BSgenome.Hsapiens.UCSC.hg17

January 10, 2024

---

**BSgenome.Hsapiens.UCSC.hg17**

*Full genome sequences for Homo sapiens (UCSC version hg17)*

---

**Description**

Full genome sequences for Homo sapiens (Human) as provided by UCSC (hg17, May 2004) 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/hg17/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.Hsapiens.UCSC.hg17

geno <- BSgenome.Hsapiens.UCSC.hg17
seqlengths(geno)
geno$chr1 # same as genome[["chr1"]]

# Upstream sequences
# Starting with BioC 3.0, the upstream1000, upstream2000, and
# upstream5000 sequences for hg17 are not included in the BSgenome data
# package anymore. However they can easily be extracted from the full
# genome sequences with something like:

library(GenomicFeatures)
txdb <- makeTranscriptDbFromUCSC(hg17, "knownGene")
gn <- sort(genes(txdb))
up1000 <- flank(gn, width=1000)
up1000seqs <- getSeq(geno, 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")
Index

* data
  BSgenome.Hsapiens.UCSC.hg17, 1
* package
  BSgenome.Hsapiens.UCSC.hg17, 1

available.genomes, /
BSgenome, /
BSgenome.Hsapiens.UCSC.hg17, 1
BSgenome.Hsapiens.UCSC.hg17-package
  (BSgenome.Hsapiens.UCSC.hg17), 1
BSgenomeForge, /
DNAString, /
Hsapiens (BSgenome.Hsapiens.UCSC.hg17), 1