

Package ‘genomes’

June 26, 2025

Type Package
Title Genome sequencing project metadata
Version 3.39.0
Date 2015-12-21
Author Chris Stubben
Maintainer Chris Stubben <stubben@lanl.gov>
License GPL-3
Depends readr, curl
biocViews Annotation, Genetics
Description Download genome and assembly reports from NCBI
git_url <https://git.bioconductor.org/packages/genomes>
git_branch devel
git_last_commit 52cdcc6
git_last_commit_date 2025-04-15
Repository Bioconductor 3.22
Date/Publication 2025-06-26

Contents

genus	1
reports	2
species	3
Index	4

genus	<i>Extract the genus name</i>
-------	-------------------------------

Description

Extracts the genus name from a scientific name

Usage

genus(x)

Arguments

x A vector of scientific names

Details

Removes single quotes, brackets and candidate qualifiers.

Value

A vector of genus names

Author(s)

Chris Stubben

See Also

[species](#)

Examples

```
genus("[Bacillus] selenitireducens")
```

reports

Genome and assembly reports

Description

Genome and assembly reports from the NCBI genomes FTP

Usage

```
reports(file, assembly = FALSE, ...)
```

Arguments

file file name, if missing then the files in the FTP directory are listed
assembly use ASSEMBLY_REPORTS directory, default is GENOME_REPORTS
... additional options passed to read_delim

Details

Uses read_delim in the readr package to read genome or assembly reports in the genomes FTP

Value

A list of files if file name is missing, otherwise a data.frame with class c("tbl_df", "tbl", "data.frame").
If dplyr is loaded, then printing will return the first ten rows and not the first 10,000.

Author(s)

Chris Stubben

References

See ftp://ftp.ncbi.nih.gov/genomes/GENOME_REPORTS and ftp://ftp.ncbi.nih.gov/genomes/ASSEMBLY_REPORTS

Examples

```
reports()
## Not run:
proks <- reports("prokaryotes.txt")

## End(Not run)
```

species

Extract the species name

Description

Extracts the species name from a scientific name

Usage

```
species(x)
```

Arguments

x A vector of scientific names

Details

Removes single quotes, brackets and candidate qualifiers.

Value

A vector of species names

Author(s)

Chris Stubben

See Also

[genus](#)

Examples

```
species("Candidatus Carsonella ruddii PV")
```

Index

* **methods**

- genus, [1](#)
- reports, [2](#)
- species, [3](#)

genus, [1](#), [3](#)

reports, [2](#)

species, [2](#), [3](#)