

Package ‘curatedMetagenomicData’

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Type Package

Title Curated Metagenomic Data of the Human Microbiome

Version 1.2.2

Author Lucas Schiffer <schiffer.lucas@gmail.com>,
Edoardo Pasolli <edoardo.pasolli@unitn.it>,
Levi Waldron <lwaldron.research@gmail.com>,
Faizan Malik <faizankmalik2012@yahoo.com>,
Nicola Segata <nicola.segata@unitn.it>,
Valerie Obenchain <Valerie.Obenchain@roswellpark.org>,
Morgan Martin <martin.morgan@roswellpark.org>

Maintainer Lucas Schiffer <schiffer.lucas@gmail.com>

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 (>= 3.3.0), dplyr (>= 0.5.0), phyloseq (>= 1.18.0), Biobase (>= 2.34.0), ExperimentHub (>= 1.0.0), AnnotationHub (>= 2.6.0), magrittr

Imports BiocInstaller, utils, tidyr, metagenomeSeq

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

VignetteBuilder knitr

biocViews Homo_sapiens_Data, ReproducibleResearch, MicrobiomeData

RoxygenNote 6.0.1

NeedsCompilation no

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combined_metadata	<i>Combined metadata of all studies in curatedMetagenomicData</i>
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Description

The combined sample level metadata of all studies in curatedMetagenomicData.

Usage

```
combined_metadata
```

Format

A data.frame with 2875 rows and 128 variables:

dataset_name Dataset name
sampleID Sample identifier
subjectID Subject identifier
first Identifier associated with the sampleID
repeat Samples with the same repeat number were acquired from the same subject
stooltexture Stool texture
daysafteronset Days after onset of diarrhea
hus Hemolytic-uremic syndrome
stec_count Colony counts of STEC from samples (low < 10⁴; moderate 10⁴ to 10⁶; high > 10⁶ colony-forming units/mL)
shigatoxin2elisa Shiga-toxin 2 enzyme-linked immunosorbent assay
readsmillions Number of original reads (millions)

nonhuman Percentage of sequenced reads that did not align against the humane refence genome and thus were used in futher analysis

stec_coverage Average coverage of the chromosome of the STEC O104:H4 reference genome

stxab_detected Shiga-toxin gene detected

stx_ratio Ratio of reads mapping to the Shiga-toxin genes to the reads mapping to STEC chromosomal loci

typingdata Whether information on the serotype (H4) and the multilocus sequence type for the outbreak strain could be recovered from the sample sequences

c_difficile_frequency Prediceted abundance of Clostridium difficile relative to other bacterial species detected in the sample in the MetaPhlAn analysis

disease Disease presence and type

bodysite Bodysite of acquisition

country Country of acquisition

sequencing_technology Sequencing technology

pubmedid Identifier of the main publication in PubMed

number_reads Number of final reads

age Subject age (years)

gender Subject gender

camp Camp name

total_initial_reads Number of initial reads

quality_control Number of reads after quality control

pasi Psoriasis Area and Severity Index (PASI)

bsa Body surface area (BSA)

age_of_onset Age of disease onset

arthritis Has the subject arthritis

type Psoriasis type

antibiotic_usage Has the subject used antibiotics

population Subject population

bmi Body mass index (kg/m²)

bmi_class Body mass index class

16s_rrna 16S rRNA analysis performed in the study

shotgun_metagenome Shotgun metagenomic analysis performed in the study

ethnicity Subject ethnicity

classification Classification

gad-antibodies Glutamic acid decarboxylase antibodies (for units see Bingley et al. Diabetes 52; 1128-1136; 2003)

whr Waist-to-hip ratio (cm/cm)

wc Waist circumference (cm)

cholesterol Cholesterol (mmol/L)

triglycerides Triglycerides (mmol/L)

hdl High-density lipoprotein (mmol/L)

ldl Low-density lipoprotein (mmol/L)
creatinine Creatinine (?mol/L)
y-gt ?-glutamyltransferase (?kat/L)
fasting_glucose Fasting glucose (mmol/L)
fasting_insulin Fasting Insulin (mU/L)
hba1c Glycosylated hemoglobin A1c (mmol/mol)
adiponectin Adiponectin (mg/L)
leptin Leptin (?g/L)
glp-1 Glucagon-like peptide 1 (pmol/L)
fgf-19 Fibroblast growth factor 19 (pg/ml)
hsgrp High-sensitivity C-reactive protein (mg/L)
c-peptide C-peptide (nmol/L)
tnfa Tumor necrosis factor ? (ng/L)
il-1 Interleukin 1 (pg/ml)
cd163 Cluster of differentiation 163 (ng/ml)
statins Statins
insulin Insulin
oral_anti-diabetic_medication Oral anti-diabetic medication (meth: metformin; sulph: sulphonylurea)
years_in_sweden Years in Sweden
designation Sample designation
age_range Subject age range (years)
site_symmetry Syte and symmetry of sample acquisition
affected Affected syte
method Acquisition method
site_characteristic Syte characteristic
estimated_median_insert_size Estimated median insert size
reported_as_failed_qc Number of reads reported as failed QC
uniquely_align_to_human Number of reads uniquely aligned to human
non_uniquely_align_to_human_with_0_2_mismatches Number of reads non-uniquely aligned to human with 0-2 mismatches
reads_removed_because_of_read_pair_trimming_discrepancy Number of reads removed because of read pair trimming discrepancy
too_short_after_quality_trimming(<50bp) Number of reads too short after quality trimming (<50bp)
tnm_stage TNM stage of the tumor
ajcc_stage AJCC stage of the tumor (na: no classification for healthy controls or adenomas)
localization Localization of the tumor/adenoma (rc: right colon; lc: left colon; lc/rc: multiple localizations; sigma: sigma; rectum: rectum)
fobt Result of the fecal occult blood test (FOBT)
wif-1_gene_methylation_test Result of the wif-1 gene methylation test
group Sample group (control: healthy controls and patients with small adenomas; crc: patients with CRC; na: patients with large adenoma not included)

stage Acquisition stage/phase
cirrhotic Is the subject cirrhotic
hbv_related Cirrhosis related to HBV
alcohol_related Cirrhosis related to alcohol
other_causes_related Cirrhosis related to other causes
inr INR
crea Crea (umol/L)
alb Alb (g/L)
tb TB (umol/L)
pt PT (S)
ascites Ascites
he HE
ctp CTP
meld MELD
antivirus Antivirus
beta-blocker beta-blocker
paired_end_insert_size Paired-end insert size (bp)
read_length Read length (bp)
matched_reads Number of matched reads
uniquely_matching_reads Number of uniquely matching reads
uniquely_matched_reads Number of uniquely matched reads (two paired end reads that matched the same gene were counted as one read)
gene_number Gene number
gene_number_for_11M_uniquely_matched_reads Gene number for 11 M uniquely matched reads
hitchip_probe_number HITChip probe number
gene_count_class Gene count class
hitchip_probe_class HITChip Probe class
height Subject height (cm)
weight Subject weight (kg)
diabetic Is the subject diabetic
fbg Fasting blood glucose (mmol/L)
sbp Systolic blood pressure (mm Hg)
dbp Diastolic blood pressure (mm Hg)
fins Fasting serum insulin (mU/L)
fcp Fasting serum C-peptide (ng/ml)
hbalc Glycosylated hemoglobin HbA1c (%)
tg Triglyceride (mmol/L)
tcho Total cholesterol (mmol/L)
sampling_day Sampling day (relative to September 20th 2007)
dfmp Known consumers of a defined fermented milk product (DFMP)
mgs_richness MGS richness
mgs_profile_matched_sample_pairs MGS profile matched sample pairs
visit_number Visit number
snprnt SNPRNT
wmsphase Acquisition stage/phase

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 approximately 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 ordinary 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_Mi.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)
```

Arguments

eset	An eset object
simplify	if TRUE the most detailed clade name is used
relab	if FALSE, values are multiplied by read depth to approximate counts, if TRUE (default) values kept as relative abundances between 0 and 100%.

Value

A phyloseq object

Examples

```
LomanNJ_2013_Mi.metaphlan_bugs_list.stool() %>%
  ExpressionSet2phyloseq()
```

HMP_2012

Data from the HMP_2012 study

Description

Data from the HMP_2012 study

Datasets

HMP_2012.genefamilies_relab.anterior_nares: An ExpressionSet with 93 samples and 1,964,481 features specific to the anterior_nares bodysite

HMP_2012.genefamilies_relab.buccal_mucosa: An ExpressionSet with 119 samples and 1,964,481 features specific to the buccal_mucosa bodysite

HMP_2012.genefamilies_relab.hard_palate: An ExpressionSet with 1 sample and 1,964,481 features specific to the hard_palate bodysite

HMP_2012.genefamilies_relab.keratinized_gingiva: An ExpressionSet with 6 samples and 1,964,481 features specific to the keratinized_gingiva bodysite

HMP_2012.genefamilies_relab.l_retroauricular_crease: An ExpressionSet with 9 samples and 1,964,481 features specific to the l_retroauricular_crease bodysite

HMP_2012.genefamilies_relab.mid_vagina: An ExpressionSet with 2 samples and 1,964,481 features specific to the mid_vagina bodysite

HMP_2012.genefamilies_relab.palatine_tonsils: An ExpressionSet with 6 samples and 1,964,481 features specific to the palatine_tonsils bodysite

HMP_2012.genefamilies_relab.posterior_fornix: An ExpressionSet with 62 samples and 1,964,481 features specific to the posterior_fornix bodysite

HMP_2012.genefamilies_relab.r_retroauricular_crease: An ExpressionSet with 18 samples and 1,964,481 features specific to the r_retroauricular_crease bodysite

HMP_2012.genefamilies_relab.saliva: An ExpressionSet with 5 samples and 1,964,481 features specific to the saliva bodysite

HMP_2012.genefamilies_relab.stool: An ExpressionSet with 147 samples and 1,964,481 features specific to the stool bodysite

HMP_2012.genefamilies_relab.subgingival_plaque: An ExpressionSet with 7 samples and 1,964,481 features specific to the subgingival_plaque bodysite

HMP_2012.genefamilies_relab.supragingival_plaque: An ExpressionSet with 128 samples and 1,964,481 features specific to the supragingival_plaque bodysite

HMP_2012.genefamilies_relab.throat: An ExpressionSet with 7 samples and 1,964,481 features specific to the throat bodysite

HMP_2012.genefamilies_relab.tongue_dorsum: An ExpressionSet with 136 samples and 1,964,481 features specific to the tongue_dorsum bodysite

HMP_2012.genefamilies_relab.vaginal_introitus: An ExpressionSet with 3 samples and 1,964,481 features specific to the vaginal_introitus bodysite

HMP_2012.marker_abundance.anterior_nares: An ExpressionSet with 93 samples and 162,108 features specific to the anterior_nares bodysite

HMP_2012.marker_abundance.buccal_mucosa: An ExpressionSet with 119 samples and 162,108 features specific to the buccal_mucosa bodysite

HMP_2012.marker_abundance.hard_palate: An ExpressionSet with 1 sample and 162,108 features specific to the hard_palate bodysite

HMP_2012.marker_abundance.keratinized_gingiva: An ExpressionSet with 6 samples and 162,108 features specific to the keratinized_gingiva bodysite

HMP_2012.marker_abundance.l_retroauricular_crease: An ExpressionSet with 9 samples and 162,108 features specific to the l_retroauricular_crease bodysite

HMP_2012.marker_abundance.mid_vagina: An ExpressionSet with 2 samples and 162,108 features specific to the mid_vagina bodysite

HMP_2012.marker_abundance.palatine_tonsils: An ExpressionSet with 6 samples and 162,108 features specific to the palatine_tonsils bodysite

HMP_2012.marker_abundance.posterior_fornix: An ExpressionSet with 62 samples and 162,108 features specific to the posterior_fornix bodysite

HMP_2012.marker_abundance.r_retroauricular_crease: An ExpressionSet with 18 samples and 162,108 features specific to the r_retroauricular_crease bodysite

HMP_2012.marker_abundance.saliva: An ExpressionSet with 5 samples and 162,108 features specific to the saliva bodysite

HMP_2012.marker_abundance.stool: An ExpressionSet with 147 samples and 162,108 features specific to the stool bodysite

HMP_2012.marker_abundance.subgingival_plaque: An ExpressionSet with 7 samples and 162,108 features specific to the subgingival_plaque bodysite

HMP_2012.marker_abundance.supragingival_plaque: An ExpressionSet with 128 samples and 162,108 features specific to the supragingival_plaque bodysite

HMP_2012.marker_abundance.throat: An ExpressionSet with 7 samples and 162,108 features specific to the throat bodysite

HMP_2012.marker_abundance.tongue_dorsum: An ExpressionSet with 136 samples and 162,108 features specific to the tongue_dorsum bodysite

HMP_2012.marker_abundance.vaginal_introitus: An ExpressionSet with 3 samples and 162,108 features specific to the vaginal_introitus bodysite

HMP_2012.marker_presence.anterior_nares: An ExpressionSet with 93 samples and 158,646 features specific to the anterior_nares bodysite

HMP_2012.marker_presence.buccal_mucosa: An ExpressionSet with 119 samples and 158,646 features specific to the buccal_mucosa bodysite

HMP_2012.marker_presence.hard_palate: An ExpressionSet with 1 sample and 158,646 features specific to the hard_palate bodysite

HMP_2012.marker_presence.keratinized_gingiva: An ExpressionSet with 6 samples and 158,646 features specific to the keratinized_gingiva bodysite

HMP_2012.marker_presence.l_retroauricular_crease: An ExpressionSet with 9 samples and 158,646 features specific to the l_retroauricular_crease bodysite

HMP_2012.marker_presence.mid_vagina: An ExpressionSet with 2 samples and 158,646 features specific to the mid_vagina bodysite

HMP_2012.marker_presence.palatine_tonsils: An ExpressionSet with 6 samples and 158,646 features specific to the palatine_tonsils bodysite

HMP_2012.marker_presence.posterior_fornix: An ExpressionSet with 62 samples and 158,646 features specific to the posterior_fornix bodysite

HMP_2012.marker_presence.r_retroauricular_crease: An ExpressionSet with 18 samples and 158,646 features specific to the r_retroauricular_crease bodysite

HMP_2012.marker_presence.saliva: An ExpressionSet with 5 samples and 158,646 features specific to the saliva bodysite

HMP_2012.marker_presence.stool: An ExpressionSet with 147 samples and 158,646 features specific to the stool bodysite

HMP_2012.marker_presence.subgingival_plaque: An ExpressionSet with 7 samples and 158,646 features specific to the subgingival_plaque bodysite

HMP_2012.marker_presence.supragingival_plaque: An ExpressionSet with 128 samples and 158,646 features specific to the supragingival_plaque bodysite

HMP_2012.marker_presence.throat: An ExpressionSet with 7 samples and 158,646 features specific to the throat bodysite

HMP_2012.marker_presence.tongue_dorsum: An ExpressionSet with 136 samples and 158,646 features specific to the tongue_dorsum bodysite

HMP_2012.marker_presence.vaginal_introitus: An ExpressionSet with 3 samples and 158,646 features specific to the vaginal_introitus bodysite

HMP_2012.metaphlan_bugs_list.anterior_nares: An ExpressionSet with 93 samples and 1,988 features specific to the anterior_nares bodysite

HMP_2012.metaphlan_bugs_list.buccal_mucosa: An ExpressionSet with 119 samples and 1,988 features specific to the buccal_mucosa bodysite

HMP_2012.metaphlan_bugs_list.hard_palate: An ExpressionSet with 1 sample and 1,988 features specific to the hard_palate bodysite

HMP_2012.metaphlan_bugs_list.keratinized_gingiva: An ExpressionSet with 6 samples and 1,988 features specific to the keratinized_gingiva bodysite

HMP_2012.metaphlan_bugs_list.l_retroauricular_crease: An ExpressionSet with 9 samples and 1,988 features specific to the l_retroauricular_crease bodysite

HMP_2012.metaphlan_bugs_list.mid_vagina: An ExpressionSet with 2 samples and 1,988 features specific to the mid_vagina bodysite

HMP_2012.metaphlan_bugs_list.palatine_tonsils: An ExpressionSet with 6 samples and 1,988 features specific to the palatine_tonsils bodysite

HMP_2012.metaphlan_bugs_list.posterior_fornix: An ExpressionSet with 62 samples and 1,988 features specific to the posterior_fornix bodysite

HMP_2012.metaphlan_bugs_list.r_retroauricular_crease: An ExpressionSet with 18 samples and 1,988 features specific to the r_retroauricular_crease bodysite

HMP_2012.metaphlan_bugs_list.saliva: An ExpressionSet with 5 samples and 1,988 features specific to the saliva bodysite

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

HMP_2012.metaphlan_bugs_list.subgingival_plaque: An ExpressionSet with 7 samples and 1,988 features specific to the subgingival_plaque bodysite

HMP_2012.metaphlan_bugs_list.supragingival_plaque: An ExpressionSet with 128 samples and 1,988 features specific to the supragingival_plaque bodysite

HMP_2012.metaphlan_bugs_list.throat: An ExpressionSet with 7 samples and 1,988 features specific to the throat bodysite

HMP_2012.metaphlan_bugs_list.tongue_dorsum: An ExpressionSet with 136 samples and 1,988 features specific to the tongue_dorsum bodysite

HMP_2012.metaphlan_bugs_list.vaginal_introitus: An ExpressionSet with 3 samples and 1,988 features specific to the vaginal_introitus bodysite

HMP_2012.pathabundance_relab.anterior_nares: An ExpressionSet with 93 samples and 23,271 features specific to the anterior_nares bodysite

HMP_2012.pathabundance_relab.buccal_mucosa: An ExpressionSet with 119 samples and 23,271 features specific to the buccal_mucosa bodysite

HMP_2012.pathabundance_relab.hard_palate: An ExpressionSet with 1 sample and 23,271 features specific to the hard_palate bodysite

HMP_2012.pathabundance_relab.keratinized_gingiva: An ExpressionSet with 6 samples and 23,271 features specific to the keratinized_gingiva bodysite

HMP_2012.pathabundance_relab.l_retroauricular_crease: An ExpressionSet with 9 samples and 23,271 features specific to the l_retroauricular_crease bodysite

HMP_2012.pathabundance_relab.mid_vagina: An ExpressionSet with 2 samples and 23,271 features specific to the mid_vagina bodysite

HMP_2012.pathabundance_relab.palatine_tonsils: An ExpressionSet with 6 samples and 23,271 features specific to the palatine_tonsils bodysite

HMP_2012.pathabundance_relab.posterior_fornix: An ExpressionSet with 62 samples and 23,271 features specific to the posterior_fornix bodysite

HMP_2012.pathabundance_relab.r_retroauricular_crease: An ExpressionSet with 18 samples and 23,271 features specific to the r_retroauricular_crease bodysite

HMP_2012.pathabundance_relab.saliva: An ExpressionSet with 5 samples and 23,271 features specific to the saliva bodysite

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

HMP_2012.pathabundance_relab.subgingival_plaque: An ExpressionSet with 7 samples and 23,271 features specific to the subgingival_plaque bodysite

HMP_2012.pathabundance_relab.supragingival_plaque: An ExpressionSet with 128 samples and 23,271 features specific to the supragingival_plaque bodysite

HMP_2012.pathabundance_relab.throat: An ExpressionSet with 7 samples and 23,271 features specific to the throat bodysite

HMP_2012.pathabundance_relab.tongue_dorsum: An ExpressionSet with 136 samples and 23,271 features specific to the tongue_dorsum bodysite

HMP_2012.pathabundance_relab.vaginal_introitus: An ExpressionSet with 3 samples and 23,271 features specific to the vaginal_introitus bodysite

HMP_2012.pathcoverage.anterior_nares: An ExpressionSet with 93 samples and 23,271 features specific to the anterior_nares bodysite

HMP_2012.pathcoverage.buccal_mucosa: An ExpressionSet with 119 samples and 23,271 features specific to the buccal_mucosa bodysite

HMP_2012.pathcoverage.hard_palate: An ExpressionSet with 1 sample and 23,271 features specific to the hard_palate bodysite

HMP_2012.pathcoverage.keratinized_gingiva: An ExpressionSet with 6 samples and 23,271 features specific to the keratinized_gingiva bodysite

HMP_2012.pathcoverage.l_retroauricular_crease: An ExpressionSet with 9 samples and 23,271 features specific to the l_retroauricular_crease bodysite

HMP_2012.pathcoverage.mid_vagina: An ExpressionSet with 2 samples and 23,271 features specific to the mid_vagina bodysite

HMP_2012.pathcoverage.palatine_tonsils: An ExpressionSet with 6 samples and 23,271 features specific to the palatine_tonsils bodysite

HMP_2012.pathcoverage.posterior_fornix: An ExpressionSet with 62 samples and 23,271 features specific to the posterior_fornix bodysite

HMP_2012.pathcoverage.r_retroauricular_crease: An ExpressionSet with 18 samples and 23,271 features specific to the r_retroauricular_crease bodysite

HMP_2012.pathcoverage.saliva: An ExpressionSet with 5 samples and 23,271 features specific to the saliva bodysite

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

HMP_2012.pathcoverage.subgingival_plaque: An ExpressionSet with 7 samples and 23,271 features specific to the subgingival_plaque bodysite

HMP_2012.pathcoverage.supragingival_plaque: An ExpressionSet with 128 samples and 23,271 features specific to the supragingival_plaque bodysite

HMP_2012.pathcoverage.throat: An ExpressionSet with 7 samples and 23,271 features specific to the throat bodysite

HMP_2012.pathcoverage.tongue_dorsum: An ExpressionSet with 136 samples and 23,271 features specific to the tongue_dorsum bodysite

HMP_2012.pathcoverage.vaginal_introitus: An ExpressionSet with 3 samples and 23,271 features specific to the vaginal_introitus bodysite

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

An EDA figure is available in the HTML documentation

Source

Title: Self-esteem: a comparative study of adolescents from mainstream and minority religious groups in Pakistan.

Author: Iqbal S, Ahmad R, Ayub N

Lab: Department of Psychology, Abdul Haq Campus, Federal Urdu University for Arts, Science and Technology, Karachi, Pakistan. shahiq_psy@yahoo.com

PMID: 22699828

Examples

```
HMP_2012.genefamilies_relab.anterior_nares()
```

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 1,415,610 features specific to the stool bodysite

KarlssonFH_2013.marker_abundance.stool: An ExpressionSet with 145 samples and 101,168 features specific to the stool bodysite

KarlssonFH_2013.marker_presence.stool: An ExpressionSet with 145 samples and 95,322 features specific to the stool bodysite

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

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

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

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

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.genefamilies_relab.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 1,519,376 features specific to the stool bodysite

LeChatelierE_2013.marker_abundance.stool: An ExpressionSet with 292 samples and 130,621 features specific to the stool bodysite

LeChatelierE_2013.marker_presence.stool: An ExpressionSet with 292 samples and 117,258 features specific to the stool bodysite

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

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

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

Exploratory Data Analysis

An EDA figure is available in the HTML documentation

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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, Denariáz 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.genefamilies_relab.stool()
```

LomanNJ_2013_Hi	<i>Data from the LomanNJ_2013_Hi study</i>
-----------------	--

Description

Data from the LomanNJ_2013_Hi study

Datasets

LomanNJ_2013_Hi.genefamilies_relab.stool: An ExpressionSet with 44 samples and 718,320 features specific to the stool bodysite

LomanNJ_2013_Hi.marker_abundance.stool: An ExpressionSet with 44 samples and 56,689 features specific to the stool bodysite

LomanNJ_2013_Hi.marker_presence.stool: An ExpressionSet with 44 samples and 53,443 features specific to the stool bodysite

LomanNJ_2013_Hi.metaphlan_bugs_list.stool: An ExpressionSet with 44 samples and 736 features specific to the stool bodysite

LomanNJ_2013_Hi.pathabundance_relab.stool: An ExpressionSet with 44 samples and 8,716 features specific to the stool bodysite

LomanNJ_2013_Hi.pathcoverage.stool: An ExpressionSet with 44 samples and 8,716 features specific to the stool bodysite

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_Hi.genefamilies_relab.stool()
```

LomanNJ_2013_Mi

Data from the LomanNJ_2013_Mi study

Description

Data from the LomanNJ_2013_Mi study

Datasets

LomanNJ_2013_Mi.genefamilies_relab.stool: An ExpressionSet with 9 samples and 337,637 features specific to the stool bodysite

LomanNJ_2013_Mi.marker_abundance.stool: An ExpressionSet with 9 samples and 24,228 features specific to the stool bodysite

LomanNJ_2013_Mi.marker_presence.stool: An ExpressionSet with 9 samples and 22,710 features specific to the stool bodysite

LomanNJ_2013_Mi.metaphlan_bugs_list.stool: An ExpressionSet with 9 samples and 399 features specific to the stool bodysite

LomanNJ_2013_Mi.pathabundance_relab.stool: An ExpressionSet with 9 samples and 4,606 features specific to the stool bodysite

LomanNJ_2013_Mi.pathcoverage.stool: An ExpressionSet with 9 samples and 4,606 features specific to the stool bodysite

Exploratory Data Analysis

An EDA figure is available in the HTML documentation

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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_Mi.genefamilies_relab.stool()
```

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 1,730,384 features specific to the stool bodysite

NielsenHB_2014.marker_abundance.stool: An ExpressionSet with 396 samples and 222,838 features specific to the stool bodysite

NielsenHB_2014.marker_presence.stool: An ExpressionSet with 396 samples and 188,447 features specific to the stool bodysite

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

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

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

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, Boumezeur 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, Boumezeur 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, Denariáz 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.genefamilies_relab.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 1,192,382 features specific to the stool bodysite

Obregon_TitoAJ_2015.marker_abundance.stool: An ExpressionSet with 58 samples and 195,320 features specific to the stool bodysite

Obregon_TitoAJ_2015.marker_presence.stool: An ExpressionSet with 58 samples and 150,347 features specific to the stool bodysite

Obregon_TitoAJ_2015.metaphlan_bugs_list.stool: An ExpressionSet with 58 samples and 1,548 features specific to the stool bodysite

Obregon_TitoAJ_2015.pathabundance_relab.stool: An ExpressionSet with 58 samples and 10,438 features specific to the stool bodysite

Obregon_TitoAJ_2015.pathcoverage.stool: An ExpressionSet with 58 samples and 10,438 features specific to the stool bodysite

Exploratory Data Analysis

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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.genefamilies_relab.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 3,956,473 features specific to the skin bodysite

OhJ_2014.marker_abundance.skin: An ExpressionSet with 291 samples and 202,658 features specific to the skin bodysite

OhJ_2014.marker_presence.skin: An ExpressionSet with 291 samples and 184,915 features specific to the skin bodysite

OhJ_2014.metaphlan_bugs_list.skin: An ExpressionSet with 291 samples and 2,461 features specific to the skin bodysite

OhJ_2014.pathabundance_relab.skin: An ExpressionSet with 291 samples and 48,536 features specific to the skin bodysite

OhJ_2014.pathcoverage.skin: An ExpressionSet with 291 samples and 48,536 features specific to the skin bodysite

Exploratory Data Analysis

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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.genefamilies_relab.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 1,690,774 features specific to the stool bodysite

QinJ_2012.marker_abundance.stool: An ExpressionSet with 363 samples and 132,934 features specific to the stool bodysite

QinJ_2012.marker_presence.stool: An ExpressionSet with 363 samples and 125,127 features specific to the stool bodysite

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

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

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

Exploratory Data Analysis

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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.genefamilies_relab.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 1,747,534 features specific to the stool bodysite

QinN_2014.marker_abundance.stool: An ExpressionSet with 237 samples and 132,775 features specific to the stool bodysite

QinN_2014.marker_presence.stool: An ExpressionSet with 237 samples and 126,097 features specific to the stool bodysite

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

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

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

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.genefamilies_relab.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 788,641 features specific to the stool bodysite

RampelliS_2015.marker_abundance.stool: An ExpressionSet with 38 samples and 50,395 features specific to the stool bodysite

RampelliS_2015.marker_presence.stool: An ExpressionSet with 38 samples and 47,456 features specific to the stool bodysite

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

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

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

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.genefamilies_relab.stool()
```

TettAJ_2016

Data from the TettAJ_2016 study

Description

Data from the TettAJ_2016 study

Datasets

TettAJ_2016.genefamilies_relab.left_ear: An ExpressionSet with 22 samples and 1,183,854 features specific to the left_ear bodysite

TettAJ_2016.genefamilies_relab.left_elbow: An ExpressionSet with 26 samples and 1,183,854 features specific to the left_elbow bodysite

TettAJ_2016.genefamilies_relab.right_ear: An ExpressionSet with 26 samples and 1,183,854 features specific to the right_ear bodysite

TettAJ_2016.genefamilies_relab.right_elbow: An ExpressionSet with 23 samples and 1,183,854 features specific to the right_elbow bodysite

TettAJ_2016.marker_abundance.left_ear: An ExpressionSet with 22 samples and 64,040 features specific to the left_ear bodysite

TettAJ_2016.marker_abundance.left_elbow: An ExpressionSet with 26 samples and 64,040 features specific to the left_elbow bodysite

TettAJ_2016.marker_abundance.right_ear: An ExpressionSet with 26 samples and 64,040 features specific to the right_ear bodysite

TettAJ_2016.marker_abundance.right_elbow: An ExpressionSet with 23 samples and 64,040 features specific to the right_elbow bodysite

TettAJ_2016.marker_presence.left_ear: An ExpressionSet with 22 samples and 57,429 features specific to the left_ear bodysite

TettAJ_2016.marker_presence.left_elbow: An ExpressionSet with 26 samples and 57,429 features specific to the left_elbow bodysite

TettAJ_2016.marker_presence.right_ear: An ExpressionSet with 26 samples and 57,429 features specific to the right_ear bodysite

TettAJ_2016.marker_presence.right_elbow: An ExpressionSet with 23 samples and 57,429 features specific to the right_elbow bodysite

TettAJ_2016.metaphlan_bugs_list.left_ear: An ExpressionSet with 22 samples and 1,004 features specific to the left_ear bodysite

TettAJ_2016.metaphlan_bugs_list.left_elbow: An ExpressionSet with 26 samples and 1,004 features specific to the left_elbow bodysite

TettAJ_2016.metaphlan_bugs_list.right_ear: An ExpressionSet with 26 samples and 1,004 features specific to the right_ear bodysite

TettAJ_2016.metaphlan_bugs_list.right_elbow: An ExpressionSet with 23 samples and 1,004 features specific to the right_elbow bodysite

TettAJ_2016.pathabundance_relab.left_ear: An ExpressionSet with 22 samples and 21,899 features specific to the left_ear bodysite

TettAJ_2016.pathabundance_relab.left_elbow: An ExpressionSet with 26 samples and 21,899 features specific to the left_elbow bodysite

TettAJ_2016.pathabundance_relab.right_ear: An ExpressionSet with 26 samples and 21,899 features specific to the right_ear bodysite

TettAJ_2016.pathabundance_relab.right_elbow: An ExpressionSet with 23 samples and 21,899 features specific to the right_elbow bodysite

TettAJ_2016.pathcoverage.left_ear: An ExpressionSet with 22 samples and 21,899 features specific to the left_ear bodysite

TettAJ_2016.pathcoverage.left_elbow: An ExpressionSet with 26 samples and 21,899 features specific to the left_elbow bodysite

TettAJ_2016.pathcoverage.right_ear: An ExpressionSet with 26 samples and 21,899 features specific to the right_ear bodysite

TettAJ_2016.pathcoverage.right_elbow: An ExpressionSet with 23 samples and 21,899 features specific to the right_elbow bodysite

Exploratory Data Analysis

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Source

Title: Experimental metagenomics and ribosomal profiling of the human skin microbiome

Author: NA

Lab: NA

PMID: 27623553

Examples

```
TettAJ_2016.genefamilies_relab.left_ear()
```

ZellerG_2014

Data from the ZellerG_2014 study

Description

Data from the ZellerG_2014 study

Datasets

ZellerG_2014.genefamilies_relab.stool: An ExpressionSet with 156 samples and 1,796,274 features specific to the stool bodysite

ZellerG_2014.marker_abundance.stool: An ExpressionSet with 156 samples and 130,272 features specific to the stool bodysite

ZellerG_2014.marker_presence.stool: An ExpressionSet with 156 samples and 126,622 features specific to the stool bodysite

ZellerG_2014.metaphlan_bugs_list.stool: An ExpressionSet with 156 samples and 1,505 features specific to the stool bodysite

ZellerG_2014.pathabundance_relab.stool: An ExpressionSet with 156 samples and 17,888 features specific to the stool bodysite

ZellerG_2014.pathcoverage.stool: An ExpressionSet with 156 samples and 17,888 features specific to the stool bodysite

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.genefamilies_relab.stool()
```

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