BSgenome.Celegans.UCSC.ce6

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BSgenome.Celegans.UCSC.ce6

*Full genome sequences for Caenorhabditis elegans (UCSC version ce6)*

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**Description**

Full genome sequences for Caenorhabditis elegans (Worm) as provided by UCSC (ce6, May 2008) and stored in Biostrings objects.

**Note**

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

chromFa.tar.gz from ftp://hgdownload.cse.ucsc.edu/goldenPath/ce6/bigZips/

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 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.Celegans.UCSC.ce6
genome <- BSgenome.Celegans.UCSC.ce6
seqlengths(genome)
genome$chrI # same as genome["chrI"]

### Upstream sequences

### Starting with BioC 3.0, the upstream1000, upstream2000, and
### upstream5000 sequences for ce6 are not included in the BSgenome data
### package anymore. However they can easily be extracted from the full
### genome sequences with something like:

library(TxDb.Celegans.UCSC.ce6.ensGene)
txdb <- TxDb.Celegans.UCSC.ce6.ensGene
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

### 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
  BSgenome.Celegans.UCSC.ce6, 1

*Topic package
  BSgenome.Celegans.UCSC.ce6, 1

available.genomes, 1

BSgenome, 1
BSgenome.Celegans.UCSC.ce6, 1
BSgenome.Celegans.UCSC.ce6-package
  (BSgenome.Celegans.UCSC.ce6), 1
BSgenomeForge, 1

Celegans (BSgenome.Celegans.UCSC.ce6), 1

DNAString, 1