

Package ‘metagenomeFeatures’

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Title Exploration of marker-gene sequence taxonomic annotations

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Description metagenomeFeatures was developed for use in exploring the taxonomic annotations for a marker-gene metagenomic sequence dataset. The package can be used to explore the taxonomic composition of a marker-gene database or annotated sequences from a marker-gene metagenome experiment.

Depends R (>= 3.5), Biobase (>= 2.17.8)

License Artistic-2.0

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'DNAStringSetOrNull-class.R' 'mgDb-class.R'
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'mgDb_method_select.R' 'mgDb_method_annotateFeatures.R'
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VignetteBuilder knitr

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annotateFeatures	<i>Annotating metagenome data with taxonomic information</i>
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Description

This method is used to create a [mgFeatures](#) class object

Usage

```
annotateFeatures(mgdb, ...)

## S4 method for signature 'MgDb'
annotateFeatures(mgdb, query)
```

Arguments

mgdb	MgDb class object
...	additional arguments passed to select function
query	A data frame with experimental data to annotate with taxonomic information, must include column named "Key" with database ids. Or a vector of database Keys of entries to include in mgFeatures-class object.

Value

mgFeatures-class object

Examples

```
## MgDb with mock community ids
gg85 <- get_gg13.8_85MgDb()
## generating mgFeatures object
data(mock_query_df)
mock_mgF <- annotateFeatures(gg85, mock_query_df)
```

get_gg13.8_85MgDb	<i>MgDb-class object with Greengenes Database Version 13.8 85% OTUs</i>
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Description

Example [MgDb-class](#) object with Greengenes Database Version 13.8 85% OTUs.

Usage

```
get_gg13.8_85MgDb()
```

Value

MgDb-class object

Examples

```
get_gg13.8_85MgDb()
```

MgDb-accessor	<i>MgDb-class accessors</i>
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Description

Accessors for [MgDb-class](#) object slots. mgDb_seq - sequence slot, mgDb_taxa - taxa slot, mgDb_tree - phylogenetic tree slot, and mgDb_meta - metadata slot.

Usage

```
mgDb_tree(mgdb)
```

```
mgDb_seq(mgdb)
```

```
mgDb_taxa(mgdb)
```

```
mgDb_meta(mgdb)
```

Arguments

mgdb MgDb-class object.

Value

appropriate class object for the slot accessed

Examples

```
gg85 <- get_gg13.8_85MgDb()
mgDb_seq(gg85)
mgDb_taxa(gg85)
mgDb_tree(gg85)
mgDb_meta(gg85)
```

MgDb-class

Metagenome Database class

Description

The MgDb-class object contains sequence, taxonomic data, and a phylogenetic tree (optional) for a 16S rRNA taxonomic database, see the **greengenes13.5MgDb** package as an example database. The `get_gg13.8_85MgDb()` function in **metagenomeFeatures** exports a small subset of the database in the **greengenes13.5MgDb** annotation package as an example MgDb-class object.

Value

MgDb-class object

Slots

`seq` database reference sequences
`tree` reference phylogenetic tree
`taxa` database taxonomy
`metadata` associated metadata for the database

Note

Currently the only database with a MgDb package is the **Greengenes database** (version 13.5), additional packages are planned.

Examples

```
# example MgDb-class object, Greengenes 13.8 85% OTUs database.
gg85 <- get_gg13.8_85MgDb()
```

MgDb-methods

Display summary of MgDb-class object

Description

Display summary of MgDb-class object

Usage

```
## S4 method for signature 'MgDb'  
show(object)
```

Arguments

object MgDb-class object

Value

MgDb-class summary

Examples

```
gg85 <- get_gg13.8_85MgDb()  
show(gg85)
```

mgDb_select

Querying MgDb objects

Description

Function for querying [MgDb-class](#) class objects, user defines the taxonomic levels (keytype) and a vector of taxonomic names (keys) being selected. If specific database ids are being selected for use keytype="Keys". Additionally, users can specify whether they want only the taxonomic and sequence data, or both.

Usage

```
mgDb_select(mgdb, type, ...)  
  
## S4 method for signature 'MgDb'  
mgDb_select(mgdb, type, keys = NULL, keytype = NULL,  
          columns = "all")
```

Arguments

mgdb	MgDb class object
type	either "taxa", "seq", "tree", "all" or a character vector of types. "taxa", "seq", and "tree" only query the reference taxonomy, sequences, and phylogenetic tree respectively. "all" queries the reference taxonomy, sequence, and phylogenetic tree.
...	additional arguments passed to select function
keys	specific taxonomic groups to select for
keytype	taxonomic level of keys
columns	keytypes in taxonomy database to return, all by default

Value

returned object depends on type: 'taxa' - dataframe with taxa information; 'seq' - DNAStrngSet with sequence data; 'tree' - phylogenetic tree of class phylo; 'all' - list with the dataframe, DNAS-trngSet, and phylo.

Examples

```
gg85 <- get_gg13.8_85MgDb()
# select taxa only
mgDb_select(gg85, type = "taxa",
            keys = c("Vibrionaceae", "Enterobacteriaceae"),
            keytype = "Family")

# select seq only
mgDb_select(gg85, type = "seq",
            keys = c("Vibrionaceae", "Enterobacteriaceae"),
            keytype = "Family")

# select all taxa, seq, and tree
mgDb_select(gg85, type = "all",
            keys = c("Vibrionaceae", "Enterobacteriaceae"),
            keytype = "Family")
```

mgFeatures-accessors *mgFeatures accessors*

Description

Accessors for [mgFeatures](#)-class object slots.

mgF_seq - refDbSeq slot,
mgF_taxa - taxa slot,
mgF_tree - phylogenetic tree slot, and
mgF_meta - metadata slot.

Usage

```
mgF_tree(mgF)
```

```
mgF_seq(mgF)
```

```
mgF_taxa(mgF)
```

```
mgF_meta(mgF)
```

Arguments

mgF mgFeatures-class object.

Value

appropriate class object for the slot accessed

Examples

```
data(mock_mgF)
mgF_seq(mock_mgF)
mgF_taxa(mock_mgF)
mgF_tree(mock_mgF)
mgF_meta(mock_mgF)
```

mgFeatures-class	<i>Class mgFeature</i>
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Description

Class defines taxonomic annotation and reference sequence data for classified OTUs. The class extends the [DataFrame](#) class with a slot with a subset of the reference database sequences and phylogenetic tree for taxonomically classified OTUs, along with an additional slot for metadata including information on the database source.

Usage

```
mgFeatures(taxa = data.frame(), tree = NULL, seq = NULL, metadata)
```

Arguments

taxa	a DataFrame-class or object that can be coerced into a DataFrame
tree	a phylo-class object with phylogenetic tree
seq	DNAStrngSet-object with feature sequences
metadata	a list

Value

mgFeature class object
mgFeatures-class object

Examples

```
data(mock_mgF)
mgFeatures(taxa = data.frame(), metadata = list())
```

mgFeatures-methods *mgFeatures-class subset method*

Description

mgFeatures-class subset method

Usage

```
## S4 method for signature 'mgFeatures'
x[i, j, ..., drop = FALSE]
```

Arguments

x	Object to extract elements
i, j	element indices to extract or replace
...	other parameters to subset function
drop	default to FALSE

mock_mgF *Example mgFeatures class object*

Description

Example [mgFeatures-class](#) object generated using the [annotateFeatures MgDb-class](#) method. The dataset contains the OTU ids and Greengenes database version 13.5 ids. Specifically, the OTU centers came from a mock community dataset from the study Bokulich et al. 2013, the OTU ids were extracted from a biom file downloaded from QIITA (<https://qiita.ucsd.edu>).

Usage

```
mock_mgF
```

Format

```
mgFeatures
```

Details

Bokulich, Nicholas A., et al. "Quality-filtering vastly improves diversity estimates from Illumina amplicon sequencing." *Nature methods* 10.1 (2013): 57-59.

Source

<https://qiita.ucsd.edu>

Examples

```
data(mock_mgF)
```

mock_query_df	<i>Example Query Data Frame</i>
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Description

Example query_df for use in generating a `mgFeatures-class` object using the `annotateFeatures` `MgDb-class` method. The dataset contains the OTU ids and Greengenes database version 13.5 ids. Specifically, the OTU centers came from a mock community dataset from the study Bokulich et al. 2013, the OTU ids were extracted from a biom file downloaded from QIITA (<https://qiita.ucsd.edu>).

Usage

```
mock_query_df
```

Format

```
data.frame
```

Details

Bokulich, Nicholas A., et al. "Quality-filtering vastly improves diversity estimates from Illumina amplicon sequencing." *Nature methods* 10.1 (2013): 57-59.

Source

<https://qiita.ucsd.edu>

Examples

```
data(mock_query_df)
```

newMgDb	<i>MgDb</i>
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Description

```
MgDb
```

Usage

```
newMgDb(db_file, tree, metadata)
```

Arguments

db_file	SQLite filename with database taxonomy and sequence data
tree	newick filename with database tree data
metadata	list with database metadata

Value

MbDb class object

Examples

```

metadata_file <- system.file("extdata", 'gg13.8_85_metadata.RData',
  package = "metagenomeFeatures")
load(metadata_file)

gg_db_file <- system.file("extdata", 'gg13.8_85.sqlite',
  package = "metagenomeFeatures")

gg_tree_file <- system.file("extdata", "gg13.8_85.tre",
  package = "metagenomeFeatures")

## Creating a new MgDb class object with gg13.8_85 data
newMgDb(db_file = gg_db_file,
  tree = gg_tree_file,
  metadata = metadata)

```

qiita_study_94_gg_ids *QIITA Dataset For this vignette we are using 16S rRNA data from Rousk et al. 2010, a soil microbiome study, <https://qiita.ucsd.edu/study/description/94>. A BIOM and qiime mapping file for the study can be obtained from QIITA. A vector of Green-genes for the study cluster centers is included in this package for use in this vignette.*

Description

data(qiita_study_94_gg_ids)

Usage

qiita_study_94_gg_ids

Format

An object of class character of length 2305.

taxa_ *MgDb-class Taxa slot helper functions*

Description

Helper functions for for **MgDb**-class taxa slot. taxa_columns - taxa slot column names, taxa_keytypes - taxa slot keytypes (values used with taxa_columns and mgDb_select functions), and taxa_keys - database values for a specific keytype.

Usage

```
taxa_keys(mgdb, keytype)

## S4 method for signature 'MgDb'
taxa_keys(mgdb, keytype)

taxa_columns(mgdb)

## S4 method for signature 'MgDb'
taxa_columns(mgdb)

taxa_keytypes(mgdb)

## S4 method for signature 'MgDb'
taxa_keytypes(mgdb)
```

Arguments

mgdb	MgDb-class object.
keytype	character string specifying keys to return

Value

appropriate class object for the slot accessed

Examples

```
gg85 <- get_gg13.8_85MgDb()
taxa_columns(gg85)
taxa_keytypes(gg85)
taxa_keys(gg85, keytype = "Phylum")
```

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