

# Genominator

March 24, 2012

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ExpData-class      *Class "ExpData"*

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## Description

A class for representing experimental data organized along a genome.

## Objects from the Class

The preferred way to construct objects of class `ExpData` is to use the constructor function `ExpData(dbFilename = "filename.db", tablename = "tablename")`

## Slots

`dbFilename`: A "character" containing the filename of the SQLite database.

`tablename`: A "character" containing the tablename of the relevant SQLite table.

`indexColumns`: A "character", listing which columns (and in which order) in the table has been indexed.

`mode`: A "character" indicating whether the database is in read or write mode. Write mode implies read mode.

`chrMap`: A "character" which is a placeholder, for now.

`.tmpFile`: A "character". Only for developers..

## Details

For all practical purposes, the class may be considered to point to a specific table in an SQLite database. A connection to the database is opened automatically and a pool of connections is maintained.

## Methods

`ExpData(dbFilename, tablename, mode, indexColumns, pragma)` A constructor function. The last three arguments are for expert users.

`getDbConnection` Returns a connection to the database associated with the `ExpData` object.

`getDbFilename` Returns the filename of the database associated with the `ExpData` object.

`getTablename` Returns the tablename of the `ExpData` object

`getSchema` Returns the schema of the table associated with the `ExpData` object.

`getIndexColumns` Returns the `indexColumns` of the object.

`getColnames` Returns all columns (argument `all = TRUE`) or all columns except the `indexColumns` (argument `all = FALSE`).

`listTables` Returns all vector of tables in a database.

`getMode` Returns the mode of the `ExpData` object.

[ `signature(x = "ExpData")`: subsetting of the object. `ExpData` objects do not have row-names.

\$ `signature(x = "ExpData")`: selects a column of the table.

**head** `signature(x = "ExpData")`: prints the first 10 rows of the object.

**initialize** `signature(.Object = "ExpData")`: The initialize method; use the constructor function `ExpData` instead.

**show** `signature(object = "ExpData")`: the show method.

**Author(s)**

James Bullard <bullard@berkeley.edu>, Kasper Daniel Hansen <khansen@jhsph.edu>

**See Also**

The package vignettes.

**Examples**

```
showClass("ExpData")
```

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Genominator-package

*Data backend for Genomic data*

---

**Description**

This package implements a data backend for genomic data, ie. data mapped to a genome with chromosome, location and possibly strand information. The data is stored in an SQLite database.

We are primarily using the package for analyzing mRNA-Seq data generated from a Solexa machine, but have also used it in part of a larger project incorporating Solexa data, tiling array data from various experiments and cDNA sequencing data.

It interfaces well with the `GenomeGraphs` package.

Read the package vignettes for extensive use cases.

To cite this package, please see the output of `citation("Genominator")`.

**Author(s)**

James Bullard <bullard@stat.berkeley.edu>, Kasper Daniel Hansen <khansen@jhsph.edu>

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addPrimingWeights *Adding priming weights to an AlignedRead object.*

---

### Description

This function adds priming weights to an AlignedRead object.

### Usage

```
addPrimingWeights(aln, weights = NULL, overwrite = FALSE, ...)
```

### Arguments

aln	An object of class AlignedRead.
weights	A vector of weights as produced by <code>computePrimingWeights</code> .
overwrite	A logical, will a weights entry in the alignData of the aln argument be overwritten?
...	These arguments are passed to <code>computePrimingWeights</code> and are only used if weights are NULL.

### Details

If the weights are not supplied, the weights are calculated using the aln object itself.

### Value

An object of class AlignedRead with a weights component in its alignData slot.

### Author(s)

Kasper Daniel Hansen <khansen@jhsp.h.edu>.

### References

Hansen, K. D., Brenner, S. E. and Dudoit, S (2010) Biases in Illumina transcriptome sequencing caused by random hexamer priming. *Nucleic Acids Res*, doi:10.1093/nar/gkq224

### See Also

`computePrimingWeights` and the extended example in the 'Working with ShortRead' vignette.

### Examples

```
if(require(ShortRead)) {
  bwt.file <- system.file("extdata", "bowtie", "s_1_aligned_bowtie.txt",
                          package="ShortRead")
  aln <- readAligned(bwt.file, type = "Bowtie")
  weights <- computePrimingWeights(aln, weightsLength = 2L)
  aln <- addPrimingWeights(aln, weights = weights)
  head(alignData(aln)$weights)
}
```

---

aggregateExpData     *Collapse data into unique entries*

---

### Description

Collapses data based on unique combinations of values in a set of columns, by default adding a column giving counts of data entries with a particular combination.

### Usage

```
aggregateExpData(expData, by = getIndexColumns(expData),
  tablename = NULL, deleteOriginal = FALSE, overwrite = FALSE,
  verbose = getOption("verbose"), colname = "counts",
  aggregator = paste("count(", by[1], ")", sep = ""))
```

### Arguments

expData	An object of class ExpData.
by	Vector containing column names used to define unique entries.
tablename	Name of database table to write output data to.
deleteOriginal	Logical indicating whether original database table in ExpData object should be deleted.
overwrite	Logical indicating whether database table referred to in tablename argument should be overwritten.
verbose	Logical indicating whether details should be printed.
colname	Name of column for recording aggregation output (by default, counts).
aggregator	SQLite code used for aggregating. See Details for more information.

### Details

By default this function counts instances of data entries with a particular combination of the values in the set of columns indicated in the `by` argument. Other SQLite commands can be indicated using the `aggregator` argument.

### Value

Returns an ExpData object.

### Author(s)

James Bullard <bullard@berkeley.edu>, Kasper Daniel Hansen <khansen@jhsph.edu>

### See Also

See `Genominator` vignette for more information.

**Examples**

```

N <- 10000 # the number of observations.
df <- data.frame(chr = sample(1:16, size = N, replace = TRUE),
                location = sample(1:1000, size = N, replace = TRUE),
                strand = sample(c(1L,-1L), size = N, replace = TRUE))
eDataRow <- aggregateExpData(importToExpData(df, dbFilename = tempfile(),
                                           tablename = "ex_tbl", overwrite = TRUE))

```

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applyMapped	<i>Apply a function over mapped data.</i>
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**Description**

Apply a function over each element of a list containing data subsets, organized by annotation, with an additional argument for the annotation element associated with the list item.

**Usage**

```
applyMapped(mapped, annoData, FUN, bindAnno = FALSE)
```

**Arguments**

mapped	A list of data subsets, typically the return value of a call to <code>splitByAnnotation</code> . Names should correspond to names of <code>annoData</code> object.
annoData	A data frame which must contain the columns <code>chr</code> , <code>start</code> , <code>end</code> and <code>strand</code> which specifies annotation regions of interest.
FUN	A function of two arguments, the first being an element of <code>mapped</code> , the second being the corresponding element of <code>annoData</code> .
bindAnno	Logical indicating whether annotation information should be included in the output. If <code>TRUE</code> it assumes the output of <code>FUN</code> is conformable into a <code>data.frame</code> .

**Value**

If `bindAnno` is `FALSE`, returns a list containing the output of `FUN` for each element of the original `mapped` argument. If `bindAnno` is `TRUE`, returns a data frame, containing annotation information and output of `FUN`.

**Author(s)**

James Bullard <bullard@berkeley.edu>, Kasper Daniel Hansen <khansen@jhsph.edu>

**See Also**

See `Genominator` vignette for more information.

**Examples**

```
ed <- ExpData(system.file(package = "Genominator", "sample.db"),
              tablename = "raw")
data("yeastAnno")
s <- splitByAnnotation(ed, yeastAnno[1:100,],
                      what = getColnames(ed, all = FALSE),
                      ignoreStrand = TRUE, addOverStrand = TRUE)

## compute the per-base rate for this dataset.
applyMapped(s, yeastAnno, function(dta, anno) {
  colSums(dta, na.rm = TRUE)/(anno$end - anno$start + 1)
}, bindAnno = TRUE)[1:4,]
```

---

collapseExpData      *Combine multiple data sets*

---

**Description**

This function takes a dataset with data from multiple experiments, and combines the data across multiple experiments according to a user-specified function.

**Usage**

```
collapseExpData(expData, tablename = NULL,
               what = getColnames(expData, all = FALSE), groups = "COL",
               collapse = c("sum", "avg", "weighted.avg"), overwrite = FALSE,
               deleteOriginal = FALSE, verbose = getOption("verbose"))
```

**Arguments**

expData	An object of class ExpData.
tablename	Name of database table to write output data to.
what	Data columns to apply collapse function to.
groups	Vector of length what indicating how columns should be grouped when applying collapse function.
collapse	Function to apply to grouped columns.
overwrite	Logical indicating whether database referred to in tablename argument should be overwritten.
deleteOriginal	Logical indicating whether original database in ExpData object should be deleted.
verbose	Logical indicating whether details should be printed.

**Details**

This function can be thought of as similar to `tapply`, operating over the entries in the data set, applying the function specified in the `collapse` argument, grouping the data as indicated in the `groups` argument.

**Value**

Returns an object of class `ExpData`.

**Author(s)**

James Bullard <bullard@berkeley.edu>, Kasper Daniel Hansen <khansen@jhsph.edu>

**See Also**

See `Genominator` vignette for more information.

**Examples**

```
ed <- ExpData(system.file(package = "Genominator", "sample.db"),
              tablename = "raw")
nd <- importToExpData(head(ed, -1), dbFilename = tempfile(),
                     tablename = "collapsed")
head(nd)
cd <- collapseExpData(nd, tablename = "bio", overwrite = TRUE,
                     groups = c("mut", "mut", "wt", "wt"))
head(cd)
```

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computeCoverage	<i>Compute effort-coverage values</i>
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**Description**

Compute fraction coverage obtained for a certain degree of sequencing effort.

**Usage**

```
computeCoverage(expData, annoData,
               cutoff = function(x, anno, group) { x > 10 },
               effort = seq(1e+05, 5e+07, length = 20),
               smooth = function(probs) { probs },
               groups = rep("ALL", length(what)),
               what = getColnames(expData, all = FALSE),
               totals = summarizeExpData(expData, what = what, verbose = verbose),
               ignoreStrand = FALSE, verbose = getOption("verbose"), ...)
```

**Arguments**

expData	An <code>ExpData</code> object.
annoData	A data frame which must contain the columns <code>chr</code> , <code>start</code> , <code>end</code> and <code>strand</code> which specifies annotation regions of interest.
cutoff	A predicate which determines when a region of annotation has been "sequenced". This function takes three arguments <code>x</code> = number of reads in region, <code>anno</code> = the annotation description of the region, <code>group</code> = the group it is in.
effort	Effort is a vector of how much sequencing has been done.

smooth	A function which takes as input the vector of probabilities and must return the probabilities.
groups	The different groups for which to calculate coverage.
what	The different columns, must be the same length as the groups.
totals	The lane totals, or some other totals. This allows us to estimate the sampling probability vector.
ignoreStrand	Whether or not to add over strands.
verbose	Do you want to see output.
...	Extra argument passed to cutoff.

### Details

This argument is pretty general as different ways of specifying the arguments allows one to compute "coverage" under a lot of different definitions.

### Value

Returns an object of class `genominator.coverage`. Pretty much you'll want to call `plot` on this object.

### Author(s)

James Bullard <bullard@berkeley.edu>, Kasper Daniel Hansen <khansen@jhsph.edu>

### See Also

See the [plot.genominator.coverage](#) for the plotting method and the `Genominator` vignette for details.

### Examples

```
ed <- ExpData(system.file(package = "Genominator", "sample.db"),
              tablename = "raw")
data("yeastAnno")
a <- computeCoverage(ed, yeastAnno, effort = 2^(5:18),
                    cutoff = function(x, ...) x > 1, smooth = FALSE)
names(a)
```

---

computePrimingWeights

*Compute weights to correct for random hexamer priming.*

---

### Description

This function computes weights used to correct for random hexamer priming, as per the reference.

### Usage

```
computePrimingWeights(aln, biasedIndex = 1:2, unbiasedIndex = 24:29,
                      weightsLength = 7L, returnSep = FALSE)
```



**Arguments**

aln                    An object of class AlignedRead.

biasedIndex        A vector of start positions for the biased k-mers.

unbiasedIndex      A vector of start positions for the unbiased k-mers.

weightsLength      The length of the k-mers.

returnSep          A logical indicating whether the numerator and denominator of the weights should be return or the weights themselves.

**Value**

If returnSep = FALSE a named vector of weights. Otherwise a list with two elements giving the numerator (p\_unbiased) and the denominator (p\_biased) of the weights.

**Author(s)**

Kasper Daniel Hansen <khansen@jhspsh.edu>.

**References**

Hansen, K. D., Brenner, S. E. and Dudoit, S (2010) Biases in Illumina transcriptome sequencing caused by random hexamer priming. Nucleic Acids Res, doi:10.1093/nar/gkq224

**See Also**

[addPrimingWeights](#) and the extended example in the 'Working with ShortRead' vignette.

**Examples**

```
if(require(ShortRead)) {
  bwt.file <- system.file("extdata", "bowtie", "s_1_aligned_bowtie.txt",
                          package="ShortRead")
  aln <- readAligned(bwt.file, type = "Bowtie")
  weights <- computePrimingWeights(aln, weightsLength = 2L)
  aln <- addPrimingWeights(aln, weights = weights)
  head(alnData(aln)$weights)
}
```

---

getRegion

*Select a region from an ExpData object.*

---

**Description**

This function selects a subset of the data that falls into a particular contiguous genomic region.

**Usage**

```
getRegion(expData, chr, start, end, strand, what = "*",
          whereClause = "", verbose = getOption("verbose"))
```

**Arguments**

<code>expData</code>	An object of class <code>ExpData</code> .
<code>chr</code>	Chromosome number of desired region.
<code>start</code>	Start position of desired region. If omitted, it is set to 0.
<code>end</code>	End position of desired region. If omitted, it is set to 1e12.
<code>strand</code>	Strand of desired region. Values of 1 or -1 return data from forward or reverse strand. A value of 0 or a missing argument returns data from any strand, including data with missing strand information.
<code>what</code>	A vector of column names specifying which columns of the data should be returned. Defaults to all columns.
<code>whereClause</code>	Additional filtration criteria, customizable to refer to additional data columns. See <a href="#">Details</a> for more explanation.
<code>verbose</code>	Logical indicating whether details should be printed.

**Details**

The argument `whereClause` should be a string indicating a subset of the data to be selected, using SQL syntax. For example, if you have a column called `category`, you could specify `category = 1` to select only those data entries where `category` has a value of 1. This function operates as a database query, and this argument can include logical combinations of multiple criteria.

**Value**

Returns a data frame containing the data from the desired region, with the desired columns.

**Author(s)**

James Bullard <bullard@berkeley.edu>, Kasper Daniel Hansen <khansen@jhspsh.edu>

**See Also**

See `Genominator` vignette for more information.

**Examples**

```
ed <- ExpData(system.file(package = "Genominator", "sample.db"),
              tablename = "raw")
c1 <- getRegion(ed, chr = 1)
dim(c1)
head(c1)
```

---

```
importFromAlignedReads
```

*Import aligned reads to database*

---

## Description

This function takes a named list of `AlignedRead` objects (from the **ShortRead** package) and creates an `ExpData` object from them, with one column for each list element. Column names are taken from list names, which must be unique.

## Usage

```
importFromAlignedReads(x, chrMap, dbFilename,
  tablename, overwrite = TRUE, deleteIntermediates = TRUE,
  readPosition = c("5prime", "left", "center"),
  verbose = getOption("verbose"), ...)
```

## Arguments

- |                                  |   |
|----------------------------------|---|
| <code>x</code>                   | This argument can be one of two things: either a named list of objects of class <code>AlignedRead</code> or a named character vector of filenames. In both cases, the names of the object are used as column names in the resulting database (not that it is not easy to change those names). Therefore the names of <code>x</code> needs to be present and non-empty and also to satisfy the requirements of column names in SQLite. If <code>x</code> is a list of <code>AlignedRead</code> , the column names needs to be unique. If <code>x</code> is a character vector of filenames, the names do not have to be unique, in which case two filenames with the same (column) name gets collapsed into the same column. |
| <code>chrMap</code>              | A vector of chromosome names from the aligned output. On importation to the database, chromosome names will be converted to integers corresponding to position within the <code>chrMap</code> vector.   |
| <code>dbFilename</code>          | The filename of the database to which the data will be imported.  |
| <code>tablename</code>           | Name of database table to write output data to.   |
| <code>overwrite</code>           | Logical indicating whether database table referred to in <code>tablename</code> argument should be overwritten.   |
| <code>deleteIntermediates</code> | Logical indicating whether intermediate database tables constructed in the process should be removed.   |
| <code>readPosition</code>        | How each read is assigned a unique genomic location. Default is "5prime" indicating that the location is the position of the 5' end of the reads, "left" indicates that the position of the left part of the read is used (5' end for reads mapping to the forward strand, 3' for reads mapping to the reverse strand), "center" indicates that the position of the center of the read is used.   |
| <code>verbose</code>             | Logical indicating whether details should be printed.   |
| <code>...</code>                 | Additional arguments to be passed to <code>readAligned</code> from <b>ShortRead</b> .   |

**Details**

The reads are aggregated and joined to form a database where each file/list element is a column. Positions are stored as the position of the 5' end of the reads (note that this differs from the convention for the `AlignedRead` class from **ShortRead**.) This can be changed by the `readPosition` argument.

If the `x` argument is a character vector of filenames, the function will require enough memory to parse each input file in turn. If there are duplicates in names of `x` the function requires enough memory to parse all files with the same column name at the same time.

If the `AlignedRead` class object has a `weights` column in its `alignData` slot, this `weights` column is used as the data to aggregate over.

**Value**

Outputs an object of class `ExpData` with a column for each element of the `x` argument.

**Author(s)**

James Bullard <bullard@berkeley.edu>, Kasper Daniel Hansen <khansen@jhsp.h.edu>

**See Also**

See `Genominator` vignette for more information. See also [ExpData-class](#), [AlignedRead-class](#) and [readAligned](#).

**Examples**

```
## Not run:
require(ShortRead)
require(yeastRNASeq)
data("yeastAligned")
chrMap <- levels(chromosome(yeastAligned[[1]]))
eData <- importFromAlignedReads(yeastAligned, chrMap = chrMap,
                               dbFilename = tempfile(), tablename = "raw",
                               overwrite = TRUE)

## End(Not run)
```

---

importToExpData      *Import data to database*

---

**Description**

This function imports data from a data frame to a table in a database.

**Usage**

```
importToExpData(df, dbFilename, tablename, overwrite = FALSE,
                verbose = getOption("verbose"), columns = NULL)
```

**Arguments**

df	A data frame containing data to be imported. Must have columns chr, location and strand.
dbFilename	The filename of the database to which the data will be imported.
tablename	Name of database table to write output data to.
overwrite	Logical indicating whether database table referred to in tablename argument should be overwritten.
verbose	Logical indicating whether details should be printed.
columns	Vector of column names of columns to be imported.

**Value**

Returns an object of class ExpData.

**Author(s)**

James Bullard <bullard@berkeley.edu>, Kasper Daniel Hansen <khansen@jhsph.edu>

**See Also**

See Genominator vignette for more information. See also [ExpData-class](#).

**Examples**

```
N <- 10000 # the number of observations.
df <- data.frame(chr = sample(1:16, size = N, replace = TRUE),
                location = sample(1:1000, size = N, replace = TRUE),
                strand = sample(c(1L,-1L), size = N, replace = TRUE))
eDataRaw <- importToExpData(df, dbFilename = tempfile(),
                           tablename = "ex_tbl", overwrite = TRUE)
```

---

joinExpData                      *Merge ExpData objects*

---

**Description**

This function merges multiple ExpData object into one in an efficient manner.

**Usage**

```
joinExpData(expDataList, fields = NULL, tablename = "aggtable",
            overwrite = TRUE, deleteOriginals = FALSE,
            verbose = getOption("verbose"))
```

**Arguments**

expDataList	List of ExpData objects. Must all be contained in the same database.
fields	A named list whose names correspond to tables of ExpData objects and whose entries indicate the column names to be pulled from each table.
tablename	Name of database table to write output data to.
overwrite	Logical indicating whether database table referred to in tablename argument should be overwritten.
deleteOriginals	Logical indicating whether original database tables in ExpData objects should be deleted.
verbose	Logical indicating whether details should be printed.

**Value**

An object of class ExpData containing data columns from all the original ExpData objects.

**Author(s)**

James Bullard <bullard@berkeley.edu>, Kasper Daniel Hansen <khansen@jhsph.edu>

**See Also**

See Genominator vignette for more information.

**Examples**

```
N <- 10000 # the number of observations.
df1 <- data.frame(chr = sample(1:16, size = N, replace = TRUE),
                 location = sample(1:1000, size = N, replace = TRUE),
                 strand = sample(c(1L,-1L), size = N, replace = TRUE))
df2 <- data.frame(chr = sample(1:16, size = N, replace = TRUE),
                 location = sample(1:1000, size = N, replace = TRUE),
                 strand = sample(c(1L,-1L), size = N, replace = TRUE))

eDataRaw1 <- aggregateExpData(importToExpData(df1, dbFilename = "my.db",
                                             tablename = "ex_tbl_1", overwrite = TRUE))
eDataRaw2 <- aggregateExpData(importToExpData(df1, dbFilename = "my.db",
                                             tablename = "ex_tbl_2", overwrite = TRUE))
jd <- joinExpData(list(eDataRaw1, eDataRaw2), tablename = "combined",
                    fields = list("ex_tbl_1" = c("counts" = "e1"),
                                  "ex_tbl_2" = c("counts" = "e2")))

head(jd)
```

---

makeGeneRepresentation

*Compute a gene representation from annotation.*

---

**Description**

Computing a gene representation from annotation using a variety of methods.

**Usage**

```
makeGeneRepresentation(annoData, type = c("UIgene", "Ugene", "ROCE",
"background"), gene.id = "ensembl_gene_id", transcript.id = "ensembl_transcript_
```

**Arguments**

<code>annoData</code>	A data frame which must contain the columns <code>chr</code> , <code>start</code> , <code>end</code> and <code>strand</code> which specifies annotation regions of interest, and optionally additional columns.
<code>type</code>	The type of gene representation, see details.
<code>gene.id</code>	The column in <code>annoData</code> that holds the gene identifiers (only needed for certain types of representation).
<code>transcript.id</code>	The column in <code>annoData</code> that holds the transcript identifiers (only needed for certain types of representation).
<code>bind.columns</code>	A character vector of column names that will be kept in the return object. It is assumed (but not checked) that these values are constant for all regions in a gene.
<code>ignoreStrand</code>	Is strand ignored? Little testing has been done for the value 'TRUE'.
<code>verbose</code>	Want verbose output?

**Details**

A union representation (Ugene) is simply the union of all bases of all transcripts of the gene, with bases belonging to other genes removed.

A union-intersection representation (UIgene) for a gene is defined as bases that are annotated as belonging to all transcripts of the gene, and not to any other gene.

Regions of constant expression (ROCE) are regions where one would assume that the expression is constant. They are best explained by an example: if transcript A goes from 1 to 4 and transcript B goes from 1 to 6 there are two ROCEs, one from 1 to 4 and one from 5 to 6. It is possible to define ROCEs independent of the gene concept, but in its current implementation regions belonging to more than one gene are removed.

Background is essentially the complement of the annotation.

**Value**

A `data.frame` with rownames and columns `chr`, `strand`, `start`, `end`, and possibly additional columns.

**Author(s)**

James Bullard <bullard@berkeley.edu>, Kasper Daniel Hansen <khansen@jhsph.edu>

**Examples**

```
data(yeastAnno)
ui <- makeGeneRepresentation(yeastAnno, type = "background")
```

---

`mergeWithAnnotation`*Combine data with annotation*

---

### Description

This function creates a data frame containing the data and the corresponding annotation information for each data row included in the annotation.

### Usage

```
mergeWithAnnotation(expData, annoData, what = "*",  
  ignoreStrand = FALSE, splitBy = NULL, verbose = getOption("verbose"))
```

### Arguments

<code>expData</code>	An object of class <code>ExpData</code> .
<code>annoData</code>	A data frame which must contain the columns <code>chr</code> , <code>start</code> , <code>end</code> and <code>strand</code> which specifies annotation regions of interest.
<code>what</code>	Which columns of <code>expData</code> to include.
<code>ignoreStrand</code>	Logical indicating whether strand should be ignored. If <code>TRUE</code> , data from either strand that falls into an annotation region is included.
<code>splitBy</code>	Field on which merged data frame should be split before returning.
<code>verbose</code>	Logical indicating whether details should be printed.

### Details

Generally this function is good for creating a list of data split by some annotation feature, which can then be applied across.

### Value

If `splitBy` is `NULL`, returns a data frame containing the data from `expData` that fall into regions defined by `annoData`, and which includes the annotation information, with columns as specified by `what`. If `splitBy` is non-`NULL`, returns a list of data frames with an element for each unique value of `splitBy` field.

### Author(s)

James Bullard <bullard@berkeley.edu>, Kasper Daniel Hansen <khansen@jhsph.edu>

### See Also

See `Genominator vignette` for more information.

### Examples

```
ed <- ExpData(system.file(package = "Genominator", "sample.db"),  
  tablename = "raw")  
data("yeastAnno")  
mergeWithAnnotation(ed, yeastAnno[1:5,])
```



---

```
plot.genominator.coverage
      Create coverage plot
```

---

## Description

S3 method to plot `genominator.coverage` object. Shows coverage as a function of plotting effort.

## Usage

```
plot.genominator.coverage(x, type = "l", col = NULL,
  draw.totals = TRUE, draw.legend = TRUE, legend.location = NULL, ...)
```

## Arguments

<code>x</code>	An object of class <code>genominator.coverage</code> , as returned by <code>computeCoverage</code> .
<code>type</code>	Plot type. See <code>plot</code> .
<code>col</code>	Vector of plotting colors.
<code>draw.totals</code>	Logical indicating whether totals should be drawn.
<code>draw.legend</code>	Logical indicating whether legend should be drawn.
<code>legend.location</code>	Vector giving x and y coordinates of legend position.
<code>...</code>	Additional arguments for lower-level functions.

## Value

This method is used for its side effect.

## Author(s)

James Bullard <bullard@berkeley.edu>, Kasper Daniel Hansen <khansen@jhsph.edu>

## See Also

See `Genominator` vignette for more information. See also `computeCoverage`.

## Examples

```
ed <- ExpData(system.file(package = "Genominator", "sample.db"),
  tablename = "raw")
data("yeastAnno")
a <- computeCoverage(ed, yeastAnno, effort = 2^(5:18),
  cutoff = function(x, ...) x > 1)
plot(a, lwd = 5, col = "grey")
plot(a, draw.totals = FALSE)
ygroups <- rep(c("mut", "wt"), c(2,2))
b <- computeCoverage(ed, yeastAnno, groups = ygroups,
  effort = 2^(5:18), cutoff = function(x, ...) x > 1)
plot(b)
b <- computeCoverage(ed, yeastAnno, groups = ygroups,
```

```

        effort = 2^(5:18), cutoff = function(x, ...) x > 3,
        smooth = function(probs) {
          probs = probs + min(probs[probs!=0])
          probs = probs/sum(probs)
        })
plot(b)

```

---

```

plot.genominator.goodness.of.fit
      Create goodness-of-fit quantile-quantile plot

```

---

### Description

S3 method to plot `genominator.goodness.of.fit` object. Creates a quantile-quantile plot of the observed versus theoretical quantiles of goodness-of-fit statistics based on a chi-squared distribution.

### Usage

```

plot.genominator.goodness.of.fit(x, chisq = FALSE, plotCol = TRUE,
  qqline = FALSE, xlab = "theoretical quantiles",
  ylab = "observed quantiles", main, pch = 16, cex = 0.75, ...)

```

### Arguments

<code>x</code>	An object of class <code>genominator.goodness.of.fit</code> , as returned by <a href="#">regionGoodnessOfFit</a>
<code>chisq</code>	Logical indicating whether chi-squared statistics should be plotted (as opposed to p-values from a chi-squared distribution).
<code>plotCol</code>	Logical indicating whether points at extreme quantiles should be colored.
<code>qqline</code>	Logical indicating whether a qqline should be added, this is a line through the 25%- and 75%-quantiles.
<code>xlab</code>	X-axis label for plot.
<code>ylab</code>	Y-axis label for plot.
<code>main</code>	Main label for plot.
<code>pch</code>	Plotting character type for plot.
<code>cex</code>	A numerical value giving the amount by which plotting text and symbols should be magnified relative to the default. See <a href="#">par</a> .
<code>...</code>	Additional arguments for lower-level functions, namely <a href="#">plot</a> .

### Details

This function constructs a quantile-quantile plot comparing the distribution of observed statistics to either the uniform 0,1 distribution or the appropriate chi-squared distribution. This plotting function provides a tool to assess whether replicate lanes, flow cells, sample preparations, etc. fit the model described in [regionGoodnessOfFit](#).

### Value

This method is used for its side effect.

**Author(s)**

James Bullard <bullard@berkeley.edu>, Kasper Daniel Hansen <khansen@jhsph.edu>

**See Also**

See Genominator vignette for more information. See also [regionGoodnessOfFit](#).

**Examples**

```
ed <- ExpData(system.file(package = "Genominator", "sample.db"),
              tablename = "raw")
data("yeastAnno")
plot(regionGoodnessOfFit(ed, yeastAnno), chisq = TRUE)
```

---

regionGoodnessOfFit-methods

*Calculate goodness-of-fit statistics*

---

**Description**

A generic method for calculating chi-squared goodness-of-fit statistics (See details). Dispatches on either a `data.frame` or an `ExpData` object.

**Usage**

```
## S4 method for signature 'data.frame'
regionGoodnessOfFit(obj,
                    denominator = colSums(obj),
                    groups = rep("A", ncol(obj)))

## S4 method for signature 'ExpData'
regionGoodnessOfFit(obj, annoData,
                    groups = rep("A", length(what)),
                    what = getColnames(obj, all = FALSE),
                    denominator = c("regions", "lanes"),
                    verbose = getOption("verbose"))
```

**Arguments**

<code>obj</code>	<code>data.frame</code> or <code>ExpData</code>
<code>annoData</code>	A <code>data.frame</code> of annotation.
<code>groups</code>	A factor or character vector describing which are the replicates.
<code>denominator</code>	How to scale the columns to take into account sequencing depth.
<code>what</code>	Which columns to choose from the database. Default is all data columns.
<code>verbose</code>	Whether or not debugging / timing info should be printed.

**Details**

This function implements the homogenous Poisson model across lanes as described in the article cited below. This model corresponds to common expression parameter across lanes scaled by a lane-specific offset. Goodness of fit to this model across replicates is a good indication of Poisson variation across lanes. Deviation from this is an indication of overdispersion between replicate lanes.

**Value**

An list containing the statistics and degrees of freedom. See details. Technically, an S3 object with class `genominator.goodness.of.fit`

**Methods**

`signature(obj = "ExpData")` Here `obj` represents the results of a call to `summarizeByAnnotation` or a `data.frame` with columns representing samples and rows representing regions, i.e. genes. Denominator is how we scale each column, therefore it this must be `true: length(denominator) == ncol(obj)`. Finally, `groups` determines how columns are aggregated across one another, i.e. which columns are replicates.

`signature(obj = "data.frame")` Here `annoData` is an annotation data frame. `groups` is as above. `what` represents the columns to select choose. `denominator` is either the total lane counts, or the lane counts restricted to `annoData`, or a vector of length `length(groups)`

**References**

James H. Bullard, Elizabeth A. Purdom, Kasper D. Hansen, Steffen Durinck, and Sandrine Dudoit, "Statistical Inference in mRNA-Seq: Exploratory Data Analysis and Differential Expression" (April 2009). U.C. Berkeley Division of Biostatistics Working Paper Series. Working Paper 247. <http://www.bepress.com/ucbbiostat/paper247>

**Examples**

```
ed <- ExpData(system.file(package = "Genominator", "sample.db"),
              tablename = "raw")
data("yeastAnno")
names(regionGoodnessOfFit(ed, yeastAnno))
```

---

`splitByAnnotation` *Split data into a list by annotation element.*

---

**Description**

This function splits the data into a list of matrices, by annotation element.

**Usage**

```
splitByAnnotation(expData, annoData, what = "*",
                  ignoreStrand = FALSE, expand = FALSE,
                  addOverStrands = FALSE, verbose = getOption("verbose"))
```

**Arguments**

<code>expData</code>	An object of class <code>ExpData</code> .
<code>annoData</code>	A data frame which must contain the columns <code>chr</code> , <code>start</code> , <code>end</code> and <code>strand</code> which specifies annotation regions of interest.
<code>what</code>	Vector of names of columns of <code>expData</code> to be included in output.
<code>ignoreStrand</code>	Logical indicating whether strand should be ignored. If <code>TRUE</code> , data that falls into the annotation region, regardless of strand, is included.
<code>expand</code>	Logical indicating whether positions with no data should be included in output. If <code>TRUE</code> , lines are added to the output to give a value for each position, even if this value is 0.
<code>addOverStrands</code>	Logical indicating whether data should be added across strands. Only applies when <code>expand</code> is <code>TRUE</code> .
<code>verbose</code>	Logical indicating whether details should be printed.

**Details**

This function retrieves the data contained in the regions of the `annoData` object. The return object may be significant in size.

**Value**

Returns a list of length equal to the number of annotation entries split upon. Each list element is either a matrix of data, or a list with data matrices for each strand included (if `expand` is `TRUE` and `addOverStrands` is `FALSE`).

**Author(s)**

James Bullard <bullard@berkeley.edu>, Kasper Daniel Hansen <khansen@jhsphe.edu>

**See Also**

See `Genominator vignette` for more information.

**Examples**

```
ed <- ExpData(system.file(package = "Genominator", "sample.db"),
              tablename = "raw")
data("yeastAnno")
splitByAnnotation(ed, yeastAnno[1:30,])
```

---

`summarizeByAnnotation`

*Summarize data based on genome annotation.*

---

**Description**

This function creates a summarization of columns of the data using specified SQLite functions, applying these summarization function to regions defined in an annotation data frame.

**Usage**

```
summarizeByAnnotation(expData, annoData,
  what = getColnames(expData, all = FALSE), fxs = c("TOTAL"),
  groupBy = NULL, splitBy = NULL, ignoreStrand = FALSE, bindAnno = FALSE,
  preserveColnames = TRUE, verbose = getOption("verbose"))
```

**Arguments**

<code>expData</code>	An object of class <code>ExpData</code> .
<code>annoData</code>	A data frame which must contain the columns <code>chr</code> , <code>start</code> , <code>end</code> and <code>strand</code> which specifies annotation regions of interest.
<code>what</code>	Vector of names of data columns to be summarized.
<code>fxs</code>	Vector of strings giving the names of SQLite functions to call on the data column(s).
<code>groupBy</code>	Character vector referring to a column in <code>annoData</code> . Regions will be aggregated over distinct values of this column. Setting this argument will set <code>bindAnno</code> to <code>TRUE</code> . If <code>splitBy</code> is set, <code>meta.id</code> will override.
<code>splitBy</code>	String indicating column of <code>annoData</code> object on which to split results.
<code>ignoreStrand</code>	Logical indicating whether strand should be taken into account in aggregation. If <code>TRUE</code> strand will be ignored.
<code>bindAnno</code>	Logical indicating whether annotation information should be included in the output.
<code>preserveColnames</code>	Logical indicating whether column names should be preserved. Only possible when a single function is being applied.
<code>verbose</code>	Logical indicating whether details should be printed.

**Details**

Most of the computation is done using SQLite. Depending on the use case, this approach may be significantly faster and use much less memory than the alternative: use `splitByAnnotation` to retrieve a list with all the data and then use R to summarize over each element of the list. It is (naturally) constrained to the use of operations expressible in (SQLite) SQL.

If `meta.id` is set to a column in `annoData`, all regions with the same value of the `meta.id` will be joined together; a standard use case is labelling exons of a gene.

**Value**

If `splitBy` is not specified, returns a data frame containing results of aggregation functions performed on each region defined in `annoData`. If `splitBy` is specified, returns a list of data frames with one entry for each unique value of the column which was split on.

**Author(s)**

James Bullard <bullard@berkeley.edu>, Kasper Daniel Hansen <khansen@jhsp.h.edu>

**References**

The SQLite website [http://www.sqlite.org/lang\\_aggfunc.html](http://www.sqlite.org/lang_aggfunc.html) has details on what mathematical functions are implemented.

**See Also**

See `Genominator` vignette for more information, as well as the [ExpData-class](#).

**Examples**

```
ed <- ExpData(system.file(package = "Genominator", "sample.db"),
              tablename = "raw")
data("yeastAnno")
summarizeByAnnotation(ed, yeastAnno[1:50,])
```

---

summarizeExpData     *Summarize a data column*

---

**Description**

This function returns a summary of one or more data columns, as indicated by a particular SQLite query function.

**Usage**

```
summarizeExpData(expData, what = getColnames(expData, all = FALSE),
                 fxs = c("TOTAL"), preserveColnames = TRUE, whereClause = "",
                 verbose = getOption("verbose"))
```

**Arguments**

<code>expData</code>	An object of class <code>ExpData</code> .
<code>what</code>	Vector of names of data columns to be summarized.
<code>fxs</code>	Vector of strings giving the names of SQLite functions to call on the data column.
<code>preserveColnames</code>	Logical indicating whether column names should be preserved.
<code>whereClause</code>	Additional filtration criteria, customizable to refer to additional data columns. See <a href="#">Details</a> for more explanation.
<code>verbose</code>	Logical indicating whether details should be printed.

**Details**

The argument `whereClause` should be a string indicating a subset of the data to be selected. For example, if you have a column called `category`, you could specify `"category = 1"` to select only those data entries where `category` has a value of 1. This function operates as a database query, and thus the argument can include logical combinations of multiple criteria using SQL boolean operators.

**Value**

A vector with results of summarization.

**Author(s)**

James Bullard <bullard@berkeley.edu>, Kasper Daniel Hansen <khansen@jhsph.edu>

## References

The available SQLite functions are listed here: [http://www.sqlite.org/lang\\_aggfunc.html](http://www.sqlite.org/lang_aggfunc.html)

## See Also

See Genominator vignette for more information.

## Examples

```
ed <- ExpData(system.file(package = "Genominator", "sample.db"),
              tablename = "raw")
summarizeExpData(ed)
summarizeExpData(ed, fxs = c("MIN", "MAX", "AVG"))
```

---

validAnnotation      *Check for validity of a annotation object.*

---

## Description

Checks whether a data.frame satisfy the requirements for an annotation object.

## Usage

```
validAnnotation(annoData)
```

## Arguments

annoData      A data.frame.

## Value

This function throws an error if the data.frame is not valid.

## Author(s)

James Bullard <bullard@berkeley.edu>, Kasper Daniel Hansen <khansen@berkeley.edu>

## See Also

The Genominator user guide.

## Examples

```
data(yeastAnno)
validAnnotation(yeastAnno)
```



---

`yeastAnno`*Example datasets from Genominator*

---

### Description

3 example datasets from Genominator; 2 contain annotation information from yeast and 1 contain actual data from yeast as well. A bigger dataset is available in the experimental data package `yeastRNASeq`.

### Usage

```
data(yeastAnno)
data(yeastAnno.sources)
data(chr1_yeast)
```

### Format

`yeastAnno` is a data frame with 7124 observations on the following 5 variables: `chr`, `start`, `end`, `strand`, `gene_biotype`.

`yeastAnno.sources` is a list with four components names `ensembl.gene`, `ensembl.transcript`, `ucsc.sgdGene`, `ucsc.ensGene` containing annotation on yeast from 2 different sources (Ensembl and UCSC), each sources has two different queries (one gene-level, one transcript-level). The annotation was obtained in January 2010 and should not be used for analysis.

`chr1_yeast` is a data frame containing mock data in yeast from two different samples (labelled `mRNA_1` and `mRNA_2`), linked to distinct genomic locations. There may be several data values linked to each genomic location.

### Source

Ensembl and UCSC January 2010.

### See Also

There is a discussion of the `yeastAnno.sources` in the `withShortRead` vignette.

### Examples

```
data(yeastAnno)
head(yeastAnno)
data(yeastAnno.sources)
names(yeastAnno.sources)
head(yeastAnno.sources$ensembl.gene)
data(chr1_yeast)
head(chr1_yeast)
```

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