

# Package ‘GenomicScores’

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**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** 1.0.2

**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

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## R topics documented:

GScores-class . . . . .	2
scores . . . . .	3
<b>Index</b>	<b>6</b>

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GScores-class

*The GenomicScores package and the GScores class*


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## 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.

**Author(s)**

R. Castelo

**See Also**

[phastCons100way.UCSC.hg19](#) [phastCons100way.UCSC.hg38](#)

**Examples**

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

  gsco <- phastCons100way.UCSC.hg19
  gsco
  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))
```

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scores

*Accessing genomic scores*

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**Description**

Functions to access genomic scores through GScores objects.

**Usage**

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

## Arguments

<code>x</code>	A character vector of length 1 specifying the genomic scores resource to fetch. The function <code>availableGScores()</code> shows the available genomic scores resources.
<code>object</code>	A <code>GScores</code> object.
<code>ranges</code>	A <code>GenomicRanges</code> object with positions from where to retrieve genomic scores.
<code>scores.only</code>	Flag set to <code>FALSE</code> (default) when scores are return in a metadata column called <code>scores</code> from the input <code>GenomicRanges</code> object. When set to <code>TRUE</code> , the only the numeric vector of scores is returned.
<code>...</code>	In the call to the <code>scores()</code> method one can additionally set the following arguments: <ul style="list-style-type: none"> <li>• <code>summaryFunFunction</code> to summarize genomic scores when more than one position is retrieved. By default, this is set to the arithmetic mean, i.e., the <code>mean()</code> function.</li> <li>• <code>cachingFlag</code> setting whether genomic scores per chromosome should be kept cached in memory (<code>TRUE</code>, default) or not (<code>FALSE</code>). The latter option minimizes the memory footprint but slows down the performance when the <code>scores()</code> method is called multiple times.</li> </ul>

## 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

```
## accessing genomic scores from an annotation package
if (require(phastCons100way.UCSC.hg19)) {
  library(GenomicRanges)

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

## accessing genomic scores from AnnotationHub resources
## Not run:
```

```
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](#)