BSgenome.Celegans.UCSC.ce2
May 1, 2024

Full genome sequences for Caenorhabditis elegans (UCSC version ce2)

Description
Full genome sequences for Caenorhabditis elegans (Worm) as provided by UCSC (ce2, Mar. 2004) and stored in Biostrings objects.

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

chromFa.zip from http://hgdownload.cse.ucsc.edu/goldenPath/ce2/bigZips/

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

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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.ce2

```r
geno <- BSgenome.Celegans.UCSC.ce2
seqlengths(genome)
genome$chrI  # same as genome[["chrI"]]
```

# Upstream sequences

Starting with BioC 3.0, the upstream1000, upstream2000, and upstream5000 sequences for ce2 are not included in the BSgenome data package anymore. However they can easily be extracted from the full genome sequences with something like:

```r
library(GenomicFeatures)
txdb <- makeTranscriptDbFromUCSC("ce2", "refGene")
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:

```r
if (interactive())
  vignette("GenomeSearching", package="BSgenome")
```
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