Description

Oryza sativa full genome as provided by MSU (MSU7 Genome Release) and stored in Biostrings objects.

Note

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

ftp://ftp.plantbiology.msu.edu/pub/data/Eukaryotic_Projects/o_sativa/annotation_dbs/pseudomolecules/version_7.0/all.dir/all.con

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

Examples

BSgenome.Osativa.MSU.MSU7
genome <- BSgenome.Osativa.MSU.MSU7
seqlengths(genome)
genome$Chr1 # same as genome["Chr1"]

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

for (seqname in seqnames(genome)) {
  cat("Checking sequence", seqname, "...
  seq <- genome[[seqname]]
  checkOnlyNsInGaps(seq)
  cat("OK
")
}

## 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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