

Package ‘GenomicFiles’

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Title Parallel queries distributed by file or by range

Description This package provides infrastructure for parallel queries distributed 'by file' or 'by range'. User defined map and reduce functions provide added flexibility for data combination and manipulation.

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Description

Use `BamFileViews()` to reference a set of disk-based BAM files to be processed

Constructor

```
BamFileViews(fileList, fileSample=DataFrame(row.names=make.unique(basename(path(fileList))))),
```

This constructor is a generic function with dispatch on argument `fileList`. Methods exist for [BamFileList](#) and `character` (vector of file names).

Accessors

All accessor-like methods defined for `GenomicFileViews` objects work on `BamFileViews` objects. See `?GenomicFileViews` for details.

- `fileList(x)`; `fileList(x) <- value`
- `fileSample(x)`; `fileSample(x) <- value`
- `fileRange(x)`; `fileRange(x) <- value`
- `fileExperiment(x)`; `fileExperiment(x) <- value`
- `yieldSize(x)`; `yieldSize(x) <- value`

Methods

`"["`: Subset the object by `fileRange` or `fileSample`.

reduceByFile Computations are distributed in parallel by files in `fileList` with the option to provide `MAP` and `REDUCE` functions across ranges and / or files.

reduceByRange Computations are distributed in parallel by ranges in `fileRange` with the option to provide `MAP` and `REDUCE` functions across ranges and / or files.

summarizeOverlaps Computations are distributed in parallel by files in `fileList`. Ranges in the `fileRange` slot take precedence over ranges in `param`. The return value is a `SummarizedExperiment` object.

countBam Computations are distributed in parallel by files in `fileList`. Ranges in the `fileRange` slot take precedence over ranges in `param`. The return value is a list of `data.frames`, one per file.

scanBam Computations are distributed in parallel by files in `fileList`. Ranges in the `fileRange` slot take precedence over ranges in `param`. The return value is a list of lists, one per file.

Arguments

- fileList: A character() vector of BAM path names or a [BamFileList](#).
- fileSample: A [DataFrame](#) instance with as many rows as length(fileList), containing sample information associated with each path.
- fileRange: A [GRanges](#), or missing instance with ranges defined on the spaces of the BAM files. Ranges are *not* validated against the BAM files.
- fileExperiment: A list() containing additional information about the experiment.
- yieldSize: An integer specifying number of records to process
- .views_on_file: An environment; currently under development
- ...: Additional arguments.
- x, object: An instance of BamFileViews.
- value: An object of appropriate type to replace content.
- i: During subsetting, a logical or numeric index into fileRange.
- j: During subsetting, a logical or numeric index into fileSample and fileList.
- file: An instance of BamFileViews.
- index: Not used.
- param: An optional [ScanBamParam](#) instance to further influence scanning or counting.

Slots

Inherited from GenomicFileViews class:

- fileList
- fileSample
- fileRange
- fileExperiment
- yieldSize
- .views_on_file

Author(s)

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See Also

- [GenomicFileViews-class](#) class.
- [reduceByFile](#) and [reduceByRange](#) methods.

Examples

```
if (.Platform$OS.type != "windows") {
## -----
## BamFileView Objects
## -----
library(RNAseqData.HNRNPC.bam.chr14)
```

```

fls <- RNAseqData.HNRNPC.bam.chr14_BAMFILES
gr <- GRanges("chr14", IRanges(1:10*5, width = 2))
bfv <- BamFileViews(fl, fileRange = gr)

## Dimensions of the object are ranges by samples (files).
bfv
bfv[1:5,]
fileList(bfv)
fileRange(bfv)

## -----
## Identify unique junctions (gaps in CIGAR) across files
## -----

fls <- RNAseqData.HNRNPC.bam.chr14_BAMFILES
gr <- GRanges("chr14", IRanges(c(1.9e7, 2e7), width = 90000))
bfv <- BamFileViews(fl, fileRange=gr)
param <- ScanBamParam()

MAP = function(FILE, RANGE, ..., param) {
  require(GenomicAlignments)
  bamWhich(param) <- RANGE
  readGAlignmentPairs(FILE, param = param)
}
REDUCE = function(MAPPED, ...) {
  summarizeJunctions(do.call(c, unname(MAPPED)))
}
reduceByRange(bfv, MAP, REDUCE, param=param)

## -----
## countBam(), scanBam(), summarizeOverlaps()
## -----
## countBam(), scanBam() and summarizeOverlaps() are implemented
## for BamFileViews objects as a convenience. These do not use the
## reduceBy* and MAP/REDUCE functions but simply apply the function in
## parallel to each file in fileList defined by the ranges in fileRange.

## summarizeOverlaps()
library(TxDb.Hsapiens.UCSC.hg19.knownGene)
tx <- transcripts(TxDb.Hsapiens.UCSC.hg19.knownGene)

fls <- RNAseqData.HNRNPC.bam.chr14_BAMFILES
gr <- GRanges("chr14", IRanges(c(24656731, 104160127, 104160241),
                               width = 200))
bfv <- BamFileViews(fl, fileRange=gr)

res = summarizeOverlaps(tx, bfv, singleEnd = FALSE, inter.feature = FALSE)
colSums(assays(res)$counts)

## countBam()
head(countBam(bfv))

## scanBam()

```

```

scn <- scanBam(bfv)
lapply(scn[[1]], names)
}

```

BigWigFileViews *Views into a set of BigWig files*

Description

Use `BigWigFileViews()` to reference a set of disk-based BigWig files to be processed (e.g., queried using [coverage](#)) as a single ‘experiment’.

Constructor

```
BigWigFileViews(fileList, fileSample=DataFrame(row.names=make.unique(basename(path(fileList))))
```

This constructor is a generic function with dispatch on argument `fileList`. Methods exist for [BigWigFileList](#) and character (vector of file names).

Accessors

All accessor-like methods defined for `GenomicFileViews` objects work on `BigWigFileViews` objects. See `?GenomicFileViews` for details.

- `fileList(x)`; `fileList(x) <- value`
- `fileSample(x)`; `fileSample(x) <- value`
- `fileRange(x)`; `fileRange(x) <- value`
- `fileExperiment(x)`; `fileExperiment(x) <- value`
- `yieldSize(x)`; `yieldSize(x) <- value`

Subsetting

`"["`: Subset the object by `fileRange` or `fileSample`.

Other methods

In the code snippets below, `x` and `object` are `BigWigFileViews` objects.

```
coverage(x, ..., by = "file", summarize = TRUE, as = "RleList"):
```

Computes coverage with the `import` function from `rtracklayer` for each file in `fileList(x)` and each range in `fileRange(x)`. Work is divided in parallel as specified in the `by` argument. Results are returned as a list unless `summarize=TRUE` in which case the data are in the `assays` slot of a `SummarizedExperiment` object. Data type are controlled with the `as` argument. See `?import,BigWigFile-method` for details.

```
summary(object, ..., by = "file", summarize = TRUE):
```

Computes summary statistics with the `summary` function from `rtracklayer` for each file in `fileList(object)` and each range in `fileRange(object)`. Work is divided in parallel as specified in the `by` argument. Results are returned as a list unless `summarize=TRUE` in which case the data are in the `assays` slot of a `SummarizedExperiment` object. Summary statistics are controlled with the `type` argument passed to `summary`. See `?summary,BigWigFile-method` for details.

Arguments

fileList: A character() vector of BigWig path names or a [BigWigFileList](#).

fileSample: A [DataFrame](#) instance with as many rows as length(fileList), containing sample information associated with each path.

fileRange: A [GRanges](#), or missing instance with ranges defined on the spaces of the BigWig files. Ranges are *not* validated against the BigWig files.

fileExperiment: A list() containing additional information about the experiment.

yieldSize: An integer specifying number of records to process

.views_on_file: An environment; currently under development

...: Additional arguments.

x, object: An instance of BigWigFileViews.

value: An object of appropriate type to replace content.

i: During subsetting, a logical or numeric index into fileRange.

j: During subsetting, a logical or numeric index into fileSample and fileList.

file: An instance of BigWigFileViews.

index: Not used.

Slots

Inherited from GenomicFileViews class:

- fileList
- fileSample
- fileRange
- fileExperiment
- yieldSize
- .views_on_file

Author(s)

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See Also

- [GenomicFileViews-class](#).

Examples

```
if (.Platform$OS.type != "windows") {
  register(SerialParam())

  ## -----
  ## BigWigFileView Objects
  ## -----
}
```

```

fl <- system.file("tests", "test.bw", package = "rtracklayer")
gr <- GRanges(Rle(c("chr2", "chr19"), c(4, 2)),
              IRanges(1 + c(200, 250, 500, 550, 1450, 1750), width=100))
bwfv <- BigWigFileViews(c(fl, fl), fileRange=gr)

## Object dimensions are range by sample (files).
bwfv
fileList(bwfv)
fileRange(bwfv)

## Subset by range(s) or sample(s).
bwfv[1:3,]
bwfv[1:3,2]

## -----
## coverage()
## -----
## coverage() on a BigWigFileViews object returns coverage for all
## files in fileList() for the ranges in fileRange().

## When summarize = FALSE results are returned as a list. The
## by argument specifies grouping by range or by file.
cv1 <- coverage(bwfv, by = "file", summarize = FALSE)
length(cv1)
elementLengths(cv1)

cv2 <- coverage(bwfv, by = "range", summarize = FALSE)
length(cv2)
elementLengths(cv2)

## When summarize = TRUE output is a SummarizedExperiment.
cv3 <- coverage(bwfv, summarize = TRUE)
assays(cv3)

## FIXME: improve show method for Lists in a matrix
## FIXME: assays as List should respect withDimnames
assays(cv3, withDimnames=TRUE)[[1]]

## -----
## summary()
## -----
## summary() on a BigWigFileViews object returns the type statistic
## for all files in fileList() for the ranges in fileRange().

sm1 <- summary(bwfv, type = "mean", by = "file", summarize = TRUE)
sm2 <- summary(bwfv, type = "max", by = "range", summarize = FALSE)

## -----
## reduceByRange() and reduceByFile()
## -----
## reduceByRange() and reduceByFile() allow detailed control of how
## data are extracted and combined through the use of MAP and REDUCE
## functions.

```

```

## In this example a summary operation FUN is applied to the
## coverage from each range.
coverage_summary <- function(X, MAP, REDUCE, FUN = mean, ...) {
  MAP <- function(FILE, RANGE, ...) {
    FUN(import(FILE, selection=RANGE, as="NumericList"))
  }
  REDUCE <- function(MAPPED, ...) unlist(MAPPED)
  reduceByRange(X, MAP, REDUCE)
}

coverage_summary(bwfv, MAP, REDUCE)
coverage_summary(bwfv, MAP, REDUCE, FUN = median)
}

```

FaFileViews

Views into a set of Fasta files

Description

Use `FaFileViews()` to reference a set of disk-based Fasta files to be processed

Constructor

`FaFileViews(fileList, fileSample=DataFrame(row.names=make.unique(basename(path(fileList))))),`
This constructor is a generic function with dispatch on argument `fileList`. Methods exist for [FaFileList](#) and character (vector of file names).

Accessors

All accessor-like methods defined for `GenomicFileViews` objects work on `FaFileViews` objects. See `?GenomicFileViews` for details.

- `fileList(x)`; `fileList(x) <- value`
- `fileSample(x)`; `fileSample(x) <- value`
- `fileRange(x)`; `fileRange(x) <- value`
- `fileExperiment(x)`; `fileExperiment(x) <- value`
- `yieldSize(x)`; `yieldSize(x) <- value`

Methods

`"["`: Subset the object by `fileRange` or `fileSample`.

reduceByFile Parallel computations are distributed by files in `fileList` with the option to provide MAP and REDUCE functions across ranges and / or files.

reduceByRange Parallel computations are distributed by ranges in `fileRange` with the option to provide MAP and REDUCE functions across ranges and / or files.

Arguments

fileList: A character() vector of Fasta path names or a [FaFileList](#).

fileSample: A [DataFrame](#) instance with as many rows as length(fileList), containing sample information associated with each path.

fileRange: A [GRanges](#), or missing instance with ranges defined on the spaces of the Fasta files. Ranges are *not* validated against the Fasta files.

fileExperiment: A list() containing additional information about the experiment.

yieldSize: An integer specifying number of records to process

.views_on_file: An environment; currently under development

...: Additional arguments.

x, object: An instance of FaFileViews.

value: An object of appropriate type to replace content.

i: During subsetting, a logical or numeric index into fileRange.

j: During subsetting, a logical or numeric index into fileSample and fileList.

file: An instance of FaFileViews.

index: Not used.

param: Unused option for FaFileViews object. fileRange are used to specify ranges to query.

Slots

Inherited from GenomicFileViews class:

- fileList
- fileSample
- fileRange
- fileExperiment
- yieldSize
- .views_on_file

Author(s)

Martin Morgan <mtmorgan@fhcrc.org> and Valerie Obenchain <vobencha@fhcrc.org>

See Also

- [GenomicFileViews-class](#).

Examples

```
## -----
## FaFileView Objects
## -----

fa <- system.file("extdata", "ce2dict1.fa", package="Rsamtools",
                 mustWork=TRUE)
ffv <- FaFileViews(c(fa, fa), fileRange=scanFaIndex(fa))
```

```
MAP <- function(FILE, RANGE, ...) {
  require(Rsamtools)
  scanFa(FILE, RANGE)
}
reduceByRange(ffv, MAP)
```

GenomicFileViews *Views into a set of files*

Description

GenomicFileViews is a VIRTUAL class used to reference a set of disk-based files to be queried across views (ranges).

Objects from the Class

GenomicFileViews is a VIRTUAL class not intended for instantiation by the user. The class serves as a parent for concrete subclasses such as BamFileViews, FaFileViews, TabixFileViews etc.

Slots

fileList List of of length ≥ 2 containing the file path and index names. List names must include 'path' and 'index'.

fileSample A [DataFrame](#) instance with as many rows as `length(fileList)`, containing sample information associated with each path.

fileRange A [GRanges](#) instance with ranges defined on the spaces (genomic position) of the files.

fileExperiment A list containing additional information about the experiment.

yieldSize An integer specifying the data chunk size.

.views_on_file An environment. Under construction / future use.

Accessors

In the code snippets below, `x` is a GenomicFileViews object.

`itemfileList(x)`, `fileList(x) <- value` Get or set the `fileList` on `x`. `value` must be a List with list elements appropriate for the subclass.

fileSample, `fileSample(x) <- value` Get or set the `fileSample` on `x`. `value` must be a [DataFrame](#) instance with as many rows as `length(fileList)`, containing sample information associated with each file.

fileRange, `fileRange(x) <- value` Get or set the `fileSample` on `x`. `value` must be a [GRanges](#) instance.

fileExperiment, `fileExperiment(x) <- value` Get or set the `fileExperiment` on `x`. `value` must be a `list()`.

yieldSize, `yieldSize(x) <- value` Get or set the `yieldSize` on `x`. `value` must be an integer.

names, `names(x) <- value` Get or set the `names` on `x`. These are the column names of the GenomicFileViews instance corresponding to the paths in `fileList`.

dimnames, `dimnames(x) <- value` Get or set the row and column names on `x`.

Methods

In the code snippets below, `x` is a `GenomicFileViews` object.

[Subset the object by `fileRange` or `fileSample`.

show Compactly display the object.

reduceByFile Parallel computations are distributed by files in `fileList` with the option to provide MAP and REDUCE functions across ranges and / or files.

reduceByRange Parallel computations are distributed by ranges in `fileRange` with the option to provide MAP and REDUCE functions across ranges and / or files.

Author(s)

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See Also

- [BamFileViews-class](#) class.
- [BigWigFileViews-class](#) class.
- [reduceByFile](#) and [reduceByRange](#) methods.

Examples

```
f1 <- system.file("extdata", "ex1.bam", package="Rsamtools",
                 mustWork=TRUE)
bfv <- BamFileViews(f1, fileRange = GRanges("seq1", IRanges(1, 10)))
showClass(class(bfv))

## See ?BamFileViews, ?BigWigFileViews, ?reduceBy for additional examples.
```

reduceBy

Distribute parallel computations across files

Description

Distribute parallel computations across files with the option to provide MAP and REDUCE functions across ranges and / or files.

Usage

```
## S4 method for signature GenomicFileViews
reduceByFile(X, MAP, REDUCE, ..., init, ITERATE=FALSE)

## S4 method for signature GenomicFileViews
reduceByRange(X, MAP, REDUCE, ..., init, ITERATE=FALSE)
```

Arguments

X	A GenomicFileViews object.
MAP	A function applied to the files in <code>fileList</code> or ranges in <code>fileRange</code> . MAP should have (at minimum) the two arguments RANGE and FILE. Signature is as follows: MAP = function(FILE, RANGE, ...) MAP can be used without a REDUCE function. In this case results from <code>reduceByRange</code> and <code>reduceByFile</code> are the same but returned in different order with different geometry (lists and list elements are different lengths).
REDUCE	A function applied to the output of MAP which (usually) performs an aggregation. The function signature of REDUCE depends on when aggregation occurs. When ITERATE is FALSE REDUCE is applied after the mapping step is complete; the signature requires a single argument (MAPPED below). When ITERATE is TRUE data are aggregated while MAP iterates through the files or ranges; the signature requires two arguments (X and Y below). <ul style="list-style-type: none"> • ITERATE = FALSE : MAPPED is the complete output from MAP. REDUCE = function(MAPPED, ...) • ITERATE = TRUE : X is the result from the last reduce step and Y is the most recent yield from MAP. REDUCE = function(X, Y, ...)
init	An (optional) initial value for REDUCE. Applicable when ITERATE = TRUE. <code>init</code> must be an object of the same type as the elements returned from MAP. REDUCE logically adds <code>init</code> to the start (when proceeding left to right) or end of results obtained with MAP. See ?Reduce for details.
ITERATE	A logical specifying if reduction should be performed during the mapping step (TRUE) or after (FALSE).
...	Arguments passed to other methods.

Details

Computations are distributed in parallel by file or by range by specifying `reduceByFile` or `reduceByRange`. In the distributed step, both `reduceByFile` and `reduceByRange` use MAP and REDUCE functions to further process and combine the data. MAP and REDUCE are based on the list-processing combinators from functional programming in the same spirit as Map and Reduce in base R. The all-caps designation of MAP and REDUCE is used to distinguish the functions in `GenomicFileViews`.

In the case of `reduceByRange` the mapping occurs between a single range and all files. The reduce step combines the results across files within the single range. With `reduceByFile` the mapping occurs between a single file and all ranges. The reduce step combines results across ranges within a single file.

The ITERATE argument controls when the REDUCE function is applied. When TRUE, REDUCE is applied while MAP iterates through the files or ranges; when FALSE, REDUCE is applied after MAP has processed all files or ranges.

- `reduceByRange` Computations are distributed in parallel over the ranges in `fileRange`. Each worker `lapply()`s the MAP function to a single range over all files. The output is a list the length of `fileRange` with each list element the length of `fileList`.

ITERATE = FALSE: Each worker applies REDUCE to MAP output from a single range, across all files; independent combination across files.

ITERATE = TRUE: Each worker applies REDUCE as MAP iterates through each file, single range; dependent combination across files.

- `reduceByFile` Computations are distributed in parallel by file. Each worker lapply()s the MAP function over all ranges in a single file. The output is a list the length of `fileList` with each list element the length of `fileRange`.

ITERATE = FALSE: Each worker applies REDUCE to MAP output from a single file, across all ranges; independent combination across ranges.

ITERATE = TRUE: Each worker applies REDUCE as MAP iterates through each range, a single file; dependent combination across ranges.

Value

A [list](#) object.

Author(s)

Martin Morgan <mtmorgan@fhcrc.org> and Valerie Obenchain <vobencha@fhcrc.org>

See Also

- [GenomicFileViews-class](#)
- [Map](#)
- [Reduce](#)

Examples

```
if (.Platform$OS.type != "windows") {

  bw <- system.file("tests", "test.bw", package = "rtracklayer")

  ## -----
  ## MAP only:
  ## -----
  gr <- GRanges(c("chr2", "chr19", "chr19"),
               IRanges(c(1, 1400, 1700), width=10))
  bwfv <- BigWigFileViews(c(bw, bw), fileRange=gr)
  MAP = function(FILE, RANGE, ...) {
    import(FILE, selection=RANGE, as="NumericList")
  }

  ## reduceByRange():
  ## List length is the number of ranges, list element lengths are
  ## the number of files.
  reduceByRange(bwfv, MAP)

  ## reduceByFile():
  ## List length is the number of files, list element lengths are
  ## the number of ranges.
```

```

reduceByFile(bwfv, MAP)

## -----
## MAP, REDUCE and ITERATE:
## -----
## This simple example demonstrates the use of ITERATE to
## control when output from MAP is aggregated.

gr <- tileGenome(seqlengths(BigWigFile(bw)),
                 tilewidth = 1e7,
                 cut.last.tile.in.chrom = TRUE)
bwv <- BigWigFileViews(c(bw, bw), fileRange = gr)
MAP = function(FILE, RANGE, ...) TRUE

## REDUCE is applied after MAP is complete.
REDUCE = function(MAPPED, ...) sum(unlist(MAPPED))
result1 <- reduceByRange(bwv, MAP, REDUCE)

## REDUCE is applied while MAP iterates though each file.
REDUCE = function(X, Y, ...) X + Y
result2 <- reduceByRange(bwv, MAP, REDUCE, ITERATE = TRUE)

stopifnot(identical(result1, result2))

## -----
## t-test at point locations across files:
## -----

library(genefilter)
gr <- tileGenome(seqlengths(BigWigFile(bw)),
                 tilewidth = 1e7,
                 cut.last.tile.in.chrom=TRUE)
bwv <- BigWigFileViews(c(bw, bw, bw, bw), fileRange = gr)
grp <- factor(c(1, 2, 2, 1))

MAP = function(FILE, RANGE, ...) {
  stopifnot(length(RANGE) == 1)
  v <- Views(import(FILE, selection = RANGE, asRle = TRUE),
             as(RANGE, "RangesList"))
  as.vector(Filter(length, v)[[1]][[1]])
}
REDUCE = function(MAPPED, ..., grp) {
  m <- simplify2array(MAPPED)
  idx <- which(rowSums(m) != 0)
  df <- rowttests(m[idx,], grp)
  cbind(offset=idx - 1, df)
}
result3 <- reduceByRange(bwv, MAP, REDUCE, grp = grp)

## Each list element contains the data.frame output
## from rowttests():
result3[[1]]

```

```

## -----
## mean per-file:
## -----

gr <- GRanges(c("chr2", "chr19", "chr19"),
              IRanges(c(1, 1400, 1700), width = 1000))
bwv <- BigWigFileViews(c(bw, bw, bw), fileRange = gr)

MAP = function(FILE, RANGE, ...) {
  v <- Filter(length, {
    Views(import(FILE, selection=RANGE, asRle = TRUE),
          as(RANGE, "RangesList"))
  })
  c(n = as.numeric(sum(unlist(width(v))))),
    sum = as.numeric(sum(sapply(v, sum))))
}
REDUCE = function(X, Y, ..., FILE)
  c(n = X[["n"]] + Y[["n"]], sum = X[["sum"]] + Y[["sum"]])

result4 <- reduceByFile(bwv, MAP, REDUCE, ITERATE = TRUE)
}

```

registry-utils

Functions for creating and searching a registry of file types.

Description

Functions for creating and searching a registry of file types based on file extension.

Usage

```

registerFileType(type, package, regex)
findTypeRegistry(fnames)
makeFileType(fnames, ..., regex=findTypeRegistry(fnames))

```

Arguments

type	The List class the file is associated with such as BamFileList, BigWigFileList, FaFileList.
package	The package where the List class (type) is defined.
regex	A regular expression that uniquely identifies the file extension.
fnames	A character vector of file names.
...	Additional arguments passed to the List-class constructor (e.g., yieldSize for BamFileList).

Details

- `registerFileType` The `registerFileType` function adds entries to the file type register created at load time. The point of the register is for discovery of file type (class) by file extension. These are List-type classes (e.g., `BamFileList`) that occupy the `fileList` slot of a `GenomicFileViews` class (e.g., `BamFileViews`).

Each List class entry in the register is associated with (1) a regular expression that identifies the file extension, (2) a class and (3) the package where the class is defined. At load time the register is populated with classes known to `GenomicFileViews`. New classes / file types can be added to the register with `registerFileType` by providing these three pieces of information.

- `findTypeRegistry` Searches the registry for a match to the extension of `fname`. Internal use only.
- `makeFileType` Performs a look-up in the file registry based on the supplied regular expression; returns an object of the associated class. Internal use only.

Value

`registerFileType`: NULL

`findTypeRegistry`: The regular expression associated with the file.

`makeFileType`: A List-type object defined in the registry.

Examples

```
## At load time the registry is populated with file types
## known to GenomicFileViews.
sapply(as.list(.fileTypeRegistry), "[", "type")

## Add a new class to the file register.
## Not run: registerFileType(NewClassList, NewPackage, "\.NewExtension$")
```


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