Full genome sequences for Mus musculus (Mouse) as provided by UCSC (mm9, Jul. 2007) and stored in Biostrings objects.

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

chromFa.tar.gz from http://hgdownload.cse.ucsc.edu/goldenPath/mm9/bigZips/

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

The Bioconductor Dev Team

• 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.Mmusculus.UCSC.mm9
genome <- BSgenome.Mmusculus.UCSC.mm9
seqlengths(genome)
genome$chr1 # same as genome[["chr1"]]

## Upstream sequences
library(TxDb.Mmuseculus.UCSC.mm9.knownGene)
txdb <- TxDb.Mmuseculus.UCSC.mm9.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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