Pan troglodytes (Chimp) full genome as provided by UCSC (panTro2, Mar. 2006) and stored in Biostrings objects.

Note

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

AGAPS masks: gap.txt.gz from ftp://hgdownload.cse.ucsc.edu/goldenPath/panTro2/database/
RM masks: http://hgdownload.cse.ucsc.edu/goldenPath/panTro2/bigZips/chromOut.tar.gz
TRF masks: http://hgdownload.cse.ucsc.edu/goldenPath/panTro2/bigZips/chromTrf.tar.gz

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-class, DNAString-class, available.genomes, BSgenomeForge

Examples

Ptroglodytes
seqlengths(Ptroglodytes)
Ptroglodytes$chr1 # same as Ptroglodytes[["chr1"]]

if ("AGAPS" %in% masknames(Ptroglodytes)) {
  ## Check that the assembly gaps contain only Ns:
  checkOnlyNsInGaps <- function(seq) {
  |
## Replace all masks by the inverted AGAPS mask

```r
masks(seq) <- gaps(masks(seq)["AGAPS"])
unique_letters <- uniqueLetters(seq)
if (any(unique_letters != "N"))
  stop("assembly gaps contain more than just Ns")
```

## A message will be printed each time a sequence is removed
## from the cache:
```r
options(verbose=TRUE)

for (seqname in seqnames(Ptroglodytes)) {
  cat("Checking sequence", seqname, "...")
  seq <- Ptrogloydyses[[seqname]]
  checkOnlyNsInGaps(seq)
  cat("OK\n")
}
```

## 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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