Package 'RMAPPER'

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Type Package

Title R interface to the MAPPER database of transcription factor binding sites

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Depends methods

Suggests RCurl

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Description The RMAPPER package allows you to retrieve a set of predicted transcription factor binding sites from the MAPPER database (http://genome.ufl.edu/mapper/) through a simple HTTP request.

biocViews Annotation, Genetics

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R topics documented:

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hits   *Hits details*

Description

Function displaying the detailed information on the sequence and other properties of each hit returned from the MAPPER RPC interface query.

Usage

hits(x)

Arguments

x   x – mapperHits object returned from readMAPPER

References

http://genome.ufl.edu/mapper/

See Also

readMAPPER.

Examples

see readMAPPER

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mapperHits-class   *Class "mapperHits" – holds collection of hits from MAPPER*

Description

A data frame and some metadata about a MAPPER query from http://genome.ufl.edu/mapper. The data frame holds the predicted transcription factor binding sites from MAPPER.

Objects from the Class

Objects can be created by calls of the form new("mapperHits", ...). These are annotated data frames.

Slots

query: character string that provides information on the query generating the object

hits: Object of class "data.frame" providing information on the sequence and other properties of each hit.

Methods

query signature(x = "mapperHits"): ...

hits signature(x = "mapperHits"): ...

show signature(object = "mapperHits"): ...

Author(s)

VJ Carey <stvjc@channing.harvard.edu>

References

http://genome.ufl.edu/mapper/

See Also

readMAPPER.

Examples

see readMAPPER

query	Character string that provides information on the query generating the object

Description

Function displaying the exact query to the MAPPER RPC interface.

Usage

query(x)

Arguments

x	x – mapperHits object returned from readMAPPER

References

http://genome.ufl.edu/mapper/

See Also

readMAPPER.

Examples

see readMAPPER

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readMAPPER   *Retrieve a set of predicted transcription factor binding sites from the*
                                MAPPER database

Description

The MAPPER RPC interface allows you to retrieve a set of predicted transcription factor binding sites from the MAPPER database through a simple HTTP request. This package provides a function to retrieve predicted TFBS from R.

Usage

readMAPPER(stub = paste(urlpath, "db-rpc?", sep = ""), ...)

Arguments

stub   stub – a string giving the URL handle up to the db-rpc selector (optional)

...   . . . – all the query parameters (see Details).

Details

Currently (9/10) the RPC interface to MAPPER defines the following parameters. You can use any of these as keywords (with bindings supplied using "=", e.g., gene="CRP") to the readMAPPER function.

gene - you can use either NCBI GeneID or mRNA accession number; gene names should work too, but this is not recommended because there often are multiple forms of the same gene. [required, unless 'list' is specified]

models - a comma-separated list of model names (to restrict the output to these models only) [required, unless 'list' is specified]

score - the score threshold (0 by default)

perc - the percentile (one of 50, 80, 85, 90, 95). Only hits with scores above the desired percentile for each model are returned.

eval - the E-value threshold (25 by default)

pbases - how many basepairs to look at (default: 2000). See pstart.

pstart - what pbases is relative to (either T for transcript start or C for coding sequence start - remember that in the db we have hits for the region from 10,000 bp upstream of transcript start to 50bp after coding sequence start)

sort - how to sort the results: either M (by model accession), N (factor name), E (by E-value), S (by score), P (by position, the default)

org - two letter organism code

list - returns a list of all TF names with the corresponding model accession numbers. All other parameters are ignored.

If you issue rmapperHelp(), you will get a help page in text.

Value

An instance of the mapperHits class.

Author(s)

Vince Carey <stvjc@channing.harvard.edu>

References

http://genome.ufl.edu/mapper/

See Also

mapperHits-class query hits

Examples

```
# Run an example retrieving data from the MAPPER RPC interface for gene ID = NM_009696
mh = readMAPPER(gene="NM_009696", perc="95", models="M00027")
# Display the mapperHits object returned by readMAPPER
mh
# Display the exact query that was issued to the MAPPER RPC interface
query(mh)
# Display the details of hits from the query
hits(mh)
```

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rmapperFactorTable   *MAPPER Factor Table*

Description

Function to display a table listing the transcription factor/s known to MAPPER with the corresponding model accession numbers.

Usage

```
rmapperFactorTable(tf)
```

Arguments

tf   tf – a specific transcription factor, i.e. "AbaA" or "*" for all transcription factors

References

http://genome.ufl.edu/mapper/

Examples

```
# Display all transcription factors and their model accession numbers
rmapperFactorTable("*")
# Display a specific transcription factor and its model accession numbers
rmapperFactorTable("AbaA")
# Display transcription factors "Ab..." and their model accession numbers
rmapperFactorTable("Ab")
```

rmapperHelp	*Help*

Description

Function to call the MAPPER backdoor interface help page.

Usage

    rmapperHelp()

References

http://genome.ufl.edu/mapper/

Examples

    # Display the help page
    rmapperHelp()

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