Package 'HMP2Data'

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Title 16s rRNA sequencing data from the Human Microbiome Project 2

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Description HMP2Data is a Bioconductor package of the Human Microbiome Project 2 (HMP2) 16S rRNA sequencing data. Processed data is provided as phyloseq, SummarizedExperiment, and MultiAssayExperiment class objects. Individual matrices and data.frames used for building these S4 class objects are also provided in the package.

Depends R (>= 3.6.0)

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Encoding UTF-8

LazyData false

BugReports https://github.com/jstansfield0/HMP2Data/issues

URL https://github.com/jstansfield0/HMP2Data

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Contents

IBD16S . . . 2
IBD16S_mtx . . . 3
IBD16S_samp . . . 3
IBD16S_tax . . . 4
momspi16S . . . 4
momspi16S_mtx . . . 5
momspi16S_samp . . . 5
momspi16S_tax . . . 6
momspiCytokines . . . 6
momspiCyto_mtx . . . 7
momspiCyto_samp . . . 7
momspiMultiAssay . . . 8
patient_table . . . 9
T2D16S . . . 9
T2D16S_mtx . . . 10
T2D16S_samp . . . 11
T2D16S_tax . . . 11
table_two . . . 11
visit_table . . . 12

Index **13**

`IBD16S` *Create HMP2 16S sequencing data for Inflammatory Bowel Disease (IBD) phyloseq object*

Description

The HMP2 study gathered data on the microbiome for patients with different disease. This dataset contains 16S rRNA data for 196 patients with IBD over multiple visits.

Usage

```
IBD16S()
```

Format

A phyloseq object with 982 taxa and 178 samples.

OTU Table: A counts matrix for the rRNA-seq results.

Sample Data:
Project Name of the project
sample_id Sample identifier
subject_id Subject identifier See colnames(sample_data(IBD16S())) for remaining values.

Taxonomy Table: Taxonomy table for the taxa identified.

Value

a phyloseq object

Examples

```
IBD <- IBD16S()
```

`IBD16S_mtx` *IBD16S_mtx*

Description

Matrix of OTU values for 16S rRNA data for IBD

Usage

```
IBD16S_mtx
```

Format

An object of class `matrix` (inherits from `array`) with 982 rows and 178 columns.

`IBD16S_samp` *IBD16S_samp*

Description

Sample data for IBD16S data

Usage

```
IBD16S_samp
```

Format

An object of class `data.frame` with 178 rows and 490 columns.

IBD16S_tax *IBD16S_tax*

Description

Taxonomy data for IBD 16S data

Usage

```
IBD16S_tax
```

Format

An object of class `matrix` (inherits from `array`) with 982 rows and 6 columns.

momspi16S *Construct MOMS-PI 16S rRNA phyloseq object*

Description

The Multi-Omic Microbiome Study-Pregnancy Initiative (MOMS-PI) was funded by the NIH Roadmap HUman Microbiome Project to understand the impact of the vaginal microbiome on pregnancy and the fetal microbiome. This longitudinal study contains samples from various body sites of 596 women. This phyloseq object contains the 16S rRNA sequencing data that was collected. Also contained are the taxa data and participant metadata.

Usage

```
momspi16S()
```

Format

A phyloseq object with 7,665 taxa and 9,107 samples.

OTU Table: A counts matrix for the rRNA-seq results.

Sample Data:

file_id File identifier
md5 md5 hash for the file
size file size
urls URL for the file
sample_id Sample identifier
file_name Filename which the sample was taken from
subject_id Participant identifier
sample_body_site Body site of the sample

visit_number Visit number
subject_gender Participant gender
subject_race Participant race
study_full_name Name of the study
project_name Name of project

Taxonomy Table: Taxonomy table for the taxa identified.

Value

a phyloseq object

Examples

```
momspi <- momspi16S()
```

`momspi16S_mtx` *momspi16S_mtx*

Description

16S rRNA OTU matrix for MOMS-PI data

Usage

```
momspi16S_mtx
```

Format

An object of class `matrix` (inherits from `array`) with 7665 rows and 9107 columns.

`momspi16S_samp` *momspi16S_samp*

Description

Sample data for MOMS-PI 16S data

Usage

```
momspi16S_samp
```

Format

An object of class `data.frame` with 9107 rows and 13 columns.

momspi16S_tax *momspi16S_tax*

Description

Taxonomy data for MOMS-PI 16S data

Usage

```
momspi16S_tax
```

Format

An object of class `matrix` (inherits from `array`) with 7665 rows and 7 columns.

momspiCytokines *Create MOMS-PI cytokines SummarizedExperiment object*

Description

The Multi-Omic Microbiome Study-Pregnancy Initiative (MOMS-PI) was funded by the NIH Roadmap HUman Microbiome Project to understand the impact of the vaginal microbiome on pregnancy and the fetal microbiome. This longitudinal study contains samples from three body sites of 116 women. This summarizedExperiment object contains the cytokine data that was collected and the participant metadata.

Usage

```
momspiCytokines()
```

Format

A SummarizedExperiment object with 29 features and 1396 samples.

colData:

file_id File identifier
md5 md5 hash for the file
size file size
urls URL for the file
sample_id Sample identifier
file_name Filename which the sample was taken from
subject_id Participant identifier
sample_body_site Body site of the sample
visit_number Visit number

subject_gender Participant gender
subject_race Participant race
study_full_name Name of the study
project_name Name of project

Value

A SummarizedExperiment object

Examples

```
momspiCyto <- momspiCytokines()
```

`momspiCyto_mtx` *momspiCyto_mtx*

Description

Cytokines matrix for MOMS-PI data

Usage

```
momspiCyto_mtx
```

Format

An object of class `matrix` (inherits from `array`) with 29 rows and 1396 columns.

`momspiCyto_samp` *momspiCyto_samp*

Description

Sample data for MOMS-PI cytokines data

Usage

```
momspiCyto_samp
```

Format

An object of class `data.frame` with 1396 rows and 13 columns.

momspiMultiAssay *Make MOMS-PI MultiAssayExperiment*

Description

Construct MultiAssayExperiment for MOMS-PI 16S rRNA and cytokines data.

Usage

```
momspiMultiAssay()
```

Format

A MultiAssayExperiment object with a 16S rRNA matrix and Cytokine matrix

16S: A counts matrix for the 16S rRNA-seq results.

cytokines: A counts matrix for the cytokines results.

colData:

file_id File identifier
md5 md5 hash for the file
size file size
urls URL for the file
sample_id Sample identifier
file_name Filename which the sample was taken from
subject_id Participant identifier
sample_body_site Body site of the sample
visit_number Visit number
subject_gender Participant gender
subject_race Participant race
study_full_name Name of the study
project_name Name of project

Value

A multiAssay Experiment object

Examples

```
momspiMA <- momspiMultiAssay()
```

patient_table *Generate patient summary table for HMP2 sample data*

Description

This function allows you to produce a summary table for the HMP2Data data sets.

Usage

```
patient_table(x)
```

Arguments

x	A named list of phyloseq or SummarizedExperiment objects.

Value

A knitr::kable table.

Examples

```
patient_table(list(momspi16S = momspi16S(),
  momspiCytokines = momspiCytokines(),
  IBD16S = IBD16S(), T2D16S = T2D16S()))
```

T2D16S *Create HMP2 16S sequencing data for Type 2 Diabetes (T2D) phyloseq object*

Description

The HMP2 study gathered data on the microbiome for patients with different disease. This dataset contains 16S rRNA data for 79 patients with T2D over multiple visits.

Usage

```
T2D16S()
```

Format

A phyloseq object with 12,062 taxa and 2,208 samples.

OTU Table: A counts matrix for the rRNA-seq results.

Sample Data:

file_id File identifier

md5 md5 hash for the file
size file size
urls URL for the file
sample_id Sample identifier
file_name Filename which the sample was taken from
subject_id Participant identifier
sample_body_site Body site of the sample
visit_number Visit number
subject_gender Participant gender
subject_race Participant race
study_full_name Name of the study
project_name Name of project

Taxonomy Table: Taxonomy table for the taxa identified.

Value

a phyloseq object

Examples

```
T2D <- T2D16S()
```

`T2D16S_mtx` *T2D16S_mtx*

Description

T2D 16S rRNA matrix

Usage

```
T2D16S_mtx
```

Format

An object of class `matrix` (inherits from `array`) with 12062 rows and 2208 columns.

T2D16S_samp *T2D16S_samp*

Description

T2D 16S sample data

Usage

```
T2D16S_samp
```

Format

An object of class `data.frame` with 2208 rows and 13 columns.

T2D16S_tax *T2D16S_tax*

Description

Taxonomy data for T2D 16S data

Usage

```
T2D16S_tax
```

Format

An object of class `matrix` (inherits from `array`) with 12062 rows and 7 columns.

table_two *Generate demographic summary table for HMP2 sample data*

Description

This function allows you to produce a summary table for the HMP2Data data sets.

Usage

```
table_two(x)
```

Arguments

x	A named list of phyloseq or SummarizedExperiment objects.

Value

A knitr::kable table.

Examples

```
table_two(list(momspi16S = momspi16S(),
  momspiCytokines = momspiCytokines(),
  IBD16S = IBD16S(), T2D16S = T2D16S()))
```

`visit_table` *Make table of visits*

Description

This function allows you to produce a summary table for the HMP2Data visits.

Usage

```
visit_table(x)
```

Arguments

x	A named list of phyloseq or SummarizedExperiment objects.

Value

A knitr::kable table.

Examples

```
visit_table(list(momspi16S = momspi16S(),
  momspiCytokines = momspiCytokines(),
  IBD16S = IBD16S(), T2D16S = T2D16S()))
```

Index

∗ **datasets**
IBD16S_mtx, 3
IBD16S_samp, 3
IBD16S_tax, 4
momspi16S_mtx, 5
momspi16S_samp, 5
momspi16S_tax, 6
momspiCyto_mtx, 7
momspiCyto_samp, 7
T2D16S_mtx, 10
T2D16S_samp, 11
T2D16S_tax, 11

IBD16S, 2
IBD16S_mtx, 3
IBD16S_samp, 3
IBD16S_tax, 4

momspi16S, 4
momspi16S_mtx, 5
momspi16S_samp, 5
momspi16S_tax, 6
momspiCyto_mtx, 7
momspiCyto_samp, 7
momspiCytokines, 6
momspiMultiAssay, 8

patient_table, 9

T2D16S, 9
T2D16S_mtx, 10
T2D16S_samp, 11
T2D16S_tax, 11
table_two, 11

visit_table, 12