Description

Drosophila melanogaster full genome as provided by UCSC (dm3, Apr. 2006) and stored in Biostrings objects.

Note

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

sequences: chromFa.tar.gz, upstream1000.fa.gz, upstream2000.fa.gz, upstream5000.fa.gz
from http://hgdownload.cse.ucsc.edu/goldenPath/dm3/bigZips/
AGAPS masks: all the chr*_gap.txt.gz files from ftp://hgdownload.cse.ucsc.edu/goldenPath/dm3/database/
TRF masks: http://hgdownload.cse.ucsc.edu/goldenPath/dm3/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

Dmelanogaster
seqlengths(Dmelanogaster)
Dmelanogaster$chr2L # same as Dmelanogaster["chr2L"]

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

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

```r
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:
```r
options(verbose=TRUE)
```

```r
for (seqname in seqnames(Dmelanogaster)) {
  cat("Checking sequence", seqname, "...
  seq <- Dmelanogaster[[seqname]]
  checkOnlyNsInGaps(seq)
  cat("OK
"
  }
```

## See the GenomeSearching vignette in the BSgenome software package for some examples of genome-wide motif searching using Biostrings and the BSgenome data packages:
```r
if (interactive())
  vignette("GenomeSearching", package="BSgenome")
```
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