RMAPPER

March 24, 2012

`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
```

`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)

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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
```

`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)
```

`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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