

# Package ‘SummarizedBenchmark’

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<http://bioconductor.org/packages/SummarizedBenchmark/>

**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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addMethod	<i>Add method to BenchDesign object</i>
-----------	---

---

### Description

Takes a [BenchDesign](#) object and the definition of a new method for benchmarking and returns the original [BenchDesign](#) with the new method included.

At a minimum, a method label (`label =`), and the workhorse function for the method (`func =`) must be specified for the new method.

Parameters for the method must be specified as a [quos](#) named list of `parameter = value` pairs mapping entries in the benchmarking data to the function parameters. For users familiar with the [ggplot2](#) package, this can be viewed similar to the `aes =` mapping of data to geometry parameters.

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`.

### Usage

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

### Arguments

<code>bd</code>	<a href="#">BenchDesign</a> object.
<code>label</code>	Character name for the method.
<code>func</code>	Primary function to be benchmarked.
<code>params</code>	Named quosure list created using <a href="#">quos</a> of <code>parameter = value</code> pairs to be passed to <code>func</code> .
<code>post</code>	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> )
<code>meta</code>	Optional metadata information for method to be included in <code>colData</code> of <a href="#">SummarizedBenchmark</a> object generated using <code>link{buildBench}</code> . See Details for more information. Ignored if <code>NULL</code> . (default = <code>NULL</code> )

### Details

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 `quo`, e.g. `list(pkg_func = quo(p.adjust))`.

### Value

Modified `BenchDesign` object with new method added.

### Author(s)

Patrick Kimes

### See Also

[modifyMethod](#), [expandMethod](#), [dropMethod](#)

### 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 performance metric to 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 <code>SummarizedBenchmark</code> 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.

**evalFunction** A function that calculates a performance metric. It should contain at least two arguments, `query` and `truth`, where `query` is the output vector of a method and `truth` is the vector of true values. If additional parameters are specified, they must contain default values. If `NULL`, the `'evalMetric'` string must be the name of a predefined metric available through `'availableMetrics()$function'`.

**Value**

A [SummarizedBenchmark](#) object.

**Author(s)**

Alejandro Reyes

**See Also**

[availableMetrics](#), [performanceMetrics](#)

**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)
```

```
assayNames<- , SummarizedBenchmark, character-method  
Set assay names in SummarizedBenchmark object
```

---

### Description

Modifies the assay names of a [SummarizedBenchmark](#) object.

### Usage

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

### Arguments

x	A <a href="#">SummarizedBenchmark</a> object.
...	Futher arguments, perhaps used by methods.
value	A character vector.

### Value

Modified [SummarizedBenchmark](#) object.

### Author(s)

Alejandro Reyes

### See Also

[SummarizedBenchmark](#)

### Examples

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

---

```
availableMetrics      List pre-defined metrics for SummarizedBenchmark objects
```

---

### 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.

**Author(s)**

Alejandro Reyes

**Examples**

```
availableMetrics()
```

---

BDData

*Create a new BDData object*

---

**Description**

Initializes a new BDData object of benchmarking data.

Data sets are stored as BDData objects within BenchDesign objects as well as SummarizedBenchmark objects. However, because data is directly specified to the BenchDesign constructor, there is usually no need to call the BDData constructor to create completely new data objects.

The BDData constructor is most useful for extracting the data sets contained in BenchDesign objects as well as SummarizedBenchmark objects. By default, the BDData object stored in SummarizedBenchmark objects will be MD5 hashes rather than the complete original data set. [compareBDData](#) can be used to compare various forms of BDData, as shown in the examples below.

**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

**See Also**

[BDData-class](#), [BenchDesign](#)

**Examples**

```
## construct from data.frame
datadf <- data.frame(x = 1:5, y = runif(5))
bdd_df <- BDData(datadf)
bdd_df

## construct from MD5 hash of data.frame
bdd_md5 <- BDData(digest::digest(datadf))
bdd_md5

## compare two BDData objects
compareBDData(bdd_df, bdd_md5)

## note that the data is the same, i.e. the MD5 hashes match, but the
## data types ("data" vs. "md5has") are different
```

---

BDData-class

*BDData class*

---

**Description**

Container for data in a BenchDesign object.

**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

**See Also**

[BDData](#), [BenchDesign-class](#), [BDMethod-class](#), [BDMethodList-class](#)



---

BDData<-                      *Set data in BenchDesign object*

---

### Description

Adds, removes or replaces [BDData](#) in [BenchDesign](#) object. Data can be removed by setting the value to NULL.

### Usage

```
BDData(x) <- value
```

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

### Arguments

x                      [BenchDesign](#) object.  
value                  [BDData](#) or NULL.

### Value

modified [BenchDesign](#) object

### Author(s)

Patrick Kimes

### See Also

[BDData](#)

### Examples

```
bd <- BenchDesign()  
BDData(bd) <- BDData(data.frame(x1 = runif(5)))  
bd
```

---

BDMETHOD                      *Create a new BDMETHOD object*

---

### Description

Initializes a new [BenchDesign](#) method object for benchmarking.

New [BDMETHOD](#) objects are typically not directly constructed as they have limited use outside of [BenchDesign](#) objects. Instead, methods in a [BenchDesign](#) object are more commonly created, modified or removed using function calls on the [BenchDesign](#), e.g. using [addMethod](#) to add a new method object.

The constructor can also be used to access [BDMETHOD](#) objects stored in [BDMETHODList](#) and [BenchDesign](#) objects.

**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, ...)

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

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

```

**Arguments**

x	main method function or function quosure. Alternative, may be a <a href="#">BDMETHODList</a> or <a href="#">BenchDesign</a> object from which the <a href="#">BDMETHOD</a> should be extracted.
params	list of quosures specifying function parameters. (default = <code>rlang::quos()</code> )
post	list of functions to be applied to the output of x. (default = <code>NULL</code> )
meta	list of metadata. (default = <code>NULL</code> )
...	other parameters.
i	integer index or character name of <a href="#">BDMETHOD</a> in <a href="#">BDMETHODList</a> or <a href="#">BenchDesign</a> object.

**Value**

[BDMETHOD](#) object

**Author(s)**

Patrick Kimes

**See Also**

[BDMETHOD-class](#), [BenchDesign](#), [BDMETHODList](#)

**Examples**

```

## create a simple BDMETHOD
bdm1 <- BDMETHOD(x = base::mean)

## create a more complex BDMETHOD
bdm2 <- BDMETHOD(x = function(x) { x^2 }, post = base::sqrt,
  meta = list(note = "simple example"))

## construct a BenchDesign with the BDMETHOD objects
bd <- BenchDesign(method1 = bdm1, method2 = bdm2)

```

```
## access a BDMETHOD in the BenchDesign
BDMETHOD(bd, "method1")
```

---

 BDMETHOD-class

*BDMETHOD class*


---

### Description

Container for individual methods to be compared as part of a benchmark experiment defined in a BenchDesign object. In the SummarizedBenchmark framework, methods are defined by a unique combination of functions, parameters, and any relevant meta data.

New BDMETHOD objects can be created using the [BDMETHOD](#) constructor.

### 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

### See Also

[BDMETHOD](#), [BenchDesign-class](#), [BDMETHODList-class](#), [BDDATA-class](#)

---

 BDMETHOD<-

*Set method in list or BenchDesign object*


---

### Description

Adds, replaces or removes a named [BDMETHOD](#) method in a [BDMETHODList](#) or [BenchDesign](#) object with a specified [BDMETHOD](#) object.

An existing method can be removed by setting the value to NULL.

## Usage

```
BDMETHOD(x, i) <- value

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

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

## Arguments

x	<a href="#">BenchDesign</a> or <a href="#">BDMETHODList</a> object.
i	character name of method.
value	<a href="#">BDMETHOD</a> or NULL.

## Value

modified [BenchDesign](#) object

## Author(s)

Patrick Kimes

## See Also

[BDMETHOD](#)

## Examples

```
bd <- BenchDesign()
BDMETHOD(bd, "avg") <- BDMETHOD(x = base::mean)
bd
```

---

BDMETHODList

*Create a new BDMETHODList object*

---

## Description

Initializes a new SimpleList of BenchDesign method ([BDMETHOD](#)) objects.

Similar to [BDMETHOD](#) objects, [BDMETHODList](#) typically do not need to be directly constructed. Because the list of methods is only useful as part of a [BenchDesign](#) object, it is more common to simply manipulate the list of methods through calls to the corresponding [BenchDesign](#), e.g. [addMethod](#) to add a new method to the list.

The constructor can also be used to access the [BDMETHODList](#) list of methods in a [BenchDesign](#) object.

**Usage**

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

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

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

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

**Arguments**

...	a named list of <a href="#">BDMETHOD</a> objects
x	a <a href="#">BenchDesign</a> or <a href="#">SummarizedBenchmark</a> object to extract the list of methods from. (default = NULL)

**Value**

BDMETHODList object

**Author(s)**

Patrick Kimes

**See Also**

[BDMETHODList-class](#), [BenchDesign](#), [BDMETHOD](#)

**Examples**

```
## construct an empty list
bdml <- BDMETHODList()

## construct a list with BDMETHOD objects
bdml <- BDMETHODList(m_method = BDMETHOD(base::mean),
                    s_method = BDMETHOD(function(x) { x^2 })))
bdml

## construct a BenchDesign with a BDMETHODList
bd <- BenchDesign(methods = bdml)

## access the BDMETHODList in the BenchDesign
BDMETHODList(bd)
```

---

BDMETHODList-class      *BDMETHODList class*

---

### Description

Extension of the SimpleList class to contain a list of BDMETHOD objects. The class serves as the primary container for the set of methods in the BenchDesign class.

New BDMETHODList objects can be created using the [BDMETHODList](#) constructor.

### Author(s)

Patrick Kimes

### See Also

[BDMETHODList](#), [BenchDesign-class](#), [BDMETHOD-class](#), [BDDATA-class](#)

---

BDMETHODList<-      *Set method list in BenchDesign object*

---

### Description

Replaces the [BDMETHODList](#) list of methods in a [BenchDesign](#) object with a specified [BDMETHODList](#) object.

### Usage

```
BDMETHODList(x) <- value
```

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

### Arguments

x                      BenchDesign object.  
value                  [BDMETHODList](#) list of methods.

### Value

modified BenchDesign object

### Author(s)

Patrick Kimes

### See Also

[BDMETHOD](#), [BDMETHODList](#)

**Examples**

```
bd <- BenchDesign()
BDMETHODList(bd) <- BDMETHODList(avg = BDMETHOD(x = base::mean))
bd
```

---

BenchDesign

---

*Create a new BenchDesign object*


---

**Description**

Initializes a new BenchDesign object of benchmarking methods and data.

The BenchDesign class serves as the core container for methods and data used for benchmarking in the SummarizedBenchmark package. The object can be initialized with a list of methods to be benchmarked, a default benchmarking data set, both or neither. Methods must be passed to the constructor as BDMETHOD or BDMETHODList objects.

The constructor can also be used to access the BenchDesign stored in a SummarizedBenchmark object.

**Usage**

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

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

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

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

```
BenchDesign(methods, data)
```

**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

**See Also**

[BenchDesign-class](#), [BDMETHOD](#), [BDMETHODList](#)

## Examples

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

## with data - data must be a named argument
datadf <- data.frame(pval = runif(20), x1 = rnorm(20))
bd <- BenchDesign(data = datadf)

## with two methods and data
method_bh <- BDMethod(stats::p.adjust, params = rlang::quos(p = pval, method = "BH"))
method_bf <- BDMethod(stats::p.adjust, params = rlang::quos(p = pval, method = "bonferroni"))
bd <- BenchDesign(bh = method_bh, bonf = method_bf,
                 data = datadf)

## with BDMethodList and data
bdml <- BDMethodList(bh = method_bh, bonf = method_bf)
bd <- BenchDesign(methods = bdml, data = datadf)
```

---

BenchDesign-class      *BenchDesign class*

---

## Description

Along with the SummarizedBenchmark class, one of the two main classes of the Summarized-Benchmark package. The BenchDesign class serves as a container for both the set of methods to be benchmarked and optionally the data to be used for benchmarking.

Methods are organized as BDMethod objects and stored in as a list using the BDMethodList class. The BDData class is used to store benchmarking data, or in some cases, just the MD5 hash of the original data set. Any list object, including data.frame objects, can be specified for data. More details on the component classes are provided in the corresponding class documentation.

For details on how to create new BenchDesign objects, see the documentation for the [BenchDesign](#) constructor.

## Slots

`data` a list containing the data to be used in the benchmark.

`methods` a BDMethodList list of BDMethod objects to be compared in the benchmark.

## Author(s)

Patrick Kimes

## See Also

[BenchDesign](#), [BDMethod-class](#), [BDMethodList-class](#), [BDData-class](#)



---

buildBench	<i>Execute BenchDesign</i>
------------	----------------------------

---

## Description

Function to evaluate methods defined in a [BenchDesign](#) on a supplied data set to generate a [SummarizedBenchmark](#) of benchmarking results. 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

bd	<a href="#">BenchDesign</a> object.
data	Data set to be used for benchmarking, will take priority over data set specified to <a href="#">BenchDesign</a> object. Ignored if NULL. (default = NULL)
truthCols	Character vector of column names in data set corresponding to ground truth values for each assay. If specified, column will be added to the <code>groundTruth</code> <code>DataFrame</code> of the returned <a href="#">SummarizedBenchmark</a> object. If the <a href="#">BenchDesign</a> includes only a single assay, the same name will be used for the assay. If the <a href="#">BenchDesign</a> 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)
ftCols	Vector of character names of columns in data set that should be included as feature data (row data) in the returned <a href="#">SummarizedBenchmark</a> object. (default = NULL)
sortIDs	Whether the output of each method should be merged and sorted using IDs. See <a href="#">Details</a> for more information. (default = FALSE)
keepData	Whether to store the data as part of the <a href="#">BenchDesign</a> slot of the returned <a href="#">SummarizedBenchmark</a> object. If FALSE, a MD5 hash of the data will be stored with the <a href="#">BenchDesign</a> slot. (default = FALSE)
catchErrors	logical whether errors produced by methods during evaluation should be caught and printed as a message without stopping the entire build process. (default = TRUE)
parallel	Whether to use parallelization for evaluating each method. Parallel execution is performed using <b>BiocParallel</b> . Parameters for parallelization should be specified with <a href="#">register</a> or through the <code>BPPARAM</code> parameter. (default = FALSE)
BPPARAM	Optional <code>BiocParallelParam</code> 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 = 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 `sortIDs = 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

## See Also

`updateBench`

## 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	<i>Compare BDData objects</i>
---------------	-------------------------------

---

**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

**See Also**

[compareBenchDesigns](#)

**Examples**

```
## compare data with same MD5 hash value
bdd1 <- BDData(data.frame(x = 1:10))
bdd1h <- hashBDData(bdd1)
compareBDData(bdd1, bdd1h)
```

```
## compare different data, both same type
bdd2 <- BDData(data.frame(x = 2:11))
bdd2h <- hashBDData(bdd2)
compareBDData(bdd1, bdd2)
compareBDData(bdd1h, bdd2h)
```

```
## compare completely different data
compareBDData(bdd1, bdd2h)
```

---

compareBDMMethod	<i>Compare BDMMethod objects</i>
------------------	----------------------------------

---

**Description**

Simple comparison of two BDMMethod objects based on meta data.

**Usage**

```
compareBDMMethod(x, y)
```

**Arguments**

x	a BDMMethod object
y	a BDMMethod object

**Value**

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

**Author(s)**

Patrick Kimes

**See Also**

[compareBenchDesigns](#)

**Examples**

```
bdm1 <- BDMMethod(stats::rnorm, params = rlang::quos(n = 100))
bdm2 <- BDMMethod(stats::rt, params = rlang::quos(n = 100, df = 1))

compareBDMMethod(bdm1, bdm2)
```

---

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).



```

      post = sd)
compareBenchDesigns(bd1, bd2)

```

---

dropMethod

*Remove method from BenchDesign object*


---

### Description

Takes a [BenchDesign](#) object and the name of an existing method and returns a reduced [BenchDesign](#) object with the method removed.

### Usage

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

### Arguments

bd                    [BenchDesign](#) object.  
label                 Character name of method.

### Value

Modified [BenchDesign](#) object with specified method dropped.

### Author(s)

Patrick Kimes

### See Also

[modifyMethod](#), [expandMethod](#), [addMethod](#)

### 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"))
BDMethodList(bench)

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

```

---

`estimateMetricsForAssay`*Estimate performance metrics in SummarizedBenchmark object*

---

### 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

<code>object</code>	A <code>SummarizedBenchmark</code> object.
<code>assay</code>	A string with an assay name. Indicates the assay that should be given as input to this performance metric.
<code>evalMetric</code>	A string with the name of the evaluation metric.
<code>addColData</code>	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.
<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 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.
<code>tidy</code>	Logical (default: FALSE). If TRUE, a long formatted <code>data.frame</code> is returned.
<code>...</code>	Additional parameters passed to the performance functions.
<code>rerun</code>	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

**See Also**[availableMetrics](#), [performanceMetrics](#)**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 )

```

---

 expandMethod

*Expand method in BenchDesign object*


---

**Description**

Takes a [BenchDesign](#) object, the name of an existing method, and new parameter specifications, and returns a modified [BenchDesign](#) object with new methods added. The named method is "expanded" to multiple methods according to the specified set of parameters.

**Usage**

```

expandMethod(bd, label, params, onlyone = NULL, .replace = FALSE,
             .overwrite = FALSE)

```

**Arguments**

bd	<a href="#">BenchDesign</a> object.
label	Character name of method to be expanded.
params	Named list of quosure lists specifying the label of the new methods to be added to the <a href="#">BenchDesign</a> , and the set of parameters to overwrite in the original method definition for each new method. Alternatively, if <code>onlyone</code> is non-NULL, a single quosure list with <code>name = value</code> pairs specifying the label of the new methods and the values to use for overwriting the parameter specified in <code>onlyone</code> .
onlyone	Character name of a parameter to be modified. Only specify if just a single parameter should be replaced in the original method definition. Ignored if NULL. (default = NULL)



`.replace` Logical whether original label method should be removed. (default = FALSE)  
`.overwrite` Logical whether to overwrite the existing list of parameters (TRUE) or to simply add the new parameters to the existing list (FALSE). (default = FALSE)

**Value**

Modified [BenchDesign](#) object with new methods with specified parameters added.

**Author(s)**

Patrick Kimes

**See Also**

[modifyMethod](#), [addMethod](#), [dropMethod](#)

**Examples**

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

## add basic 'padjust' method
bench <- addMethod(bench, label = "padjust",
                  func = p.adjust,
                  params = rlang::quos(p = pval, method = "none"))

## modify multiple parameters - params is a list of quosure lists
newparams <- list(bonf = rlang::quos(p = round(pval, 5), method = "bonferonni"),
                 bh = rlang::quos(p = round(pval, 3), method = "BH"))
bench_exp <- expandMethod(bench, label = "padjust", params = newparams)
BDMethodList(bench_exp)

## only modify a single parameter - params is a quosure list
newparams <- rlang::quos(bonf = "bonferonni", BH = "BH")
bench_exp <- expandMethod(bench, label = "padjust", onlyone = "method", params = newparams)
BDMethodList(bench_exp)
```

---

groundTruths

*Get ground truths in SummarizedBenchmark object*

---

**Description**

Method to get groundTruths in SummarizedBenchmark object.

**Usage**

```
groundTruths(object, ...)

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

**Arguments**

object            a SummarizedBenchmark object.  
 ...              further arguments, perhaps used by methods.

**Value**

modified BenchDesign object

**Author(s)**

Alejandro Reyes

---

*groundTruths<-            Set ground truths in SummarizedBenchmark object*

---

**Description**

Method to set groundTruths in SummarizedBenchmark object.

**Usage**

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

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

**Arguments**

object            a SummarizedBenchmark object.  
 ...              futher arguments, perhaps used by methods.  
 value             replacement set of ground truths.

**Value**

modified BenchDesign object

**Author(s)**

Alejandro Reyes, Patrick Kimes

---

hashBDData	<i>Hash data in BDData object</i>
------------	-----------------------------------

---

**Description**

Replaces data stored in a [BDData](#) object with the MD5 hash of the data. If the data was already a MD5 hash, the original object is returned unchanged. The method can be called directly on [BenchDesign](#) objects to hash the underlying data as well.

**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

---

mcols<- , SummarizedBenchmark-method	<i>Set meta data columns in SummarizedBenchmark object</i>
--------------------------------------	--

---

**Description**

Modifies the mcols slot of a [SummarizedBenchmark](#) object.

**Usage**

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

**Arguments**

x                    A [SummarizedBenchmark](#) object.  
 ...                  Further arguments, perhaps used by methods.  
 value                A [DataFrame](#) of meta data.

**Value**

Modified [SummarizedBenchmark](#) object.

**Author(s)**

Alejandro Reyes

**See Also**

[SummarizedBenchmark](#)

---

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

---

**Description**

Takes a [BenchDesign](#) object, the name of an existing method, and new parameter specifications, and returns a modified [BenchDesign](#) object with the specified changes.

**Usage**

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

**Arguments**

bd	<a href="#">BenchDesign</a> object.
label	Character name of method to be modified.
params	Named quosure list created using <a href="#">quos</a> of parameter = value pairs to replace in the method definition. The post, and meta 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 <a href="#">BenchDesign</a> parameters). All other named parameters will be added to the list of parameters to be passed to <code>func</code> .
.overwrite	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 with single method parameters modified.

**Author(s)**

Patrick Kimes

**See Also**

[addMethod](#), [expandMethod](#), [dropMethod](#)

**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      *Get performance metrics in SummarizedBenchmark object*

---

**Description**

Given a [SummarizedBenchmark](#) object, returns a list of lists of performance metrics that have been defined for each assay. Optionally, if `assay =` is specified, performance metrics for only the specified subset of specified assays are returned.

**Usage**

```
performanceMetrics(object, ...)
```

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

**Arguments**

<code>object</code>	a <a href="#">SummarizedBenchmark</a> object.
<code>...</code>	further arguments, perhaps used by methods.
<code>assay</code>	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 metric functions.

**Author(s)**

Alejandro Reyes

**See Also**

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

**Examples**

```
data(sb)
performanceMetrics(sb)
performanceMetrics(sb, assay = "qvalue")
```

---

```
performanceMetrics<- Set performance metrics in SummarizedBenchmark object
```

---

**Description**

Replaces the list of performance metrics in a [SummarizedBenchmark](#) object with a new list of performance metric lists.

**Usage**

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

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

**Arguments**

<code>object</code>	a <a href="#">SummarizedBenchmark</a> object.
<code>...</code>	further arguments, perhaps used by methods.
<code>value</code>	a <a href="#">SimpleList</a> of the same length as the number of assays.

**Value**

Silently, the newly specified [SimpleList](#) of performance metric lists.

**Author(s)**

Alejandro Reyes

**See Also**

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

**Examples**

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

---

plotMethodsOverlap     *Plot UpSetR for 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

### See Also

[plotROC](#), [estimatePerformanceMetrics](#)

### Examples

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

## End(Not run)
```

---

plotROC	<i>Plot ROC curve for SummarizedBenchmark object</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

**See Also**

[plotMethodsOverlap](#), [estimatePerformanceMetrics](#)

**Examples**

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

## End(Not run)
```

---

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

**See Also**

[BDMETHOD-class](#), [BENCHDESIGN-class](#)

**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)
```

---

show,BDData-method     *Show BDData object*

---

**Description**

Show BDData object

**Usage**

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

**Arguments**

object                BDData object to show

**Value**

Print description of BDData object to console

---

show,BDMethod-method     *Show BDMethod object*

---

**Description**

Show BDMethod object

**Usage**

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

**Arguments**

object                BDMethod object to show

**Value**

Print description of BDMethod object to console

---

show,BDMethodList-method

*Show BDMethodList object*

---

### **Description**

Show BDMethodList object

### **Usage**

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

### **Arguments**

object           BDMethodList object to show

### **Value**

Print description of BDMethodList object to console

---

show,BenchDesign-method

*Show BenchDesign object*

---

### **Description**

Show BenchDesign object

### **Usage**

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

### **Arguments**

object           BenchDesign object to show

### **Value**

Print description of BenchDesign object to console

---

SummarizedBenchmark    *Create a new SummarizedBenchmark object*

---

## 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-class

*SummarizedBenchmark class*


---

## 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	<i>Example data.frame containing results for 50 two-sample t-tests.</i>
------	---

---

### 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	<i>Tidy BDMethod Data</i>
--------------	---------------------------

---

### Description

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

### Usage

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

## S4 method for signature 'BDMethod'
tidyBDMethod(obj, dat, eval)

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

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

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

**Arguments**

obj	BDMETHOD object, list/List of BDMETHOD 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

*Tidy up performance metrics in SummarizedBenchmark object*

---

**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

**See Also**

[estimatePerformanceMetrics](#)

**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

*Check/Update SummarizedBenchmark***Description**

Function to update or check status of [SummarizedBenchmark](#) results.

If only a [SummarizedBenchmark](#) object is specified, the function will check whether ‘func’, ‘param’, ‘meta’, ‘post’ or the ‘pkg\_vers’ of the methods in the [BenchDesign](#) stored with the [SummarizedBenchmark](#) do not match values stored in the colData. By default, no methods will be executed to update results. To actually execute updates, set `dryrun = FALSE`.

If a [BenchDesign](#) object is specified in addition to a [SummarizedBenchmark](#) object, the function will check which methods in the new [BenchDesign](#) need to be executed to update the [SummarizedBenchmark](#) results. Again, by default, no methods will be executed unless `dryrun = FALSE` is specified.

Unless `reuseParams = FALSE` is specified, the parameters of the last execution session stored in the colData of the [SummarizedBenchmark](#) object will be used.

**Usage**

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

**Arguments**

sb	a <a href="#">SummarizedBenchmark</a> object
bd	a <a href="#">BenchDesign</a> 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 <a href="#">SummarizedBenchmark</a> but not in new <a href="#">BenchDesign</a> . Only used if bd is not NULL. (default = TRUE)
reuseParams	logical whether to reuse parameters from <code>buildBench</code> call used to create <a href="#">SummarizedBenchmark</a> object (if available). Directly specified <code>buildBench</code> parameters still take precedence. (default = TRUE)
...	optional parameters to pass to <a href="#">buildBench</a> .

**Value**

SummarizedBenchmark object.



**Author(s)**

Patrick Kimes

**See Also**

[buildBench](#)

**Examples**

```
## load example SummarizedBenchmark object
data(allSB)
sb <- allSB[[1]]

## check if results are out of date
updateBench(sb)

## modify BenchDesign
bd <- BenchDesign(sb)
bd <- dropMethod(bd, "kallisto-default")

## check if results need to be updated with new BenchDesign
updateBench(sb, bd)
```

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