Package ‘GenomicScores’

April 25, 2017

Type Package

Title Infrastructure to work with genomewide position-specific scores

Description Provide infrastructure to store and access genomewide position-specific scores within R and Bioconductor.

Version 1.0.0

License Artistic-2.0

Depends R (>= 3.4), S4Vectors (>= 0.7.21), GenomicRanges, methods, BiocGenerics (>= 0.13.8)

Imports utils, XML, IRanges (>= 2.3.23), BSgenome, GenomeInfoDb, AnnotationHub

Suggests BiocStyle, knitr, rmarkdown, BSgenome.Hsapiens.UCSC.hg19, phastCons100way.UCSC.hg19, VariantAnnotation, TxDb.Hsapiens.UCSC.hg19.knownGene

VignetteBuilder knitr

URL https://github.com/rcastelo/GenomicScores

BugReports https://github.com/rcastelo/GenomicScores/issues

Encoding UTF-8

biocViews Infrastructure, Genetics, Annotation, Sequencing, Coverage

NeedsCompilation no

Author Robert Castelo [aut, cre],
Pau Puigdevall [ctb]

Maintainer Robert Castelo <robert.castelo@upf.edu>

R topics documented:

    GScores-class .............................................................. 2
    scores ................................................................. 3

Index 6
GScores-class

The GenomicScores package and the GScores class

Description

Provide support to store and retrieve genomic scores associated to nucleotide positions along a genome.

Usage

```
GScores(provider, provider_version, download_url, download_date, reference_genome, data_pkgname, data_dirpath, data_serialized_objnames)
```

Arguments

- `provider`: Data provider.
- `provider_version`: Version of the data, as given by the data provider.
- `download_url`: URL from where data were downloaded.
- `download_date`: Date when data were downloaded.
- `reference_genome`: GenomeDescription object containing information about the reference genome to where data belongs to.
- `data_pkgname`: Name of the package storing the data.
- `data_dirpath`: Path to the directory where the actual data is stored.
- `data_serialized_objnames`: Serialized object names.

Details

The GenomicScores package defines the GScores class and associated methods to provide support to annotation packages and resources that store genomic scores. In the context of the GenomicScores package, genomic scores are numeric values associated to physical nucleotide positions along a genome, such as UCSC phastCons conservation scores for human. Two such annotation packages are:

- `phastCons100way.UCSC.hg19`: Nucleotide-level phastCons conservation scores from the UCSC Genome Browser calculated from multiple genome alignments from the human genome version hg19 to 99 vertebrate species.
- `phastCons100way.UCSC.hg38`: Nucleotide-level phastCons conservation scores from the UCSC Genome Browser calculated from multiple genome alignments from the human genome version hg38 to 99 vertebrate species.

Value

The GScores() constructor function returns a GScores-class object. In principle, the end-user needs not to call this function.
scores

Author(s)

R. Castelo

See Also

phastCons100way.UCSC.hg19 phastCons100way.UCSC.hg38

Examples

```r
## supporting annotation packages with genomic scores
if (require(phastCons100way.UCSC.hg19)) {
  library(GenomicRanges)

  gsco <- phastCons100way.UCSC.hg19
  scores(gsco, GRanges(seqnames="chr7", IRanges(start=117232380, width=5)))
}

## supporting AnnotationHub resources
## Not run:
availableGScores()
 gsco <- getGScores("phastCons100way.UCSC.hg19")
 scores(gsco, GRanges(seqnames="chr7", IRanges(start=117232380, width=5)))

## End(Not run)

## meta information about a GScores object
provider(gsco)
providerVersion(gsco)
organism(gsco)
seqlevelsStyle(gsco)
seqinfo(gsco)
head(seqnames(gsco))
head(seqlengths(gsco))
```

scores

Accessing genomic scores

Description

Functions to access genomic scores through GScores objects.

Usage

availableGScores()
getGScores(x)
```r
## S4 method for signature 'GScores,GenomicRanges'
scores(object, ranges, scores.only, ...)
```
Arguments

- **x**: A character vector of length 1 specifying the genomic scores resource to fetch. The function `availableGScores()` shows the available genomic scores resources.
- **object**: A GScores object.
- **ranges**: A GenomicRanges object with positions from where to retrieve genomic scores.
- **scores.only**: Flag set to FALSE (default) when scores are returned in a metadata column called `scores` from the input GenomicRanges object. When set to TRUE, the only the numeric vector of scores is returned.

In the call to the `scores()` method one can additionally set the following arguments:

- **summaryFunFunction** to summarize genomic scores when more than one position is retrieved. By default, this is set to the arithmetic mean, i.e., the `mean()` function.
- **cachingFlag** setting whether genomic scores per chromosome should be kept cached in memory (TRUE, default) or not (FALSE). The latter option minimizes the memory footprint but slows down the performance when the `scores()` method is called multiple times.

Details

The method `scores()` takes as first argument a GScores-class object that can be loaded from an annotation package or from an AnnotationHub resource. These two possibilities are illustrated in the examples below.

Value

The function `availableGScores()` returns a character vector with the names of the AnnotationHub resources corresponding to different available sets of genomic scores. The function `getGScores()` return a GScores object. The method `scores()` returns a numeric vector.

Author(s)

R. Castelo

See Also

`phastCons100way.UCSC.hg19` `phastCons100way.UCSC.hg38`

Examples

```r
## accessing genomic scores from an annotation package
if (require(phastCons100way.UCSC.hg19)) {
  library(GenomicRanges)
  gsc0 <- phastCons100way.UCSC.hg19
  gsc0
  scores(gsc0, GRanges(seqnames="chr7", IRanges(start=117232380, width=5)))
}
## accessing genomic scores from AnnotationHub resources
## Not run:
```
scores

availableGScores()
gsco <- getGScores("phastCons100way.UCSC.hg19")
scores(gsco, GRanges(seqnames="chr7", IRanges(start=117232380, width=5)))

## End(Not run)
Index

*Topic datasets*
  - `GScores-class`, 2
  - `scores`, 3

availableGScores (scores), 3

`GenomicScores (GScores-class)`, 2
`getGScores (scores)`, 3
`GScores (GScores-class)`, 2
`GScores-class`, 2

`organism, GScores-method`
  - `(GScores-class)`, 2

`phastCons100way.UCSC.hg19`, 3, 4
`phastCons100way.UCSC.hg38`, 3, 4
`provider, GScores-method`
  - `(GScores-class)`, 2
`providerVersion, GScores-method`
  - `(GScores-class)`, 2

`referenceGenome, GScores-method`
  - `(GScores-class)`, 2

`scores`, 3
`scores, GScores, GenomicRanges-method`
  - `(scores)`, 3
`seqinfo, GScores-method (GScores-class)`, 2

`seqlengths, GScores-method`
  - `(GScores-class)`, 2
`seqlevelsStyle, GScores-method`
  - `(GScores-class)`, 2
`seqnames, GScores-method`
  - `(GScores-class)`, 2
`show, GScores-method (GScores-class)`, 2