

# Package ‘SummarizedBenchmark’

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**Type** Package

**Title** Classes and methods for performing benchmark comparisons

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**Description** This package defines the BenchDesign and SummarizedBenchmark classes for building, executing, and evaluating benchmark experiments of computational methods. The SummarizedBenchmark class extends the RangedSummarizedExperiment object, and is designed to provide infrastructure to store and compare the results of applying different methods to a shared data set. This class provides an integrated interface to store metadata such as method parameters and software versions as well as ground truths (when these are available) and evaluation metrics.

**biocViews** Software, Infrastructure

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**R topics documented:**

addMethod	2
addPerformanceMetric	4
allSB	5
availableMetrics	5
BDData	6
BDData-class	6
BDMethod	7
BDMethod-class	8
BDMethodList	8
BDMethodList-accessors	9
BDMethodList-class	10
BenchDesign	10
BenchDesign-accessors	11
BenchDesign-class	12
buildBench	12
compareBDData	14
compareBDMethod	15
compareBenchDesigns	15
dropMethod	16
estimateMetricsForAssay	17
expandMethod	19
hashBDData	20
modifyMethod	21
performanceMetrics	22
plotMethodsOverlap	23
plotROC	24
printMethod	24
sb	25
SummarizedBenchmark	26
SummarizedBenchmark-accessors	27
SummarizedBenchmark-class	28
tdat	29
tidyBDMethod	29
tidyUpMetrics	30
updateBench	31
<b>Index</b>	<b>33</b>

---

addMethod

*Add new method to BenchDesign object*


---

**Description**

This function takes a `BenchDesign` object and returns a modified object with the specified method included. At a minimum, a string name for the method, `label`, and the workhorse function for the method, `func`, must be specified in addition to the primary `BenchDesign` object.

**Usage**

```
addMethod(bd, label, func, params = rlang::quos(), post = NULL,
          meta = NULL)
```

**Arguments**

bd	BenchDesign object.
label	Character name for the method.
func	Primary function to be benchmarked.
params	Named quosure list created using <code>rlang::quos</code> of <code>parameter = value</code> pairs to be passed to <code>func</code> .
post	Optional post-processing function that takes results of <code>func</code> as input. Ignored if <code>NULL</code> . If multiple assays (metrics) should be generated for each method, this can be accomplished by specifying a named list of post-processing functions, one for each assay. (default = <code>NULL</code> )
meta	Optional metadata information for method to be included in <code>colData</code> of <code>SummarizedBenchmark</code> object generated using <code>buildBench</code> . See <code>Details</code> for more information. Ignored if <code>NULL</code> . (default = <code>NULL</code> )

**Details**

The inputs for the call to `label` should be specified as `parameter = value` pairs, where the value can be any fixed value, variable, or column in the `bdata` of the `BenchDesign` object.

An optional secondary function, `post`, can be specified if the output of the workhorse function, `func`, needs to be further processed. As an example, `post` may be a simple "getter" function for accessing the column of interest from the large object returned by `func`.

The optional `meta` parameter accepts a named list of metadata tags to be included for the method in the resulting `SummarizedBenchmark` object. This can be useful for two primary cases. First, it can help keep analyses better organized by allowing the specification of additional information that should be stored with methods, e.g. a tag for "method type" or descriptive information on why the method was included in the comparison. Second, and more importantly, the `meta` parameter can be used to overwrite the package and version information that is automatically extracted from the function specified to `func`. This is particularly useful when the function passed to `func` is a wrapper for a script in (or outside of) R, and the appropriate package and version information can't be directly pulled from `func`. In this case, the user can either manually specify the `"pkg_name"` and `"pkg_vers"` values to `meta` as a list, or specify a separate function that should be used to determine the package name and version. If a separate function should be used, it should be passed to `meta` as a list entry with the name `pkg_func` and first quoted using `rlang::quo`, e.g. `list(pkg_func = quo(p.adjust))`.

**Value**

A copy of the originally supplied `BenchDesign` with the new method added.

**Author(s)**

Patrick Kimes

**Examples**

```
## create example data set of p-values
df <- data.frame(pval = runif(100))

## example calculating qvalue from pvalues

## using standard call
```

```
qv <- qvalue::qvalue(p = df$pval)
qv <- qv$qvalue

## adding same method to BenchDesign
bench <- BenchDesign(data = df)
bench <- addMethod(bench,
  label = "qv",
  func = qvalue::qvalue,
  post = function(x) { x$qvalue },
  params = rlang::quos(p = pval))
```

---

`addPerformanceMetric` *Add a performance metric definition to a [SummarizedBenchmark](#) object.*

---

## Description

This is a function to define performance metrics for benchmarking methods. The function is saved into the `performanceMetrics` slot.

## Usage

```
addPerformanceMetric(object, evalMetric, assay, evalFunction = NULL)
```

## Arguments

<code>object</code>	A <a href="#">SummarizedBenchmark</a> object.
<code>evalMetric</code>	A string with the name of the evaluation metric.
<code>assay</code>	A string with an assay name. Indicates the assay that should be given as input to this performance metric.
<code>evalFunction</code>	A function that calculates a performance metric. It should contain at least two arguments, <code>query</code> and <code>truth</code> , where <code>query</code> is the output vector of a method and <code>truth</code> is the vector of true values. If additional parameters are specified, they must contain default values. If <code>NULL</code> , the <code>'evalMetric'</code> string must be the name of a predefined metric available through <code>'availableMetrics()'\$function'</code> .

## Value

A [SummarizedBenchmark](#) object.

## Author(s)

Alejandro Reyes

## Examples

```
data( sb )
sb <- addPerformanceMetric(
  object=sb,
  assay="qvalue",
  evalMetric="TPR",
  evalFunction = function( query, truth, alpha=0.1 ){
    goodHits <- sum( (query < alpha) & truth == 1 )
    goodHits / sum(truth == 1)
  }
)
```

---

allSB

*SummarizedBenchmark object of isoform quantification results*

---

## Description

This object is a SummarizedBenchmark object containing isoform quantifications from salmon, sailfish and kallisto from 4 mouse samples (2 hearts and 2 brains) part of the Mouse BodyMap. Its generation is described in one of the vignettes of this package.

## Source

Mouse BodyMap (Li et al, 2014). SRA accession numbers SRR5273705, SRR5273689, SRR5273699 and SRR5273683.

## Examples

```
data(quantSB)
```

---

availableMetrics

*availableMetrics*

---

## Description

This function returns a data frame summarizing the default performance metrics provided in this package. The data.frame contains three columns, 'functions' is the name of the performance metric, 'description' is longer description of the performance metric and 'requiredTruth' is logical depending on whether the performance metrics require ground truths.

## Usage

```
availableMetrics()
```

## Value

A data.frame summarizing the default performance metrics provided in this package.

**Examples**

```
availableMetrics()
```

---

 BDData

*Create a new BDData*


---

**Description**

Initialized a new BDData object for benchmarking methods.

**Usage**

```
BDData(data)
```

```
## S4 method for signature 'ANY'
```

```
BDData(data)
```

```
## S4 method for signature 'BenchDesign'
```

```
BDData(data)
```

```
## S4 method for signature 'SummarizedBenchmark'
```

```
BDData(data)
```

```
## S4 method for signature 'BDData'
```

```
BDData(data)
```

**Arguments**

data                    a list object of data or MD5 hash string

**Value**

BDData object

**Author(s)**

Patrick Kimes

---

 BDData-class

*BDMETHOD class*


---

**Description**

Container for individual methods to be compared as part of a BenchDesign object.

**Usage**

```
## S4 method for signature 'BDData'
```

```
show(object)
```

**Arguments**

object            BDData object to show

**Slots**

data a list or MD5 hash of the data.

type a character string indicating whether the data slot contains the 'data' or a 'md5hash' of the data.

**Author(s)**

Patrick Kimes

---

 BDMETHOD

*Create a new BDMETHOD*


---

**Description**

Initializes a new BenchDesign method (BDMETHOD) object for benchmarking methods.

**Usage**

```
BDMETHOD(x, params = rlang::quos(), post = NULL, meta = NULL, ...)
```

```
## S4 method for signature 'quosure'
```

```
BDMETHOD(x, params = rlang::quos(), post = NULL,
  meta = NULL, ...)
```

```
## S4 method for signature '`function`'
```

```
BDMETHOD(x, params = rlang::quos(), post = NULL,
  meta = NULL, ...)
```

**Arguments**

x                    main method function or function quosure

params              list of quosures specifying function parameters. (default = `codrlang::quos()`)

post                list of functions to be applied to the output of x. (default = `NULL`)

meta                list of meta data. (default = `NULL`)

...                 other parameters.

**Value**

BDMETHOD object

---

BDMETHOD-class	<i>BDMETHOD class</i>
----------------	-----------------------

---

**Description**

Container for individual methods to be compared as part of a BenchDesign object.

**Usage**

```
## S4 method for signature 'BDMETHOD'
show(object)
```

**Arguments**

object            BDMETHOD object to show

**Slots**

f a function to be benchmarked  
 fc a captured expression of the function f  
 params a list of quosures specifying function parameters  
 post a list of functions to be applied to the output of f  
 meta a list of meta data

**Author(s)**

Patrick Kimes

---

BDMETHODList	<i>Create a new BDMETHODList</i>
--------------	----------------------------------

---

**Description**

Initialized a new SimpleList of BenchDesign method (BDMETHOD) objects.

**Usage**

```
BDMETHODList(..., x = NULL)
```

```
## S4 method for signature 'ANY'
BDMETHODList(..., x = NULL)
```

**Arguments**

...            a named list of BDMETHOD objects  
 x            a BenchDesign or SummarizedBenchmark object to extract the BDMETHODList from. (default = NULL)



**Value**

BDMETHODList object

**Author(s)**

Patrick Kimes

**Examples**

```
BDMETHODList()
```

---

BDMETHODList-accessors

*BDMETHODList Accessors*

---

**Description**

These methods can be used to access, set, and remove elements of a BDMETHODList object.

**Usage**

```
## S4 replacement method for signature 'BDMETHODList,character,BDMETHOD'  
BDMETHOD(x, i) <- value
```

```
## S4 replacement method for signature 'BDMETHODList,character,`NULL`'  
BDMETHOD(x, i) <- value
```

```
## S4 method for signature 'BDMETHODList'  
BDMETHOD(x, i = 1)
```

**Arguments**

x	BDMETHODList object.
i	character name or integer index of a BDMETHOD object. (Note: must be a character name for replacement operations.)
value	replacement object, either BDMETHOD or NULL object.

**Value**

modified BDMETHODList object

**Author(s)**

Patrick Kimes

---

BDMETHOD-list-class      *BDMETHOD class*

---

### Description

Extension of the SimpleList class to contain a list of BDMETHOD objects.

### Usage

```
## S4 method for signature 'BDMETHOD'
show(object)
```

### Arguments

object                      BDMETHOD object to show

### Author(s)

Patrick Kimes

---

BenchDesign                      *Create a new BenchDesign*

---

### Description

Initializes a new BenchDesign object for benchmarking methods.

### Usage

```
BenchDesign(..., methods = NULL, data = NULL)
```

```
## S4 method for signature 'ANY'
BenchDesign(..., methods = NULL, data = NULL)
```

### Arguments

...                      named set of BDMETHOD objects and/or unnamed BenchDesign objects. Only the methods of any BenchDesign object will be used, and the data slot of the objects will be ignored.

methods                      named set of BDMETHOD objects and/or unnamed BenchDesign objects as a list. (default = NULL)

data                      optional data.frame or other list object to be used in the benchmark. (default = NULL)

### Value

BenchDesign object.

**Author(s)**

Patrick Kimes

**Examples**

```
## with no input
bd <- BenchDesign()

## with toy data.frame
df <- data.frame(x1 = rnorm(20), y1 = rnorm(20))
bd <- BenchDesign(data = df)
```

---

BenchDesign-accessors *BenchDesign Accessors*

---

**Description**

These methods can be used to access, set, and remove elements of a BenchDesign object.

**Usage**

```
BDData(x) <- value

BDMETHOD(x, i) <- value

BDMETHODList(x) <- value

## S4 replacement method for signature 'BenchDesign,BDDataOrNULL'
BDData(x) <- value

## S4 replacement method for signature 'BenchDesign,character,BDMETHOD'
BDMETHOD(x, i) <- value

## S4 replacement method for signature 'BenchDesign,character,`NULL`'
BDMETHOD(x, i) <- value

## S4 replacement method for signature 'BenchDesign,BDMETHODList'
BDMETHODList(x) <- value

## S4 method for signature 'BenchDesign'
BDMETHOD(x, i = 1)

## S4 method for signature 'BenchDesign'
BDMETHODList(..., x = NULL)
```

**Arguments**

x	BenchDesign object.
value	replacement object, either BDData, BDMETHOD, BDMETHODList or NULL object.

`i` character name or integer index of a BDMethod object. (Note: must be a character name for replacement operations.)

`...` Further arguments, perhaps used by methods

**Value**

modified BenchDesign object

**Author(s)**

Patrick Kimes

---

BenchDesign-class      *BenchDesign class*

---

**Description**

Container for benchmark methods and data.

**Usage**

```
## S4 method for signature 'BenchDesign'
show(object)
```

**Arguments**

`object`      BenchDesign object to show

**Slots**

`data` a list containing the data to be used in the benchmark.  
`methods` a list of BDMethods to be compared in the benchmark.

**Author(s)**

Patrick Kimes

---

buildBench      *Make SummarizedBenchmark from BenchDesign*

---

**Description**

Function to evaluate BenchDesign methods on supplied data set to generate a SummarizedBenchmark. In addition to the results of applying each method on the data, the returned SummarizedBenchmark also includes metadata for the methods in the `colData` of the returned object, metadata for the data in the `rowData`, and session information in the metadata.

**Usage**

```
buildBench(bd, data = NULL, truthCols = NULL, ftCols = NULL,
           sortIDs = FALSE, keepData = FALSE, catchErrors = TRUE,
           parallel = FALSE, BPPARAM = bpparam())
```

**Arguments**

<code>bd</code>	BenchDesign object.
<code>data</code>	Data set to be used for benchmarking, will take priority over data set specified to BenchDesign object. Ignored if NULL. (default = NULL)
<code>truthCols</code>	Character vector of column names in data set corresponding to ground truth values for each assay. If specified, column will be added to the groundTruth DataFrame of the returned SummarizedBenchmark object. If the BenchDesign includes only a single assay, the same name will be used for the assay. If the BenchDesign includes multiple assays, to map data set columns with assays, the vector must have names corresponding to the assay names specified to the <code>post</code> parameter at each <code>addMethod</code> call. (default = NULL)
<code>ftCols</code>	Vector of character names of columns in data set that should be included as feature data (row data) in the returned SummarizedBenchmark object. (default = NULL)
<code>sortIDs</code>	Whether the output of each method should be merged and sorted using IDs. See Details for more information. (default = FALSE)
<code>keepData</code>	Whether to store the data as part of the BenchDesign slot of the returned SummarizedBenchmark object. If FALSE, a MD5 hash of the data will be stored with the BenchDesign slot. (default = FALSE)
<code>catchErrors</code>	logical whether errors produced by methods during evaluation should be caught and printed as a message without stopping the entire build process. (default = TRUE)
<code>parallel</code>	Whether to use parallelization for evaluating each method. Parallel execution is performed using BiocParallel. Parameters for parallelization should be specified with <code>BiocParallel::register</code> or through the BPPARAM parameter. (default = FALSE)
<code>BPPARAM</code>	Optional BiocParallelParam instance to be used when <code>parallel</code> is TRUE. If not specified, the default instance from the parameter registry is used.

**Details**

Parallelization is performed across methods. Therefore, there is currently no benefit to specifying more cores than the total number of methods in the BenchDesign object.

By default, errors thrown by individual methods in the BenchDesign are caught during evaluation and handled in a way that allows `buildBench` to continue running with the other methods. The error is printed as a message, and the corresponding column in the returned SummarizedBenchmark object is set to NA. Since many benchmarking experiments can be time and computationally intensive, having to rerun the entire analysis due to a single failed method can be frustrating. Default error catching was included to alleviate these frustrations. However, if this behavior is not desired, setting `catchErrors = FALSE` will turn off error handling.

If `sortIDs` is TRUE, each method must return a named vector or list. The names will be used to align the output of each method in the returned SummarizedBenchmark. Missing values from each method will be set to NA. This can be useful if the different methods return overlapping, but

not identical, results. If `truthCols` is also specified, and sorting by IDs is necessary, rather than specifying 'TRUE', specify the string name of a column in the data to use to sort the method output to match the order of `truthCols`.

When a method specified in the `BenchDesign` does not have a postprocessing function specified to 'post', the trivial base: `identity` function is used as the default postprocessing function.

### Value

SummarizedBenchmark object.

### Author(s)

Patrick Kimes

### Examples

```
## with toy data.frame
df <- data.frame(pval = rnorm(100))
bench <- BenchDesign(data = df)

## add methods
bench <- addMethod(bench, label = "bonf", func = p.adjust,
                  params = rlang::quos(p = pval, method = "bonferroni"))
bench <- addMethod(bench, label = "BH", func = p.adjust,
                  params = rlang::quos(p = pval, method = "BH"))

## evaluate benchmark experiment
sb <- buildBench(bench)

## evaluate benchmark experiment w/ data sepecified
sb <- buildBench(bench, data = df)
```

---

compareBDData

*Compare BDData objects*

---

### Description

Simple comparison of two `BDData` objects based on comparing both type and data hash.

### Usage

```
compareBDData(x, y)
```

### Arguments

`x` a `BDData` or `BenchDesign` object  
`y` a `BDData` or `BenchDesign` object

### Value

list of two values giving agreement of "data" and "type".

**Author(s)**

Patrick Kimes

---

compareBDMETHOD	<i>Compare BDMETHOD objects</i>
-----------------	---------------------------------

---

**Description**

Simple comparison of two BDMETHOD objects based on meta data.

**Usage**

```
compareBDMETHOD(x, y)
```

**Arguments**

x	a BDMETHOD object
y	a BDMETHOD object

**Value**

logical value indicating whether the two objects produced the same meta data.

**Author(s)**

Patrick Kimes

---

compareBenchDesigns	<i>Compare BenchDesign objects</i>
---------------------	------------------------------------

---

**Description**

Comparison of BenchDesign objects and BenchDesign method information stored in SummarizedBenchmark objects. Inputs can be either BenchDesign or SummarizedBenchmark objects. If SummarizedBenchmark objects are specified, the method metadata stored in the colData will be used for the comparison. If only a single SummarizedBenchmark object is specified, the colData information will be compared with the BenchDesign object in the BenchDesign slot of the object. To compare the BenchDesign slots of SummarizedBenchmark objects, the BenchDesigns should be extracted with BenchDesign(sb) and passed as inputs (see Examples).

**Usage**

```

compareBenchDesigns(x, y = NULL, ...)

## S4 method for signature 'SummarizedBenchmark,missing'
compareBenchDesigns(x, y = NULL,
  ...)

## S4 method for signature 'SummarizedBenchmark,SummarizedBenchmark'
compareBenchDesigns(x,
  y = NULL, ...)

## S4 method for signature 'SummarizedBenchmark,BenchDesign'
compareBenchDesigns(x,
  y = NULL, ...)

## S4 method for signature 'BenchDesign,SummarizedBenchmark'
compareBenchDesigns(x,
  y = NULL, ...)

## S4 method for signature 'BenchDesign,BenchDesign'
compareBenchDesigns(x, y = NULL, ...)

```

**Arguments**

x	a SummarizedBenchmark or BenchDesign object
y	an optional second SummarizedBenchmark or BenchDesign object (default = NULL)
...	other parameters

**Value**

list of comparison results

**Author(s)**

Patrick Kimes

---

dropMethod

*Remove method from BenchDesign object*

---

**Description**

This function takes a BenchDesign object and the name of a method already defined in the object, and returns a reduced BenchDesign object with the specified method removed.

**Usage**

```
dropMethod(bd, label)
```



**Arguments**

bd                    BenchDesign object.  
label                Character name of method to be modified.

**Value**

Modified BenchDesign object.

**Author(s)**

Patrick Kimes

**Examples**

```
## empty BenchDesign
bench <- BenchDesign()

## add methods
bench <- addMethod(bench, label = "bonf", func = p.adjust,
                  params = rlang::quos(p = pval, method = "bonferroni"))
bench <- addMethod(bench, label = "BH", func = p.adjust,
                  params = rlang::quos(p = pval, method = "BH"))

## remove methods
bench <- dropMethod(bench, label = "bonf")
```

---

estimateMetricsForAssay

*Estimate performance metrics.*

---

**Description**

These functions estimate the performance metrics, either passed as arguments or added previously with the [addPerformanceMetric](#) function. The function will estimate the performance metric for each method.

**Usage**

```
estimateMetricsForAssay(object, assay, evalMetric = NULL,
                        addColData = FALSE, evalFunction = NULL, tidy = FALSE, ...)

estimatePerformanceMetrics(object, addColData = FALSE, tidy = FALSE,
                           rerun = TRUE, ...)
```

**Arguments**

object                A [SummarizedBenchmark](#) object.  
assay                 A string with an assay name. Indicates the assay that should be given as input to this performance metric.  
evalMetric            A string with the name of the evaluation metric.

addColData	Logical (default: FALSE). If TRUE, the results are added to the <code>colData</code> slot of the <code>SummarizedExperiment</code> object and the object is returned. If FALSE, only a <code>DataFrame</code> with the results is returned.
evalFunction	A function that calculates a performance metric. It should contain at least two arguments, <code>query</code> and <code>truth</code> , where <code>query</code> is the output vector of a method and <code>truth</code> is the vector of ground true values. If additional parameters are specified, they must contain default values. If this parameter is passed, the metrics in the object are ignored and only this evaluation metric is estimated.
tidy	Logical (default: FALSE). If TRUE, a long formatted <code>data.frame</code> is returned.
...	Additional parameters passed to the performance functions.
rerun	Logical (default: TRUE). By default, all performance metrics are recalculated everytime that <code>estimatePerformanceMetrics</code> is called. If FALSE, performance metrics will only be calculated for newly added methods or modified methods.

### Value

Either a `SummarizedBenchmark` object, a `DataFrame` or a `data.frame`.

### Functions

- `estimateMetricsForAssay`: Estimate performance metrics for a given assay
- `estimatePerformanceMetrics`: Estimate performance metrics for all assays

### Author(s)

Alejandro Reyes

### Examples

```
data( sb )
sb <- addPerformanceMetric(
  object=sb,
  assay="qvalue",
  evalMetric="TPR",
  evalFunction = function( query, truth, alpha=0.1 ){
    goodHits <- sum( (query < alpha) & truth == 1 )
    goodHits / sum(truth == 1)
  }
)

qvalueMetrics <- estimateMetricsForAssay( sb, assay="qvalue" )
allMetrics <- estimatePerformanceMetrics( sb )
allMetricsTidy <- estimatePerformanceMetrics( sb, tidy=TRUE )
```



```

## modify multiple parameters, "p" and "method"
bench_exp <- expandMethod(bench, label = "padjust",
                        params = list(
                          bonf = rlang::quos(p = round(pval, 5),
                                                method = "bonferonni"),
                          bh = rlang::quos(p = round(pval, 3),
                                             method = "BH")))
printMethods(bench_exp)

## only modify a single parameter using the 'onlyone=' parameter
bench_exp <- expandMethod(bench, label = "padjust",
                        onlyone = "method",
                        params = rlang::quos(bonf = "bonferonni",
                                             BH = "BH"))
printMethods(bench_exp)

```

---

hashBDData

*Convert BDData to BDData with MD5 Hash*


---

### Description

Simple converting function to replace data object in BDData object with MD5 hash value.

### Usage

```

hashBDData(object)

## S4 method for signature 'BDData'
hashBDData(object)

## S4 method for signature 'BenchDesign'
hashBDData(object)

```

### Arguments

object            a BDData or BenchDesign object

### Value

an object of the same class as object with data converted to a MD5 hash.

### Author(s)

Patrick Kimes

---

modifyMethod	<i>Modify definition of method in BenchDesign object</i>
--------------	--

---

### Description

This function takes a BenchDesign object and the name of a method already defined in the object, and returns a modified BenchDesign object with the specified changes made only to the named method. At a minimum, a string name for the method, `label`, must be specified in addition to the primary BenchDesign object.

### Usage

```
modifyMethod(bd, label, params, .overwrite = FALSE)
```

### Arguments

<code>bd</code>	BenchDesign object.
<code>label</code>	Character name of method to be modified.
<code>params</code>	Named quosure list created using <code>rlang::quos</code> of <code>parameter = value</code> pairs to replace in the method definition. The <code>post</code> , and <code>meta</code> parameters of the method can be modified using the special keywords, <code>bd.post</code> , and <code>bd.meta</code> (the prefix denoting that these values should modify BenchDesign parameters). All other named parameters will be added to the list of parameters to be passed to <code>func</code> .
<code>.overwrite</code>	Logical whether to overwrite the complete existing list of parameters to be passed to <code>func</code> (TRUE), or to simply add the new parameters to the existing list and only replace overlapping parameters (FALSE). (default = FALSE)

### Value

Modified BenchDesign object.

### Author(s)

Patrick Kimes

### Examples

```
## empty BenchDesign
bench <- BenchDesign()

## add method
bench <- addMethod(bench, label = "qv",
  func = qvalue::qvalue,
  post = function(x) { x$qvalue },
  meta = list(note = "storey's q-value"),
  params = rlang::quos(p = pval))

## modify method 'meta' property of 'qv' method
bench <- modifyMethod(bench, label = "qv",
  params = rlang::quos(bd.meta =
    list(note = "Storey's q-value")))
```

```
## verify that method has been updated
printMethod(bench, "qv")
```

---

performanceMetrics     *Accessor and replacement functions for the slot 'performanceMetrics' of a SummarizedBenchmark object.*

---

### Description

Accessor and replacement functions for the slot 'performanceMetrics' of a SummarizedBenchmark object.

### Usage

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

## S4 method for signature 'SummarizedBenchmark'
performanceMetrics(object, assay = NULL)

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

### Arguments

object	a SummarizedBenchmark object.
...	Futher arguments, perhaps used by methods
value	A SimpleList of the same length as the number of assays
assay	A character string indicating an assay name

### Value

A SimpleList with one element for each assay. Each element of the list contains a list of performance functions.

### Author(s)

Alejandro Reyes

### See Also

[addPerformanceMetric](#), [estimatePerformanceMetrics](#)

## Examples

```
data( sb )
performanceMetrics( sb )
performanceMetrics( sb, assay="qvalue" )
performanceMetrics( sb ) <- SimpleList( qvalue=list(), logFC=list() )
```

---

plotMethodsOverlap      *Calls UpSetR for qvalues of a [SummarizedBenchmark](#) object.*

---

## Description

This function looks for an assay, called by default 'qvalue', and given an alpha threshold, it binarizes the assay matrix depending on whether its values are below the alpha threshold. Then it uses the function [upset](#) to plot the overlaps. The plot is only generated if at least 2 methods have observations that pass the alpha threshold.

## Usage

```
plotMethodsOverlap(object, assay = "qvalue", alpha = 0.1, ...)
```

## Arguments

object	A <a href="#">SummarizedBenchmark</a> object.
assay	The name of an assay.
alpha	An alpha value.
...	Further arguments passed to <a href="#">upset</a>

## Value

An upseR plot.

## Author(s)

Alejandro Reyes

## Examples

```
data( sb )
## Not run:
plotMethodsOverlap(sb)

## End(Not run)
```

---

plotROC	<i>Plotting ROC curves</i>
---------	----------------------------

---

**Description**

This function inputs a [SummarizedBenchmark](#) object, looks for an assay called 'qvalue' and plots receiver operating characteristic curves for each of the methods to benchmark.

**Usage**

```
plotROC(object, assay = "qvalue")
```

**Arguments**

object	A <a href="#">SummarizedBenchmark</a> object.
assay	An assay name.

**Value**

A ggplot object.

**Author(s)**

Alejandro Reyes

**Examples**

```
data( sb )  
## Not run:  
plotROC( sb )  
  
## End(Not run)
```

---

printMethod	<i>Pretty print methods in a BenchDesign</i>
-------------	--

---

**Description**

Print out details about a method included in the BenchDesign. The printMethods function is just a wrapper to call printMethod on all methods in the BenchDesign.

**Usage**

```
printMethod(bd, n = NULL)  
  
printMethods(bd)
```



**Arguments**

bd                    BenchDesign object.  
n                     name of a method in the BenchDesign to show.

**Value**

Brief description is returned to console.

**Author(s)**

Patrick Kimes  
Patrick Kimes

**Examples**

```
## create empty BenchDesign
bench <- BenchDesign()

## currently no methods
printMethods(bench)

## add method
bench <- addMethod(bench, label = "method_a", p.adjust)
bench <- addMethod(bench, label = "method_b", qvalue::qvalue)

## show a single method
printMethod(bench, "method_a")

## show all methods
printMethods(bench)
```

---

sb

*SummarizedBenchmark example*

---

**Description**

This object contains the example data from the iCOBRA package reformatted as a SummarizedBenchmark object. It consists of differential expression results from DESeq2 edgeR and limma-voom.

**Source**

Example data from the iCOBRA package.

**Examples**

```
data(sb)
```

---

SummarizedBenchmark     *Constructor function for SummarizedBenchmark objects.*

---

### Description

Function to construct SummarizedBenchmark objects.

### Usage

```
SummarizedBenchmark(assays, colData, ftData = NULL, groundTruth = NULL,  
  performanceMetrics = NULL, BenchDesign = NULL, ...)
```

### Arguments

assays	A list containing outputs of the methods to be benchmark. Each element of the list must contain a matrix or data.frame of $n \times m$ , $n$ being the number of features tested (e.g. genes) and $m$ being the number of methods in the benchmark. Each element of the list must contain a single assay (the outputs of the methods). For example, for a benchmark of differential expression methods, one assay could contain the q-values from the different methods and another assay could be the estimated log fold changes.
colData	A <a href="#">DataFrame</a> describing the annotation of the methods. These could include version of the software or the parameters used to run them.
ftData	A <a href="#">DataFrame</a> object describing the rows. This parameter is equivalent to the parameter rowData of a SummarizedExperiment.
groundTruth	If present, a <a href="#">DataFrame</a> containing the ground truths. If provided, the number of columns must be the same as the number of assays (NA's are accepted). The names of the columns should have the same names as the assays.
performanceMetrics	A <a href="#">SimpleList</a> of the same length as the number of assays. Each element of the list must be a list of functions. Each function must contain the parameters 'query' and 'truth'.
BenchDesign	A <a href="#">BenchDesign</a> containing the code used to construct the object. (default = NULL)
...	Additional parameters passed to <a href="#">SummarizedExperiment</a> .

### Value

A [SummarizedBenchmark](#) object.

### Author(s)

Alejandro Reyes

### Examples

```
## loading the example data from iCOBRA  
library(iCOBRA)  
data(cobradata_example)
```

```
## a bit of data wrangling and reformatting
assays <- list(
  qvalue=cobradata_example@padj,
  logFC=cobradata_example@score )
assays[["qvalue"]]$DESeq2 <- p.adjust(cobradata_example@pval$DESeq2, method="BH")
groundTruth <- DataFrame( cobradata_example@truth[,c("status", "logFC")] )
colnames(groundTruth) <- names( assays )
colData <- DataFrame( method=colnames(assays[[1]]) )
groundTruth <- groundTruth[rownames(assays[[1]]),]

## constructing a SummarizedBenchmark object
sb <- SummarizedBenchmark(
  assays=assays, colData=colData,
  groundTruth=groundTruth )
colData(sb)$label <- rownames(colData(sb))
```

---

SummarizedBenchmark-accessors

*Accessor and replacement functions for the slots of a Summarized-Benchmark object.*

---

## Description

Accessor and replacement functions for the slots of a SummarizedBenchmark object.

## Usage

```
groundTruths(object, ...)

groundTruths(object, ...) <- value

## S4 replacement method for signature 'SummarizedBenchmark,character'
assayNames(x, ...) <- value

## S4 replacement method for signature 'SummarizedBenchmark'
mcols(x, ...) <- value

## S4 method for signature 'SummarizedBenchmark'
groundTruths(object, ...)

## S4 replacement method for signature 'SummarizedBenchmark'
groundTruths(object, ...) <- value

## S4 method for signature 'SummarizedBenchmark'
BDMethodList(..., x = NULL)

## S4 method for signature 'SummarizedBenchmark'
BenchDesign(methods, data)
```

**Arguments**

object	a SummarizedBenchmark object.
...	Futher arguments, perhaps used by methods
value	A character vector.
x	A SummarizedBenchmark object.
methods	A SummarizedBenchmark object.
data	A data set to be used.

**Value**

Either a SummarizedBenchmark object or a slot of the SummarizedBenchmark object.

**Author(s)**

Alejandro Reyes

**See Also**

[performanceMetrics](#)

**Examples**

```
data( sb )
assayNames( sb )[2] <- "log2FC"
```

---

SummarizedBenchmark-class

*SummarizedBenchmark class documentation*

---

**Description**

Extension of the [RangedSummarizedExperiment](#) to store the output of different methods intended for the same purpose in a given dataset. For example, a differential expression analysis could be done using **limma**-voom, **edgeR** and **DESeq2**. The SummarizedBenchmark class provides a framework that is useful to store, benchmark and compare results.

**Slots**

**performanceMetrics** A [SimpleList](#) of the same length as the number of [assays](#) containing performance functions to be compared with the ground truths.

**BenchDesign** A [BenchDesign](#) originally used to generate the results in the object.

**Author(s)**

Alejandro Reyes

## Examples

```
## loading the example data from iCOBRA
library(iCOBRA)
data(cobradata_example)

## a bit of data wrangling and reformatting
assays <- list(
  qvalue=cobradata_example@padj,
  logFC=cobradata_example@score )
assays[["qvalue"]]$DESeq2 <- p.adjust(cobradata_example@pval$DESeq2, method="BH")
groundTruth <- DataFrame( cobradata_example@truth[,c("status", "logFC")] )
colnames(groundTruth) <- names( assays )
colData <- DataFrame( method=colnames(assays[[1]]) )
groundTruth <- groundTruth[rownames(assays[[1]]),]

## constructing a SummarizedBenchmark object
sb <- SummarizedBenchmark(
  assays=assays, colData=colData,
  groundTruth=groundTruth )
```

---

tdat

*Example data.frame containing results for 50 two-sample t-tests.*


---

## Description

Example data.frame containing results for 50 two-sample t-tests.

## Format

a data.frame that contains the results of 50 simulated two-sample t-tests, with each row corresponding to an independent test. The data.frame includes the following 5 columns: 1. H = binary 0/1 whether data for the test was simulated under the null (0) or alternative (1) 2. test\_statistic = test-statistics of the t-test 3. effect\_size = mean difference between the two sample groups 4. pval = p-value of the t-test 5. SE = standard error of the t-test

## Examples

```
data(tdat)
```

---

tidyBDMethod

*Tidy BDMethod Data*


---

## Description

A helper function to extract information for a single or multiple BDMethod object or a list of BDMethod objects.

**Usage**

```
tidyBDMMethod(obj, dat = NULL, eval = FALSE, label = FALSE)

## S4 method for signature 'BDMMethod'
tidyBDMMethod(obj, dat, eval)

## S4 method for signature 'list'
tidyBDMMethod(obj, dat = NULL, eval = FALSE,
  label = FALSE)

## S4 method for signature 'SimpleList'
tidyBDMMethod(obj, dat = NULL, eval = FALSE,
  label = FALSE)

## S4 method for signature 'BenchDesign'
tidyBDMMethod(obj, dat = NULL, eval = FALSE,
  label = FALSE)
```

**Arguments**

obj	BDMMethod object, list/List of BDMMethod objects (e.g. a BDMethodList), or a BenchDesign object
dat	optional data object to use when evaluating any unevaluated expressions in bdm meta data. (default = NULL)
eval	logical whether to evaluate any quosures in the meta slot of the BDMethod objects. (default = FALSE)
label	logical whether to add a "label" column to the resulting table containing the names of the methods if obj was specified as a named list. (default = FALSE)

**Details**

If any quosures are specified to the "meta" slot of a BDMethod object, the quosure is converted to a text string using `rlang::quo_text`.

**Value**

A named vector of meta data if only a single BDMethod object specified, else a tibble of meta data for the specified list of methods.

**Author(s)**

Patrick Kimes

---

tidyUpMetrics

*Reformat performance metrics to a long format.*

---

**Description**

This function takes as input a SummarizedBenchmark object, extracts the estimated performance metrics and reformats them into a long-formatted data frame.

**Usage**

```
tidyUpMetrics(object)
```

**Arguments**

object            A [SummarizedBenchmark](#) object.

**Value**

A tidy data.frame

**Author(s)**

Alejandro Reyes

**Examples**

```
data( "sb", package="SummarizedBenchmark" )
sb <- estimateMetricsForAssay( sb, assay="qvalue", evalMetric="rejections",
  evalFunction=function( query, truth, alpha=0.1 ){
    sum( query < alpha )
  },
  addColData=TRUE )
tidyUpMetrics( sb )
```

---

updateBench

*Update SummarizedBenchmark object*

---

**Description**

Update SummarizedBenchmark results with new methods.

**Usage**

```
updateBench(sb, bd = NULL, dryrun = TRUE, version = FALSE,
  keepAll = TRUE, reuseParams = TRUE, ...)
```

**Arguments**

sb	a SummarizedBenchmark object
bd	a BenchDesign object
dryrun	logical whether to just print description of what would be updated rather than actually running any methods. (default = TRUE)
version	logical whether to re-run methods with only package version differences. (default = FALSE)
keepAll	logical whether to keep methods run in original SummarizedBenchmark but not in new BenchDesign. Only used if bd is not NULL. (default = TRUE)
reuseParams	logical whether to reuse parameters from buildBench call used to create SummarizedBenchmark object (if available). Directly specified buildBench parameters still take precedence. (default = TRUE)
...	optional parameters to pass to <a href="#">buildBench</a> .

**Value**

SumamrizedBenchmark object.

**Author(s)**

Patrick Kimes



# Index

## \*Topic **SummarizedBenchmark**

sb, [25](#)

## \*Topic **data**

allSB, [5](#)

sb, [25](#)

tdata, [29](#)

addMethod, [2](#)

addPerformanceMetric, [4](#), [17](#), [22](#)

allSB, [5](#)

allSB, quantSB (allSB), [5](#)

assayNames

(SummarizedBenchmark-accessors),  
[27](#)

assayNames, SummarizedBenchmark-method  
(SummarizedBenchmark-accessors),  
[27](#)

assayNames<-, SummarizedBenchmark, character-method  
(SummarizedBenchmark-accessors),  
[27](#)

assays, [28](#)

availableMetrics, [5](#)

BDDData, [6](#)

BDDData, ANY-method (BDDData), [6](#)

BDDData, BDDData-method (BDDData), [6](#)

BDDData, BenchDesign-method (BDDData), [6](#)

BDDData, SummarizedBenchmark-method  
(BDDData), [6](#)

BDDData-class, [6](#)

BDDData<- (BenchDesign-accessors), [11](#)

BDDData<-, BenchDesign, BDDDataOrNULL-method  
(BenchDesign-accessors), [11](#)

BDMethod, [7](#)

BDMethod, BDMethodList-method  
(BDMethodList-accessors), [9](#)

BDMethod, BenchDesign-method  
(BenchDesign-accessors), [11](#)

BDMethod, function-method (BDMethod), [7](#)

BDMethod, quosure-method (BDMethod), [7](#)

BDMethod-class, [8](#)

BDMethod<- (BenchDesign-accessors), [11](#)

BDMethod<-, BDMethodList, character, BDMethod-method  
(BDMethodList-accessors), [9](#)

BDMethod<-, BDMethodList, character, NULL-method  
(BDMethodList-accessors), [9](#)

BDMethod<-, BenchDesign, character, BDMethod-method  
(BenchDesign-accessors), [11](#)

BDMethod<-, BenchDesign, character, NULL-method  
(BenchDesign-accessors), [11](#)

BDMethodList, [8](#)

BDMethodList, ANY-method (BDMethodList),  
[8](#)

BDMethodList, BenchDesign-method  
(BenchDesign-accessors), [11](#)

BDMethodList, SummarizedBenchmark-method  
(SummarizedBenchmark-accessors),  
[27](#)

BDMethodList-accessors, [9](#)

BDMethodList-class, [10](#)

BDMethodList<- (BenchDesign-accessors),  
[11](#)

BDMethodList<-, BenchDesign, BDMethodList-method  
(BenchDesign-accessors), [11](#)

BenchDesign, [10](#), [26](#), [28](#)

BenchDesign, ANY-method (BenchDesign), [10](#)

BenchDesign, SummarizedBenchmark-method  
(SummarizedBenchmark-accessors),  
[27](#)

BenchDesign-accessors, [11](#)

BenchDesign-class, [12](#)

buildBench, [12](#), [31](#)

coerce (BDMethodList), [8](#)

colData, [18](#)

compareBDDData, [14](#)

compareBDMethod, [15](#)

compareBenchDesigns, [15](#)

compareBenchDesigns, BenchDesign, BenchDesign-method  
(compareBenchDesigns), [15](#)

compareBenchDesigns, BenchDesign, SummarizedBenchmark-method  
(compareBenchDesigns), [15](#)

compareBenchDesigns, SummarizedBenchmark, BenchDesign-method  
(compareBenchDesigns), [15](#)

compareBenchDesigns, SummarizedBenchmark, missing-method  
(compareBenchDesigns), [15](#)

compareBenchDesigns, SummarizedBenchmark, SummarizedBenchmark-method  
(compareBenchDesigns), [15](#)

- data.frame, [18](#)
- DataFrame, [18](#), [26](#)
- dropMethod, [16](#)
- estimateMetricsForAssay, [17](#)
- estimatePerformanceMetrics, [18](#), [22](#)
- estimatePerformanceMetrics  
(estimateMetricsForAssay), [17](#)
- expandMethod, [19](#)
- groundTruths  
(SummarizedBenchmark-accessors),  
[27](#)
- groundTruths, SummarizedBenchmark-method  
(SummarizedBenchmark-accessors),  
[27](#)
- groundTruths<-  
(SummarizedBenchmark-accessors),  
[27](#)
- groundTruths<- , SummarizedBenchmark-method  
(SummarizedBenchmark-accessors),  
[27](#)
- hashBDDData, [20](#)
- hashBDDData, BDDData-method (hashBDDData),  
[20](#)
- hashBDDData, BenchDesign-method  
(hashBDDData), [20](#)
- mcols<- , SummarizedBenchmark-method  
(SummarizedBenchmark-accessors),  
[27](#)
- modifyMethod, [21](#)
- performanceMetrics, [22](#), [28](#)
- performanceMetrics, SummarizedBenchmark-method  
(performanceMetrics), [22](#)
- performanceMetrics<-  
(performanceMetrics), [22](#)
- performanceMetrics<- , SummarizedBenchmark, SimpleList-method  
(performanceMetrics), [22](#)
- plotMethodsOverlap, [23](#)
- plotROC, [24](#)
- printMethod, [24](#)
- printMethods (printMethod), [24](#)
- RangedSummarizedExperiment, [28](#)
- sb, [25](#)
- show, BDDData-method (BDDData-class), [6](#)
- show, BDMMethod-method (BDMMethod-class), [8](#)
- show, BDMethodList-method  
(BDMethodList-class), [10](#)
- show, BenchDesign-method  
(BenchDesign-class), [12](#)
- SimpleList, [26](#), [28](#)
- SummarizedBenchmark, [4](#), [17](#), [18](#), [23](#), [24](#), [26](#),  
[26](#), [31](#)
- SummarizedBenchmark-accessors, [27](#)
- SummarizedBenchmark-class, [28](#)
- SummarizedExperiment, [18](#), [26](#)
- tdat, [29](#)
- tidyBDMMethod, [29](#)
- tidyBDMMethod, BDMMethod-method  
(tidyBDMMethod), [29](#)
- tidyBDMMethod, BenchDesign-method  
(tidyBDMMethod), [29](#)
- tidyBDMMethod, list-method  
(tidyBDMMethod), [29](#)
- tidyBDMMethod, SimpleList-method  
(tidyBDMMethod), [29](#)
- tidyUpMetrics, [30](#)
- truthdat (sb), [25](#)
- txi (sb), [25](#)
- updateBench, [31](#)
- upset, [23](#)