroup cohorts, such as normal patients to be compared against the
disease cohorts being used for class discovery.

- `...` Fallthrough parameters to BiocParallel::bpmapply. This can also be used to
customize the call to stats::cor.test used for calculating the cluster thresholds.
validateModel, GeneFuModel, CohortList-method

Evaluate the Performance of a List of Trained KTSP Models from a PCOSP Model

Description
Evaluate the Performance of a List of Trained KTSP Models from a PCOSP Model

Usage
## S4 method for signature 'GeneFuModel, CohortList'
validateModel(model, valData, ...)

Arguments
- **model**: A GeneFuModel with a DataFrame of gene coefficients in the models slot.
- **valData**: A CohortList containing one or more SurvivalExperiments. The first assay in each SurvivalExperiment will be classified using all top scoring KTSP models in models(model).
- **...**: Fallthrough arguments to BiocParallel::bplapply, use this to configure the parallelization settings for this function. For example to specify BPARAM.

Value
The model object with the validationStats and validationData slots occupied.

See Also
- BiocParallel::bplapply, switchBox::SWAP.KTSP.Classify

Examples
```r
data(sampleTrainedPCOSPmodel)
data(samplePCOSPpredList)

# Set parallelization settings
BiocParallel::register(BiocParallel::SerialParam())

# Validate model
validatedPCOSPmodel <- validateModel(sampleTrainedPCOSPmodel, valData=samplePCOSPpredList)
```
validateModel, GeneFuModel, SurvivalExperiment-method

Validate a GeneFuModel object with a single SurvivalExperiment object.

Description

Validate a GeneFuModel object with a single SurvivalExperiment object.

Usage

```r
## S4 method for signature 'GeneFuModel,SurvivalExperiment'
validateModel(model, valData)
```

Arguments

- `model`: A GeneFuModel object which has been trained using `trainModel`.
- `valData`: A SurvivalExperiment object to validate the model with.

Value

The GeneModel with the validation statistics in the `validationStats` slot and the validation data in the `validationData` slot.

validateModel, PCOSP_or_RLS_or_RGA, CohortList-method

Evaluate the Performance of a List of Trained KTSP Models from a PCOSP Model

Description

Evaluate the Performance of a List of Trained KTSP Models from a PCOSP Model

Usage

```r
## S4 method for signature 'PCOSP_or_RLS_or_RGA,CohortList'
validateModel(model, valData, ...)
```

Arguments

- `model`: A PCOSP model which has been trained using `trainModel`.
- `valData`: A CohortList containing one or more SurvivalExperiments. The first assay in each SurvivalExperiment will be classified using all top scoring KTSP models in `models(model)`.
- `...`: Fallthrough arguments to `BiocParallel::bplapply`, use this to configure the parallelization settings for this function. For example to specify `BPARAM`. 
Validate a PCOSP model with a single SurvivalExperiment object.

Validate a PCOSP model with a single SurvivalExperiment object.

Usage

```r
## S4 method for signature 'PCOSP_or_RLS_or_RGA,SurvivalExperiment'
validateModel(model, valData)
```

Arguments

- `model` A PCOSP model which has been trained using trainModel.
- `valData` A SurvivalExperiment to validate the model with.

Value

The PCOSP model with the validation statistics in the validationStats slot and the validation data in the validationData slot.
validationData

Examples

```r
data(sampleTrainedPCOSPmodel)
data(samplePCOSPpredList)

# Set parallelization settings
BiocParallel::register(BiocParallel::SerialParam())

# Validate model
validatedPCOSPmodel <- validateModel(sampleTrainedPCOSPmodel, valData=samplePCOSPpredList)
```

validationData  
*Accessor for the validationData slot of an S4 object*

Description

Accessor for the validationData slot of an S4 object

Usage

```r
validationData(object, ...)
```

Arguments

- **object**  
  An S4 object

- **...**  
  Allow definition of new arguments to this generic.

Value

A list- or list-like object containing one or more sets of validation data.

Examples

```r
data(CSPC_MAE)
set.seed(1987)
metaclustModel <- ConMetaclustModel(CSPC_MAE, randomSeed=1987)
validationData(metaclustModel)
```
validationData,S4Model-method

Accessor for the validationData slot of an S4Model object

Description

Accessor for the validationData slot of an S4Model object.

Usage

## S4 method for signature 'S4Model'
validationData(object)

Arguments

object An S4Model object

Value

A List- or list-like object containing one or more sets of validation data.

validationData,SurvivalModel-method

Accessor for the validationData slot of a SurvivalModel object.

Description

Accessor for the validationData slot of a SurvivalModel object.

Usage

## S4 method for signature 'SurvivalModel'
validationData(object)

Arguments

object A SurvivalModel object.

Value

A CohortList object containing the datasets used to compute validation statistics for this model.

Examples

data(samplePCOSPmodel)
validationData(samplePCOSPmodel)
validationData<-

__validationData<-__

Generic for setting the validationData slot on an S4 object

**Description**

Generic for setting the validationData slot on an S4 object

**Usage**

validationData(object, ...) <- value

**Arguments**

<table>
<thead>
<tr>
<th>argument</th>
<th>description</th>
</tr>
</thead>
<tbody>
<tr>
<td>object</td>
<td>An S4 object.</td>
</tr>
<tr>
<td>...</td>
<td>Allow definition of additional parameters to this generic.</td>
</tr>
<tr>
<td>value</td>
<td>A data.frame of validation statistics.</td>
</tr>
</tbody>
</table>

**Value**

None, updates the object

**Examples**

data(CSPC_MAE)
set.seed(1987)
metaclustModel <- ConMetaclustModel(CSPC_MAE, randomSeed=1987)
validationData(metaclustModel) <- list(cohort1='This should be cohort data')

validationData<-,S4Model,List_or_list_or_NULL-method

__Setter Method for the validationData of an S4Model Object.__

**Description**

Setter Method for the validationData of an S4Model Object.

**Usage**

```r
## S4 replacement method for signature 'S4Model,List_or_list_or_NULL'
validationData(object) <- value
```

**Arguments**

<table>
<thead>
<tr>
<th>argument</th>
<th>description</th>
</tr>
</thead>
<tbody>
<tr>
<td>object</td>
<td>An S4Model object.</td>
</tr>
<tr>
<td>value</td>
<td>A List- or list-like object containing the new validation data for the S4Model object.</td>
</tr>
</tbody>
</table>
validationData<-,SurvivalModel,CohortList-method

Setter for the validationData slot of a SurvivalModel object with a CohortList.

Description
Setter for the validationData slot of a SurvivalModel object with a CohortList.

Usage
## S4 replacement method for signature 'SurvivalModel,CohortList'
validationData(object) <- value

Arguments

  object       A SurvivalModel model.
  value        A CohortList of validation cohorts for the SurvivalModel model.

Value
None, updates the object.

Examples
data(samplePCOSPmodel)
validationData(samplePCOSPmodel) <- validationData(samplePCOSPmodel)

validationStats  Accessor for the validationStats slot of an S4 object

Description
Accessor for the validationStats slot of an S4 object

Usage
validationStats(object, ...)

Arguments

object An S4 object
... Allow definition of new arguments to this generic.

Value

A data.frame of validation statistics for the validation data provided to validateModel function for a given S4 object.

Examples

data(CSPC_MAE)
set.seed(1987)
metaclustModel <- ConMetaclustModel(CSPC_MAE, randomSeed=1987)
validationStats(metaclustModel)
**validationStats**<-

Accessor for the validationStats slot of a SurvivalModel object.

**Description**

Accessor for the validationStats slot of a SurvivalModel object.

**Usage**

```r
## S4 method for signature 'SurvivalModel'
validationStats(object)
```

**Arguments**

- `object` A SurvivalModel object to get validation statistics from.

**Value**

A data.table of validation statistics for the SurvivalModel object.

**Examples**

```r
data(samplePCOSPmodel)
validationStats(samplePCOSPmodel)
```

---

**validationStats<-**

Setter for the validationStats slot on an S4 object

**Description**

Setter for the validationStats slot on an S4 object

**Usage**

```r
validationStats(object, ...) <- value
```

**Arguments**

- `object` An S4 object.
- `...` Allow definition of additional parameters to this generic.
- `value` A DataFrame- or data.frame-like object of validation statistics.
ValidationStats<- S4Model,DFrame_or_data.frame_data.frame_data.table_or_NULL-method

Value
None, updates the object

Examples
data(CSPC_MAE)
set.seed(1987)
metaclustModel <- ConMetaclustModel(CSPC_MAE, randomSeed=1987)
validationStats(metaclustModel) <- data.frame()

validationStats<-,SurvivalModel,data.frame-method

Description
Setter for the validationStats slot of a SurvivalModel object with a data.frame

Usage
## S4 replacement method for signature 'SurvivalModel,data.frame'
validationStats(object) <- value

Arguments
object An S4Model object.
value A DataFrame- or data.frame-like object of validation statistics.

Value
None, updates the object
validationStats<-,SurvivalModel.data.frame-method

Arguments

- **object**: A SurvivalModel model.
- **value**: A data.frame of validation statistics for a SurvivalModel object.

Value

None, updated the object.

Examples

```r
data(samplePCOSPmodel)
validationStats(samplePCOSPmodel) <- data.frame()
```
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