BSgenome.Hsapiens.UCSC.hg17
April 26, 2017

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.

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

## Upstream sequences
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library(GenomicFeatures)
txdb <- makeTranscriptDbFromUCSC("hg17", "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

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