BSgenome.Hsapiens.UCSC.hg38

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Description

Full genomic sequences for Homo sapiens as provided by UCSC (genome hg38, based on assembly GRCh38.p14 since 2023/01/31). The sequences are stored in DNAString objects.

Note

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

hg38.p14.2bit, downloaded from https://hgdownload.soe.ucsc.edu/goldenPath/hg38/bigZips/p14/ on Feb 1st, 2023

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

Author(s)

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See Also

- BSgenome objects in the BSgenome software package.
- The seqinfo getter and Seqinfo objects in the GenomeInfoDb package.
- The seqlevelsStyle getter and setter in the GenomeInfoDb package.
- DNAString objects in the Biostrings package.
- The available.genomes function in the BSgenome software package.
- The BSgenomeForge vignette (vignette("BSgenomeForge")) in the BSgenome software package for how to create a BSgenome data package.
Examples

BSgenome.Hsapiens.UCSC.hg38
bsg <- BSgenome.Hsapiens.UCSC.hg38
head(seqlengths(bsg))
seqinfo(bsg)

## Access individual sequences:

bsg$chr1 # same as bsg[["chr1"]]
alphabetFrequency(bsg[["chr1"]])

bsg[["chrM"]]] # same as bsg$chrM
reverseComplement(bsg$chrM)

# Switch the sequence names back and forth between UCSC and NCBI
# ----------------------------------------------------------------------------------------------------------

# IMPORTANT NOTE: Even though hg38 is officially based on the
# GRCh38.p14 assembly (this is as of Jan 31, 2023, hg38 was based on
# GRCh38.p13 before that), it contains 2 sequences that do not belong
# to GRCh38.p14: chr11_KQ759759v1_fix and chr22_KQ759762v1_fix
# These 2 foreign sequences belong to GRCh38.p13 (they are named
# HG107_PATCH and HG1311_PATCH there), but they've been replaced with
# sequences HG107_HG2565_PATCH and HG1311_HG2539_PATCH in GRCh38.p14.

seqinfo(bsg)
seqlevelsStyle(bsg) # UCSC

# --- switch to NCBI names ---

bsg0 <- bsg
seqlevelsStyle(bsg) <- "NCBI"
bsg
seqinfo(bsg)
bsg[["1"]])

# Surprise!
table(genome(bsg)) # 2 sequences belong to GRCh38.p13!
foreign_idx <- which(genome(bsg) == "GRCh38.p13")
seqinfo(bsg)[seqnames(bsg)[foreign_idx]]
seqlevelsStyle(bsg) # NCBI

# --- switch back ---

seqlevelsStyle(bsg) <- "UCSC"
bsg
stopifnot(identical(bsg0, bsg))
seqinfo(bsg)[seqnames(bsg)[foreign_idx]]

# ----------------------------------------------------------------------------------------------------------
# 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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