BSgenome.Tguttata.UCSC.taeGut1.masked

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`BSgenome.Tguttata.UCSC.taeGut1.masked`
Full masked genome sequences for Taeniopygia guttata (UCSC version taeGut1)

Description

Full genome sequences for Taeniopygia guttata (Zebra finch) as provided by UCSC (taeGut1, Jul. 2008) and stored in Biostrings objects. The sequences are the same as in BSgenome.Tguttata.UCSC.taeGut1, except that each of them has the 2 following masks on top: (1) the mask of assembly gaps (AGAPS mask), and (2) the mask of intra-contig ambiguities (AMB mask). Both masks are "active" by default.

Note

The masks in this BSgenome data package were made from the following source data files:

`AGAPS masks: all the chr*_gap.txt.gz files from http://hgdownload.cse.ucsc.edu/goldenPath/taeGut1/data`

See `?BSgenome.Tguttata.UCSC.taeGut1` in the **BSgenome.Tguttata.UCSC.taeGut1** package for information about how the sequences were obtained.

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.Tguttata.UCSC.taeGut1 in the **BSgenome.Tguttata.UCSC.taeGut1** package for information about how the sequences were obtained.
- BSgenome objects and the `available.genomes` function in the **BSgenome** software package.
- MaskedDNAString 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.Tguttata.UCSC.taeGut1.masked
genome <- BSgenome.Tguttata.UCSC.taeGut1.masked
seqlengths(genome)
genome$chr1  # a MaskedDNAString object!
## To get rid of the masks altogether:
unmasked(genome$chr1)  # same as BSgenome.Tguttata.UCSC.taeGut1$chr1

if ("AGAPS" %in% masknames(genome)) {

  ## Check that the assembly gaps contain only Ns:
  checkOnlyNsInGaps <- function(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\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:
if (interactive())
    vignette("GenomeSearching", package="BSgenome")
```

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