BSgenome.Mmusculus.UCSC.mm9

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Mmusculus  
*Mus musculus* full genome (UCSC version mm9)

Description

*Mus musculus* full genome as provided by UCSC (mm9, Jul. 2007) and stored in Biostrings objects.

Note

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

- sequences: chromFa.tar.gz, upstream1000.fa.gz, upstream2000.fa.gz, upstream5000.fa.gz from http://hgdownload.cse.ucsc.edu/goldenPath/mm9/bigZips/
- AGAPS masks: all the chr*_gap.txt.gz files from ftp://hgdownload.cse.ucsc.edu/goldenPath/mm9/database/
- RM masks: http://hgdownload.cse.ucsc.edu/goldenPath/mm9/bigZips/chromOut.tar.gz
- TRF masks: http://hgdownload.cse.ucsc.edu/goldenPath/mm9/bigZips/chromTrf.tar.gz

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-class, DNAString-class, available.genomes, BSgenomeForge

Examples

Mmusculus
seqlengths(Mmusculus)
Mmusculus$chr1  # same as Mmusculus[["chr1"]]

if ("AGAPS" %in% masknames(Mmusculus)) {
    ## Check that the assembly gaps contain only Ns:
    checkOnlyNsInGaps <- function(seq)
    {
        ## Replace all masks by the inverted AGAPS mask
mMuskus

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(MMuskus)) {
  cat("Checking sequence", seqname, "...")
  seq <- MMuskus[[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")
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