BSgenome.Hsapiens.UCSC.hg18

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BSgenome.Hsapiens.UCSC.hg18
Full genome sequences for Homo sapiens (UCSC version hg18)

Description

Full genome sequences for Homo sapiens (Human) as provided by UCSC (hg18, Mar. 2006) and stored in Biostrings objects.

Note

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

 chromFa.zip from http://hgdownload.cse.ucsc.edu/goldenPath/hg18/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.Hsapiens.UCSC.hg18
genome <- BSgenome.Hsapiens.UCSC.hg18
seqlengths(genome)
genome$chr1 # same as genome[["chr1"]]

## Upstream sequences
## Starting with BioC 3.0, the upstream1000, upstream2000, and upstream5000 sequences for hg18 are not included in the BSgenome data package anymore. However they can easily be extracted from the full genome sequences with something like:

library(TxDB.Hsapiens.UCSC.hg18.knownGene)
txdb <- TxDb.Hsapiens.UCSC.hg18.knownGene
gn <- sort(genes(txdb))
up1000 <- flank(gn, width=1000)
up1000seqs <- getSeq(genome, up1000)

## Genome-wide motif searching
## See the GenomeSearching vignette in the BSgenome software 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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