

BSgenome.Dmelanogaster.UCSC.dm3

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Drosophila melanogaster (Fly) full genome (UCSC version dm3)

Description

Drosophila melanogaster (Fly) 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/>

RM masks: <http://hgdownload.cse.ucsc.edu/goldenPath/dm3/bigZips/chromOut.tar.gz>

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)

The Bioconductor Dev Team

See Also

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

Examples

```
BSgenome.Dmelanogaster.UCSC.dm3
genome <- BSgenome.Dmelanogaster.UCSC.dm3
seqlengths(genome)
genome$chr2L # same as genome[["chr2L"]]

if ("AGAPS" %in% masknames(genome)) {
```

```
## 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(genome)) {
  cat("Checking sequence", seqname, "... ")
  seq <- genome[[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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