Package 'curatedMetagenomicData'

April 12, 2018

Type Package

Title Curated Metagenomic Data of the Human Microbiome

Version 1.8.1

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Description The curatedMetagenomicData package provides microbial taxonomic, functional, and gene marker abundance for samples collected from different bodysites.

URL https://github.com/waldronlab/curatedMetagenomicData

BugReports https://github.com/waldronlab/curatedMetagenomicData/issues

License Artistic-2.0

Encoding UTF-8

LazyData true

Depends R (>= 3.4.0), dplyr (>= 0.5.0), Biobase (>= 2.37.0),
ExperimentHub (>= 1.3.0), AnnotationHub (>= 2.9.0)

Imports utils, tidyr, magrittr, methods, S4Vectors

Suggests BiocInstaller, devtools, roxygen2, testthat, covr, knitr,
rmarkdown, BiocCheck, BiocStyle, BiocParallel, readr, RISmed,
ggplot2, metagenomeSeq, phyloseq, ape

VignetteBuilder knitr

biocViews Homo_sapiens_Data, ReproducibleResearch, MicrobiomeData

RoxygenNote 6.0.1

NeedsCompilation no

R topics documented:

AsnicarF_2017   *Data from the AsnicarF_2017 study*

Description

Data from the AsnicarF_2017 study

Datasets

AsnicarF_2017.genefamilies_relab.milk: An ExpressionSet with 8 samples and 752,977 features specific to the milk body site

AsnicarF_2017.genefamilies_relab.stool: An ExpressionSet with 16 samples and 752,977 features specific to the stool body site

AsnicarF_2017.marker_abundance.milk: An ExpressionSet with 8 samples and 53,228 features specific to the milk body site

AsnicarF_2017.marker_abundance.stool: An ExpressionSet with 16 samples and 53,228 features specific to the stool body site

AsnicarF_2017.marker_presence.milk: An ExpressionSet with 8 samples and 50,192 features specific to the milk body site

AsnicarF_2017.marker_presence.stool: An ExpressionSet with 16 samples and 50,192 features specific to the stool body site

AsnicarF_2017.metaphlan_bugs_list.milk: An ExpressionSet with 8 samples and 799 features specific to the milk body site

AsnicarF_2017.metaphlan_bugs_list.stool: An ExpressionSet with 16 samples and 799 features specific to the stool body site

AsnicarF_2017.pathabundance_relab.milk: An ExpressionSet with 8 samples and 9,274 features specific to the milk body site

AsnicarF_2017.pathabundance_relab.stool: An ExpressionSet with 16 samples and 9,274 features specific to the stool body site

AsnicarF_2017.pathcoverage.milk: An ExpressionSet with 8 samples and 9,274 features specific to the milk body site

AsnicarF_2017.pathcoverage.stool: An ExpressionSet with 16 samples and 9,274 features specific to the stool body site

Exploratory Data Analysis

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An EDA figure is available in the HTML documentation

Source

Title: Studying Vertical Microbiome Transmission from Mothers to Infants by Strain-Level Metagenomic Profiling.

Author: Asnicar F, Manara S, Zolfo M, Truong DT, Scholz M, Armanini F, Ferretti P, Gorfer V, Pedrotti A, Tett A, Segata N

Lab: Centre for Integrative Biology, University of Trento, Trento, Italy.

PMID: 28144631

Examples

```
AsnicarF_2017.metaphlan_bugs_list.milk()
```

| BritoIL_2016 | *Data from the BritoIL_2016 study* |

Description

Data from the BritoIL_2016 study

Datasets

BritoIL_2016.genefamilies_relab.oralcavity: An ExpressionSet with 140 samples and 1,825,268 features specific to the oralcavity body site

BritoIL_2016.genefamilies_relab.stool: An ExpressionSet with 172 samples and 1,825,268 features specific to the stool body site

BritoIL_2016.marker_abundance.oralcavity: An ExpressionSet with 140 samples and 162,905 features specific to the oralcavity body site

BritoIL_2016.marker_abundance.stool: An ExpressionSet with 172 samples and 162,905 features specific to the stool body site

BritoIL_2016.marker_presence.oralcavity: An ExpressionSet with 140 samples and 156,452 features specific to the oralcavity body site

BritoIL_2016.marker_presence.stool: An ExpressionSet with 172 samples and 156,452 features specific to the stool body site

BritoIL_2016.metaphlan_bugs_list.oralcavity: An ExpressionSet with 140 samples and 1,864 features specific to the oralcavity body site

BritoIL_2016.metaphlan_bugs_list.stool: An ExpressionSet with 172 samples and 1,864 features specific to the stool body site

BritoIL_2016.pathabundance_relab.oralcavity: An ExpressionSet with 140 samples and 22,539 features specific to the oralcavity body site

BritoIL_2016.pathabundance_relab.stool: An ExpressionSet with 172 samples and 22,539 features specific to the stool body site

BritoIL_2016.pathcoverage.oralcavity: An ExpressionSet with 140 samples and 22,539 features specific to the oralcavity body site

BritoIL_2016.pathcoverage.stool: An ExpressionSet with 172 samples and 22,539 features specific to the stool body site

Exploratory Data Analysis

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An EDA figure is available in the HTML documentation

Source

Title: Mobile genes in the human microbiome are structured from global to individual scales.

Author: Brito IL, Yilmaz S, Huang K, Xu L, Jupiter SD, Jenkins AP, Naisilisili W, Tamminen M, Smillie CS, Wortman JR, Birren BW, Xavier RJ, Blainey PC, Singh AK, Gevers D, Alm EJ

Lab: NA

PMID: 27409808

Examples

```
BritoIL_2016.metaphlan_bugs_list.oralcavity()
```

Castro-NallarE_2015   *Data from the Castro-NallarE_2015 study*

Description

Data from the Castro-NallarE_2015 study

Datasets

Castro-NallarE_2015.genefamilies_relab.oralcavity: An ExpressionSet with 32 samples and 588,014 features specific to the oralcavity body site

Castro-NallarE_2015.marker_abundance.oralcavity: An ExpressionSet with 32 samples and 51,679 features specific to the oralcavity body site

Castro-NallarE_2015.marker_presence.oralcavity: An ExpressionSet with 32 samples and 49,093 features specific to the oralcavity body site

Castro-NallarE_2015.metaphlan_bugs_list.oralcavity: An ExpressionSet with 32 samples and 755 features specific to the oralcavity body site

Castro-NallarE_2015.pathabundance_relab.oralcavity: An ExpressionSet with 32 samples and 9,237 features specific to the oralcavity body site

Castro-NallarE_2015.pathcoverage.oralcavity: An ExpressionSet with 32 samples and 9,237 features specific to the oralcavity body site

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Source

Title: Composition, taxonomy and functional diversity of the oropharynx microbiome in individuals with schizophrenia and controls.

Author: Castro-Nallar E, Bendall ML, Pérez-Losada M, Sabuncyan S, Severance EG, Dickerson FB, Schroeder JR, Yolken RH, Crandall KA

Lab: Computational Biology Institute, George Washington University , Ashburn, VA , USA ; Center for Bioinformatics and Integrative Biology, Universidad Andres Bello, Facultad de Ciencias Biologicas , Santiago , Chile.

PMID: 26336637

Examples

```
`Castro-NallarE_2015.metaphlan_bugs_list.oralcavity`()
```

ChngKR_2016   *Data from the ChngKR_2016 study*

Description

Data from the ChngKR_2016 study

Datasets

ChngKR_2016.genefamilies_relab.skin: An ExpressionSet with 78 samples and 823,859 features specific to the skin body site

ChngKR_2016.marker_abundance.skin: An ExpressionSet with 78 samples and 89,597 features specific to the skin body site

ChngKR_2016.marker_presence.skin: An ExpressionSet with 78 samples and 85,656 features specific to the skin body site

ChngKR_2016.metaphlan_bugs_list.skin: An ExpressionSet with 78 samples and 1,219 features specific to the skin body site

ChngKR_2016.pathabundance_relab.skin: An ExpressionSet with 78 samples and 10,995 features specific to the skin body site

ChngKR_2016.pathcoverage.skin: An ExpressionSet with 78 samples and 10,995 features specific to the skin body site

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Source

Title: Whole metagenome profiling reveals skin microbiome-dependent susceptibility to atopic dermatitis flare.

Author: Chng KR, Tay AS, Li C, Ng AH, Wang J, Suri BK, Matta SA, McGovern N, Janela B, Wong XF, Sio YY, Au BV, Wilm A, De Sessions PF, Lim TC, Tang MB, Ginhoux F, Connolly JE, Lane EB, Chew FT, Common JE, Nagarajan N

Lab: Genome Institute of Singapore, Singapore 138672, Singapore.

PMID: 27562258

Examples

```
ChngKR_2016.metaphlan_bugs_list.skin()
```

---

cmdValidVersions   *Get valid data versions*

Description

Get valid data versions

Usage

```
cmdValidVersions()
```

Value

An integer vector of data versions, in the format YYYYMMDD, read from inst/extdata/versions.txt.

Examples

```
cmdValidVersions()
max(cmdValidVersions())  #latest version
stopifnot(is(cmdValidVersions(), "integer"))
```

---

combined_metadata   *Combined metadata of all studies in curatedMetagenomicData*

Description

The combined sample level metadata of all studies in curatedMetagenomicData.

Usage

```
combined_metadata
```

Format

A data.frame with 6058 rows and 80 variables:

NA NA

sampleID Sample identifier.

subjectID Subject identifier.

body_site Bodysite of acquisition.

antibiotics_current_use Subject is currently taking antibiotics.

study_condition The main disease or condition under study; control for controls.

disease Semicolon-delimited vector of conditions; Use healthy only if subject is known to be healthy; CRC=colorectal cancer.

age Subject age (years).

infant_age Infant age (days); should be used for infants < 2 years old.

age_category Age category: newborn < 1 year; 1 <= child < 12; 12 <= schoolage < 19; 19 <= adult <= 65; senior > 65.

gender Subject gender.

country Country of acquisition using ISO3 code from http://www.fao.org/countryprofiles/iso3list/en/.

non_westernized Subject belongs to a non-westernized community.

sequencing_platform This will be modified as new sequencing platforms are added to the database.

DNA_extraction_kit DNA extraction kit.

PMID Identifier of the main publication in PubMed.

number_reads Number of final reads - calculated from raw data.

number_bases Total number of bases sequenced in the sample.

minimum_read_length Minimum read length - calculated from raw data.

median_read_length Median read length - calculated from raw data.

pregnant Pregnancy of the subject (men: no).

lactating Lactating subjects (men: no).

NCBI_accession Semicolon-separated vector of NCBI accessions.

BMI Body mass index (kg/m2).

antibiotics_family Family of antibiotics currently used; Semicolon-separated.

momeducat Years of education of the mother of the subject.

alcohol Subject is reported as a drinker.

flg-genotype Any term for filaggrin-protein genotype.

disease_subtype Disease subtype; CD=Chrohn's Disease.

hdl Curators must use mg/l.

triglycerides Curators must use mg/l.

hba1c Curators must use %.

ldl Curators must use mg/l.

tnm TNM classification for colorectal-cancer.

body_subsite Subsite of body site of acquisition.

visit_number Visit number for studies with repeated visits.

days_from_first_collection Used for time series studies.

c-peptide Curators must use ng/ml.

family A number identifying the family subjects belong; not corrected for meta-analyses.

cholesterol Curators must use mg/dl.

glucose Curators must use mg/dl.

mumps Subject has been through mumps in life.

adiponectin Curators must use mg/l.

insulin(cat) Insulin intake as a boolean.

fgf-19 Curators must use pg/ml.

hscrp High-sensitivity C-reactive protein test result.

leptin Curators must use micrograms/l.

glutamate_decarboxylase_2_antibody Glutamic acid decarboxylase (GAD65) antibody assay.

creatinine Curators must use micro-mol/l.

il-1 Curators must use pg/ml.

cd163 Curators must use ng/ml.

glp-1 Curators must use pmol/l.

hitchip_probe_class High/Low species content onthe HIT-chip probe.

hitchip_probe_number HIT-chip probe score.

protein_intake Indication about the protein intake in the Mongolians diet.

days_after_onset Days from the onset of the disease.

stec_count Amount of STEC colonies detected.

shigatoxin_2_elisa Enzyme-linked immunosorbent assay for Shiga-toxigenic E.coli.

stool_texture Texture of the stool at sampling time.

ferm_milk_prod_consumer Dfmp means yes (defined milk product).

mgs_richness Metagenomic species richness.

location Free-form additional location information.

dyastolic_p Measured in mm/Hg.

systolic_p Measured in mm/Hg.

prothrombin_time Prothrombin time in seconds.

creatine Curators must use micro-mol/l.

inr International normalized ratio.

ctp Cytidine triphosphate level.

albumine Albumine level; curators must use g/l.

bilubirin Bilubirin; curators must use mg/dl.

smoker Currently a smoker at sampling.

ever_smoker Ever been a smoker.

birth_control_pil Use of the birth-control-pils at the sampling time (men: no).

hla_drb12 Hla_drb12 allele.

hla_dqa12 Hla_dqa12 allele.

hla_dqa11 Hla_dqa11 allele.

hla_drb11 Hla_drb11 allele.

start_solidfood First day of solid food introduction (newborns).

ajcc AJCC staging for colorectal-cancer.

fobt Fecal occult blood test.

Source

See dataset specific help functions for source information

---

curatedMetagenomicData

Curated Metagenomic Data of the Human Microbiome

Description

The curatedMetagenomicData package provides taxonomic, functional, and gene marker abundance for samples collected from different bodysites. It provides data from aproximately 3000 human microbiome samples that has been highly processed, refined, and curated such that analysis that might otherwise require a computing cluster can be done on an ordianary laptop.

Usage

```
curatedMetagenomicData(x = "*", dryrun = TRUE, counts = FALSE,
  bugs.as.phyloseq = FALSE, x.is.glob = TRUE)
```

Arguments

x	A character vector of dataset names, regexes, or globs, that will be matched to available datasets. If x.is.glob is TRUE (default), wildcards such as "*" and "?" are supported (see ?glob2rx), otherwise, regexes are supported (see ?grep)
dryrun	= TRUE Only return the names of datasets to be downloaded, not the datasets themselves. If FALSE, return the datasets rather than the names.
counts	= FALSE If TRUE, relative abundances will be multiplied by read depth, then rounded to the nearest integer.
bugs.as.phyloseq	
	= FALSE If TRUE, tables of taxonomic abundance (metaphlan datasets) will be converted to phyloseq objects for use with the phyloseq package.
x.is.glob	= TRUE Set to FALSE to actually download the datasets

Value

A list of ExpressionSet and/or phyloseq objects

Examples

```
curatedMetagenomicData()
curatedMetagenomicData("ZellerG*")
curatedMetagenomicData("ZellerG.+marker", x.is.glob=FALSE)
curatedMetagenomicData("ZellerG_2014.metaphlan_bugs_list.stool", dryrun=FALSE)
curatedMetagenomicData("ZellerG_2014.metaphlan_bugs_list.stool",
        counts=TRUE, dryrun=FALSE, bugs.as.phyloseq=TRUE)
```

ExpressionSet2MRexperiment

Convert   an   ExpressionSet   object   to   a metagenomeSeq::MRexperiment-class object

---

Description

Convert an ExpressionSet object to a metagenomeSeq::MRexperiment-class object

Usage

```
ExpressionSet2MRexperiment(eset, simplify = TRUE)
```

Arguments

eset   An eset object

simplify   if TRUE the most detailed clade name is used, instead of the original metaPhlAn2 names which contain the full taxonomy.

Value

A metagenomeSeq::MRexperiment-class object

Examples

```
eset <- LomanNJ_2013.metaphlan_bugs_list.stool()
ExpressionSet2MRexperiment(eset)
```

ExpressionSet2phyloseq

Convert an ExpressionSet object to a phyloseq object

Description

Convert an ExpressionSet object to a phyloseq object

Usage

```
ExpressionSet2phyloseq(eset, simplify = TRUE, relab = TRUE,
  phylogenetictree = FALSE)
```

Arguments

`eset`	An eset object
`simplify`	if TRUE, only the most detailed level of the taxonomy is kept in the names, for example species or strain. Default is TRUE because the full taxonomy is provided by the tax_table of the phyloseq object.
`relab`	if FALSE, values are multiplied by read depth to approximate counts, if TRUE (default) values kept as relative abundances between 0 and 100%.
`phylogenetictree`	
	if TRUE, a phylogenetic tree will be attached to the phyloseq object. Note, this will remove all clades not associated with a genome, e.g. kingdoms, phyla, etc. It will remove any feature that can't be matched to the Newick tree included in inst/extdata; see ?getMetaphlanTree.

Value

A phyloseq object

Examples

```
eset <- LomanNJ_2013.metaphlan_bugs_list.stool()
ExpressionSet2phyloseq(eset)
ExpressionSet2phyloseq(eset, relab=FALSE)

## Using a phylogenetic tree
library(phyloseq)
(pseq <- ExpressionSet2phyloseq(eset, phylogenetictree = TRUE))
unwt <- UniFrac(pseq, weighted=FALSE, normalized=TRUE, parallel=FALSE, fast=TRUE)
plot(hclust(unwt))
wt <- UniFrac(pseq, weighted=TRUE, normalized=FALSE, parallel=FALSE, fast=TRUE)
plot(hclust(wt))
```

FengQ_2015   *Data from the FengQ_2015 study*

Description

Data from the FengQ_2015 study

Datasets

FengQ_2015.genefamilies_relab.stool: An ExpressionSet with 154 samples and 1,627,981 features specific to the stool body site

FengQ_2015.marker_abundance.stool: An ExpressionSet with 154 samples and 140,519 features specific to the stool body site

FengQ_2015.marker_presence.stool: An ExpressionSet with 154 samples and 130,216 features specific to the stool body site

FengQ_2015.metaphlan_bugs_list.stool: An ExpressionSet with 154 samples and 1,547 features specific to the stool body site

FengQ_2015.pathabundance_relab.stool: An ExpressionSet with 154 samples and 16,866 features specific to the stool body site

FengQ_2015.pathcoverage.stool: An ExpressionSet with 154 samples and 16,866 features specific to the stool body site

Exploratory Data Analysis

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Source

Title: Gut microbiome development along the colorectal adenoma-carcinoma sequence.

Author: Feng Q, Liang S, Jia H, Stadlmayr A, Tang L, Lan Z, Zhang D, Xia H, Xu X, Jie Z, Su L, Li X, Li X, Li J, Xiao L, Huber-Schönauer U, Niederseer D, Xu X, Al-Aama JY, Yang H, Wang J, Kristiansen K, Arumugam M, Tilg H, Datz C, Wang J

Lab: [1] BGI-Shenzhen, Shenzhen 518083, China [2] Department of Biology, University of Copenhagen, Ole Maaloes Vej 5, 2200 Copenhagen, Denmark.

PMID: 25758642

Examples

```
FengQ_2015.metaphlan_bugs_list.stool()
```

---

getMetaphlanTree   *Title Return a phylogenetic tree for MetaPhlAn2 bugs*

Description

Title Return a phylogenetic tree for MetaPhlAn2 bugs

Usage

```
getMetaphlanTree(removeGCF = TRUE, simplify = TRUE)
```

Arguments

removeGCF	remove "|GCF_nnnnnnnnn" from the end of tip labels. Default is TRUE.
simplify	if TRUE, only the most detailed level of the taxonomy is kept in the names, for example species or strain. Default is TRUE.

Details

The phylogenetic tree was built with PhyloPhlAn, using all the genomes from MetaPhlAn2. Clades that had more than one leaf per species were cleaned and a new tree generated with these selected genomes. Labels are in the form: "taxonomy|genome_ID". The Newick file of the tree is stored in the package as inst/extdata/metaphlan2_selected.tree.reroot.nwk.bz2. Thanks to Francesco Asnicar <f.asnicar@unitn.it> for generating this tree.

Value

a phylogenetic tree of class ape::phylo

Examples

```
tree <- getMetaphlanTree()
summary(tree)
getMetaphlanTree(simplify = FALSE)
getMetaphlanTree(simplify = FALSE, removeGCF = FALSE)
```

HanniganGD_2017   *Data from the HanniganGD_2017 study*

Description

Data from the HanniganGD_2017 study

Datasets

HanniganGD_2017.genefamilies_relab.stool: An ExpressionSet with 82 samples and 709,894 features specific to the stool body site

HanniganGD_2017.marker_abundance.stool: An ExpressionSet with 82 samples and 57,511 features specific to the stool body site

HanniganGD_2017.marker_presence.stool: An ExpressionSet with 82 samples and 52,996 features specific to the stool body site

HanniganGD_2017.metaphlan_bugs_list.stool: An ExpressionSet with 82 samples and 716 features specific to the stool body site

HanniganGD_2017.pathabundance_relab.stool: An ExpressionSet with 82 samples and 8,500 features specific to the stool body site

HanniganGD_2017.pathcoverage.stool: An ExpressionSet with 82 samples and 8,500 features specific to the stool body site

Source

Title: NA

Author: NA

Lab: NA

PMID: NA

Examples

```
HanniganGD_2017.metaphlan_bugs_list.stool()
```

Heitz-BuschartA_2016   *Data from the Heitz-BuschartA_2016 study*

Description

Data from the Heitz-BuschartA_2016 study

Datasets

Heitz-BuschartA_2016.genefamilies_relab.stool: An ExpressionSet with 53 samples and 1,110,454 features specific to the stool body site

Heitz-BuschartA_2016.marker_abundance.stool: An ExpressionSet with 53 samples and 80,864 features specific to the stool body site

Heitz-BuschartA_2016.marker_presence.stool: An ExpressionSet with 53 samples and 77,488 features specific to the stool body site

Heitz-BuschartA_2016.metaphlan_bugs_list.stool: An ExpressionSet with 53 samples and 1,011 features specific to the stool body site

Heitz-BuschartA_2016.pathabundance_relab.stool: An ExpressionSet with 53 samples and 10,281 features specific to the stool body site

Heitz-BuschartA_2016.pathcoverage.stool: An ExpressionSet with 53 samples and 10,281 features specific to the stool body site

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Source

Title: Integrated multi-omics of the human gut microbiome in a case study of familial type 1 diabetes.

Author: Heintz-Buschart A, May P, Laczny CC, Lebrun LA, Bellora C, Krishna A, Wampach L, Schneider JG, Hogan A, de Beaufort C, Wilmes P

Lab: Luxembourg Centre for Systems Biomedicine, 7 avenue des Hauts-Fourneaux, 4362 Esch-sur-Alzette, Luxembourg.

PMID: 27723761

Examples

```
`Heitz-BuschartA_2016.metaphlan_bugs_list.stool`()
```

HMP_2012   *Data from the HMP_2012 study*

Description

Data from the HMP_2012 study

Datasets

HMP_2012.genefamilies_relab.nasalcavity: An ExpressionSet with 91 samples and 1,964,480 features specific to the nasalcavity body site

HMP_2012.genefamilies_relab.oralcavity: An ExpressionSet with 506 samples and 1,964,480 features specific to the oralcavity body site

HMP_2012.genefamilies_relab.stool: An ExpressionSet with 147 samples and 1,964,480 features specific to the stool body site

HMP_2012.genefamilies_relab.vagina: An ExpressionSet with 5 samples and 1,964,480 features specific to the vagina body site

HMP_2012.marker_abundance.nasalcavity: An ExpressionSet with 91 samples and 162,107 features specific to the nasalcavity body site

HMP_2012.marker_abundance.oralcavity: An ExpressionSet with 506 samples and 162,107 features specific to the oralcavity body site

HMP_2012.marker_abundance.stool: An ExpressionSet with 147 samples and 162,107 features specific to the stool body site

HMP_2012.marker_abundance.vagina: An ExpressionSet with 5 samples and 162,107 features specific to the vagina body site

HMP_2012.marker_presence.nasalcavity: An ExpressionSet with 91 samples and 158,645 features specific to the nasalcavity body site

HMP_2012.marker_presence.oralcavity: An ExpressionSet with 506 samples and 158,645 features specific to the oralcavity body site

HMP_2012.marker_presence.stool: An ExpressionSet with 147 samples and 158,645 features specific to the stool body site

HMP_2012.marker_presence.vagina: An ExpressionSet with 5 samples and 158,645 features specific to the vagina body site

HMP_2012.metaphlan_bugs_list.nasalcavity: An ExpressionSet with 91 samples and 1,988 features specific to the nasalcavity body site

HMP_2012.metaphlan_bugs_list.oralcavity: An ExpressionSet with 506 samples and 1,988 features specific to the oralcavity body site

HMP_2012.metaphlan_bugs_list.stool: An ExpressionSet with 147 samples and 1,988 features specific to the stool body site

HMP_2012.metaphlan_bugs_list.vagina: An ExpressionSet with 5 samples and 1,988 features specific to the vagina body site

HMP_2012.pathabundance_relab.nasalcavity: An ExpressionSet with 91 samples and 23,271 features specific to the nasalcavity body site

HMP_2012.pathabundance_relab.oralcavity: An ExpressionSet with 506 samples and 23,271 features specific to the oralcavity body site

HMP_2012.pathabundance_relab.stool: An ExpressionSet with 147 samples and 23,271 features specific to the stool body site

HMP_2012.pathabundance_relab.vagina: An ExpressionSet with 5 samples and 23,271 features specific to the vagina body site

HMP_2012.pathcoverage.nasalcavity: An ExpressionSet with 91 samples and 23,271 features specific to the nasalcavity body site

HMP_2012.pathcoverage.oralcavity: An ExpressionSet with 506 samples and 23,271 features specific to the oralcavity body site

HMP_2012.pathcoverage.stool: An ExpressionSet with 147 samples and 23,271 features specific to the stool body site

HMP_2012.pathcoverage.vagina: An ExpressionSet with 5 samples and 23,271 features specific to the vagina body site

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Source

Title: Structure, function and diversity of the healthy human microbiome.

Author: Huttenhower C, Gevers D, Knight R, Abubucker S, Badger JH, Chinwalla AT, Creasy HH, Earl AM, FitzGerald MG, Fulton RS, Giglio MG, Hallsworth-Pepin K, Lobos EA, Madupu R, Magrini V, Martin JC, Mitreva M, Muzny DM, Sodergren EJ, Versalovic J, Wollam AM, Worley KC, Wortman JR, Young SK, Zeng Q, Aagaard KM, Abolude OO, Allen-Vercoe E, Alm EJ, Alvarado L, Andersen GL, Anderson S, Appelbaum E, Arachchi HM, Armitage G, Arze CA, Ayvaz T, Baker CC, Begg L, Belachew T, Bhonagiri V, Bihan M, Blaser MJ, Bloom T, Bonazzi V, Brooks J, Buck GA, Buhay CJ, Busam DA, Campbell JL, Canon SR, Cantarel BL, Chain PS, Chen IM, Chen L, Chhibba S, Chu K, Ciulla DM, Clemente JC, Clifton SW, Conlan S, Crabtree J, Cutting MA, Davidovics NJ, Davis CC, DeSantis TZ, Deal C, Delehaunty KD, Dewhirst FE, Deych E, Ding Y, Dooling DJ, Dugan SP, Dunne WM, Durkin A, Edgar RC, Erlich RL, Farmer CN, Farrell RM, Faust K, Feldgarden M, Felix VM, Fisher S, Fodor AA, Forney LJ, Foster L, Di Francesco V, Friedman J, Friedrich DC, Fronick CC, Fulton LL, Gao H, Garcia N, Giannoukos

G, Giblin C, Giovanni MY, Goldberg JM, Goll J, Gonzalez A, Griggs A, Gujja S, Haake SK, Haas BJ, Hamilton HA, Harris EL, Hepburn TA, Herter B, Hoffmann DE, Holder ME, Howarth C, Huang KH, Huse SM, Izard J, Jansson JK, Jiang H, Jordan C, Joshi V, Katancik JA, Keitel WA, Kelley ST, Kells C, King NB, Knights D, Kong HH, Koren O, Koren S, Kota KC, Kovar CL, Kyrpides NC, La Rosa PS, Lee SL, Lemon KP, Lennon N, Lewis CM, Lewis L, Ley RE, Li K, Liolios K, Liu B, Liu Y, Lo CC, Lozupone CA, Lunsford R, Madden T, Mahurkar AA, Mannon PJ, Mardis ER, Markowitz VM, Mavromatis K, McCorrison JM, McDonald D, McEwen J, McGuire AL, McInnes P, Mehta T, Mihindukulasuriya KA, Miller JR, Minx PJ, Newsham I, Nusbaum C, O'Laughlin M, Orvis J, Pagani I, Palaniappan K, Patel SM, Pearson M, Peterson J, Podar M, Pohl C, Pollard KS, Pop M, Priest ME, Proctor LM, Qin X, Raes J, Ravel J, Reid JG, Rho M, Rhodes R, Riehle KP, Rivera MC, Rodriguez-Mueller B, Rogers YH, Ross MC, Russ C, Sanka RK, Sankar P, Sathirapongsasuti J, Schloss JA, Schloss PD, Schmidt TM, Scholz M, Schriml L, Schubert AM, Segata N, Segre JA, Shannon WD, Sharp RR, Sharpton TJ, Shenoy N, Sheth NU, Simone GA, Singh I, Smillie CS, Sobel JD, Sommer DD, Spicer P, Sutton GG, Sykes SM, Tabbaa DG, Thiagarajan M, Tomlinson CM, Torralba M, Treangen TJ, Truty RM, Vishnivetskaya TA, Walker J, Wang L, Wang Z, Ward DV, Warren W, Watson MA, Wellington C, Wetterstrand KA, White JR, Wilczek-Boney K, Wu Y, Wylie KM, Wylie T, Yandava C, Ye L, Ye Y, Yooseph S, Youmans BP, Zhang L, Zhou Y, Zhu Y, Zoloth L, Zucker JD, Birren BW, Gibbs RA, Highlander SK, Methé BA, Nelson KE, Petrosino JF, Weinstock GM, Wilson RK, White O

Lab: NA

PMID: 22699609

Examples

```
HMP_2012.metaphlan_bugs_list.nasalcavity()
```

KarlssonFH_2013   *Data from the KarlssonFH_2013 study*

Description

Data from the KarlssonFH_2013 study

Datasets

KarlssonFH_2013.genefamilies_relab.stool: An ExpressionSet with 145 samples and 1,415,750 features specific to the stool body site

KarlssonFH_2013.marker_abundance.stool: An ExpressionSet with 145 samples and 101,166 features specific to the stool body site

KarlssonFH_2013.marker_presence.stool: An ExpressionSet with 145 samples and 95,324 features specific to the stool body site

KarlssonFH_2013.metaphlan_bugs_list.stool: An ExpressionSet with 145 samples and 1,140 features specific to the stool body site

KarlssonFH_2013.pathabundance_relab.stool: An ExpressionSet with 145 samples and 13,392 features specific to the stool body site

KarlssonFH_2013.pathcoverage.stool: An ExpressionSet with 145 samples and 13,392 features specific to the stool body site

Exploratory Data Analysis

An EDA figure is available in the HTML documentation

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An EDA figure is available in the HTML documentation

Source

Title: Gut metagenome in European women with normal, impaired and diabetic glucose control.

Author: Karlsson FH, Tremaroli V, Nookaew I, Bergström G, Behre CJ, Fagerberg B, Nielsen J, Bäckhed F

Lab: Department of Chemical and Biological Engineering, Chalmers University of Technology, SE-412 96 Gothenburg, Sweden.

PMID: 23719380

Examples

```
KarlssonFH_2013.metaphlan_bugs_list.stool()
```

LeChatelierE_2013 *Data from the LeChatelierE_2013 study*

Description

Data from the LeChatelierE_2013 study

Datasets

LeChatelierE_2013.genefamilies_relab.stool: An ExpressionSet with 292 samples and 1,519,375 features specific to the stool body site

LeChatelierE_2013.marker_abundance.stool: An ExpressionSet with 292 samples and 130,620 features specific to the stool body site

LeChatelierE_2013.marker_presence.stool: An ExpressionSet with 292 samples and 117,257 features specific to the stool body site

LeChatelierE_2013.metaphlan_bugs_list.stool: An ExpressionSet with 292 samples and 1,542 features specific to the stool body site

LeChatelierE_2013.pathabundance_relab.stool: An ExpressionSet with 292 samples and 13,504 features specific to the stool body site

LeChatelierE_2013.pathcoverage.stool: An ExpressionSet with 292 samples and 13,504 features specific to the stool body site

Exploratory Data Analysis

An EDA figure is available in the HTML documentation

An EDA figure is available in the HTML documentation

An EDA figure is available in the HTML documentation

An EDA figure is available in the HTML documentation

Source

Title: Richness of human gut microbiome correlates with metabolic markers.

Author: Le Chatelier E, Nielsen T, Qin J, Prifti E, Hildebrand F, Falony G, Almeida M, Arumugam M, Batto JM, Kennedy S, Leonard P, Li J, Burgdorf K, Grarup N, Jørgensen T, Brandslund I, Nielsen HB, Juncker AS, Bertalan M, Levenez F, Pons N, Rasmussen S, Sunagawa S, Tap J, Tims S, Zoetendal EG, Brunak S, Clément K, Doré J, Kleerebezem M, Kristiansen K, Renault P, Sicheritz-Ponten T, de Vos WM, Zucker JD, Raes J, Hansen T, Bork P, Wang J, Ehrlich SD, Pedersen O, Guedon E, Delorme C, Layec S, Khaci G, van de Guchte M, Vandemeulebrouck G, Jamet A, Dervyn R, Sanchez N, Maguin E, Haimet F, Winogradski Y, Cultrone A, Leclerc M, Juste C, Blottière H, Pelletier E, LePaslier D, Artiguenave F, Bruls T, Weissenbach J, Turner K, Parkhill J, Antolin M, Manichanh C, Casellas F, Boruel N, Varela E, Torrejon A, Guarner F, Denariaz G, Derrien M, van Hylckama Vlieg JE, Veiga P, Oozeer R, Knol J, Rescigno M, Brechot C, M'Rini C, Mérieux A, Yamada T

Lab: INRA, Institut National de la Recherche Agronomique, US1367 Metagenopolis, 78350 Jouy en Josas, France.

PMID: 23985870

Examples

```
LeChatelierE_2013.metaphlan_bugs_list.stool()
```

LiJ_2014	*Data from the LiJ_2014 study*

Description

Data from the LiJ_2014 study

Datasets

LiJ_2014.genefamilies_relab.stool: An ExpressionSet with 260 samples and 1,728,762 features specific to the stool body site

LiJ_2014.marker_abundance.stool: An ExpressionSet with 260 samples and 159,458 features specific to the stool body site

LiJ_2014.marker_presence.stool: An ExpressionSet with 260 samples and 144,690 features specific to the stool body site

LiJ_2014.metaphlan_bugs_list.stool: An ExpressionSet with 260 samples and 1,613 features specific to the stool body site

LiJ_2014.pathabundance_relab.stool: An ExpressionSet with 260 samples and 17,391 features specific to the stool body site

LiJ_2014.pathcoverage.stool: An ExpressionSet with 260 samples and 17,391 features specific to the stool body site

Source

Title: An integrated catalog of reference genes in the human gut microbiome.

Author: Li J, Jia H, Cai X, Zhong H, Feng Q, Sunagawa S, Arumugam M, Kultima JR, Prifti E, Nielsen T, Juncker AS, Manichanh C, Chen B, Zhang W, Levenez F, Wang J, Xu X, Xiao L, Liang S, Zhang D, Zhang Z, Chen W, Zhao H, Al-Aama JY, Edris S, Yang H, Wang J, Hansen T, Nielsen HB, Brunak S, Kristiansen K, Guarner F, Pedersen O, Dor<U+00E9> J, Ehrlich SD, Bork P, Wang J, Pons N, Le Chatelier E, Batto JM, Kennedy S, Haimet F, Winogradski Y, Pelletier E, LePaslier D, Artiguenave F, Bruls T, Weissenbach J, Turner K, Parkhill J, Antolin M, Casellas F, Borruel N, Varela E, Torrejon A, Denariaz G, Derrien M, van Hylckama Vlieg JE, Viega P, Oozeer R, Knoll J, Rescigno M, Brechot C, M'Rini C, M<U+00E9>rieux A, Yamada T, Tims S, Zoetendal EG, Kleerebezem M, de Vos WM, Cultrone A, Leclerc M, Juste C, Guedon E, Delorme C, Layec S, Khaci G, van de Guchte M, Vandemeulebrouck G, Jamet A, Dervyn R, Sanchez N, Blotti<U+00E8>re H, Maguin E, Renault P, Tap J, Mende DR

Lab: [1] 1] BGI-Shenzhen, Shenzhen, China. [2] BGI Hong Kong Research Institute, Hong Kong, China. [3] School of Bioscience and Biotechnology, South China University of Technology, Guangzhou, China. [4]., [2] 1] BGI-Shenzhen, Shenzhen, China. [2]., [3] 1] BGI-Shenzhen, Shenzhen, China. [2] Department of Biology, University of Copenhagen, Copenhagen, Denmark. [3]., [4] European Molecular Biology Laboratory, Heidelberg, Germany., [5] 1] BGI-Shenzhen, Shenzhen, China. [2] European Molecular Biology Laboratory, Heidelberg, Germany. [3] The Novo Nordisk Foundation Center for Basic Metabolic Research, Faculty of Health and Medical Sciences, University of Copenhagen, Copenhagen, Denmark., [6] INRA, Institut National de la Recherche Agronomique, Metagenopolis, Jouy en Josas, France., [7] The Novo Nordisk Foundation Center for Basic Metabolic Research, Faculty of Health and Medical Sciences, University of Copenhagen, Copenhagen, Denmark., [8] Center for Biological Sequence Analysis, Technical University of Denmark, Kongens Lyngby, Denmark., [9] Digestive System Research Unit, University Hospital Vall d'Hebron, Ciberehd, Barcelona, Spain., [10] BGI-Shenzhen, Shenzhen, China., [11] 1] Department of Genetic Medicine, Faculty of Medicine, King Abdulaziz University (KAU), Jeddah, Saudi Arabia. [2] Princess Al-Jawhara AlBrahim Centre of Excellence in Research of Hereditary Disorders (PACER-HD), Faculty of Medicine, KAU, Jeddah, Saudi Arabia., [12] 1] Princess Al-Jawhara AlBrahim Centre of Excellence in Research of Hereditary Disorders (PACER-HD), Faculty of Medicine, KAU, Jeddah, Saudi Arabia. [2] Department of Biological Sciences, Faculty of Science, King Abdulaziz University (KAU), Jeddah, Saudi Arabia., [13] 1] BGI-Shenzhen, Shenzhen, China. [2] Princess Al-Jawhara AlBrahim Centre of Excellence in Research of Hereditary Disorders (PACER-HD), Faculty of Medicine, KAU, Jeddah, Saudi Arabia. [3] James D. Watson Institute of Genome Science, Hangzhou, China., [14] 1] BGI-Shenzhen, Shenzhen, China. [2] James D. Watson Institute of Genome Science, Hangzhou, China., [15] Department of Biology, University of Copenhagen, Copenhagen, Denmark., [16] NA, [17] 1] INRA, Institut National de la Recherche Agronomique, Metagenopolis, Jouy en Josas, France. [2] Centre for Host-Microbiome Interactions, Dental Institute Central Office, King's College London, Guy's Hospital, London Bridge, UK., [18] NA, [19] 1] BGI-Shenzhen, Shenzhen, China. [2] Department of Biology, University of Copenhagen, Copenhagen, Denmark. [3] The Novo Nordisk Foundation Center for Basic Metabolic Research, Faculty of Health and Medical Sciences, University of Copenhagen, Copenhagen, Denmark. [4] Princess Al-Jawhara AlBrahim Centre of Excellence in Research of Hereditary Disorders (PACER-HD), Faculty of Medicine, KAU, Jeddah, Saudi Arabia. [5] Macau University of Science and Technology, Macau, China.

PMID: 24997786

Examples

```
LiJ_2014.metaphlan_bugs_list.stool()
```

LiuW_2016   *Data from the LiuW_2016 study*

Description

Data from the LiuW_2016 study

Datasets

LiuW_2016.genefamilies_relab.stool: An ExpressionSet with 110 samples and 1,178,616 features specific to the stool body site

LiuW_2016.marker_abundance.stool: An ExpressionSet with 110 samples and 81,028 features specific to the stool body site

LiuW_2016.marker_presence.stool: An ExpressionSet with 110 samples and 76,593 features specific to the stool body site

LiuW_2016.metaphlan_bugs_list.stool: An ExpressionSet with 110 samples and 1,078 features specific to the stool body site

LiuW_2016.pathabundance_relab.stool: An ExpressionSet with 110 samples and 12,647 features specific to the stool body site

LiuW_2016.pathcoverage.stool: An ExpressionSet with 110 samples and 12,647 features specific to the stool body site

Exploratory Data Analysis

An EDA figure is available in the HTML documentation

An EDA figure is available in the HTML documentation

Source

Title: Unique Features of Ethnic Mongolian Gut Microbiome revealed by metagenomic analysis.

Author: Liu W, Zhang J, Wu C, Cai S, Huang W, Chen J, Xi X, Liang Z, Hou Q, Zhou B, Qin N, Zhang H

Lab: Key Laboratory of Dairy Biotechnology and Engineering, Education Ministry of P. R. China, Department of Food Science and Engineering, Inner Mongolia Agricultural University, Hohhot 010018, China.

PMID: 27708392

Examples

```
LiuW_2016.metaphlan_bugs_list.stool()
```

LomanNJ_2013 *Data from the LomanNJ_2013 study*

Description

Data from the LomanNJ_2013 study

Datasets

LomanNJ_2013.genefamilies_relab.stool: An ExpressionSet with 43 samples and 716,332 features specific to the stool body site

LomanNJ_2013.marker_abundance.stool: An ExpressionSet with 43 samples and 56,517 features specific to the stool body site

LomanNJ_2013.marker_presence.stool: An ExpressionSet with 43 samples and 53,285 features specific to the stool body site

LomanNJ_2013.metaphlan_bugs_list.stool: An ExpressionSet with 43 samples and 736 features specific to the stool body site

LomanNJ_2013.pathabundance_relab.stool: An ExpressionSet with 43 samples and 8,657 features specific to the stool body site

LomanNJ_2013.pathcoverage.stool: An ExpressionSet with 43 samples and 8,657 features specific to the stool body site

Exploratory Data Analysis

An EDA figure is available in the HTML documentation

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An EDA figure is available in the HTML documentation

Source

Title: A culture-independent sequence-based metagenomics approach to the investigation of an outbreak of Shiga-toxigenic Escherichia coli O104:H4.

Author: Loman NJ, Constantinidou C, Christner M, Rohde H, Chan JZ, Quick J, Weir JC, Quince C, Smith GP, Betley JR, Aepfelbacher M, Pallen MJ

Lab: Institute of Microbiology and Infection, University of Birmingham, Birmingham, England.

PMID: 23571589

Examples

```
LomanNJ_2013.metaphlan_bugs_list.stool()
```

---

mergeData   *Title Merge a list of curatedMetagenomicData datasets*

Description

This function merges a list of ExpressionSet objects produced by the curatedMetagenomicData()
function into a single ExpressionSet. It is recommended to use this functions only on a list of
datasets of the same data type (for example, all metaphlan_bugs_list datasets).

Usage

```
mergeData(obj, sampledelim = ":", studycolname = "studyID")
```

Arguments

obj   A list or SimpleList containing an ExpressionSet in each element

sampledelim   If a character vector of length one is provided, for example ":" (default) then
               sample names in the merged ExpressionSet will combine study identifier with
               sample identifier in the form studyID:sampleID. If not a character vector of
               length one, then sample names from the original studies will be preserved. Can
               be set to NULL to keep the sample names of the original studies.

studycolname   If a character vector of length one is provided (default: studyID), a column with
               this name will be added to the phenoData, containing study IDs taken from the
               names of the ExpressionSet object.

Value

an ExpressionSet object

Examples

```
oral <- c("BritoIL_2016.metaphlan_bugs_list.oralcavity",
          "Castro-NallarE_2015.metaphlan_bugs_list.oralcavity")
esl <- curatedMetagenomicData(oral, dryrun = FALSE)
eset <- mergeData(esl)
eset
pseq <- ExpressionSet2phyloseq(eset)
pseq
```

NielsenHB_2014   *Data from the NielsenHB_2014 study*

Description

Data from the NielsenHB_2014 study

Datasets

NielsenHB_2014.genefamilies_relab.stool: An ExpressionSet with 396 samples and 1,730,383 features specific to the stool body site

NielsenHB_2014.marker_abundance.stool: An ExpressionSet with 396 samples and 222,837 features specific to the stool body site

NielsenHB_2014.marker_presence.stool: An ExpressionSet with 396 samples and 188,446 features specific to the stool body site

NielsenHB_2014.metaphlan_bugs_list.stool: An ExpressionSet with 396 samples and 1,939 features specific to the stool body site

NielsenHB_2014.pathabundance_relab.stool: An ExpressionSet with 396 samples and 17,280 features specific to the stool body site

NielsenHB_2014.pathcoverage.stool: An ExpressionSet with 396 samples and 17,280 features specific to the stool body site

Exploratory Data Analysis

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Source

Title: Identification and assembly of genomes and genetic elements in complex metagenomic samples without using reference genomes.

Author: Nielsen HB, Almeida M, Juncker AS, Rasmussen S, Li J, Sunagawa S, Plichta DR, Gautier L, Pedersen AG, Le Chatelier E, Pelletier E, Bonde I, Nielsen T, Manichanh C, Arumugam M, Batto JM, Quintanilha Dos Santos MB, Blom N, Borruel N, Burgdorf KS, Boumezbeur F, Casellas F, Doré J, Dworzynski P, Guarner F, Hansen T, Hildebrand F, Kaas RS, Kennedy S, Kristiansen K, Kultima JR, Léonard P, Levenez F, Lund O, Moumen B, Le Paslier D, Pons N, Pedersen O, Prifti E, Qin J, Raes J, Sørensen S, Tap J, Tims S, Ussery DW, Yamada T, Renault P, Sicheritz-Ponten T, Bork P, Wang J, Brunak S, Ehrlich SD, Nielsen HB, Almeida M, Juncker AS, Rasmussen S, Li J, Sunagawa S, Plichta DR, Gautier L, Pedersen AG, Le Chatelier E, Pelletier E, Bonde I, Nielsen T, Manichanh C, Arumugam M, Batto JM, Quintanilha Dos Santos MB, Blom N, Borruel N, Burgdorf KS, Boumezbeur F, Casellas F, Doré J, Dworzynski P, Guarner F, Hansen T, Hildebrand F, Kaas RS, Kennedy S, Kristiansen K, Kultima JR, Leonard P, Levenez F, Lund O, Moumen B, Le Paslier D, Pons N, Pedersen O, Prifti E, Qin J, Raes J, Sørensen S, Tap J, Tims S, Ussery DW, Yamada T, Renault P, Sicheritz-Ponten T, Bork P, Wang J, Brunak S, Ehrlich SD, Jamet A, Mérieux A, Cultrone A, Torrejon A, Quinquis B, Brechot C, Delorme C, M'Rini C, de Vos WM, Maguin E, Varela E, Guedon E, Gwen F, Haimet F, Artiguenave F, Vandemeulebrouck G, Denariaz G, Khaci G, Blottière H, Knol J, Weissenbach J, van Hylckama Vlieg JE, Torben J, Parkhill J, Turner K, van de Guchte M, Antolin M, Rescigno M, Kleerebezem M, Derrien M, Galleron N, Sanchez N, Grarup N, Veiga P, Oozeer R, Dervyn R, Layec S, Bruls T, Winogradski Y, Erwin G Z

Lab: [1] Center for Biological Sequence Analysis, Technical University of Denmark, Kongens Lyngby, Denmark. [2] Novo Nordisk Foundation Center for Biosustainability, Technical University of Denmark, Kongens Lyngby, Denmark. [3].

PMID: 24997787

Examples

```
NielsenHB_2014.metaphlan_bugs_list.stool()
```

Obregon-TitoAJ_2015   *Data from the Obregon-TitoAJ_2015 study*

Description

Data from the Obregon-TitoAJ_2015 study

Datasets

Obregon-TitoAJ_2015.genefamilies_relab.stool: An ExpressionSet with 58 samples and 1,192,381 features specific to the stool body site

Obregon-TitoAJ_2015.marker_abundance.stool: An ExpressionSet with 58 samples and 195,319 features specific to the stool body site

Obregon-TitoAJ_2015.marker_presence.stool: An ExpressionSet with 58 samples and 150,346 features specific to the stool body site

Obregon-TitoAJ_2015.metaphlan_bugs_list.stool: An ExpressionSet with 58 samples and 1,548 features specific to the stool body site

Obregon-TitoAJ_2015.pathabundance_relab.stool: An ExpressionSet with 58 samples and 10,438 features specific to the stool body site

Obregon-TitoAJ_2015.pathcoverage.stool: An ExpressionSet with 58 samples and 10,438 features specific to the stool body site

Exploratory Data Analysis

An EDA figure is available in the HTML documentation

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Source

>   **Title:** Subsistence strategies in traditional societies distinguish gut microbiomes.

>   **Author:** Obregon-Tito AJ, Tito RY, Metcalf J, Sankaranarayanan K, Clemente JC, Ursell LK, Zech Xu Z, Van Treuren W, Knight R, Gaffney PM, Spicer P, Lawson P, Marin-Reyes L, Trujillo-Villarroel O, Foster M, Guija-Poma E, Troncoso-Corzo L, Warinner C, Ozga AT, Lewis CM

>   **Lab:** [1] Department of Anthropology, University of Oklahoma, Dale Hall Tower, 521 Norman, Oklahoma 73019, USA [2] Universidad Cientifica del Sur, Lima 18, Peru [3] City of Hope, NCI-designated Comprehensive Cancer Center, Duarte, California 91010, USA.

>   **PMID:** 25807110

Examples

```
`Obregon-TitoAJ_2015.metaphlan_bugs_list.stool`()
```

OhJ_2014   *Data from the OhJ_2014 study*

Description

>   Data from the OhJ_2014 study

Datasets

>   **OhJ_2014.genefamilies_relab.skin:** An ExpressionSet with 291 samples and 3,956,472 features specific to the skin body site

>   **OhJ_2014.marker_abundance.skin:** An ExpressionSet with 291 samples and 202,657 features specific to the skin body site

>   **OhJ_2014.marker_presence.skin:** An ExpressionSet with 291 samples and 184,914 features specific to the skin body site

>   **OhJ_2014.metaphlan_bugs_list.skin:** An ExpressionSet with 291 samples and 2,461 features specific to the skin body site

>   **OhJ_2014.pathabundance_relab.skin:** An ExpressionSet with 291 samples and 48,536 features specific to the skin body site

>   **OhJ_2014.pathcoverage.skin:** An ExpressionSet with 291 samples and 48,536 features specific to the skin body site

Exploratory Data Analysis

>   An EDA figure is available in the HTML documentation

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>   An EDA figure is available in the HTML documentation

Source

Title: Biogeography and individuality shape function in the human skin metagenome.

Author: Oh J, Byrd AL, Deming C, Conlan S, Kong HH, Segre JA, Barnabas B, Blakesley R, Bouffard G, Brooks S, Coleman H, Dekhtyar M, Gregory M, Guan X, Gupta J, Han J, Ho SL, Legaspi R, Maduro Q, Masiello C, Maskeri B, McDowell J, Montemayor C, Mullikin J, Park M, Riebow N, Schandler K, Schmidt B, Sison C, Stantripop M, Thomas J, Thomas P, Vemulapalli M, Young A

Lab: Translational and Functional Genomics Branch, National Human Genome Research Institute, NIH, Bethesda, Maryland 20892, USA.

PMID: 25279917

Examples

```
OhJ_2014.metaphlan_bugs_list.skin()
```

QinJ_2012   *Data from the QinJ_2012 study*

Description

Data from the QinJ_2012 study

Datasets

QinJ_2012.genefamilies_relab.stool: An ExpressionSet with 363 samples and 1,690,773 features specific to the stool body site

QinJ_2012.marker_abundance.stool: An ExpressionSet with 363 samples and 132,933 features specific to the stool body site

QinJ_2012.marker_presence.stool: An ExpressionSet with 363 samples and 125,126 features specific to the stool body site

QinJ_2012.metaphlan_bugs_list.stool: An ExpressionSet with 363 samples and 1,588 features specific to the stool body site

QinJ_2012.pathabundance_relab.stool: An ExpressionSet with 363 samples and 18,478 features specific to the stool body site

QinJ_2012.pathcoverage.stool: An ExpressionSet with 363 samples and 18,478 features specific to the stool body site

Exploratory Data Analysis

An EDA figure is available in the HTML documentation
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An EDA figure is available in the HTML documentation
An EDA figure is available in the HTML documentation
An EDA figure is available in the HTML documentation

Source

Title: A metagenome-wide association study of gut microbiota in type 2 diabetes.

Author: Qin J, Li Y, Cai Z, Li S, Zhu J, Zhang F, Liang S, Zhang W, Guan Y, Shen D, Peng Y, Zhang D, Jie Z, Wu W, Qin Y, Xue W, Li J, Han L, Lu D, Wu P, Dai Y, Sun X, Li Z, Tang A, Zhong S, Li X, Chen W, Xu R, Wang M, Feng Q, Gong M, Yu J, Zhang Y, Zhang M, Hansen T, Sanchez G, Raes J, Falony G, Okuda S, Almeida M, LeChatelier E, Renault P, Pons N, Batto JM, Zhang Z, Chen H, Yang R, Zheng W, Li S, Yang H, Wang J, Ehrlich SD, Nielsen R, Pedersen O, Kristiansen K, Wang J

Lab: BGI-Shenzhen, Shenzhen 518083, China.

PMID: 23023125

Examples

```
QinJ_2012.metaphlan_bugs_list.stool()
```

QinN_2014   *Data from the QinN_2014 study*

Description

Data from the QinN_2014 study

Datasets

QinN_2014.genefamilies_relab.stool: An ExpressionSet with 237 samples and 1,747,533 features specific to the stool body site

QinN_2014.marker_abundance.stool: An ExpressionSet with 237 samples and 132,774 features specific to the stool body site

QinN_2014.marker_presence.stool: An ExpressionSet with 237 samples and 126,096 features specific to the stool body site

QinN_2014.metaphlan_bugs_list.stool: An ExpressionSet with 237 samples and 1,512 features specific to the stool body site

QinN_2014.pathabundance_relab.stool: An ExpressionSet with 237 samples and 19,418 features specific to the stool body site

QinN_2014.pathcoverage.stool: An ExpressionSet with 237 samples and 19,418 features specific to the stool body site

Exploratory Data Analysis

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Source

Title: Alterations of the human gut microbiome in liver cirrhosis.

Author: Qin N, Yang F, Li A, Prifti E, Chen Y, Shao L, Guo J, Le Chatelier E, Yao J, Wu L, Zhou J, Ni S, Liu L, Pons N, Batto JM, Kennedy SP, Leonard P, Yuan C, Ding W, Chen Y, Hu X, Zheng B, Qian G, Xu W, Ehrlich SD, Zheng S, Li L

Lab: [1] State Key Laboratory for Diagnosis and Treatment of Infectious Disease, The First Affiliated Hospital, College of Medicine, Zhejiang University, 310003 Hangzhou, China [2] Collaborative Innovation Center for Diagnosis and Treatment of Infectious Diseases, Zhejiang University, 310003 Hangzhou, China [3].

PMID: 25079328

Examples

```
QinN_2014.metaphlan_bugs_list.stool()
```

RampelliS_2015   *Data from the RampelliS_2015 study*

Description

Data from the RampelliS_2015 study

Datasets

RampelliS_2015.genefamilies_relab.stool: An ExpressionSet with 38 samples and 788,640 features specific to the stool body site

RampelliS_2015.marker_abundance.stool: An ExpressionSet with 38 samples and 50,394 features specific to the stool body site

RampelliS_2015.marker_presence.stool: An ExpressionSet with 38 samples and 47,455 features specific to the stool body site

RampelliS_2015.metaphlan_bugs_list.stool: An ExpressionSet with 38 samples and 727 features specific to the stool body site

RampelliS_2015.pathabundance_relab.stool: An ExpressionSet with 38 samples and 6,798 features specific to the stool body site

RampelliS_2015.pathcoverage.stool: An ExpressionSet with 38 samples and 6,798 features specific to the stool body site

Exploratory Data Analysis

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Source

Title: Metagenome Sequencing of the Hadza Hunter-Gatherer Gut Microbiota.

Author: Rampelli S, Schnorr SL, Consolandi C, Turroni S, Severgnini M, Peano C, Brigidi P, Crittenden AN, Henry AG, Candela M

Lab: Department of Pharmacy and Biotechnology, University of Bologna, Bologna 40126, Italy.

PMID: 25981789

Examples

```
RampelliS_2015.metaphlan_bugs_list.stool()
```

RaymondF_2016 *Data from the RaymondF_2016 study*

Description

Data from the RaymondF_2016 study

Datasets

RaymondF_2016.genefamilies_relab.stool: An ExpressionSet with 72 samples and 1,060,132 features specific to the stool body site

RaymondF_2016.marker_abundance.stool: An ExpressionSet with 72 samples and 72,992 features specific to the stool body site

RaymondF_2016.marker_presence.stool: An ExpressionSet with 72 samples and 70,705 features specific to the stool body site

RaymondF_2016.metaphlan_bugs_list.stool: An ExpressionSet with 72 samples and 834 features specific to the stool body site

RaymondF_2016.pathabundance_relab.stool: An ExpressionSet with 72 samples and 8,562 features specific to the stool body site

RaymondF_2016.pathcoverage.stool: An ExpressionSet with 72 samples and 8,562 features specific to the stool body site

Exploratory Data Analysis

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Source

Title: The initial state of the human gut microbiome determines its reshaping by antibiotics.

Author: Raymond F, Ouameur AA, Déraspe M, Iqbal N, Gingras H, Dridi B, Leprohon P, Plante PL, Giroux R, Bérubé NA, Frenette J, Boudreau DK, Simard JL, Chabot I, Domingo MC, Trottier S, Boissinot M, Huletsky A, Roy PH, Ouellette M, Bergeron MG, Corbeil J

Lab: Centre de Recherche en Infectiologie, CHU de Quebec-Universite Laval, Quebec, Canada.

PMID: 26359913

Examples

```
RaymondF_2016.metaphlan_bugs_list.stool()
```

SchirmerM_2016   *Data from the SchirmerM_2016 study*

Description

Data from the SchirmerM_2016 study

Datasets

SchirmerM_2016.genefamilies_relab.stool: An ExpressionSet with 471 samples and 1,396,085 features specific to the stool body site

SchirmerM_2016.marker_abundance.stool: An ExpressionSet with 471 samples and 104,930 features specific to the stool body site

SchirmerM_2016.marker_presence.stool: An ExpressionSet with 471 samples and 101,457 features specific to the stool body site

SchirmerM_2016.metaphlan_bugs_list.stool: An ExpressionSet with 471 samples and 1,177 features specific to the stool body site

SchirmerM_2016.pathabundance_relab.stool: An ExpressionSet with 471 samples and 12,707 features specific to the stool body site

SchirmerM_2016.pathcoverage.stool: An ExpressionSet with 471 samples and 12,707 features specific to the stool body site

Exploratory Data Analysis

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Source

Title: Linking the Human Gut Microbiome to Inflammatory Cytokine Production Capacity.

Author: Schirmer M, Smeekens SP, Vlamakis H, Jaeger M, Oosting M, Franzosa EA, Horst RT, Jansen T, Jacobs L, Bonder MJ, Kurilshikov A, Fu J, Joosten LA, Zhernakova A, Huttenhower C, Wijmenga C, Netea MG, Xavier RJ

Lab: NA

PMID: 27984736

Examples

```
SchirmerM_2016.metaphlan_bugs_list.stool()
```

TettAJ_2016 *Data from the TettAJ_2016 study*

Description

Data from the TettAJ_2016 study

Datasets

TettAJ_2016.genefamilies_relab.skin: An ExpressionSet with 97 samples and 1,183,853 features specific to the skin body site

TettAJ_2016.marker_abundance.skin: An ExpressionSet with 97 samples and 64,039 features specific to the skin body site

TettAJ_2016.marker_presence.skin: An ExpressionSet with 97 samples and 57,428 features specific to the skin body site

TettAJ_2016.metaphlan_bugs_list.skin: An ExpressionSet with 97 samples and 1,004 features specific to the skin body site

TettAJ_2016.pathabundance_relab.skin: An ExpressionSet with 97 samples and 21,899 features specific to the skin body site

TettAJ_2016.pathcoverage.skin: An ExpressionSet with 97 samples and 21,899 features specific to the skin body site

Exploratory Data Analysis

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> An EDA figure is available in the HTML documentation

Source

> **Title:** NA
>
> **Author:** NA
>
> **Lab:** NA
>
> **PMID:** NA

Examples

```
TettAJ_2016.metaphlan_bugs_list.skin()
```

VatanenT_2016 *Data from the VatanenT_2016 study*

Description

> Data from the VatanenT_2016 study

Datasets

> **VatanenT_2016.genefamilies_relab.stool:** An ExpressionSet with 785 samples and 1,719,634 features specific to the stool body site
>
> **VatanenT_2016.marker_abundance.stool:** An ExpressionSet with 785 samples and 135,979 features specific to the stool body site
>
> **VatanenT_2016.marker_presence.stool:** An ExpressionSet with 785 samples and 131,625 features specific to the stool body site
>
> **VatanenT_2016.metaphlan_bugs_list.stool:** An ExpressionSet with 785 samples and 1,584 features specific to the stool body site
>
> **VatanenT_2016.pathabundance_relab.stool:** An ExpressionSet with 785 samples and 19,236 features specific to the stool body site
>
> **VatanenT_2016.pathcoverage.stool:** An ExpressionSet with 785 samples and 19,236 features specific to the stool body site

Exploratory Data Analysis

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Source

Title: Variation in Microbiome LPS Immunogenicity Contributes to Autoimmunity in Humans.

Author: Vatanen T, Kostic AD, d'Hennezel E, Siljander H, Franzosa EA, Yassour M, Kolde R, Vlamakis H, Arthur TD, Hämäläinen AM, Peet A, Tillmann V, Uibo R, Mokurov S, Dorshakova N, Ilonen J, Virtanen SM, Szabo SJ, Porter JA, Lähdesmäki H, Huttenhower C, Gevers D, Cullen TW, Knip M, Xavier RJ

Lab: NA

PMID: 27259157

Examples

```
VatanenT_2016.metaphlan_bugs_list.stool()
```

VincentC_2016   *Data from the VincentC_2016 study*

Description

Data from the VincentC_2016 study

Datasets

VincentC_2016.genefamilies_relab.stool: An ExpressionSet with 229 samples and 1,513,277 features specific to the stool body site

VincentC_2016.marker_abundance.stool: An ExpressionSet with 229 samples and 116,377 features specific to the stool body site

VincentC_2016.marker_presence.stool: An ExpressionSet with 229 samples and 110,951 features specific to the stool body site

VincentC_2016.metaphlan_bugs_list.stool: An ExpressionSet with 229 samples and 1,452 features specific to the stool body site

VincentC_2016.pathabundance_relab.stool: An ExpressionSet with 229 samples and 16,254 features specific to the stool body site

VincentC_2016.pathcoverage.stool: An ExpressionSet with 229 samples and 16,254 features specific to the stool body site

Exploratory Data Analysis

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Source

Title: Bloom and bust: intestinal microbiota dynamics in response to hospital exposures and Clostridium difficile colonization or infection.

Author: Vincent C, Miller MA, Edens TJ, Mehrotra S, Dewar K, Manges AR

Lab: Department of Microbiology and Immunology, McGill University, Montreal, Quebec, Canada.

PMID: 26975510

Examples

```
VincentC_2016.metaphlan_bugs_list.stool()
```

VogtmannE_2016   *Data from the VogtmannE_2016 study*

Description

Data from the VogtmannE_2016 study

Datasets

VogtmannE_2016.genefamilies_relab.stool: An ExpressionSet with 110 samples and 2,229,881 features specific to the stool body site

VogtmannE_2016.marker_abundance.stool: An ExpressionSet with 110 samples and 1,009,074 features specific to the stool body site

VogtmannE_2016.marker_presence.stool: An ExpressionSet with 110 samples and 986,069 features specific to the stool body site

VogtmannE_2016.metaphlan_bugs_list.stool: An ExpressionSet with 110 samples and 11,432 features specific to the stool body site

VogtmannE_2016.pathabundance_relab.stool: An ExpressionSet with 110 samples and 18,706 features specific to the stool body site

VogtmannE_2016.pathcoverage.stool: An ExpressionSet with 110 samples and 18,706 features specific to the stool body site

Exploratory Data Analysis

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Source

Title: Colorectal Cancer and the Human Gut Microbiome: Reproducibility with Whole-Genome Shotgun Sequencing.

Author: Vogtmann E, Hua X, Zeller G, Sunagawa S, Voigt AY, Hercog R, Goedert JJ, Shi J, Bork P, Sinha R

Lab: Division of Cancer Epidemiology & Genetics, National Cancer Institute, Bethesda, Maryland, United States of America.

PMID: 27171425

Examples

```
VogtmannE_2016.metaphlan_bugs_list.stool()
```

XieH_2016   *Data from the XieH_2016 study*

Description

Data from the XieH_2016 study

Datasets

XieH_2016.genefamilies_relab.stool: An ExpressionSet with 250 samples and 1,743,159 features specific to the stool body site

XieH_2016.marker_abundance.stool: An ExpressionSet with 250 samples and 142,530 features specific to the stool body site

XieH_2016.marker_presence.stool: An ExpressionSet with 250 samples and 129,776 features specific to the stool body site

XieH_2016.metaphlan_bugs_list.stool: An ExpressionSet with 250 samples and 1,551 features specific to the stool body site

XieH_2016.pathabundance_relab.stool: An ExpressionSet with 250 samples and 15,880 features specific to the stool body site

XieH_2016.pathcoverage.stool: An ExpressionSet with 250 samples and 15,880 features specific to the stool body site

Exploratory Data Analysis

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Source

Title: Shotgun Metagenomics of 250 Adult Twins Reveals Genetic and Environmental Impacts on the Gut Microbiome.

Author: Xie H, Guo R, Zhong H, Feng Q, Lan Z, Qin B, Ward KJ, Jackson MA, Xia Y, Chen X, Chen B, Xia H, Xu C, Li F, Xu X, Al-Aama JY, Yang H, Wang J, Kristiansen K, Wang J, Steves CJ, Bell JT, Li J, Spector TD, Jia H

Lab: BGI-Shenzhen, Shenzhen 518083, China; China National Genebank-Shenzhen, BGI-Shenzhen, Shenzhen 518083, China.

PMID: 27818083

Examples

```
XieH_2016.metaphlan_bugs_list.stool()
```

YuJ_2015   *Data from the YuJ_2015 study*

Description

Data from the YuJ_2015 study

Datasets

YuJ_2015.genefamilies_relab.stool: An ExpressionSet with 128 samples and 1,532,931 features specific to the stool body site

YuJ_2015.marker_abundance.stool: An ExpressionSet with 128 samples and 125,243 features specific to the stool body site

YuJ_2015.marker_presence.stool: An ExpressionSet with 128 samples and 117,525 features specific to the stool body site

YuJ_2015.metaphlan_bugs_list.stool: An ExpressionSet with 128 samples and 1,405 features specific to the stool body site

YuJ_2015.pathabundance_relab.stool: An ExpressionSet with 128 samples and 15,487 features specific to the stool body site

YuJ_2015.pathcoverage.stool: An ExpressionSet with 128 samples and 15,487 features specific to the stool body site

Exploratory Data Analysis

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Source

Title: Metagenomic analysis of faecal microbiome as a tool towards targeted non-invasive biomarkers for colorectal cancer.

Author: Yu J, Feng Q, Wong SH, Zhang D, Liang QY, Qin Y, Tang L, Zhao H, Stenvang J, Li Y, Wang X, Xu X, Chen N, Wu WK, Al-Aama J, Nielsen HJ, Kiilerich P, Jensen BA, Yau TO, Lan Z, Jia H, Li J, Xiao L, Lam TY, Ng SC, Cheng AS, Wong VW, Chan FK, Xu X, Yang H, Madsen L, Datz C, Tilg H, Wang J, Brünner N, Kristiansen K, Arumugam M, Sung JJ, Wang J

Lab: Department of Medicine & Therapeutics, State Key Laboratory of Digestive Disease, Institute of Digestive Disease, LKS Institute of Health Sciences, CUHK Shenzhen Research Institute, The Chinese University of Hong Kong, Hong Kong.

PMID: 26408641

Examples

```
YuJ_2015.metaphlan_bugs_list.stool()
```

ZellerG_2014 *Data from the ZellerG_2014 study*

Description

Data from the ZellerG_2014 study

Datasets

ZellerG_2014.genefamilies_relab.stool: An ExpressionSet with 199 samples and 2,040,556 features specific to the stool body site

ZellerG_2014.marker_abundance.stool: An ExpressionSet with 199 samples and 828,890 features specific to the stool body site

ZellerG_2014.marker_presence.stool: An ExpressionSet with 199 samples and 735,085 features specific to the stool body site

ZellerG_2014.metaphlan_bugs_list.stool: An ExpressionSet with 199 samples and 10,503 features specific to the stool body site

ZellerG_2014.pathabundance_relab.stool: An ExpressionSet with 199 samples and 19,367 features specific to the stool body site

ZellerG_2014.pathcoverage.stool: An ExpressionSet with 199 samples and 19,367 features specific to the stool body site

Exploratory Data Analysis

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Source

Title: Potential of fecal microbiota for early-stage detection of colorectal cancer.

Author: Zeller G, Tap J, Voigt AY, Sunagawa S, Kultima JR, Costea PI, Amiot A, Böhm J, Brunetti F, Habermann N, Hercog R, Koch M, Luciani A, Mende DR, Schneider MA, Schrotz-King P, Tournigand C, Tran Van Nhieu J, Yamada T, Zimmermann J, Benes V, Kloor M, Ulrich CM, von Knebel Doeberitz M, Sobhani I, Bork P

Lab: Structural and Computational Biology Unit, European Molecular Biology Laboratory, Heidelberg, Germany.

PMID: 25432777

Examples

```
ZellerG_2014.metaphlan_bugs_list.stool()
```

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