

BSgenome.Hsapiens.UCSC.hg19

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Full genome sequences for Homo sapiens (UCSC version hg19)

Description

Full genome sequences for Homo sapiens (Human) as provided by UCSC (hg19, Feb. 2009) 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/hg19/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.hg19
genome <- BSgenome.Hsapiens.UCSC.hg19
seqlengths(genome)
genome$chr1 # same as genome[["chr1"]]

## -----
## Upstream sequences
## -----
## Starting with BioC 3.0, the upstream1000, upstream2000, and
## upstream5000 sequences for hg19 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.hg19.knownGene)
txdb <- TxDb.Hsapiens.UCSC.hg19.knownGene
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.

## -----
## 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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