

BSgenome.Hsapiens.UCSC.hg17

October 16, 2009

Hsapiens

Homo sapiens full genome (UCSC version hg17)

Description

Homo sapiens full genome 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:

```
sequences: chromFa.zip, upstream1000.zip, upstream2000.zip, upstream5000.zip
from http://hgdownload.cse.ucsc.edu/goldenPath/hg17/bigZips/
AGAPS masks: all the chr*_gap.txt.gz files from ftp://hgdownload.cse.ucsc.edu/g
RM masks: http://hgdownload.cse.ucsc.edu/goldenPath/hg17/bigZips/chromOut.zip
TRF masks: http://hgdownload.cse.ucsc.edu/goldenPath/hg17/bigZips/chromTrf.zip
```

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

Author(s)

H. Pages

See Also

[BSgenome-class](#), [DNASTring-class](#), [available.genomes](#), [BSgenomeForge](#)

Examples

```
Hsapiens
seqlengths(Hsapiens)
Hsapiens$chr1 # same as Hsapiens[["chr1"]]

if ("AGAPS" %in% masknames(Hsapiens)) {

  ## Check that the assembly gaps contain only Ns:
  checkOnlyNsInGaps <- function(seq)
  {
    ## Replace all masks by the inverted AGAPS mask
```

```
    masks(seq) <- gaps(masks(seq) ["AGAPS"])
    unique_letters <- uniqueLetters(seq)
    if (any(unique_letters != "N"))
      stop("assembly gaps contain more than just Ns")
  }

  ## A message will be printed each time a sequence is removed
  ## from the cache:
  options(verbose=TRUE)

  for (seqname in seqnames(Hsapiens)) {
    cat("Checking sequence", seqname, "... ")
    seq <- Hsapiens[[seqname]]
    checkOnlyNsInGaps(seq)
    cat("OK\n")
  }
}

## 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

*Topic **data**

Hsapiens, [1](#)

*Topic **package**

Hsapiens, [1](#)

available.genomes, [1](#)

BSgenome-class, [1](#)

BSgenome.Hsapiens.UCSC.hg17
(*Hsapiens*), [1](#)

BSgenome.Hsapiens.UCSC.hg17-package
(*Hsapiens*), [1](#)

BSgenomeForge, [1](#)

DNASTring-class, [1](#)

Hsapiens, [1](#)