Description

Full genome sequences for Rattus norvegicus (Rat) as provided by UCSC (rn6, Jul. 2014) and stored in Biostrings objects.

Note

This BSgenome data package was made from the following source data files:

rn6.2bit from http://hgdownload.cse.ucsc.edu/goldenPath/rn6/bigZips/

See ?BSgenomeForge and the BSgenomeForge vignette (vignette("BSgenomeForge")) in the BSgenome software package for how to make a BSgenome data package.

Author(s)

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See Also

• BSgenome objects and the available.genomes function in the BSgenome software package.
• DNAString objects in the Biostrings package.
• The BSgenomeForge vignette (vignette("BSgenomeForge")) in the BSgenome software package for how to make a BSgenome data package.

Examples

BSgenome.Rnorvegicus.UCSC.rn6
genome <- BSgenome.Rnorvegicus.UCSC.rn6
seqlengths(genome)
genome$chr1 # same as genome[["chr1"]]

## ---------------------------------------------------------------
## Extract the upstream sequences
The upstream sequences can easily be extracted from the full genome sequences with something like:

```r
library(GenomicFeatures)
txdb <- makeTxDbFromUCSC("rn6", tablename="refGene")
up1000seqs <- extractUpstreamSeqs(genome, txdb, width=1000)
```

IMPORTANT: Make sure you use a TxDb package (or TxDb object) that contains a gene model based on rn6 or on a compatible genome (i.e. a genome with sequences identical to the sequences in rn6). Note that you can make a TxDb object from various annotation resources. See the makeTxDbFromUCSC(), makeTxDbFromBiomart(), and makeTxDbFromGFF() functions in the GenomicFeatures package for more information.

Genome-wide motif searching

See the GenomeSearching vignette in the BSgenome software package for some examples of genome-wide motif searching using Biostrings and the BSgenome data packages:

```r
if (interactive())
vignette("GenomeSearching", package="BSgenome")
```
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