

Package ‘epi2me2r’

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Type Package

Title Process Nanopore EPI2ME Output for Use in R

Version 0.1.0

Description The functions in this package take WIMP and ARMA data files generated by Oxford Nanopore EPI2ME workflows, read them, clean them, and prepare them for downstream analysis. This package was written by United States federal government employees in their official capacity. Therefore, it is not protected by copyright and is in the public domain.

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Encoding UTF-8

LazyData true

RoxygenNote 7.1.2

BugReports <https://github.com/mweinroth/epi2me2r/issues>

Imports data.table, taxonomizr, phyloseq, Biobase, metagenomeSeq

Suggests rmarkdown, knitr, reshape2, testthat (>= 3.0.0)

VignetteBuilder knitr

Config/testthat/edition 3

URL <https://mweinroth.github.io/epi2me2r/>

Depends R (>= 3.5.0)

NeedsCompilation no

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amr_raw_to_metagenomeseq

Raw AMR files plus metadata to phyloseq object

Description

Given directory and metadata, make phyloseq object. [metagenomeSeq](#) package required.

Arguments

path.to.amr.files	path to folder containing raw CSV files from ARMA CARD analysis
metadata	data.table of metadata with "filename" and "barcode" columns required
coveragenumber	Minimum percentage of a gene that must be covered. Range from 0 to 99, default = 80
keepSNP	TRUE or FALSE: whether to keep AMR gene conferred by one SNP change, default = FALSE

Value

metagenomeSeq object for downstream analysis

See Also

[metagenomeSeq](#)

Examples

```
## Not run:
amr_raw_to_phyloseq(path.to.amr.files = path/to/amr.count.table,
  metadata = metadata, coveragenumber = 80, keepSNP = FALSE)
```

```
## End(Not run)
```

amr_raw_to_phyloseq *Raw AMR files plus metadata to phyloseq object*

Description

given directory and metadata make phyloseq object [phyloseq](#) package required.

Arguments

path.to.amr.files	path to data of raw csv files from ARMA CARD analysis
metdata	data.table of metadata with "arma_filename" and "arma_barcode" columns required
coveragenumber	Minimum percentage of a gene that must be covered. Range from 0 to 99, default = 80
keepSNP	TRUE or FALSE: whether to keep AMR gene conferred by one SNP change, default = FALSE

Value

phyloseq object for downstream analysis

See Also

[phyloseq](#)

Examples

```
## Not run:  
amr_raw_to_phyloseq(path.to.amr.files = path/to/amr.count.table,  
metadata = metadata, coveragenumber = 80, keepSNP = FALSE)  
  
## End(Not run)
```

amr_read_taxonomy *assign taxonomy for phylogenetic and AMR for each read*

Description

Given raw data for AMR and WIMP, provides full AMR and taxon info for those reads that assign to both

Arguments

path.to.wimp.files
 path to folder containing raw CSV files from WIMP analysis

path.to.amr.files
 path to folder containing raw CSV files from ARMA analysis

coveragenumber Minimum percentage of a gene that must be covered. Range from 0 to 99,
 default = 80

Value

data.frame with double classified reads

Examples

```
## Not run:
amr_read_taxonomy(path.to.wimp.files = "path/to/wimp_files",
path.to.amr.files = "path/to/amr_files", coveragenumber = 80)

## End(Not run)
```

CARD_taxonomy

CARD 3.1.4 and 1.1.3 aro_index hand curated and combine

Description

A dataset with information on CARD genes in the 3.1.4 and 1.13 data releases The variables are as follows:

Usage

```
data(CARD_taxonomy)
```

Format

A data frame with 3385 rows and 13 variables

Details

- ARO Accession. ARO Accession (3000005–3005385)
- CARDversion. If the data came from 3.1.4 or 1.1.3 (3.1.3, hand-added 1.1.3)
- CVTERMID. CV TERM ID (36014–43745)
- Model Sequence ID.
- Model ID.
- Model Name.
- ARO Name.

- Protein Accession.
- DNA Accession.
- AMR Gene Family.
- Drug Class.
- Resistance Mechanism.
- mutation-associated. if the gene is mutation associated

Source

<https://card.mcmaster.ca/download>

epi2me2r	<i>epi2me2r</i> .
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Description

data for CARD db

`generate_amr_taxonomy` *Generates a taxonomy file for AMR count table*

Description

Generates a taxonomy file for AMR count table

Arguments

`amr.count.table` count of AMR genes with CVTERMID in the first row and samples on columns

`verbose` TRUE or FALSE: whether to keep all columns of AMR gene information or not. Default FALSE.

Value

data table of taxonomy of AMR genes in count table

Examples

```
## Not run:
generate_amr_taxonomy(amr.count.table = amr.count.table, verbose = FALSE)

## End(Not run)
```

```
generate_wimp_taxonomy
```

Generates a taxonomy file for WIMP court table using taxonomizr

Description

Generates a taxonomy file for WIMP court table using taxonomizr

Usage

```
generate_wimp_taxonomy(wimp.count.table)
```

Arguments

```
wimp.count.table
```

count of WIMP genes with taxID in the first row and samples on columns

Value

data table of taxonomy of WIMP genes in count table

Examples

```
## Not run:
generate_wimp_taxonomy(wimp.count.table = wimp.count.table)

## End(Not run)
```

```
read_in_amr_files
```

Convert raw AMR CSV files to data table

Description

Convert raw AMR CSV files to data table

Arguments

```
path.to.amr.files
```

path to folder containing raw CSV files from ARMA CARD analysis

```
coveragenumber
```

Minimum percentage of a gene that must be covered. Range from 0 to 99, default = 80

```
keepSNP
```

TRUE or FALSE: whether to keep AMR gene conferred by one SNP change, default = FALSE

Value

data.table of AMR genes at a specific coverage with or without SNP associated

Examples

```
## Not run:  
read_in_amr_files(path.to.amr.files = "~/Desktop/my.files/",  
coveragenumber = 80, keepSNP = FALSE)  
  
## End(Not run)
```

read_in_wimp_files *Convert raw WIMP CSV files to data table*

Description

Convert raw WIMP CSV files to data table

Usage

```
read_in_wimp_files(path.to.wimp.files)
```

Arguments

path.to.wimp.files
File path to folder containing raw WIMP files

Value

data.table of mb genes at a specific coverage

Examples

```
## Not run:  
read_in_wimp_files(path.to.wimp.files="~/Desktop/my.files")  
  
## End(Not run)
```

wimp_raw_to_metagenomeseq
Raw WIMP files plus metadata to metagenomeseq object

Description

Given WIMP directory and metadata, make phyloseq object. [metagenomeSeq](#) package required.

Usage

```
wimp_raw_to_metagenomeseq(  
  path.to.wimp.files,  
  metadata,  
  keep.unclassified = FALSE,  
  keep.human = FALSE  
)
```

Arguments

path.to.wimp.files	path to data of raw CSV files from WIMP analysis
metadata	dataframe of metadata with "filename" and "barcode" columns required
keep.unclassified	TRUE or FALSE: whether to keep reads that do not classify below phylum, default = FALSE
keep.human	TRUE or FALSE: whether to keep reads that are classified as human, default = FALSE

Value

metagenomeseq object for downstream analysis with WIMP data

See Also

[metagenomeSeq](#)

Examples

```
## Not run:  
wimp_raw_to_metagenomeseq(path.to.wimp.files = path/to/wimpfiles,  
  metadata = metadata, keep.unclassified = FALSE, keep.human = FALSE)  
  
## End(Not run)
```

wimp_raw_to_phyloseq *Raw WIMP files plus metadata to phyloseq object*

Description

Given wimp directory and metadata, make phyloseq object. [phyloseq](#) package required.

Usage

```
wimp_raw_to_phyloseq(  
  path.to.wimp.files,  
  metadata,  
  keep.unclassified = FALSE,  
  keep.human = FALSE  
)
```

Arguments

<code>path.to.wimp.files</code>	path to data of raw csv files from WIMP analysis
<code>metadata</code>	dataframe of metadata with "filename" and "barcode" columns required
<code>keep.unclassified</code>	TRUE or FALSE: whether to keep reads that do not classify below phylum, default = FALSE
<code>keep.human</code>	TRUE or FALSE: whether to keep reads that are classified as human, default = FALSE

Value

phyloseq object for downstream analysis with WIMP data

See Also

[phyloseq](#)

Examples

```
## Not run:  
wimp_raw_to_phyloseq(path.to.wimp.files = path/to/wimpfiles,  
  metadata = metadata, keep.unclassified = FALSE, keep.human = FALSE)  
  
## End(Not run)
```

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