Package ‘curatedMetagenomicData’

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Type Package

Title Curated Metagenomic Data of the Human Microbiome

Version 1.12.3

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

VignetteBuilder knitr

biocViews Homo_sapiens_Data, ReproducibleResearch, MicrobiomeData, ExperimentHub

RoxygenNote 6.1.0

git_url https://git.bioconductor.org/packages/curatedMetagenomicData

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git_last_commit_date 2018-11-04

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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 53,078 features specific to the milk body site

AsnicarF_2017.marker_abundance.stool: An ExpressionSet with 16 samples and 53,078 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

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: [1] Centre for Integrative Biology, University of Trento, Trento, Italy., [2] Azienda Provinciale per i Servizi Sanitari, Trento, Italy.

PMID: 28144631

Examples

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

`Bengtsson-PalmeJ_2015` *Data from the Bengtsson-PalmeJ_2015 study*

Description

Data from the Bengtsson-PalmeJ_2015 study

Datasets

Bengtsson-PalmeJ_2015.genefamilies_relab.stool: An ExpressionSet with 70 samples and 1,301,172 features specific to the stool body site

Bengtsson-PalmeJ_2015.marker_abundance.stool: An ExpressionSet with 70 samples and 105,814 features specific to the stool body site

Bengtsson-PalmeJ_2015.marker_presence.stool: An ExpressionSet with 70 samples and 93,375 features specific to the stool body site

Bengtsson-PalmeJ_2015.metaphlan_bugs_list.stool: An ExpressionSet with 70 samples and 1,220 features specific to the stool body site

Bengtsson-PalmeJ_2015.pathabundance_relab.stool: An ExpressionSet with 70 samples and 10,641 features specific to the stool body site

Bengtsson-PalmeJ_2015.pathcoverage.stool: An ExpressionSet with 70 samples and 10,641 features specific to the stool body site

Source

Title: The Human Gut Microbiome as a Transporter of Antibiotic Resistance Genes between Continents.

Author: Bengtsson-Palme J, Angelin M, Huss M, Kjellqvist S, Kristiansson E, Palmgren H, Larsson DG, Johansson A

Lab: [1] Department of Infectious Diseases, Institute of Biomedicine, The Sahlgrenska Academy, University of Gothenburg, Gothenburg, Sweden., [2] Department of Clinical Microbiology, Infectious Diseases, Umea University, Umea, Sweden., [3] Science for Life Laboratory, Department of Biochemistry and Biophysics, Stockholm University, Solna, Sweden., [4] Department of Mathematical Sciences, Chalmers University of Technology, Gothenburg, Sweden., [5] Laboratory for Molecular Infection Medicine Sweden, Department of Clinical Microbiology, Bacteriology, Umea University, Umea, Sweden anders.f.johansson@umu.se.

PMID: 26259788

Examples

```
`Bengtsson-PalmeJ_2015.metaphlan_bugs_list.stool`()
```

`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

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: [1] Department of Biological Engineering, Massachusetts Institute of Technology, Cambridge, MA., [2] Broad Institute of MIT and Harvard, Cambridge, MA., [3] Sandia National Laboratories, Livermore, CA., [4] Wildlife Conservation Society, Suva, Fiji., [5] Edith Cowan University, Western Australia., [6] University of Helsinki, Helsinki, Finland., [7] Massachusetts General Hospital, Boston, MA., [8] Center for Microbiome, Informatics and Therapeutics, Massachusetts Institute of Technology, Cambridge, MA.

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

Details

Note that Castro_NallarE_2015 is deprecated, use Castro-NallarE_2015 instead.

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

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: [1] Computational Biology Institute, George Washington University , Ashburn, VA , USA ; Center for Bioinformatics and Integrative Biology, Universidad Andres Bello, Facultad de Ciencias Biologicas , Santiago , Chile., [2] Computational Biology Institute, George Washington University , Ashburn, VA , USA., [3] Computational Biology Institute, George Washington University , Ashburn, VA , USA ; CIBIO-InBIO, Centro de Investigacao em Biodiversidade e Recursos Geneticos, Universidade do Porto , Vairao , USA ; Division of Emergency Medicine, Children's National Medical Center , Washington, D.C. , USA., [4] Stanley Neurovirology Laboratory, Johns Hopkins School of Medicine , Baltimore, MD , USA., [5] Sheppard Pratt Hospital , Baltimore, MD , USA., [6] Schroeder Statistical Consulting LLC , Ellicott City, MD , USA.

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 89,589 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

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: [1] Genome Institute of Singapore, Singapore 138672, Singapore., [2] Institute of Medical Biology, Singapore 138648, Singapore., [3] Institute of Molecular and Cell Biology, Singapore 138673, Singapore., [4] Department of Neurology, The First Affiliated Hospital of Zhengzhou University, Zhengzhou, Henan 450001, China., [5] Institute of Biomedical Studies, Baylor University, Waco, Texas 76798, USA., [6] Department of Biological Sciences, National University of Singapore, Singapore 117543., [7] Singapore Immunology Network, Singapore 138648, Singapore., [8] Division of Plastic, Reconstructive &Aesthetic Surgery, National University Health System, Singapore 119074, Singapore., [9] National Skin Centre, Singapore 308205, Singapore., [10] Department of Microbiology and Immunology, National University of Singapore, Singapore 117545, 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 12444 rows and 87 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.

NA NA

NA NA

NA NA

NA NA

NA NA

NA NA

NA NA

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 to treat x as a regular expression. If TRUE, ‘x‘ is provided to `glob2rx` first to generate a regular expression.

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)
```

`DavidLA_2015` *Data from the DavidLA_2015 study*

Description

Data from the DavidLA_2015 study

Datasets

DavidLA_2015.genefamilies_relab.stool: An ExpressionSet with 49 samples and 694,925 features specific to the stool body site

DavidLA_2015.marker_abundance.stool: An ExpressionSet with 49 samples and 57,862 features specific to the stool body site

DavidLA_2015.marker_presence.stool: An ExpressionSet with 49 samples and 55,487 features specific to the stool body site

DavidLA_2015.metaphlan_bugs_list.stool: An ExpressionSet with 49 samples and 892 features specific to the stool body site

DavidLA_2015.pathabundance_relab.stool: An ExpressionSet with 49 samples and 10,437 features specific to the stool body site

DavidLA_2015.pathcoverage.stool: An ExpressionSet with 49 samples and 10,437 features specific to the stool body site

Source

Title: Gut microbial succession follows acute secretory diarrhea in humans.

Author: David LA, Weil A, Ryan ET, Calderwood SB, Harris JB, Chowdhury F, Begum Y, Qadri F, LaRocque RC, Turnbaugh PJ

Lab: [1] Society of Fellows, Harvard University, Cambridge, Massachusetts, USA FAS Center for Systems Biology, Harvard University, Cambridge, Massachusetts, USA., [2] Center for Vaccine Sciences, International Centre for Diarrhoeal Disease Research, Dhaka, Bangladesh., [3] rclarocque@partners.org Peter.Turnbaugh@ucsf.edu., [4] FAS Center for Systems Biology, Harvard University, Cambridge, Massachusetts, USA rclarocque@partners.org Peter.Turnbaugh@ucsf.edu.

PMID: 25991682

Examples

```
DavidLA_2015.metaphlan_bugs_list.stool()
```

`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

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] 1] BGI-Shenzhen, Shenzhen 518083, China [2] Department of Biology, University of Copenhagen, Ole Maaloes Vej 5, 2200 Copenhagen, Denmark., [2] 1] BGI-Shenzhen, Shenzhen 518083, China [2] School of Bioscience and Biotechnology, South China University of Technology, Guangzhou 510006, China., [3] BGI-Shenzhen, Shenzhen 518083, China., [4] Department of Internal Medicine, Hospital Oberndorf, Teaching Hospital of the Paracelsus Private University of Salzburg, Paracelsusstrasse 37, 5110 Oberndorf, Austria., [5] 1] BGI-Shenzhen, Shenzhen 518083, China [2] School of Bioscience and Biotechnology, South China University of Technology, Guangzhou 510006, China [3] BGI Hong Kong Research Institute, Hong Kong, China., [6] 1] BGI-Shenzhen, Shenzhen 518083, China [2] Princess Al Jawhara Center of Excellence in the Research of Hereditary Disorders, King Abdulaziz University, Jeddah 21589, Saudi Arabia., [7] 1] BGI-Shenzhen, Shenzhen 518083, China [2] The Novo Nordisk Foundation Center for Basic Metabolic Research, Faculty of Health and Medical Sciences, University of Copenhagen, 2200 Copenhagen, Denmark., [8] First Department of Internal Medicine, Medical University Innsbruck, Anichstrasse 35, 6020 Innsbruck, Austria., [9] 1] BGI-Shenzhen, Shenzhen 518083, China [2] Department of Biology, University of Copenhagen, Ole Maaloes Vej 5, 2200 Copenhagen, Denmark [3] Princess Al Jawhara Center of Excellence in the Research of Hereditary Disorders, King Abdulaziz University, Jeddah 21589, Saudi Arabia [4] Macau University of Science and Technology, Avenida Wai long, Taipa, Macau 999078, China.

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

Details

Note that Heitz_BuschartA_2016 is deprecated, use Heitz-BuschartA_2016 instead.

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

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: [1] Luxembourg Centre for Systems Biomedicine, 7 avenue des Hauts-Fourneaux, 4362 Esch-sur-Alzette, Luxembourg., [2] Integrated BioBank of Luxembourg, 6 rue Nicolas Ernest Barble, 1210 Luxembourg, Luxembourg., [3] Department of Internal Medicine II, Saarland University Medical Center, 66421 Homburg, Germany., [4] Centre Hospitalier Emile Mayrisch, Rue Emile Mayrisch, 4240 Esch-sur-Alzette, Luxembourg., [5] Clinique Pediatrique - Centre Hospitalier de Luxembourg, 4 rue Nicolas Ernest Barble, 1210 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 93 samples and 1,964,480 features specific to the nasalcavity body site

HMP_2012.genefamilies_relab.oralcavity: An ExpressionSet with 415 samples and 1,964,480 features specific to the oralcavity body site

HMP_2012.genefamilies_relab.skin: An ExpressionSet with 27 samples and 1,964,480 features specific to the skin 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 67 samples and 1,964,480 features specific to the vagina body site

HMP_2012.marker_abundance.nasalcavity: An ExpressionSet with 93 samples and 162,107 features specific to the nasalcavity body site

HMP_2012.marker_abundance.oralcavity: An ExpressionSet with 415 samples and 162,107 features specific to the oralcavity body site

HMP_2012.marker_abundance.skin: An ExpressionSet with 27 samples and 162,107 features specific to the skin 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 67 samples and 162,107 features specific to the vagina body site

HMP_2012.marker_presence.nasalcavity: An ExpressionSet with 93 samples and 158,645 features specific to the nasalcavity body site

HMP_2012.marker_presence.oralcavity: An ExpressionSet with 415 samples and 158,645 features specific to the oralcavity body site

HMP_2012.marker_presence.skin: An ExpressionSet with 27 samples and 158,645 features specific to the skin 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 67 samples and 158,645 features specific to the vagina body site

HMP_2012.metaphlan_bugs_list.nasalcavity: An ExpressionSet with 93 samples and 1,988 features specific to the nasalcavity body site

HMP_2012.metaphlan_bugs_list.oralcavity: An ExpressionSet with 415 samples and 1,988 features specific to the oralcavity body site

HMP_2012.metaphlan_bugs_list.skin: An ExpressionSet with 27 samples and 1,988 features specific to the skin 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 67 samples and 1,988 features specific to the vagina body site

HMP_2012.pathabundance_relab.nasalcavity: An ExpressionSet with 93 samples and 23,271 features specific to the nasalcavity body site

HMP_2012.pathabundance_relab.oralcavity: An ExpressionSet with 415 samples and 23,271 features specific to the oralcavity body site

HMP_2012.pathabundance_relab.skin: An ExpressionSet with 27 samples and 23,271 features specific to the skin 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 67 samples and 23,271 features specific to the vagina body site

HMP_2012.pathcoverage.nasalcavity: An ExpressionSet with 93 samples and 23,271 features specific to the nasalcavity body site

HMP_2012.pathcoverage.oralcavity: An ExpressionSet with 415 samples and 23,271 features specific to the oralcavity body site

HMP_2012.pathcoverage.skin: An ExpressionSet with 27 samples and 23,271 features specific to the skin 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 67 samples and 23,271 features specific to the vagina body site

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

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

PMID: 23719380

Examples

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

`KosticAD_2015` *Data from the KosticAD_2015 study*

Description

Data from the KosticAD_2015 study

Datasets

KosticAD_2015.genefamilies_relab.stool: An ExpressionSet with 124 samples and 994,216 features specific to the stool body site

KosticAD_2015.marker_abundance.stool: An ExpressionSet with 124 samples and 74,501 features specific to the stool body site

KosticAD_2015.marker_presence.stool: An ExpressionSet with 124 samples and 72,708 features specific to the stool body site

KosticAD_2015.metaphlan_bugs_list.stool: An ExpressionSet with 124 samples and 869 features specific to the stool body site

KosticAD_2015.pathabundance_relab.stool: An ExpressionSet with 124 samples and 10,948 features specific to the stool body site

KosticAD_2015.pathcoverage.stool: An ExpressionSet with 124 samples and 10,948 features specific to the stool body site

Source

Title: The dynamics of the human infant gut microbiome in development and in progression toward type 1 diabetes.

Author: Kostic AD, Gevers D, Siljander H, Vatanen T, Hyötyläinen T, Hämäläinen AM, Peet A, Tillmann V, Pöhö P, Mattila I, Lähdesmäki H, Franzosa EA, Vaarala O, de Goffau M, Harmsen H, Ilonen J, Virtanen SM, Clish CB, Orešič M, Huttenhower C, Knip M, Xavier RJ, Knip M, Koski K, Koski M, Härkönen T, Ryhänen S, Siljander H, Hämäläinen A, Ormisson A, Peet A, Tillmann V, Ulich V, Kuzmicheva E, Mokurov S, Markova S, Pylova S, Isakova M, Shakurova E, Petrov V, Dorshakova NV, Karapetyan T, Varlamova T, Ilonen J, Kiviniemi M, Alnek K, Janson H, Uibo R, Salum T, von Mutius E, Weber J, Ahlfors H, Kallionpää H, Laajala E, Lahesmaa R, Lähdesmäki H, Moulder R, Nieminen J, Ruohtula T, Vaarala O, Honkanen H, Hyöty H, Kondrashova A, Oikarinen S, Harmsen HJ, De Goffau MC, Welling G, Alahuhta K, Korhonen T, Virtanen SM

Lab: [1] Broad Institute of MIT and Harvard, Cambridge, MA 02142, USA; Center for Computational and Integrative Biology, Massachusetts General Hospital and Harvard Medical School, Boston, MA 02114, USA; Department of Biostatistics, Harvard School of Public Health, Boston, MA 02115, USA., [2] Broad Institute of MIT and Harvard, Cambridge, MA 02142, USA., [3] Children's Hospital, University of Helsinki and Helsinki University Hospital, 00290 Helsinki, Finland; Research Program Unit, Diabetes and Obesity, University of Helsinki, 00290 Helsinki, Finland., [4] Broad Institute of MIT and Harvard, Cambridge, MA 02142, USA; Department of Information and Computer Science, Aalto University School of Science, 02150 Espoo, Finland., [5] Steno Diabetes Center, 2820 Gentofte, Denmark; VTT Technical Research Centre of Finland, 02044 Espoo, Finland., [6] Department of Pediatrics, Jorvi Hospital, 02740 Espoo, Finland., [7] Department of Pediatrics, University of Tartu, Estonia and Tartu University Hospital, 51014 Tartu, Estonia., [8] Faculty of Pharmacy, University of Helsinki, 00290 Helsinki, Finland; VTT Technical Research Centre of Finland, 02044 Espoo, Finland., [9] Department of Information and Computer Science, Aalto University School of Science, 02150 Espoo, Finland., [10] Department of Biostatistics, Harvard School of Public Health, Boston, MA 02115, USA., [11] Research Program Unit, Diabetes and Obesity, University of Helsinki, 00290 Helsinki, Finland., [12] Department of Medical Microbiology, University Medical Center Groningen and University of Groningen, 9713 GZ Groningen, the Netherlands., [13] Immunogenetics Laboratory, University of Turku, 20520 Turku, Finland; Department of Clinical Microbiology, University of Eastern Finland, 70211 Kuopio, Finland., [14] Department of Lifestyle and Participation, National Institute for Health and Welfare, 00271 Helsinki, Finland; School of Health Sciences, University of Tampere, 33014 Tampere, Finland; Science Centre, Pirkanmaa Hospital District, 33521 Tampere, Finland., [15] Broad Institute of MIT and Harvard, Cambridge, MA 02142, USA; Department of Biostatistics, Harvard School of Public Health, Boston, MA 02115, USA., [16] Children's Hospital, University of Helsinki and Helsinki University Hospital, 00290 Helsinki, Finland; Research Program Unit, Diabetes and Obesity, University of Helsinki, 00290 Helsinki, Finland; Folkhalsan Research Center, 00290 Helsinki, Finland; Department of Pediatrics, Tampere University Hospital, 33521 Tampere, Finland., [17] Broad Institute of MIT and Harvard, Cambridge, MA 02142, USA; Center for Computational and Integrative Biology, Massachusetts General Hospital and Harvard Medical School, Boston, MA 02114, USA; Gastrointestinal Unit and Center for the Study of Inflammatory Bowel Disease, Massachusetts General Hospital and Harvard Medical School, Boston, MA 02114, USA; Center for Microbiome Informatics and Therapeutics, Massachusetts Institute of Technology, Cambridge, MA 02139, USA. Electronic address: xavier@molbio.mgh.harvard.edu.

PMID: 25662751

Examples

```
KosticAD_2015.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

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: [1] 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, Doré 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, Mérieux 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, Blottière 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] 1] INRA, Institut National de la Recherche Agronomique, Metagenopolis, Jouy en Josas, France. [2] INRA, Institut National de la Recherche Agronomique, Unite mixte de Recherche 14121 Microbiologie de l'Alimentation au Service de la Sante, Jouy en Josas, France., [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] 1] European Molecular Biology Laboratory, Heidelberg, Germany. [2] Max Delbruck Centre for Molecular Medicine, Berlin, Germany., [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()
```

`LiJ_2017` *Data from the LiJ_2017 study*

Description

Data from the LiJ_2017 study

Datasets

LiJ_2017.genefamilies_relab.stool: An ExpressionSet with 196 samples and 1,393,787 features specific to the stool body site

LiJ_2017.marker_abundance.stool: An ExpressionSet with 196 samples and 88,651 features specific to the stool body site

LiJ_2017.marker_presence.stool: An ExpressionSet with 196 samples and 82,679 features specific to the stool body site

LiJ_2017.metaphlan_bugs_list.stool: An ExpressionSet with 196 samples and 1,150 features specific to the stool body site

LiJ_2017.pathabundance_relab.stool: An ExpressionSet with 196 samples and 11,776 features specific to the stool body site

LiJ_2017.pathcoverage.stool: An ExpressionSet with 196 samples and 11,776 features specific to the stool body site

Source

Title: Gut microbiota dysbiosis contributes to the development of hypertension.

Author: Li J, Zhao F, Wang Y, Chen J, Tao J, Tian G, Wu S, Liu W, Cui Q, Geng B, Zhang W, Weldon R, Auguste K, Yang L, Liu X, Chen L, Yang X, Zhu B, Cai J

Lab: [1] Hypertension Center, Fuwai Hospital, State Key Laboratory of Cardiovascular Disease of China, National Center for Cardiovascular Diseases of China, Chinese Academy of Medical Sciences and Peking Union Medical College, Beijing, 100037, China., [2] Department of Cardiology, Beijing ChaoYang Hospital, Capital Medical University, Beijing, 100020, China., [3] Beijing Key Laboratory of Hypertension, Beijing, 100020, China., [4] Computational Genomics Laboratory, Beijing Institutes of Life Science, Chinese Academy of Sciences, Beijing, 100101, China., [5] Novogene Bioinformatics Institute, Beijing, 100000, China., [6] Department of Cardiology, Baoding NO.1 Central Hospital, Baoding, 071000, China., [7] Department of Cardiology, The First Affiliated Hospital, Xi'an Jiaotong University, Xi'an, 710061, China., [8] Department of Cardiology Kailuan General Hospital, Hebei Union University, Tangshan, 063000, China., [9] Department of Biomedical Informatics, Centre for Noncoding RNA Medicine, School of Basic Medical Sciences, Peking University, Beijing, 100191, China., [10] Department of Biology and Biochemistry, University of Houston, Houston, TX, 77204, USA., [11] Medical Research Center, Beijing ChaoYang Hospital, Capital Medical University, Beijing, 100020, China., [12] Department of Stem Cell Engineering, Texas Heart Institute, Houston, TX, 77030, USA., [13] Tongji Hospital, Huazhong University of Science and Technology, Wuhan, Hubei, 430030, China., [14] Department of Cardiology, Beijing ChaoYang Hospital, Capital Medical University, Beijing, 100020, China. yxc6229@sina.com., [15] Beijing Key Laboratory of Hypertension, Beijing, 100020, China. yxc6229@sina.com., [16] CAS Key Laboratory of Pathogenic Microbiology and Immunology, Institute of Microbiology, Chinese Academy of Sciences, Beijing, 100101, China. zhubaoli@im.ac.cn., [17] Collaborative Innovation Center for Diagnosis and Treatment of Infectious Diseases, The First Affiliated Hospital, College of Medicine, Zhejiang University, Hangzhou, 310003, China. zhubaoli@im.ac.cn., [18] Hypertension Center, Fuwai Hospital, State Key Laboratory of Cardiovascular Disease of China, National Center for Cardiovascular Diseases of China, Chinese Academy of Medical Sciences and Peking Union Medical College, Beijing, 100037, China. caijun@fuwaihospital.org.

PMID: 28143587

Examples

```
LiJ_2017.metaphlan_bugs_list.stool()
```

`LiSS_2016` *Data from the LiSS_2016 study*

Description

Data from the LiSS_2016 study

Datasets

LiSS_2016.genefamilies_relab.stool: An ExpressionSet with 55 samples and 974,539 features specific to the stool body site

LiSS_2016.marker_abundance.stool: An ExpressionSet with 55 samples and 72,504 features specific to the stool body site

LiSS_2016.marker_presence.stool: An ExpressionSet with 55 samples and 69,172 features specific to the stool body site

LiSS_2016.metaphlan_bugs_list.stool: An ExpressionSet with 55 samples and 854 features specific to the stool body site

LiSS_2016.pathabundance_relab.stool: An ExpressionSet with 55 samples and 8,888 features specific to the stool body site

LiSS_2016.pathcoverage.stool: An ExpressionSet with 55 samples and 8,888 features specific to the stool body site

Source

Title: Durable coexistence of donor and recipient strains after fecal microbiota transplantation.

Author: Li SS, Zhu A, Benes V, Costea PI, Hercog R, Hildebrand F, Huerta-Cepas J, Nieuwdorp M, Salojärvi J, Voigt AY, Zeller G, Sunagawa S, de Vos WM, Bork P

Lab: [1] Structural and Computational Biology Unit, European Molecular Biology Laboratory, 69117 Heidelberg, Germany. School of Biotechnology and Biomolecular Sciences, University of New South Wales, 2052 Sydney, Australia., [2] Structural and Computational Biology Unit, European Molecular Biology Laboratory, 69117 Heidelberg, Germany., [3] Genomics Core Facility, European Molecular Biology Laboratory, 69117 Heidelberg, Germany., [4] Department of Vascular Medicine, Academic Medical Center, 1105 AZ Amsterdam, Netherlands. Diabetes Center, Vrije University Medical Center, 1018 HV Amsterdam, Netherlands. Wallenberg Laboratory, University of Gothenburg, 41345 Gothenburg, Sweden., [5] Department of Veterinary Biosciences, University of Helsinki, 00014 Helsinki, Finland. Department of Biosciences, University of Helsinki, 00014 Helsinki, Finland., [6] Structural and Computational Biology Unit, European Molecular Biology Laboratory, 69117 Heidelberg, Germany. Department of Applied Tumor Biology, Institute of Pathology, University Hospital Heidelberg, 69120 Heidelberg, Germany. Molecular Medicine Partnership Unit, University of Heidelberg and European Molecular Biology Laboratory, 69120 Heidelberg, Germany., [7] Structural and Computational Biology Unit, European Molecular Biology Laboratory, 69117 Heidelberg, Germany. bork@embl.de willem.devos@wur.nl sunagawa@embl.de., [8] Department of Veterinary Biosciences, University of Helsinki, 00014 Helsinki, Finland. Laboratory of Microbiology, Wageningen University, 6703 HB Wageningen, Netherlands. Immunobiology Research Program, Department of Bacteriology and Immunology, University of Helsinki, 00014 Helsinki, Finland. bork@embl.de willem.devos@wur.nl sunagawa@embl.de., [9] Structural and Computational Biology Unit, European Molecular Biology Laboratory, 69117 Heidelberg, Germany. Molecular Medicine Partnership Unit, University of Heidelberg and European Molecular Biology Laboratory, 69120 Heidelberg, Germany. Max Delbruck Centre for Molecular Medicine, 13125 Berlin, Germany. Department of Bioinformatics, Biocenter, University of Wurzburg, 97074 Wurzburg, Germany. bork@embl.de willem.devos@wur.nl sunagawa@embl.de.

PMID: 27126044

Examples

```
LiSS_2016.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

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: [1] 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., [2] RealBio Genomic Institute, Shanghai 200050, China., [3] State Key Laboratory for Diagnosis and Treatment of Infectious Disease, Collaborative Innovation Center for Diagnosis and Treatment of Infectious Diseases, the First Affiliated Hospital, Zhejiang University, Hangzhou 310003, 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

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: [1] Institute of Microbiology and Infection, University of Birmingham, Birmingham, England.

PMID: 23571589

Examples

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

`LoombaR_2017` *Data from the LoombaR_2017 study*

Description

Data from the LoombaR_2017 study

Datasets

LoombaR_2017.genefamilies_relab.stool: An ExpressionSet with 86 samples and 1,222,524 features specific to the stool body site

LoombaR_2017.marker_abundance.stool: An ExpressionSet with 86 samples and 88,649 features specific to the stool body site

LoombaR_2017.marker_presence.stool: An ExpressionSet with 86 samples and 85,505 features specific to the stool body site

LoombaR_2017.metaphlan_bugs_list.stool: An ExpressionSet with 86 samples and 1,034 features specific to the stool body site

LoombaR_2017.pathabundance_relab.stool: An ExpressionSet with 86 samples and 12,913 features specific to the stool body site

LoombaR_2017.pathcoverage.stool: An ExpressionSet with 86 samples and 12,913 features specific to the stool body site

Source

Title: Gut Microbiome-Based Metagenomic Signature for Non-invasive Detection of Advanced Fibrosis in Human Nonalcoholic Fatty Liver Disease.

Author: Loomba R, Seguritan V, Li W, Long T, Klitgord N, Bhatt A, Dulai PS, Caussy C, Bettencourt R, Highlander SK, Jones MB, Sirlin CB, Schnabl B, Brinkac L, Schork N, Chen CH, Brenner DA, Biggs W, Yooseph S, Venter JC, Nelson KE

Lab: [1] NAFLD Research Center, Department of Medicine, University of California, San Diego, La Jolla, CA 92093, USA; Division of Epidemiology, Department of Family and Preventive Medicine, University of California, San Diego, La Jolla, CA 92093, USA; Division of Gastroenterology, Department of Medicine, University of California, San Diego, La Jolla, CA 92093, USA. Electronic address: roloomba@ucsd.edu., [2] Human Longevity, San Diego, CA 92121, USA., [3] Human Longevity, San Diego, CA 92121, USA; J. Craig Venter Institute, La Jolla, CA 92037, USA., [4] NAFLD Research Center, Department of Medicine, University of California, San Diego, La Jolla, CA 92093, USA., [5] NAFLD Research Center, Department of Medicine, University of California, San Diego, La Jolla, CA 92093, USA; Division of Gastroenterology, Department of Medicine, University of California, San Diego, La Jolla, CA 92093, USA., [6] J. Craig Venter Institute, La Jolla, CA 92037, USA., [7] Liver Imaging Group, Department of Radiology, University of California, San Diego, La Jolla, CA 92093, USA., [8] J. Craig Venter Institute, Rockville, MD 20850, USA.

PMID: 28467925

Examples

```
LoombaR_2017.metaphlan_bugs_list.stool()
```

`LouisS_2016` *Data from the LouisS_2016 study*

Description

Data from the LouisS_2016 study

Datasets

LouisS_2016.genefamilies_relab.stool: An ExpressionSet with 92 samples and 814,252 features specific to the stool body site

LouisS_2016.marker_abundance.stool: An ExpressionSet with 92 samples and 53,320 features specific to the stool body site

LouisS_2016.marker_presence.stool: An ExpressionSet with 92 samples and 51,680 features specific to the stool body site

LouisS_2016.metaphlan_bugs_list.stool: An ExpressionSet with 92 samples and 657 features specific to the stool body site

LouisS_2016.pathabundance_relab.stool: An ExpressionSet with 92 samples and 7,212 features specific to the stool body site

LouisS_2016.pathcoverage.stool: An ExpressionSet with 92 samples and 7,212 features specific to the stool body site

Source

Title: Characterization of the Gut Microbial Community of Obese Patients Following a Weight-Loss Intervention Using Whole Metagenome Shotgun Sequencing.

Author: Louis S, Tappu RM, Damms-Machado A, Huson DH, Bischoff SC

Lab: [1] Institute of Clinical Nutrition, University of Hohenheim, Stuttgart, Germany., [2] Algorithms in Bioinformatics, University of Tubingen, Tubingen, Germany.

PMID: 26919743

Examples

```
LouisS_2016.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

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] 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]., [2] 1] INRA, Institut National de la Recherche Agronomique, UMR 14121 MICALIS, Jouy en Josas, France. [2] INRA, Institut National de la Recherche Agronomique, US 1367 Metagenopolis, Jouy en Josas, France. [3] Department of Computer Science, Center for Bioinformatics and Computational Biology, University of Maryland, USA. [4]., [3] 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., [4] Center for Biological Sequence Analysis, Technical University of Denmark, Kongens Lyngby, Denmark., [5] 1] BGI

Hong Kong Research Institute, Hong Kong, China. [2] BGI-Shenzhen, Shenzhen, China. [3] School of Bioscience and Biotechnology, South China University of Technology, Guangzhou, China., [6] European Molecular Biology Laboratory, Heidelberg, Germany., [7] 1] INRA, Institut National de la Recherche Agronomique, UMR 14121 MICALIS, Jouy en Josas, France. [2] INRA, Institut National de la Recherche Agronomique, US 1367 Metagenopolis, Jouy en Josas, France., [8] 1] Commissariat a l'Energie Atomique et aux Energies Alternatives, Institut de Genomique, Evry, France. [2] Centre National de la Recherche Scientifique, Evry, France. [3] Universite d'Evry Val d'Essonne, Evry, France., [9] The Novo Nordisk Foundation Center for Basic Metabolic Research, University of Copenhagen, Copenhagen, Denmark., [10] Digestive System Research Unit, University Hospital Vall d'Hebron, Ciberehd, Barcelona, Spain., [11] 1] BGI-Shenzhen, Shenzhen, China. [2] European Molecular Biology Laboratory, Heidelberg, Germany. [3] The Novo Nordisk Foundation Center for Basic Metabolic Research, University of Copenhagen, Copenhagen, Denmark., [12] Novo Nordisk Foundation Center for Biosustainability, Technical University of Denmark, Kongens Lyngby, Denmark., [13] 1] The Novo Nordisk Foundation Center for Basic Metabolic Research, University of Copenhagen, Copenhagen, Denmark. [2] Faculty of Health Sciences, University of Southern Denmark, Odense, Denmark., [14] 1] Department of Structural Biology, VIB, Brussels, Belgium. [2] Department of Bioscience Engineering, Vrije Universiteit, Brussels, Belgium., [15] National Food Institute, Division for Epidemiology and Microbial Genomics, Technical University of Denmark, Kongens Lyngby, Denmark., [16] 1] BGI-Shenzhen, Shenzhen, China. [2] Department of Biology, University of Copenhagen, Copenhagen, Denmark., [17] 1] The Novo Nordisk Foundation Center for Basic Metabolic Research, University of Copenhagen, Copenhagen, Denmark. [2] Hagedorn Research Institute, Gentofte, Denmark. [3] Institute of Biomedical Science, Faculty of Health and Medical Sciences, University of Copenhagen, Copenhagen, Denmark. [4] Faculty of Health, Aarhus University, Aarhus, Denmark., [18] 1] BGI Hong Kong Research Institute, Hong Kong, China. [2] BGI-Shenzhen, Shenzhen, China., [19] 1] Department of Bioscience Engineering, Vrije Universiteit, Brussels, Belgium. [2] Department of Microbiology and Immunology, Rega Institute, KU Leuven, Belgium. [3] VIB Center for the Biology of Disease, Leuven, Belgium., [20] Section of Microbiology, Department of Biology, University of Copenhagen, Copenhagen, Denmark., [21] Laboratory of Microbiology, Wageningen University, Wageningen, The Netherlands., [22] 1] European Molecular Biology Laboratory, Heidelberg, Germany. [2] Department of Biological Information, Tokyo Institute of Technology, Yokohama, Japan., [23] INRA, Institut National de la Recherche Agronomique, UMR 14121 MICALIS, Jouy en Josas, France., [24] 1] European Molecular Biology Laboratory, Heidelberg, Germany. [2] Max Delbruck Centre for Molecular Medicine, Berlin, Germany., [25] 1] BGI-Shenzhen, Shenzhen, China. [2] The Novo Nordisk Foundation Center for Basic Metabolic Research, University of Copenhagen, Copenhagen, Denmark. [3] Department of Biology, University of Copenhagen, Copenhagen, Denmark. [4] Princess Al Jawhara Center of Excellence in the Research of Hereditary Disorders, King Abdulaziz University, Jeddah, Saudi Arabia., [26] 1] INRA, Institut National de la Recherche Agronomique, UMR 14121 MICALIS, Jouy en Josas, France. [2] INRA, Institut National de la Recherche Agronomique, US 1367 Metagenopolis, Jouy en Josas, France. [3] King's College London, Centre for Host-Microbiome Interactions, Dental Institute Central Office, Guy's Hospital, United Kingdom.

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

Details

Note that Obregon_TitoAJ_2015 is deprecated, use Obregon-TitoAJ_2015 instead.

Datasets

Obregon-TitoAJ_2015.genefamilies_relab.stool: An ExpressionSet with 58 samples and 1,185,621 features specific to the stool body site

Obregon-TitoAJ_2015.marker_abundance.stool: An ExpressionSet with 58 samples and 96,336 features specific to the stool body site

Obregon-TitoAJ_2015.marker_presence.stool: An ExpressionSet with 58 samples and 86,352 features specific to the stool body site

Obregon-TitoAJ_2015.metaphlan_bugs_list.stool: An ExpressionSet with 58 samples and 1,094 features specific to the stool body site

Obregon-TitoAJ_2015.pathabundance_relab.stool: An ExpressionSet with 58 samples and 9,801 features specific to the stool body site

Obregon-TitoAJ_2015.pathcoverage.stool: An ExpressionSet with 58 samples and 9,801 features specific to the stool body site

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] 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., [2] 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., [4] Department of Anthropology, University of Oklahoma, Dale Hall Tower, 521 Norman, Oklahoma 73019, USA., [5] Department of Chemistry and Biochemistry, University of Colorado, Boulder, Colorado 80309, USA., [6] Departments of Pediatrics and Computer Science &Engineering University of California San Diego, La Jolla, CA 92093, USA., [7] Oklahoma Medical Research Foundation, Oklahoma City, Oklahoma 73104, USA., [8] Instituto Nacional de Salud, Lima 11, Peru, [9] Old Dominion University, Norfolk, Virginia 23529, USA., [10] Universidad Cientifica del Sur, Lima 18, Peru

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

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: [1] Translational and Functional Genomics Branch, National Human Genome Research Institute, NIH, Bethesda, Maryland 20892, USA., [2] 1] Dermatology Branch, Center for Cancer Research, National Cancer Institute, NIH, Bethesda, Maryland 20892, USA [2]., [3] 1] Translational and Functional Genomics Branch, National Human Genome Research Institute, NIH, Bethesda, Maryland 20892, USA [2].

PMID: 25279917

Examples

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

`OlmMR_2017` *Data from the OlmMR_2017 study*

Description

Data from the OlmMR_2017 study

Datasets

OlmMR_2017.genefamilies_relab.oralcavity: An ExpressionSet with 4 samples and 138,859 features specific to the oralcavity body site

OlmMR_2017.genefamilies_relab.skin: An ExpressionSet with 4 samples and 138,859 features specific to the skin body site

OlmMR_2017.genefamilies_relab.stool: An ExpressionSet with 37 samples and 138,859 features specific to the stool body site

OlmMR_2017.marker_abundance.oralcavity: An ExpressionSet with 4 samples and 10,965 features specific to the oralcavity body site

OlmMR_2017.marker_abundance.skin: An ExpressionSet with 4 samples and 10,965 features specific to the skin body site

OlmMR_2017.marker_abundance.stool: An ExpressionSet with 37 samples and 10,965 features specific to the stool body site

OlmMR_2017.marker_presence.oralcavity: An ExpressionSet with 4 samples and 9,977 features specific to the oralcavity body site

OlmMR_2017.marker_presence.skin: An ExpressionSet with 4 samples and 9,977 features specific to the skin body site

OlmMR_2017.marker_presence.stool: An ExpressionSet with 37 samples and 9,977 features specific to the stool body site

OlmMR_2017.metaphlan_bugs_list.oralcavity: An ExpressionSet with 4 samples and 201 features specific to the oralcavity body site

OlmMR_2017.metaphlan_bugs_list.skin: An ExpressionSet with 4 samples and 201 features specific to the skin body site

OlmMR_2017.metaphlan_bugs_list.stool: An ExpressionSet with 37 samples and 201 features specific to the stool body site

OlmMR_2017.pathabundance_relab.oralcavity: An ExpressionSet with 4 samples and 2,941 features specific to the oralcavity body site

OlmMR_2017.pathabundance_relab.skin: An ExpressionSet with 4 samples and 2,941 features specific to the skin body site

OlmMR_2017.pathabundance_relab.stool: An ExpressionSet with 37 samples and 2,941 features specific to the stool body site

OlmMR_2017.pathcoverage.oralcavity: An ExpressionSet with 4 samples and 2,941 features specific to the oralcavity body site

OlmMR_2017.pathcoverage.skin: An ExpressionSet with 4 samples and 2,941 features specific to the skin body site

OlmMR_2017.pathcoverage.stool: An ExpressionSet with 37 samples and 2,941 features specific to the stool body site

Source

Title: Identical bacterial populations colonize premature infant gut, skin, and oral microbiomes and exhibit different in situ growth rates.

Author: Olm MR, Brown CT, Brooks B, Firek B, Baker R, Burstein D, Soenjoyo K, Thomas BC, Morowitz M, Banfield JF

Lab: [1] Department of Plant and Microbial Biology, University of California, Berkeley, California 94720, USA., [2] Department of Surgery, University of Pittsburgh School of Medicine, Pittsburgh, Pennsylvania 15213, USA., [3] Division of Newborn Medicine, Children's Hospital of Pittsburgh and Magee-Womens Hospital of UPMC, Pittsburgh, Pennsylvania 15213, USA., [4] Department of Earth and Planetary Science, University of California, Berkeley, California 94709, USA., [5] Department of Environmental Science, Policy, and Management, University of California, Berkeley, California 94720, USA., [6] Earth Sciences Division, Lawrence Berkeley National Laboratory, Berkeley, California 94720, USA.

PMID: 28073918

Examples

```
OlmMR_2017.metaphlan_bugs_list.oralcavity()
```

`PasolliE_2018` *Data from the PasolliE_2018 study*

Description

Data from the PasolliE_2018 study

Datasets

PasolliE_2018.genefamilies_relab.stool: An ExpressionSet with 112 samples and 1,242,950 features specific to the stool body site

PasolliE_2018.marker_abundance.stool: An ExpressionSet with 112 samples and 87,770 features specific to the stool body site

PasolliE_2018.marker_presence.stool: An ExpressionSet with 112 samples and 82,466 features specific to the stool body site

PasolliE_2018.metaphlan_bugs_list.stool: An ExpressionSet with 112 samples and 1,111 features specific to the stool body site

PasolliE_2018.pathabundance_relab.stool: An ExpressionSet with 112 samples and 13,695 features specific to the stool body site

PasolliE_2018.pathcoverage.stool: An ExpressionSet with 112 samples and 13,695 features specific to the stool body site

Source

Title: NA

Author: NA

Lab: NA

PMID: NA

Examples

```
PasolliE_2018.metaphlan_bugs_list.stool()
```

`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

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: [1] 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

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] 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]., [2] 1] State Key Laboratory for Diagnosis and Treatment of Infectious Disease, The First Affiliated Hospital, College of Medicine, Zhejiang University, 310003 Hangzhou, China [2]., [3] 1] Metagenopolis, Institut National de la Recherche Agronomique, 78350 Jouy en Josas, France [2]., [4] State Key Laboratory for Diagnosis and Treatment of Infectious Disease, The First Affiliated Hospital, College of Medicine, Zhejiang University, 310003 Hangzhou, China., [5] Metagenopolis, Institut National de la Recherche Agronomique, 78350 Jouy en Josas, France., [6] 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., [7] 1] Metagenopolis, Institut National de la Recherche Agronomique, 78350 Jouy en Josas, France [2] King's College London, Centre for Host-Microbiome Interactions, Dental Institute Central Office, Guy's Hospital, London Bridge, London SE1 9RT, UK., [8] 1] Collaborative Innovation Center for Diagnosis and Treatment of Infectious Diseases, Zhejiang University, 310003 Hangzhou, China [2] Key Laboratory of Combined Multi-organ Transplantation, Ministry of Public Health, the First Affiliated Hospital, Zhejiang University, 310003 Hangzhou, China.

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

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: [1] Department of Pharmacy and Biotechnology, University of Bologna, Bologna 40126, Italy., [2] Plant Foods in Hominin Dietary Ecology Research Group, Max Planck Institute for Evolutionary Anthropology, Leipzig 04103, Germany. Electronic address: stephanie_schnorr@eva.mpg.de., [3] Institute of Biomedical Technologies, Italian National Research Council, Segrate, Milan 20090, Italy., [4] Metabolism, Anthropometry, and Nutrition Laboratory, Department of Anthropology, University of Nevada, Las Vegas, NV 89154-5003, USA., [5] Plant Foods in Hominin Dietary Ecology Research Group, Max Planck Institute for Evolutionary Anthropology, Leipzig 04103, Germany., [6] Department of Pharmacy and Biotechnology, University of Bologna, Bologna 40126, Italy. Electronic address: marco.candela@unibo.it.

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

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: [1] Centre de Recherche en Infectiologie, CHU de Quebec-Universite Laval, Quebec, Canada., [2] Institut National de Sante Publique du Quebec, Laboratoire de Sante Publique du Quebec, Montreal, 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

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 LAB, Zhernakova A, Huttenhower C, Wijmenga C, Netea MG, Xavier RJ

Lab: NA

PMID: 27984736

Examples

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

`ShiB_2015` *Data from the ShiB_2015 study*

Description

Data from the ShiB_2015 study

Datasets

ShiB_2015.genefamilies_relab.oralcavity: An ExpressionSet with 48 samples and 601,260 features specific to the oralcavity body site

ShiB_2015.marker_abundance.oralcavity: An ExpressionSet with 48 samples and 56,520 features specific to the oralcavity body site

ShiB_2015.marker_presence.oralcavity: An ExpressionSet with 48 samples and 55,414 features specific to the oralcavity body site

ShiB_2015.metaphlan_bugs_list.oralcavity: An ExpressionSet with 48 samples and 729 features specific to the oralcavity body site

ShiB_2015.pathabundance_relab.oralcavity: An ExpressionSet with 48 samples and 6,934 features specific to the oralcavity body site

Source

Title: Dynamic changes in the subgingival microbiome and their potential for diagnosis and prognosis of periodontitis.

Author: Shi B, Chang M, Martin J, Mitreva M, Lux R, Klokkevold P, Sodergren E, Weinstock GM, Haake SK, Li H

Lab: [1] Department of Molecular and Medical Pharmacology, Crump Institute for Molecular Imaging, David Geffen School of Medicine, UCLA, Los Angeles, California, USA., [2] Section of Periodontics, School of Dentistry, UCLA, Los Angeles, California, USA., [3] The Genome Institute, Washington University, St. Louis, Missouri, USA., [4] The Jackson Laboratory for Genomic Medicine, Farmington, Connecticut, USA., [5] huiying@mednet.ucla.edu.

PMID: 25691586

Examples

```
ShiB_2015.metaphlan_bugs_list.oralcavity()
```

`SmitsSA_2017` *Data from the SmitsSA_2017 study*

Description

Data from the SmitsSA_2017 study

Datasets

SmitsSA_2017.genefamilies_relab.stool: An ExpressionSet with 40 samples and 400,325 features specific to the stool body site

SmitsSA_2017.marker_abundance.stool: An ExpressionSet with 40 samples and 21,684 features specific to the stool body site

SmitsSA_2017.marker_presence.stool: An ExpressionSet with 40 samples and 19,635 features specific to the stool body site

SmitsSA_2017.metaphlan_bugs_list.stool: An ExpressionSet with 40 samples and 343 features specific to the stool body site

SmitsSA_2017.pathabundance_relab.stool: An ExpressionSet with 40 samples and 3,562 features specific to the stool body site

SmitsSA_2017.pathcoverage.stool: An ExpressionSet with 40 samples and 3,562 features specific to the stool body site

Source

Title: Seasonal cycling in the gut microbiome of the Hadza hunter-gatherers of Tanzania.

Author: Smits SA, Leach J, Sonnenburg ED, Gonzalez CG, Lichtman JS, Reid G, Knight R, Manjurano A, Changalucha J, Elias JE, Dominguez-Bello MG, Sonnenburg JL

Lab: [1] Department of Microbiology and Immunology, Stanford University School of Medicine, Stanford, CA 94305, USA., [2] Human Food Project, 53600 Highway 118, Terlingua, TX 79852, USA., [3] The Department of Twin Research and Genetic Epidemiology, King's College London, St. Thomas' Hospital, Lambeth Palace Road, London SE1 7EH, UK., [4] Department of Chemical and Systems Biology, Stanford School of Medicine, Stanford University, Stanford, CA 94025, USA., [5] Lawson Health Research Institute and Western University, London, Ontario N6A 4V2, Canada., [6] Departments of Pediatrics and Computer Science and Engineering and Center for Microbiome Innovation, University of California, San Diego, CA 92093, USA., [7] National Institute for Medical Research, Mwanza 11101, Tanzania., [8] School of Medicine and Department of Anthropology, New York University, New York, NY, USA.

PMID: 28839072

Examples

```
SmitsSA_2017.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 1,177,112 features specific to the skin body site

TettAJ_2016.marker_abundance.skin: An ExpressionSet with 97 samples and 64,205 features specific to the skin body site

TettAJ_2016.marker_presence.skin: An ExpressionSet with 97 samples and 59,833 features specific to the skin body site

TettAJ_2016.metaphlan_bugs_list.skin: An ExpressionSet with 97 samples and 1,002 features specific to the skin body site

TettAJ_2016.pathabundance_relab.skin: An ExpressionSet with 97 samples and 18,914 features specific to the skin body site

TettAJ_2016.pathcoverage.skin: An ExpressionSet with 97 samples and 18,914 features specific to the skin body site

Source

Title: Unexplored diversity and strain-level structure of the skin microbiome associated with psoriasis.

Author: Tett A, Pasolli E, Farina S, Truong DT, Asnicar F, Zolfo M, Beghini F, Armanini F, Jousson O, De Sanctis V, Bertorelli R, Girolomoni G, Cristofolini M, Segata N

Lab: [1] Centre for Integrative Biology, University of Trento, Trento, Italy., [2] Istituto G.B. Mattei, Comano, Italy., [3] NGS Facility, Laboratory of Biomolecular Sequence and Structure Analysis for Health, Centre for Integrative Biology, University of Trento, Trento, Italy., [4] Department of Medicine, Section of Dermatology, University of Verona, Verona, Italy.

PMID: 28649415

Examples

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

`ThomasAM_2018a` *Data from the ThomasAM_2018a study*

Description

Data from the ThomasAM_2018a study

Datasets

ThomasAM_2018a.genefamilies_relab.stool: An ExpressionSet with 80 samples and 1,324,452 features specific to the stool body site

ThomasAM_2018a.marker_abundance.stool: An ExpressionSet with 80 samples and 88,476 features specific to the stool body site

ThomasAM_2018a.marker_presence.stool: An ExpressionSet with 80 samples and 86,326 features specific to the stool body site

ThomasAM_2018a.metaphlan_bugs_list.stool: An ExpressionSet with 80 samples and 1,162 features specific to the stool body site

ThomasAM_2018a.pathabundance_relab.stool: An ExpressionSet with 80 samples and 8,227 features specific to the stool body site

ThomasAM_2018a.pathcoverage.stool: An ExpressionSet with 80 samples and 8,227 features specific to the stool body site

Source

Title: NA

Author: NA

Lab: NA

PMID: NA

Examples

```
ThomasAM_2018a.metaphlan_bugs_list.stool()
```

`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

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

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: [1] Department of Microbiology and Immunology, McGill University, Montreal, Quebec, Canada., [2] Genome Quebec Innovation Centre, McGill University, Montreal, Quebec, Canada., [3] Jewish General Hospital, Montreal, Quebec, Canada., [4] Devil's Staircase Consulting, North Vancouver, British Columbia, Canada., [5] New York Genome Center, New York, NY, USA., [6] Department of Human Genetics, McGill University, Montreal, Quebec, Canada., [7] School of Population and Public Health, University of British Columbia, Vancouver, British Columbia, Canada. amee.manges@ubc.ca.

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 1,511,515 features specific to the stool body site

VogtmannE_2016.marker_abundance.stool: An ExpressionSet with 110 samples and 110,990 features specific to the stool body site

VogtmannE_2016.marker_presence.stool: An ExpressionSet with 110 samples and 107,190 features specific to the stool body site

VogtmannE_2016.metaphlan_bugs_list.stool: An ExpressionSet with 110 samples and 1,296 features specific to the stool body site

VogtmannE_2016.pathabundance_relab.stool: An ExpressionSet with 110 samples and 14,809 features specific to the stool body site

VogtmannE_2016.pathcoverage.stool: An ExpressionSet with 110 samples and 14,809 features specific to the stool body site

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: [1] Division of Cancer Epidemiology & Genetics, National Cancer Institute, Bethesda, Maryland, United States of America., [2] Division of Cancer Prevention, National Cancer Institute, Bethesda, Maryland, United States of America., [3] Structural and Computational Biology Unit, European Molecular Biology Laboratory, Heidelberg, Germany., [4] Department of Applied Tumor Biology, Institute of Pathology, University Hospital Heidelberg, Heidelberg, Germany., [5] Clinical Cooperation Unit Applied Tumor Biology, German Cancer Research Center (DKFZ), Heidelberg, Germany., [6] Molecular Medicine Partnership Unit (MMPU), University Hospital Heidelberg and European Molecular Biology Laboratory, Heidelberg, Germany., [7] Genomics Core Facility, European Molecular Biology Laboratory, Heidelberg, Germany., [8] Max Delbruck Centre for Molecular Medicine, Berlin, Germany., [9] Department of Bioinformatics Biocenter, University of Wurzburg, Wurzburg, Germany.

PMID: 27171425

Examples

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

`WenC_2017` *Data from the WenC_2017 study*

Description

Data from the WenC_2017 study

Datasets

WenC_2017.genefamilies_relab.stool: An ExpressionSet with 97 samples and 1,160,257 features specific to the stool body site

WenC_2017.marker_abundance.stool: An ExpressionSet with 97 samples and 89,660 features specific to the stool body site

WenC_2017.marker_presence.stool: An ExpressionSet with 97 samples and 83,333 features specific to the stool body site

WenC_2017.metaphlan_bugs_list.stool: An ExpressionSet with 97 samples and 1,075 features specific to the stool body site

WenC_2017.pathabundance_relab.stool: An ExpressionSet with 97 samples and 11,713 features specific to the stool body site

WenC_2017.pathcoverage.stool: An ExpressionSet with 97 samples and 11,713 features specific to the stool body site

Source

Title: Quantitative metagenomics reveals unique gut microbiome biomarkers in ankylosing spondylitis.

Author: Wen C, Zheng Z, Shao T, Liu L, Xie Z, Le Chatelier E, He Z, Zhong W, Fan Y, Zhang L, Li H, Wu C, Hu C, Xu Q, Zhou J, Cai S, Wang D, Huang Y, Breban M, Qin N, Ehrlich SD

Lab: [1] Institute of Basic Research in Clinical Medicine, College of Basic Medical Science, Zhejiang Chinese Medical University, Hangzhou, 310053, China. wengcp@163.com., [2] Realbio Genomics Institute, Shanghai, 200123, China., [3] Institute of Basic Research in Clinical Medicine, College of Basic Medical Science, Zhejiang Chinese Medical University, Hangzhou, 310053, China., [4] State Key Laboratory for Diagnosis and Treatment of Infectious Diseases, Department of Infectious Diseases, the First Affiliated College of Medicine, Zhejiang University, Hangzhou, 310003, China., [5] Collaborative Innovation Center for Diagnosis and Treatment of Infectious Diseases, Zhejiang University, Hangzhou, 310003, China., [6] INRA, Institut National de la Recherche Agronomique, Metagenopolis, Jouy en Josas, 78350, France., [7] Rheumatology Division, Ambroise-Pare Hospital, AP-HP, 9, avenue Charles-de-Gaulle, 92100, Boulogne-Billancourt, France., [8] Realbio Genomics Institute, Shanghai, 200123, China. qinnan001@126.com., [9] State Key Laboratory for Diagnosis and Treatment of Infectious Diseases, Department of Infectious Diseases, the First Affiliated College of Medicine, Zhejiang University, Hangzhou, 310003, China. qinnan001@126.com., [10] Collaborative Innovation Center for Diagnosis and Treatment of Infectious Diseases, Zhejiang University, Hangzhou, 310003, China. qinnan001@126.com., [11] INRA, Institut National de la Recherche Agronomique, Metagenopolis, Jouy en Josas, 78350, France. dusko.ehrlich@jouy.inra.fr., [12] King's College London, Centre for Host-Microbiome Interactions, Dental Institute Central Office, Guy's Hospital, London Bridge, London, SE1 9RT, UK. dusko.ehrlich@jouy.inra.fr.

PMID: 28750650

Examples

```
WenC_2017.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

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: [1] BGI-Shenzhen, Shenzhen 518083, China; China National Genebank-Shenzhen, BGI-Shenzhen, Shenzhen 518083, China., [2] BGI-Shenzhen, Shenzhen 518083, China; China National Genebank-Shenzhen, BGI-Shenzhen, Shenzhen 518083, China; Shenzhen Engineering Laboratory of Detection and Intervention of Human Intestinal Microbiome, BGI-Shenzhen, Shenzhen 518083, China; Macau University of Science and Technology, Taipa, Macau 999078, China., [3] BGI-Shenzhen, Shenzhen 518083, China; China National Genebank-Shenzhen, BGI-Shenzhen, Shenzhen 518083, China; Shenzhen Engineering Laboratory of Detection and Intervention of Human Intestinal Microbiome, BGI-Shenzhen, Shenzhen 518083, China., [4] BGI-Shenzhen, Shenzhen 518083, China., [5] Department of Twin Research and Genetic Epidemiology, King's

College London, London SE1 7EH, UK., [6] BGI-Shenzhen, Shenzhen 518083, China; BGI Education Center, University of Chinese Academy of Sciences, Shenzhen 518083, China., [7] BGI-Shenzhen, Shenzhen 518083, China; Qingdao University-BGI Joint Innovation College, Qingdao University, Qingdao 266071, China., [8] BGI-Shenzhen, Shenzhen 518083, China; China National Genebank-Shenzhen, BGI-Shenzhen, Shenzhen 518083, China; Shenzhen Key Laboratory of Human Commensal Microorganisms and Health Research, BGI-Shenzhen, Shenzhen 518083, China., [9] BGI-Shenzhen, Shenzhen 518083, China; China National Genebank-Shenzhen, BGI-Shenzhen, Shenzhen 518083, China; BGI Education Center, University of Chinese Academy of Sciences, Shenzhen 518083, China., [10] BGI-Shenzhen, Shenzhen 518083, China; China National Genebank-Shenzhen, BGI-Shenzhen, Shenzhen 518083, China; James D. Watson Institute of Genome Sciences, Hangzhou 310058, China., [11] BGI-Shenzhen, Shenzhen 518083, China; Department of Biology, University of Copenhagen, Ole Maaloes Vej 5, 2200 Copenhagen, Denmark., [12] BGI-Shenzhen, Shenzhen 518083, China; Macau University of Science and Technology, Taipa, Macau 999078, China; Shenzhen Key Laboratory of Human Commensal Microorganisms and Health Research, BGI-Shenzhen, Shenzhen 518083, China., [13] BGI-Shenzhen, Shenzhen 518083, China; China National Genebank-Shenzhen, BGI-Shenzhen, Shenzhen 518083, China; Shenzhen Key Laboratory of Human Commensal Microorganisms and Health Research, BGI-Shenzhen, Shenzhen 518083, China. Electronic address: lijunhua@genomics.cn., [14] Department of Twin Research and Genetic Epidemiology, King's College London, London SE1 7EH, UK. Electronic address: tim.spector@kcl.ac.uk., [15] BGI-Shenzhen, Shenzhen 518083, China; China National Genebank-Shenzhen, BGI-Shenzhen, Shenzhen 518083, China; Macau University of Science and Technology, Taipa, Macau 999078, China; Shenzhen Key Laboratory of Human Commensal Microorganisms and Health Research, BGI-Shenzhen, Shenzhen 518083, China. Electronic address: jiahuijue@genomics.cn.

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

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: [1] 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., [2] BGI-Shenzhen, Shenzhen, China., [3] Department of Biology, University of Copenhagen, Copenhagen, Denmark., [4] Department of Veterinary Disease Biology, Faculty of Health and Medical Sciences, University of Copenhagen, Copenhagen, Denmark., [5] Princess Al Jawhara Center of Excellence in the Research of Hereditary Disorders, King Abdulaziz University, Jeddah, Saudi Arabia., [6] Department of Surgical Gastroenterology, Hvidovre Hospital, Hvidovre, Denmark., [7] National Institute of Nutrition and Seafood Research, Bergen, Norway., [8] Department of Internal Medicine, Hospital Oberndorf, Q3 Teaching Hospital of the Paracelsus Private University of Salzburg, Oberndorf, Austria., [9] First Department of Internal Medicine, Medical University Innsbruck, Innsbruck, Austria., [10] The Novo Nordisk Foundation Center for Basic Metabolic Research, Faculty of Health and Medical Sciences, University of Copenhagen, Copenhagen, Denmark., [11] Macau University of Science and Technology, Macau, China.

PMID: 26408641

Examples

```
YuJ_2015.metaphlan_bugs_list.stool()
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`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 1,847,962 features specific to the stool body site

ZellerG_2014.marker_abundance.stool: An ExpressionSet with 199 samples and 138,412 features specific to the stool body site

ZellerG_2014.marker_presence.stool: An ExpressionSet with 199 samples and 133,484 features specific to the stool body site

ZellerG_2014.metaphlan_bugs_list.stool: An ExpressionSet with 199 samples and 1,585 features specific to the stool body site

ZellerG_2014.pathabundance_relab.stool: An ExpressionSet with 199 samples and 18,579 features specific to the stool body site

ZellerG_2014.pathcoverage.stool: An ExpressionSet with 199 samples and 18,579 features specific to the stool body site

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: [1] Structural and Computational Biology Unit, European Molecular Biology Laboratory, Heidelberg, Germany., [2] Structural and Computational Biology Unit, European Molecular Biology Laboratory, Heidelberg, Germany Department of Gastroenterology and LIC-EA4393-EC2M3, APHP and UPEC Universite Paris-Est Creteil, Creteil, France., [3] Structural and Computational Biology Unit, European Molecular Biology Laboratory, Heidelberg, Germany Department of Applied Tumor Biology, Institute of Pathology University Hospital Heidelberg, Heidelberg, Germany Clinical Cooperation Unit Applied Tumor Biology, German Cancer Research Center (DKFZ), Heidelberg, Germany Molecular Medicine Partnership Unit (MMPU), University Hospital Heidelberg and European Molecular Biology Laboratory, Heidelberg, Germany., [4] Department of Gastroenterology and LIC-EA4393-EC2M3, APHP and UPEC Universite Paris-Est Creteil, Creteil, France., [5] Division of Preventive Oncology, National Center for Tumor Diseases (NCT) Heidelberg, Heidelberg, Germany German Cancer Research Center (DKFZ), Heidelberg, Germany., [6] Department of Surgery, APHP and UPEC Universite Paris-Est Creteil, Creteil, France., [7] Genomics Core Facility, European Molecular Biology Laboratory, Heidelberg, Germany., [8] Department of General, Visceral and Transplantation Surgery, University Hospital Heidelberg, Heidelberg, Germany., [9] Department of Radiology, APHP and UPEC Universite Paris-Est Creteil, Creteil, France., [10] Department of Medical Oncology, APHP and UPEC Universite Paris-Est Creteil, Creteil, France., [11] Department of Pathology and LIC-EA4393-EC2M3, APHP and UPEC Universite Paris-Est Creteil, Creteil, France., [12] Department of Biological Information, Tokyo Institute of Technology, Tokyo, Japan., [13] Department of Applied Tumor Biology, Institute of Pathology University Hospital Heidelberg, Heidelberg, Germany Clinical Cooperation Unit Applied Tumor Biology, German Cancer Research Center (DKFZ), Heidelberg, Germany Molecular Medicine Partnership Unit (MMPU), University Hospital Heidelberg and European Molecular Biology Laboratory, Heidelberg, Germany., [14] Division of Preventive Oncology, National Center for Tumor Diseases (NCT) Heidelberg, Heidelberg, Germany German Cancer Research Center (DKFZ), Heidelberg, Germany Fred Hutchinson Cancer Research Center (FHCRC), Seattle, WA, USA., [15] Department of Gastroenterology and LIC-EA4393-EC2M3, APHP and UPEC Universite Paris-Est Creteil, Creteil, France iradj.sobhani@hmn.aphp.fr bork@embl.de., [16] Structural and Computational Biology Unit, European Molecular Biology Laboratory, Heidelberg, Germany Molecular Medicine Partnership Unit (MMPU), University Hospital Heidelberg and European Molecular Biology Laboratory, Heidelberg, Germany Max Delbruck Centre for Molecular Medicine, Berlin, Germany iradj.sobhani@hmn.aphp.fr bork@embl.de.

PMID: 25432777

Examples

```
ZellerG_2014.metaphlan_bugs_list.stool()
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