Full genome sequences for Canis lupus familiaris (Dog) as provided by UCSC (canFam2, May 2005) and stored in Biostrings objects.

Note

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

chromFa.tar.gz from http://hgdownload.cse.ucsc.edu/goldenPath/canFam2/bigZips/

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 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.Cfamiliaris.UCSC.canFam2
genome <- BSgenome.Cfamiliaris.UCSC.canFam2
seqlengths(genome)
genome$chr1  # same as genome[["chr1"]]

## Upstream sequences

The upstream sequences for canFam2 (i.e. the sequences 1000 bases upstream of annotated transcription starts) can easily be extracted from the full genome sequences with something like:

library(GenomicFeatures)
txdb <- makeTranscriptDbFromUCSC("canFam2", "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:
if (interactive())
vignette("GenomeSearching", package="BSgenome")
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