BSgenome.Rnorvegicus.UCSC.rn5

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*Full genome sequences for* Rattus norvegicus (*UCSC version* rn5)

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**Description**

Full genome sequences for Rattus norvegicus (Rat) as provided by UCSC (rn5, Mar. 2012) and stored in Biostrings objects.

**Note**

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

rn5.fa.gz from http://hgdownload.cse.ucsc.edu/goldenPath/rn5/bigZips/

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

**Author(s)**

The Bioconductor Dev Team

**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.rn5
genome <- BSgenome.Rnorvegicus.UCSC.rn5
seqlengths(genome)
genome$chr1 # same as genome["chr1"]

## Upstream sequences

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## Starting with BioC 3.0, the upstream1000, upstream2000, and
## upstream5000 sequences for rn5 are not included in the BSgenome data
## package anymore. However they can easily be extracted from the full
genome sequences with something like:

```r
library(TxDb.Rnorvegicus.UCSC.rn5.refGene)
txdb <- TxDb.Rnorvegicus.UCSC.rn5.refGene
gn <- sort(genes(txdb))
up1000 <- flank(gn, width=1000)
up1000seqs <- getSeq(genome, up1000)
```

## IMPORTANT: Make sure you use a TxDb package (or TranscriptDb object),
## that contains a gene model based on the exact same reference genome
## as the BSgenome object you pass to getSeq(). Note that you can make
## your own custom TranscriptDb object from various annotation resources.
## See the makeTranscriptDbFromUCSC(), makeTranscriptDbFromBiomart(),
## and makeTranscriptDbFromGFF() functions in the GenomicFeatures
## package.

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