GenomicFeatures.Mmusculus.UCSC.mm9

March 19, 2011

`CpG.mm9` *CpG islands for mm9*

Description

Locations of the CpG islands in the Mouse genome (build mm9). Coordinates are relative to the mm9 build and are in nucleotides from the 5' end of the positive (`"+"`) strand. They are always *one-based*, that is, the coordinate of the first (or leftmost) nucleotide in the strand is 1.

Usage

```
CpG.mm9()
```

Value

A data frame with 16026 observations on the following 4 variables.

1. `chromosome`: Chromosome name as a character vector.
2. `start`: Interval start points.
3. `end`: Interval end points.
4. `ID`: An identifier.

Source

This table was obtained by downloading the following database file from UCSC (on Sep 28, 2009): `http://hgdownload.cse.ucsc.edu/goldenPath/mm9/database/cpgIslandExt.txt.gz` and by translating the start coordinates found in the file from zero-based to one-based.

The cpgIslandExt.txt.gz file is a database dump containing the UCSC track called "CpG Islands" and described here: `http://genome.ucsc.edu/cgi-bin/hgTrackUi?db=mm9&g=cpgIslandExt`

`GenomicFeatures.Mmusculus.UCSC.mm9_dbconn` *Get the connection to the built-in DB*

Description

A convenience function for getting a connection object to the annotation DB included in the GenomicFeatures.Mmusculus.UCSC.mm9 package.

Usage

```
GenomicFeatures.Mmusculus.UCSC.mm9_dbconn()
GenomicFeatures.Mmusculus.UCSC.mm9_dbfile()
```

Details

`GenomicFeatures.Mmusculus.UCSC.mm9_dbconn` returns a connection object that was created at load-time and is aimed to hold a permanent connection. It is used internally by some of the functions defined in this package. Don't call `dbDisconnect` on this connection object or you will break these functions.

See Also

`dbGetQuery`, `dbConnect`, `geneMouse`

Examples

```
library(RSQLite)

## Get Mouse genes in chromosome 1:
chr1_genes <- dbGetQuery(GenomicFeatures.Mmusculus.UCSC.mm9_dbconn(),
                         "SELECT * FROM knownGene WHERE chrom='chr1'")
## Get all the Mouse genes:
genes <- dbReadTable(GenomicFeatures.Mmusculus.UCSC.mm9_dbconn(),
                     "knownGene", row.names=NULL)
## NOTE: The recommended way to get all the Mouse genes is to use geneMouse().
```

`geneMouse` *UCSC Gene Predictions for mm9*

Description

Gene coordinates and annotations for M. musculus from UCSC. Coordinates are relative to the mm9 build and are in nucleotides from the 5' end of the positive (`"+"`) strand. They are always *one-based*, that is, the coordinate of the first (or leftmost) nucleotide in the strand is 1. Each “gene”, or row in the dataset, corresponds to a unique combination of transcript (TSS, TES and exons) and coding sequence (start and end).

Usage

```
geneMouse()
```

Value

A data frame with 49409 observations on the following 12 variables.

1. `name`: The name of the gene.
2. `chrom`: The name of the chromosome the gene is located on.
3. `strand`: The strand the gene is coded on, `"+"`, or `"-"`.
4. `txStart`: Transcription start site.
5. `txEnd`: Transcription stop site.
6. `cdsStart`: Start position of the coding sequence.
7. `cdsEnd`: End position of the coding sequence.
8. `exonCount`: The number of exons.
9. `exonStarts`: A comma separated list of the exon start positions.
10. `exonEnds`: A comma separated list of exon stop positions.
11. `proteinID`: An ID for the protein produced, missing values are coded as NA.
12. `alignID`: Unique identifier of each gene and RNA alignment pair, apparently redundant with `name`.

Note

For genes coded on the negative strand the `txStart` is really the end, and similarly for the coding regions.

Source

This table was obtained by downloading the following database file from UCSC (on Sep 28, 2009): `http://hgdownload.cse.ucsc.edu/goldenPath/mm9/database/knownGene.txt.gz` and by translating the start coordinates found in the file from zero-based to one-based.

The knownGene.txt.gz file is a database dump containing the UCSC track called "UCSC Genes" and described here: `http://genome.ucsc.edu/cgi-bin/hgTrackUi?db=mm9&g=knownGene`

See `http://genome.ucsc.edu/cgi-bin/hgTables` and Hsu F, Kent WJ, Clawson H, Kuhn RM, Diekhans M, Haussler D. The UCSC Known Genes. Bioinformatics. 2006 May 1;22(9):1036-46.

All the annotations in this package are freely available for public use, except for the Swiss-Prot/UniProt data in the knownGene table, which has the following terms of use:

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```

Examples

```
genes <- geneMouse()
str(genes)
transcripts_deprecated(genes)
```

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