BSgenome.Drerio.UCSC.danRer10

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Description

Full genome sequences for Danio rerio (Zebrafish) as provided by UCSC (danRer10, Sep. 2014) and stored in Biostrings objects.

Note

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

danRer10.2bit from http://hgdownload.soe.ucsc.edu/goldenPath/danRer10/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.Drerio.UCSC.danRer10

genome <- BSgenome.Drerio.UCSC.danRer10
head(seqlengths(genome))
genome$chr1  # same as genome["chr1"]

# Extract the upstream sequences
# The upstream sequences located in http://hgdownload.cse.ucsc.edu/goldenPath/danRer10/bigZips/
# are based on RefSeq genes (RefSeq Genes track in the Genome Browser).
# These can easily be extracted from the full genome sequences with:

library(GenomicFeatures)
refGene_txdb <- suppressWarnings(makeTxDbFromUCSC("danRer10", "refGene"))
refGene_up1000seqs <- extractUpstreamSeqs(genome, refGene_txdb)

# Note that you can make a TxDb object from various annotation resources. See the makeTxDbFromUCSC(), makeTxDbFromBiomart(), and makeTxDbFromGFF() functions in the GenomicFeatures package for more information.
# IMPORTANT: Make sure you use a TxDb package (or TxDb object) that contains a gene model based on danRer10 or on a compatible genome (i.e. a genome with sequences identical to the sequences in danRer10). See ?extractUpstreamSeqs in the GenomicFeatures package for more information.

# 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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