Package ‘rapimave’

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Title R API for MaveDB

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Description Allows programatic access to the MaveDB database of Deep Mutational Scans

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License GPL

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new.experiment *New R-API MaveDB Experiment*

Description

Internal constructor that creates an immutable new Experiment object. This function is not exported and should not be called outside of the rapimave package itself. Experiment objects are generated by the `getAllExperiments()` and `getExperiment()` methods of a rapimave object (which itself is generated using the `new.rapimave()` constructor). However, this section explains the functions that are available for these objects.

Usage

```
new.experiment(data)
```

Details

A Experiment object offers the following getter functions:

- getContributors() returns a list of users that contributed to this record.
- getURN() returns the URN of this record.
- getCreationDate() returns the date when this record was originally created.
- getModificationDate() returns the date when this record was last modified.
- getPublicationDate() returns the date when this record was published.
- getCreatedBy() returns the user who originally created this record.
- getModifiedBy() returns the user who last modified this record.
- getMetadata() returns the metadata for this record.
- getTitle() returns the title of this record.
- getShortDescription() returns a short description text of this record.
- getAbstract() returns the abstract text of this record.
- getMethods() returns the methods description text of this record.
- getKeywords() returns the list of keywords associated with this record.
- getDOIs() returns the list of Digital Object Identifiers (DOIs) associated with this record.
- getXrefSRA() returns cross-references to the NCBI Short Read Archive (SRA).
- getXRefPubmed() returns cross-references to Pubmed.
- getExperimentSet() return the accession of the ExperimentSet to which this Experiment belongs.
- getScoreSets() return the list of URNs of the Experiment's ScoreSets.

Value

a new R-API MaveDB experiment object.

Examples

```
## Not run:
mave <- new.rapimave()
exp1 <- mave$getExperiment("urn:mavedb:00000001-a")
authorIds <- exp1$getAuthors()

## End(Not run)
```

new.experimentSet *New R-API MaveDB ExperimentSet*

Description

Internal constructor that creates an immutable new ExperimentSet object. This function is not exported and should not be called outside of the rapimave package itself. ExperimentSet objects are generated by the `getAllExperimentSets()` and `getExperimentSet()` methods of a rapimave object (which itself is generated using the `new.rapimave()` constructor). However, this section explains the functions that are available for these objects.

Usage

```
new.experimentSet(data)
```

Details

A ExperimentSet object offers the following getter functions:

- getContributors() returns a list of users that contributed to this record.
- getURN() returns the URN of this record.
- getCreationDate() returns the date when this record was originally created.
- getModificationDate() returns the date when this record was last modified.
- getPublicationDate() returns the date when this record was published.
- getCreatedBy() returns the user who originally created this record.
- getModifiedBy() returns the user who last modified this record.
- getMetadata() returns the metadata for this record.
- getTitle() returns the title of this record.
- getShortDescription() returns a short description text of this record.
- getAbstract() returns the abstract text of this record.
- getMethods() returns the methods description text of this record.
- getKeywords() returns the list of keywords associated with this record.
- getDOIs() returns the list of Digital Object Identifiers (DOIs) associated with this record.
- getXrefSRA() returns cross-references to the NCBI Short Read Archive (SRA).
- getXRefPubmed() returns cross-references to Pubmed.
- getExperiments() returns the URNs of the experiments belonging to this ExperimentSet.

Value

a new R-API MaveDB ExperimentSet object.

Examples

```
## Not run:
mave <- new.rapimave()
set1 <- mave$getExperimentSet("urn:mavedb:00000001")
expURNs <- set1$getExperiments()

## End(Not run)
```

new.genome *New R-API MaveDB genome*

Description

Internal constructor that creates an immutable new genome object. This function is not exported and should not be called outside of the rapimave package itself. Genome objects are generated by the getGenome() method of a reference map object (which itself is generated using the `get.referenceMaps()` method on a target object). However, this section explains the functions that are available for these objects.

Usage

```
new.genome(data)
```

Details

A ScoreSet object offers the following getter functions:

- getShortName() returns the name of this genome object
- getSpecies() returns the species to which this genome belongs.
- getXRefEnsembl() returns the a cross-reference object for Ensembl (if it exists).
- getXrefRefseq() returns the a cross-reference object for Refseq (if it exists).

Value

a new R-API MaveDB genome object.

new.mave.filter *New MaveDB Filter Object*

Description

Constructor that creates a MaveDB filter object

Usage

```
new.mave.filter(data, verbose = TRUE)
```

Arguments

`data`	A data.frame containing a MaveDB data set containing at least the two columns "hgvs" and "score".
`verbose`	Logical. If TRUE, prints status messages while loading data.

Details

The resulting object offers a number of filter functions. All these functions return vectors of type `logical`, which can be combined with `&` and `|` to form more complex filters before being applied to the data. (See example below). The following functions are available.

- mutationCount() filters by number of mutations in the variant. Parameters `min` and `max` default to 0 and Inf respectively.
- position() filters by the (start) position of the mutations. Parameters `min` and `max` default to -Inf and Inf respectively. Parameter `multi` determines whether in case of multi-mutants, the criterium must match any or all of the individual mutations. Allowed values are "any" and "all".
- residues() filters by amino acid residues. Parameter from and to are vectors of allowed ancestral and variant amino acid residues.Parameter `multi` determines whether in case of multi-mutants, the criterium must match any or all of the individual mutations. Allowed values are "any" and "all".
- numerical() filters by numerical columns. Parameter `col` is the name of the numerical column to filter by. Parameters `min` and `max` default to -Inf and Inf respectively.
- categorical() filters by categorical columns. Parameter `col` is the name of the categorical column (of type `character` or `factor`) to filter by. Parameter values is a vector of allowed values in that column to filter for.

Value

a new MaveDB filter object

Examples

```
## Not run:
mave <- new.rapimave()
data <- mave$getScores("SCS000001A.2")
mfilter <- new.mave.filter(data)
filter <- with(mfilter,
  position(min=5,multi="all") & residues(to="Ala",multi="all") & numerical("score",min=0.1)
)
filtered.data <- data[filter,]

## End(Not run)
```

new.rapimave *MaveDB R-API client constructor*

Description

Creates an object of type rapimave.

Usage

```
new.rapimave(baseURL = "https://www.mavedb.org/api/", certifySSL = FALSE,
  encoding = "UTF-8")
```

Arguments

`baseURL`	MaveDB API base-URL. Defaults to "https://www.mavedb.org/api/"
`certifySSL`	Logical indicating whether to certify SSL certificates when querying the database. Defaults to `FALSE`.
`encoding`	A string specifying the expected character encoding used by the webservice. Defaults to "UTF-8"

Details

The resulting object offers the following functions:

- getAllUsers() returns a list of all user objects. See `new.user` for available methods on user objects.
- getUser(username) returns the user object for the given username. Usernames are usually ORCID IDs. See `https://orcid.org/` for information on ORCID. See `new.user` for available methods on user objects.
- findExperimentSets(filter) returns a list of all ExperimentSet objects that match the given filter word. See `new.experimentSet` for available methods on ExperimentSet objects.
- getAllExperimentSets() returns a list of all ExperimentSet objects. See `new.experimentSet` for available methods on ExperimentSet objects.

- getExperimentSet(urn) returns the ExperimentSet object for the given URN. ExperimentSet URNs usually follow the syntax /^urn:mavedb:\d+$/ . See `new.experimentSet` for available methods on ExperimentSet objects.
- getAllExperiments() returns a list of all Experiment objects. See `new.experiment` for available methods on Experiment objects.
- findExperiments(filter) returns a list of all Experiment objects that match the given filter word. See `new.experiment` for available methods on Experiment objects.
- getExperiment(urn) returns the Experiment object for the given URN. Experiment URNs usually follow the syntax /^urn:mavedb:\d+-\w+/ . See `new.experiment` for available methods on Experiment objects.
- getAllScoreSets() returns a list of all ScoreSet objects. See `new.scoreSet` for available methods on ScoreSet objects.
- findScoreSets(filter) returns a list of all ScoreSet objects that match the given filter word. See `new.scoreSet` for available methods on ScoreSet objects.
- getScoreSet(urn) returns the ScoreSet object for the given URN. ScoreSet URNs usually follow the syntax /^urn:mavedb:\d+-\w+-\d+$/ . See `new.scoreSet` for available methods on ScoreSet objects.
- getScores(urn) returns a `data.frame` with the scores for the given ScoreSet URN
- getCounts(urn) returns a `data.frame` with the counts for the given ScoreSet URN
- getMetadata(urn) returns a `data.frame` with the metadata for the given ScoreSet URN

Value

MaveDB R-API object with functions accessbile via the $ operator.

Examples

```
## Not run:
mave <- new.rapimave()

## End(Not run)
```

`new.refmap` *New R-API MaveDB ReferenceMap*

Description

Internal constructor that creates an immutable new ReferenceMap object. This function is not exported and should not be called outside of the rapimave package itself. ReferenceMap objects are generated by the getReferenceMap() method of a target object (which itself is generated using the `getTarget()` method on a scoreset object). However, this section explains the functions that are available for these objects.

Usage

```
new.refmap(data)
```

Details

A ScoreSet object offers the following getter functions:

- getGenome() returns the genome object for this reference map
- isPrimary() returns whether this is the primary reference map for this scoreset
- getIntervals() returns a data.frame listing the intervals in the genome to which the target is mapped.

Value

a new R-API MaveDB ReferenceMap object.

`new.scoreSet` *New R-API MaveDB ScoreSet*

Description

Internal constructor that creates an immutable new ScoreSet object. This function is not exported and should not be called outside of the rapimave package itself. ScoreSet objects are generated by the `getAllScoreSets()` and `getScoreSet()` methods of a rapimave object (which itself is generated using the `new.rapimave()` constructor). However, this section explains the functions that are available for these objects.

Usage

```
new.scoreSet(data)
```

Details

A ScoreSet object offers the following getter functions:

- getContributors() returns a list of users that contributed to this ScoreSet.
- getURN() returns the URN of this ScoreSet.
- getCreationDate() returns the date when this record was originally created.
- getModificationDate() returns the date when this record was last modified.
- getPublicationDate() returns the date when this record was published.
- getCreatedBy() returns the user who originally created this record.
- getModifiedBy() returns the user who last modified this record.
- getMetadata() returns the metadata for this record.
- getTitle() returns the title of this record.
- getShortDescription() returns a short description text of this record.
- getAbstract() returns the abstract text of this record.
- getMethods() returns the methods description text of this record.

- getKeywords() returns the list of keywords associated with this record.
- getDOIs() returns the list of Digital Object Identifiers (DOIs) associated with this record.
- getXrefSRA() returns cross-references to the NCBI Short Read Archive (SRA).
- getXRefPubmed() returns cross-references to Pubmed.
- getTarget() returns the Target object for this scoreset, which describes the molecule that that was targeted in the experiment.
- getLicence() returns the licencing information governing the use of this ScoreSet.
- getCurrentVersion() If a more up-to-date version of this ScoreSet exists, that has since replaced it, this function will return the accession of the most recent version.
- getPreviousVersion() If this ScoreSet replaces an older ScoreSet, this function returns the accession of that older ScoreSet.
- getNextVersion() If this ScoreSet was replaced by newer ScoreSet, this function returns the accession of that newer ScoreSet in versioning history. To obtain the most recent version, use `getCurrentVersion()`.
- getCountColumns() returns the column names in the count table for this ScoreSet.
- getScoreColumns() returns the column names in the score table for this ScoreSet.
- getMetaDataColumns() returns the column names in the metadata table for this ScoreSet.
- getVariantCount() returns the number of variants in this scoreset, i.e. the number of rows to be expected in the scores and counts tables.
- getExperiment() returns the URN of the experiment record to which this scoreset belongs.

Value

a new R-API MaveDB ScoreSet object.

Examples

```
## Not run:
mave <- new.rapimave()
set1 <- mave$getScoreSet("urn:mavedb:00000001-a-1")
scoreColNames <- set1$getScoreColumns()

## End(Not run)
```

`new.target` *New R-API MaveDB Target*

Description

Internal constructor that creates an immutable new Target object. This function is not exported and should not be called outside of the rapimave package itself. Target objects are generated by the getTarget() method of a scoreset object (which itself is generated using the `getAllScoreSets()` and `getScoreSet()` methods of a rapimave object). However, this section explains the functions that are available for these objects.

Usage

```
new.target(data)
```

Details

A ScoreSet object offers the following getter functions:

- getName() returns the name of the target
- getSequence() returns wildtype sequence of the target
- getXrefUniprot() returns a Xref object for Uniprot
- getXrefEnsembl() returns a Xref object for Ensembl
- getXrefRefseq() returns a Xref object for Refseq
- getReferenceMaps() returns a list of reference map objects that describe how this target maps to different reference genomes.
- getScoreset() retunrs the URN of the scoreset to which this target belongs.

Value

a new R-API MaveDB Target object.

`new.user` *New R-API MaveDB User*

Description

Internal constructor that creates an immutable new user object. This function is not exported and should not be called outside of the rapimave package itself. User objects are generated by the `getAllUsers()` and `getUser()` methods of a rapimave object (which itself is generated using the `new.rapimave()` constructor). However, this section explains the functions that are available for these objects.

Usage

```
new.user(data)
```

Details

A user object offers the following getter functions:

- getUsername() return the username.
- getFirstName() return the user's first name.
- getLastName() return the user's last name.
- getDisplayName() return the user's preferred display name.
- getExperimentSets() return the ExperimentSets attributed to the user.
- getExperiments() return the Experiments attributed to the user.
- getScoreSets() return the ScoreSets attributed to the user.

Value

a new R-API MaveDB user object.

Examples

```
## Not run:
mave <- new.rapimave()
user <- mave$getUser("0000-0003-1474-605X")
cat(user$getFirstName(),user$getLastName())

## End(Not run)
```

---

new.xref *New R-API MaveDB cross-reference*

Description

Internal constructor that creates an immutable new Xref object. This function is not exported and should not be called outside of the rapimave package itself. Xref objects are generated by various methods of a rapimave object (which itself is generated using the `new.rapimave()` constructor). However, this section explains the functions that are available for these objects.

Usage

```
new.xref(data)
```

Details

A ScoreSet object offers the following getter functions:

- getID() returns the Identifier or Accession of this cross-reference
- getURL() returns the database URL
- getDB() returns the database name
- getDBVersion() returns the database version

Value

a new R-API MaveDB Xref object.

print.rapimave *Print R-API MaveDB object*

Description

Prints a human-readable summary of a R-API MaveDB object.

Usage

```
## S3 method for class 'rapimave'
print(obj)
```

Arguments

obj	the object to print

Details

Prints a list of available functions for the object.

Examples

```
## Not run:
mave <- new.rapimave()
print(mave)

## End(Not run)
```

print.rapimaveExperiment *Print R-API MaveDB Experiment*

Description

Prints a human-readable summary of a R-API MaveDB Experiment object:

Usage

```
## S3 method for class 'rapimaveExperiment'
print(obj)
```

Arguments

obj	the Experiment object to print

Examples

```
## Not run:
mave <- new.rapimave()
print(mave$getExperiment("urn:mavedb:00000001-a"))

## End(Not run)
```

print.rapimaveExpSet *Print R-API MaveDB ExperimentSet*

Description

Prints a human-readable summary of a R-API MaveDB ExperimentSet object:

Usage

```
## S3 method for class 'rapimaveExpSet'
print(obj)
```

Arguments

obj	the ExperimentSet object to print

Examples

```
## Not run:
mave <- new.rapimave()
print(mave$getExperimentSet("urn:mavedb:00000001"))

## End(Not run)
```

print.rapimaveGenome *Print R-API MaveDB Genome object*

Description

Prints a human-readable summary of a R-API MaveDB genome object:

Usage

```
## S3 method for class 'rapimaveGenome'
print(obj)
```

Arguments

obj	the object to print

print.rapimaveRefmap *Print R-API MaveDB reference map object*

Description

Prints a human-readable summary of a R-API MaveDB reference map object:

Usage

```
## S3 method for class 'rapimaveRefmap'
print(obj)
```

Arguments

obj	the object to print

print.rapimaveScoreSet *Print R-API MaveDB ScoreSet*

Description

Prints a human-readable summary of a R-API MaveDB ScoreSet object:

Usage

```
## S3 method for class 'rapimaveScoreSet'
print(obj)
```

Arguments

obj	the ScoreSet object to print

Examples

```
## Not run:
mave <- new.rapimave()
print(mave$getScoreSet("SCS000001A.2"))

## End(Not run)
```

`print.rapimaveTarget` *Print R-API MaveDB target object*

Description

Prints a human-readable summary of a R-API MaveDB target object:

Usage

```
## S3 method for class 'rapimaveTarget'
print(obj)
```

Arguments

`obj`	the object to print

`print.rapimaveUser` *Print R-API MaveDB User*

Description

Prints a human-readable summary of a R-API MaveDB User object:

Usage

```
## S3 method for class 'rapimaveUser'
print(obj)
```

Arguments

`obj`	the User object to print

Examples

```
## Not run:
mave <- new.rapimave()
print(mave$getUser("0000-0003-1474-605X"))

## End(Not run)
```

print.rapimaveXref *Print R-API MaveDB cross-reference*

Description

Prints a human-readable summary of a R-API MaveDB cross-reference object:

Usage

```
## S3 method for class 'rapimaveXref'
print(obj)
```

Arguments

obj	the object to print

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