Package: PDATK (via r-universe)

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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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Depends R (>= 4.1), SummarizedExperiment

Imports data.table, MultiAssayExperiment, ConsensusClusterPlus, igraph, ggplotify, matrixStats, RColorBrewer, clusterRepro, CoreGx, caret, survminer, methods, S4Vectors, BiocGenerics, survival, stats, plyr, dplyr, MatrixGenerics, BiocParallel, rlang, piano, scales, survcomp, genefu, ggplot2, switchBox, reportROC, pROC, verification, utils

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`assignColDataColumn` *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

```
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.

Examples

```
SE <- SummarizedExperiment(matrix(rnorm(100), 10, 10))
updatedSE <- assignColDataColumn(SE, 'test', rep(1, 10))
```

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')
```

assignSubtypes,CohortList,list-method *Assign Subtype Annotations to a SurvivalExperiment Object*

Description

Assign Subtype Annotations to a SurvivalExperiment Object

Usage

```
## 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 to 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 colum with sample identifiers in the subtype column. Must match the name of the sample identifier in colData.
subtypeCol	A character vectoring 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

```
data(sampleCohortList)
data(cohortSubtypeDFs)

cohortList <- assignSubtypes(sampleCohortList,
  subtypes=cohortSubtypeDFs[names(sampleCohortList)],
  sampleCol='sample_name',
  subtypeCol='subtype')
```

---

assignSubtypes,SurvivalExperiment,data.frame-method

Assign Subtype Annotations to a SurvivalExperiment Object

Description

Assign Subtype Annotations to a SurvivalExperiment Object

Usage

```
## 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

```
data(sampleICGCmicro)
data(cohortSubtypeDFs)

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

---

barPlotModelComparison

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

Description

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

Usage

```
barPlotModelComparison(model1, model2, ...)
```

Arguments

model1	AnS4 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 predctions
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

```
## 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

```
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 predctions
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

```
# 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

```
# 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 relavant to a surival 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 *CohortList Class Definition*

Description

A list containing only SurvivalExperiment objects.

cohortSubtypeDFs *A list of sample subtypes for the data in sampleCohortList*

Description

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

Examples

```
data(cohortSubtypeDFs)
```

compareModels *Compare Two Mathematical Models Represented as* S4 *Objects*

Description

Compare Two Mathematical Models Represented as S4 Objects

Usage

```
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)
```

---

compareModels,ModelComparison,SurvivalModel-method

Compare Two `SurivalModel` *Objects, Returing A* `ModelComparison` *Object With Statistics Comparing the Performance of Each Model.*

Description

Compare Two `SurivalModel` Objects, Returing 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 inherting from the `SurvivalModel` class.
`model2`	Another object inherting 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

```
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 `SurivalModel` *Objects, Returing A* `ModelComparison` *Object With Statistics Comparing the Performance of Each Model.*

Description

Compare Two `SurivalModel` Objects, Returing A `ModelComparison` Object With Statistics Comparing the Performance of Each Model.

Usage

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

Arguments

`model1`	An object inherting from the `SurvivalModel` class.
`model2`	Another object inherting 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

trainData	A MultiAssayExperiment or SummarizedExperiment containing molecular data to be used for consensus clustering with ConsensusClusterPlus::ConsensusClusterPlus
...	Force subsequent parameters to be named. Not used.
randomSeed	An integer randomSeed that will be passed to the randomSeed parameter of the ConsensusClusterPlus::ConsensusClusterPlus function when training the model.

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)
experiments(CSPC_MAE) <- endoapply(experiments(CSPC_MAE), SurvivalExperiment,
    event_occurred='vital_status', survival_time='days_to_death')
coxModel <- CoxModel(CSPC_MAE, survivalPredictor='sample_type')
```

CSPC_MAE *A* MultiAssayExperiment *containing cohorts of pancreatic cancer patients, for use in package examples.*

Description

A MultiAssayExperiment containing cohorts of pancreatic cancer patients, for use in package examples.

Examples

```
data(CSPC_MAE)
```

---

densityPlotModelComparison *Render A Density Plot of Model Performance for an* S4 *Object*

Description

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.

`densityPlotModelComparison,PCOSP_or_RLS_or_RGA,PCOSP_or_RLS_or_RGA-method` *Render a Density Plot Comparing Model Performance Between Two* `PCOSP`, `RLSModel` *or* `RGAModel` *object.*

Description

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
)
```

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 whos names are one or more existing mDataTypes in `object` and `refModel` and whos 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.

dropNotCensored *Remove Censored Patient Samples from An* S4 *Object.*

Description

Remove Censored Patient Samples from An S4 Object.

Usage

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

Arguments

object	An S4 object containing survival data which needs to have patients who were not censored before some criteria.
...	Allow new parmeters to be defined for this generic.

Value

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

Examples

```
data(sampleICGCmicro)
ICGCmicro <- dropNotCensored(sampleICGCmicro)
```

dropNotCensored,CohortList-method *Remove Censored Patients from Each* SurvivalExperiemnt *in a* CohortList

Description

Remove Censored Patients from Each SurvivalExperiemnt in a CohortList

Usage

```
## 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

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

---

dropNotCensored,SurvivalExperiment-method

Remove Censored Patients from A SurvivalExperiment *Object*

Description

Remove Censored Patients from A SurvivalExperiment Object

Usage

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

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 *existingClassifierData*

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

```
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

```
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

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

Arguments

object	A CohortList of SurvivalExperiments to find common genes between.

Value

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

Examples

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

findCommonGenes,MultiAssayExperiment-method *Intersect Gene Names for All* experiments *in a* MultiAssayExperiment

Description

Intersect Gene Names for All experiments in a MultiAssayExperiment

Usage

```
## 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 `MutliAssayExperiment`.

`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

```
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)
```

`findCommonSamples,CohortList-method`
Find Common Samples in a CohortList Object where The Columns of Each Item Represent Samples

---

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)
```

---

forestPlot *Generate a forest plot from an* S4 *object*

Description

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')
```

forestPlot,ModelComparison-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 '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 forestplot.
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[c('PCSI', 'TCGA')],
  model=trainedClinicalModel)

# 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

object	A PCOSP model which has been validated with validateModel and therefore has data in the validationStats slot.
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 forestplot.
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)

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

GeneFuModel GeneFuModel *Constructor Method*

Description

GeneFuModel Constructor Method

Usage

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

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 paramater to SurvivalModel constructor.
randomSeed	An integer randomSeed that was used to train the model. Users should specify this when initializing a model to ensure reproducibilty.

Value

A GeneFuModel object, with model parameters in the

Examples

```
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

```
getModelSeed(object)
```

Arguments

`object`	An `S4` object to get the seed from.

Value

An `integer` seed to be used when training the a `SurivvalModel`.

Examples

```
data(samplePCOSPmodel)
getModelSeed(samplePCOSPmodel)
```

`getModelSeed,SurvivalModel-method`

Method for retrieving the random seed used for training a specific survival model object.

Description

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

Usage

```
## S4 method for signature 'SurvivalModel'
getModelSeed(object)
```

Arguments

`object`	A `SurvivalModel` object to get the seed from.

Value

An `integer` seed to be used when training the a `SurivalModel`.

Examples

```
data(samplePCOSPmodel)
getModelSeed(samplePCOSPmodel)
```

`getTopFeatures` *Get the Top Predictive Features from an S4 Object*

Description

Get the Top Predictive Features from an S4 Object

Usage

```
getTopFeatures(object, ...)
```

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 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

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

haiderSigScores *Classifier survival scores for Haider*

Description

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

Examples

```
# 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

```
hasColDataColumns(SE, values)
```

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

```
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

```
## 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 *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*

Description

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

```
## 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.

---

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

Description

Accessor for the models slot of an S4 object

Usage

```
models(object, ...)
```

Arguments

object	An S4 object to retrieve models from.
...	Allow new parameters to be defined for this generic.

Value

An S4 object representing a model.

Examples

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

---

models,S4Model-method *Getter for the models slot of an* S4Model *Object*

Description

Getter for the models slot of an S4Model Object

Usage

```
## S4 method for signature 'S4Model'
models(object)
```

Arguments

object	An S4Model object to retrieve models from.

Value

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

models,SurvivalModel-method *Getter for the models slot of a* SurvivalModel *object*

Description

Getter for the models slot of a SurvivalModel object

Usage

```
## 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

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

models<-,SurvivalModel,SimpleList-method *Setter for the models slot of a* SurvivalModel *object*

Description

Setter for the models slot of a SurvivalModel object

Usage

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

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(model1=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

```
## 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

```
## 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 DFrame object.

---

normalize,MultiAssayExperiment-method

Normalize the assays *of a* MutliAssayExperiment *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",
  ...,
  whichAssays = seq_along(assays(object))
)
```

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.

whichAssays	A numeric or character vector specifying the indices 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

---

normalize,SummarizedExperiment-method

Normalize the assays *in a* SummarizedExperiment *Object*

Description

Normalize the assays in a SummarizedExperiment Object

Usage

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

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 applyying 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 `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

`preprocessCaret`, `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))
```

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 subinteral 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 SurivalExperiment 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 reproducibilty.

Details

This function assumes there is only 1 assay per SurvivalExperiment.

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

plotNetworkGraph *A Generic for Plotting a Network Graph From an S4 Object*

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 metaclusters 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 with the validateModel method.
alpha	A float specifying the significance level for the plot. Non- signficiant 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 speciyfing the plot tile.

Value

A ggplot object containing the ROC curves.

Examples

```
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

```
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

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

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.

---

predictClasses *Predict Classes for New Data Based on a Train Classifier Model*

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(samplePCSIsurvExp)

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

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

predictClasses,CohortList,ClinicalModel-method
Use a Clinical GLM to Predict Classes for a CohortList *of* SurvivalExperment *Objects.*

Description

Use a Clinical GLM to Predict Classes for a CohortList of SurvivalExperment 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 paramter 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,GeneFuModel-method

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

Description

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

Usage

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

Arguments

object	A CohortList with SurvivalExperiments to predict classes for.
model	A trained GeneFuModel 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

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

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

```
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]]))
```

---

predictClasses,ConsensusMetaclusteringModel,ANY-method

Compute the Optimal Clustering Solution for a Trained ConsensusMetaclusteringModel

---

Description

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

Usage

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

Arguments

object	A MutliAssayExperiment 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")
```

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 paramter 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

```
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))
```

---

predictClasses,SurvivalExperiment,GeneFuModel-method

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

Description

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

Usage

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

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.

---

predictClasses,SurvivalExperiment,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

```
## 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

```
data(sampleTrainedPCOSPmodel)
data(samplePCSIsurvExp)

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

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

`preprocessCaret` *Preprocess Data Using the* `caret::preProcess` *method, then return the normalized data using* `predict`.

Description

Preprocess Data Using the `caret::preProcess` method, then return the normalized data using `predict`.

Usage

```
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 'SurvivelExperiment' 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 reproducibilty.

Value

A SurvivalModel object.

Examples

```
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 'SurvivelExperiment' 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 reproducibilty.

Value

A SurvivalModel object.

Examples

```
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

```
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

```
data(sampleICGCmicro)
rankFeatures(sampleICGCmicro)
```

rankFeatures,MultiAssayExperiment-method
Rank the Features in a MultiAssayExperiment *Object*

Description

Rank the Features in a MultiAssayExperiment Object

Usage

```
## 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 paramter is missing.

Value

The MultiAssayExperiment with the item featureRanks in the object metadata, which stores a DataFrame containing ranks accross 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

```
## 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 where used for each column can be found in the object mcols in the calculated_with column.

Examples

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

removeColDataFactorColumns *Remave any factor columns from the* colData *of an* S4 *object*

Description

Remave 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 columsn 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.

Examples

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

---

renameColDataColumns *Rename the columns in the* colData *slot, or do nothing if they don't match*

Description

Rename the columns in the colData slot, or do nothing if they don't match

Usage

```
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

```
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

```
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.

---

runGSEA,PCOSP,data.frame-method

Run Gene Set Enrichment Analysis On A PCOSP *Model Object.*

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 inherting 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 *A Set of Example Patient Cohorts*

Description

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

See Also

`MetaGxPancreas::loadPancreasDatasets`

Examples

```
data(sampleCohortList)
```

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

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

```
data(samplePCOSPmodel)
```

samplePCOSPpredList *Sample CohortList with PCOSP Risk Predictions*

Description

Sample CohortList with PCOSP Risk Predictions

See Also

MetaGxPancreas::loadPancreasDatasets

Examples

```
data(samplePCOSPpredList)
```

samplePCSIsurvExp *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)
```

sampleValPCOSPmodel *Sample Validated PCOSP Model for Plotting Examples*

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

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

Arguments

x	A CohortList object
subset	The row query. Defaults to TRUE, i.e., select all.
select	The column query. Defaults to TRUE, i.e., select all.
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

```
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* survival_time *and* 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 survival_time and event_occurred.

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
ICGCmicroSumExp <- as(sampleICGCmicro, 'SummarizedExperiment')
ICGCmicro <- SurvivalExperiment(ICGCmicroSumExp,
  survival_time='survival_time', event_occurred='event_occurred')
```

SurvivalExperiment-class
SurvivalExperiment Class

Description

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

`SurvivalModel` *Constructor for a SurvivalModel Object.*

Description

Constructor for a SurvivalModel Object.

Usage

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

Arguments

`trainCohorts`	A 'SurvivelExperiment' 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 reproducibilty.

Value

A `SurvivalModel` object.

Examples

```
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 relavant to a surival 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

```
## 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

```
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.

Examples

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

`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

```
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.
`...`	Fall through parameters to the `stats::glm` function.
`family`	Argument to the family parameter of `stats::glm`. Defaults to `binomial(link='logit')`. This parameter must be named.
`na.action`	Argument to the na.action paramater 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

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

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

trainedClinicalModel <- trainModel(sampleClinicalModel)
```

`trainModel,ConsensusMetaclusteringModel-method`
Train A ConsensusMetaclusteringModel

Description

Since consensus clustering is an unsuperived 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

```
## 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::ConsensusClusterP` for more options.
`clusterAlg`	The clustering algorithm to use. Defaults to 'hc'. See `?ConesnsusClusterPLus::ConsensusClusterPlu` for more options.
`plot`	An optional path to output the plots generated by each call to `ConsensusClusterPlus::ConsensusClust` 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.

trainModel,CoxModel-method
Fit Models to the trainData in a CoxModel Object

Description

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

Usage

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

Arguments

object	A CoxModel object to fit models for.

Value

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

trainModel,GeneFuModel-method
Train a GeneFuModel Object

Description

Train a GeneFuModel Object

Usage

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

Arguments

object	A GeneFuModel object to train.

Value

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

trainModel,NCSModel-method

Train a NetworkCommunitySearchModel

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 fitlered based on the specified criteria. The criteria are also stored in the modelParam slots to ensure reproducibility.

trainModel,PCOSP-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 paramters.

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 accurary required to consider a model 'top scoring'. Defaults to 0.6. Must be in the range [0, 1].
...	Fall through arguments to BiocParallel::bplapply. Use this to configure parallelization options. By default the settings inferred in BiocParallel::bpparam() will be used.

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,RGAModel-method

Train a RGAModel Based on the Data in the assays slot.

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 paramters.

Usage

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

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 paramters.

Usage

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

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	This parameter should be set to zero, since we do not expect the permuted models to perform well. Setting this higher will result in an ensemble with very few models included.
...	Fall through arguments to BiocParallel::bplapply. Use this to configure parallelization options. By default the settings inferred in BiocParallel::bpparam() will be used.

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(sampleRLSmodel)
set.seed(getModelSeed(sampleRLSmodel))

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

trainedRLSmodel <- trainModel(sampleRLSmodel, numModels=2)
```

---

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, ...)
```

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

```
## 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 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

```
data(sampleClinicalModel)
data(samplePCSIsurvExp)

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

# Train Model
trainedClinicalModel <- trainModel(sampleClinicalModel)

# Make predictions
clinicalPredSurvExp <- predictClasses(samplePCSIsurvExp,
  model=trainedClinicalModel)

# Validate model
validatedClincalModel <- validateModel(trainedClinicalModel,
  valData=clinicalPredSurvExp)
```

---

validateModel,ClinicalModel,SurvivalExperiment-method

Validate a ClinicalModel object with a single SurvivalExperiment object.

Description

Validate a ClinicalModel object with a single SurvivalExperiment object.

Usage

```
## 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

```
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)
```

---

validateModel,ConsensusMetaclusteringModel,ConsensusMetaclusteringModel-method

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

Description

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

Usage

```
## S4 method for signature
## 'ConsensusMetaclusteringModel,ConsensusMetaclusteringModel'
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.

Value

The ConsensusMetaclusteringModel from object, with the training data from valData in the validationData slot, the models from the valData object appended to the models of object, and the validationStats slot populated with pair-wise comparisons between all experiments in both model and valData.

---

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

```
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

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

Arguments

`model`	A `GenefuModel` object which has been trained using `trainModel`.
`valData`	A `SurvivalExperiment` 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

```
## 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.

Value

The model object with the validationStats and validationData slots occupied.

See Also

BiocParallel::bplapply, switchBox::SWAP.KTSP.Classify

Examples

```
data(sampleTrainedPCOSPmodel)
data(samplePCOSPpredList)

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

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

---

validateModel,PCOSP_or_RLS_or_RGA,SurvivalExperiment-method

Validate a PCOSP model with a single SurvivalExperiment object.

Description

Validate a PCOSP model with a single SurvivalExperiment object.

Usage

```
## 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 PCOSPmodel with the validation statistics in the validationStats slot and the validation data in the validationData slot.

Examples

```
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

```
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

```
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<- *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

object	An S4 object.
...	Allow definition of additional parameters to this generic.
value	A data.frame of validation statistics.

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<-,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,S4Model-method
Acessor for the validationStats *slot of an* S4Model *Object*

Description

Acessor for the validationStats slot of an S4Model Object

Usage

```
## S4 method for signature 'S4Model'
validationStats(object)
```

Arguments

object	An S4 object

Value

A data.frame of validation statistics for the validation data provided to validateModel function for a given S4Model object.

validationStats,SurvivalModel-method
Accessor for the validationStats *slot of a* SurvivalModel *object.*

Description

Accessor for the validationStats slot of a SurvivalModel object.

Usage

```
## 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

```
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

```
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.

Value

None, updates the object

Examples

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

validationStats<-,S4Model,DFrame_or_data.frame_data.table_or_NULL-method *Setter for the* validationStats *slot on an* S4Model *object*

Description

Setter for the validationStats slot on an S4Model object

Usage

```
## S4 replacement method for signature 'S4Model,DFrame_or_data.frame_data.table_or_NULL'
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`
Setter for the validationStats slot of a `SurvivalModel` *object with a* `data.frame`

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`	A `SurvivalModel` model.
`value`	A `data.frame` of validation statistics for a `SurvivelModel` object.

Value

None, updated the object.

Examples

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

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