Package ‘genomes’

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Type Package

Title Genome sequencing project metadata

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biocViews Annotation, Genetics

Description Download genome and assembly reports from NCBI

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genus *Extract the genus name*

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")
```

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