Package ‘yatah’

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Title Yet Another TAxonomy Handler

Version 0.2.1

Description Provides functions to manage taxonomy when lineages are described with strings and ranks separated with special patterns like ``|*__'' or ``;*__''.

License GPL-3

URL `https://abichat.github.io/yatah/`, `https://github.com/abichat/yatah/`

BugReports `https://github.com/abichat/yatah/issues`

Depends R (>= 2.10)

Imports ape, purrr, stats, stringr

Suggests dplyr, knitr, rmarkdown, spelling, testthat (>= 2.1.0)

VignetteBuilder knitr

Encoding UTF-8

Language en-US

LazyData true

RoxygenNote 7.2.1

NeedsCompilation no

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Repository CRAN

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R topics documented:

`abundances` *Abundance table for 199 samples.*

Description

A dataset containing the abundances of 1585 lineages among 199 patients.

Usage

```
abundances
```

Format

A data.frame with 1585 rows and 200 variables:

lineages lineage (string)

XXX abundance of each lineage in the sample XXX (double)

Source

Zeller et al., 2014 (doi: 10.15252/msb.20145645), Pasolli et al., 2017 (doi: 10.1038/nmeth.4468).

Examples

```
dim(abundances)
abundances[1:5, 1:7]
```

`all_clades` *Extract all clades present in the lineages*

Description

Extract all clades present in the lineages

Usage

```
all_clades(lineage, simplify = TRUE)
```

Arguments

`lineage`	string. Vector of lineages.
`simplify`	logical. Should the output be a vector or a dataframe?

Details

If a clade correspond to different ranks (e.g. Actinobacteria is both a phylum and a clade), it will be displayed only one time when `simplify` is set to `TRUE`. It is also the case for different clades with same name and same rank when `simplify` is set to `FALSE`.

Value

The clades present in the lineage. Vector of ordered strings or data.frame.

Examples

```
lineage1 <- "k__Bacteria|p__Verrucomicrobia|c__Verrucomicrobiae"
lineage2 <- "k__Bacteria|p__Firmicutes|c__Clostridia"
lineage3 <- "k__Bacteria|p__Actinobacteria|c__Actinobacteria"
all_clades(c(lineage1, lineage2, lineage3))
all_clades(c(lineage1, lineage2, lineage3), simplify = FALSE)
```

`is_clade` *Test if a lineage belongs to a clade*

Description

Test if a lineage belongs to a clade

Usage

```
is_clade(
  lineage,
  clade,
 rank = c(".", "kingdom", "phylum", "class", "order", "family", "genus", "species",
    "strain")
)
```

Arguments

`lineage`	string. Vector of lineages.
`clade`	string.
`rank`	string. One of `c("kingdom", "phylum", "class","order", "family", "genus", "species", "strain")` with partial matching.

Details

If `rank` is set to `.`, clade is looked for among all ranks.

Value

logical.

Examples

```
lineage1 <- "k__Bacteria|p__Verrucomicrobia|c__Verrucomicrobiae"
lineage2 <- "k__Bacteria|p__Firmicutes|c__Clostridia"
is_clade(c(lineage1, lineage2), clade = "Verrucomicrobia", rank = "phylum")
is_clade(c(lineage1, lineage2), clade = "Clostridia")
```

`is_lineage` *Test if a string is a lineage*

Description

Test if a string is a lineage

Usage

```
is_lineage(string)
```

Arguments

`string`	string to be tested as lineage.

Details

Alphanumeric character, hyphen, dots, square brackets and non-consecutive underscores are allowed in clades names.

Value

A logical.

Examples

```
is_lineage("k__Bacteria|p__Firmicutes|c__Clostridia|o__Clostridiales")
```

`is_rank` *Test if a lineage goes down to a specified rank*

Description

Test if a lineage goes down to a specified rank

Usage

```
is_rank(
  lineage,
  rank = c("kingdom", "phylum", "class", "order", "family", "genus", "species", "strain")
)
```

Arguments

`lineage`	string. Vector of lineages.
`rank`	string. One of `c("kingdom", "phylum", "class","order", "family", "genus", "species", "strain")` with partial matching.

Value

logical.

Examples

```
lineage1 <- "k__Bacteria|p__Verrucomicrobia|c__Verrucomicrobiae"
lineage2 <- "k__Bacteria|p__Firmicutes|c__Clostridia"
is_rank(c(lineage1, lineage2), "class")
is_rank(c(lineage1, lineage2), "order")
```

`last_clade` *Extract the last clade of a lineage*

Description

Extract the last clade of a lineage

Usage

```
last_clade(lineage, same = TRUE)
```

Arguments

`lineage`	string. Vector of lineages.
`same`	logical. Does the lineage have the same depth? Default to TRUE.

Value

A string. The last clades of the given lineages.

Examples

```
lineage1 <- "k__Bacteria|p__Verrucomicrobia|c__Verrucomicrobiae"
lineage2 <- "k__Bacteria|p__Firmicutes|c__Clostridia"
last_clade(c(lineage1, lineage2))
```

`last_rank` *Extract the last rank of a lineage*

Description

Extract the last rank of a lineage

Usage

```
last_rank(lineage, same = TRUE)
```

Arguments

`lineage`	string. Vector of lineages.
`same`	logical. Does the lineage have the same depth? Default to TRUE.

Value

A string. The last rank of the given lineages.

Examples

```
lineage1 <- "k__Bacteria|p__Verrucomicrobia|c__Verrucomicrobiae"
lineage2 <- "k__Bacteria|p__Firmicutes|c__Clostridia"
last_rank(c(lineage1, lineage2))
```

`taxtable` *Taxonomic table*

Description

Compute taxonomic table from lineages.

Usage

```
taxtable(lineage)
```

Arguments

`lineage`	string. Vector of lineages.

Details

Duplicated lineages are removed.

Value

A data.frame with columns corresponding to different ranks.

Examples

```
lineage1 <- "k__Bacteria|p__Verrucomicrobia|c__Verrucomicrobiae"
lineage2 <- "k__Bacteria|p__Firmicutes|c__Clostridia"
lineage3 <- "k__Bacteria|p__Firmicutes|c__Bacilli"
taxtable(c(lineage1, lineage2, lineage3))
```

`taxtree` *Taxonomic tree*

Description

Compute taxonomic tree from taxonomic table.

Usage

```
taxtree(table, collapse = TRUE, lineage_length = 1, root = "")
```

Arguments

`table`	dataframe.
`collapse`	logical. Should node with one child be vanished? Default to TRUE.
`lineage_length`	double. Lineage length from the root to the leaves. Default to 1.
`root`	character. Name of the root if there is no natural root.

Value

A phylo object.

Examples

```
lineage1 <- "k__Bacteria|p__Verrucomicrobia|c__Verrucomicrobiae"
lineage2 <- "k__Bacteria|p__Firmicutes|c__Clostridia"
lineage3 <- "k__Bacteria|p__Firmicutes|c__Bacilli"
table <- taxtable(c(lineage1, lineage2, lineage3))
taxtree(table)
```

`trim_common` *Trim lineages until the shallowest common rank.*

Description

Trim lineages until the shallowest common rank.

Usage

```
trim_common(lineage, remove_void = TRUE, only_tail = TRUE)
```

Arguments

`lineage`	string. Vector of lineages.
`remove_void`	Should void ranks be removed? Default to `TRUE`.
`only_tail`	Logical to be passed to `trim_void()`. Used only if `remove_void` is set to `TRUE`.

Value

The trimmed lineages, with same depth.

Examples

```
lineage1 <- "k__Bacteria|p__Verrucomicrobia|c__Verrucomicrobiae"
lineage2 <- "k__Bacteria|p__Firmicutes"
lineage3 <- "k__Bacteria|p__|c__Clostridia"
trim_common(c(lineage1, lineage2, lineage3), remove_void = FALSE)
trim_common(c(lineage1, lineage2, lineage3), only_tail = FALSE)
```

`trim_rank` *Trim lineages until a specified rank*

Description

Trim lineages until a specified rank

Usage

```
trim_rank(
  lineage,
 rank = c("kingdom", "phylum", "class", "order", "family", "genus", "species", "strain"),
  same = TRUE
)
```

Arguments

`lineage`	string. Vector of lineages.
`rank`	string. One of `c("kingdom", "phylum", "class","order", "family", "genus", "species", "strain")` with partial matching.
`same`	logical. Does the lineage have the same depth? Default to TRUE.

Details

Returns `NA` if a lineage is not as deep as the specified rank.

Value

The trimmed lineages. Depth could be different among them.

Examples

```
lineage1 <- "k__Bacteria|p__Verrucomicrobia|c__Verrucomicrobiae"
lineage2 <- "k__Bacteria|p__Firmicutes|c__Clostridia"
trim_rank(c(lineage1, lineage2), rank = "phylum")
trim_rank(c(lineage1, lineage2), rank = "genus")
```

`trim_void` *Trim void ranks in lineages*

Description

Trim void ranks in lineages

Usage

```
trim_void(lineage, same = TRUE, only_tail = FALSE)
```

Arguments

`lineage`	string. Vector of lineages.
`same`	logical. Does the lineage have the same depth? Default to TRUE.
`only_tail`	Logical. If `FALSE` (default), void ranks amid lineages and subranks are removed. If `TRUE`, only final void ranks are removed.

Details

If there is a void rank amid a lineage, deeper ranks will be removed. See the example with `lineage3`.

Value

The trimmed lineages. Depth could be different among them.

Examples

```
lineage1 <- "k__Bacteria|p__Verrucomicrobia|c__Verrucomicrobiae|o__|f__"
lineage2 <- "k__Bacteria|p__Firmicutes|c__"
lineage3 <- "k__Bacteria|p__|c__Verrucomicrobiae|o__|f__"
trim_void(c(lineage1, lineage2, lineage3), same = FALSE)
trim_void(c(lineage1, lineage2, lineage3), same = FALSE, only_tail = TRUE)
```

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