Package ‘curatedMetagenomicData’

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Type Package

Title Curated Metagenomic Data of the Human Microbiome

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

License Artistic-2.0

Encoding UTF-8

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

Imports BioCInstaller, utils, tidyr

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

VignetteBuilder knitr

biocViews Homo_sapiens_Data, ReproducibleResearch, MicrobiomeData

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NeedsCompilation no

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- QinJ_2012.pathcoverage
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- QinN_2014.marker_abundance
Curated Metagenomic Data of the Human Microbiome

Description

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

ExpressionSet2phyloseq

Convert an ExpressionSet object to a phyloseq object

Usage

ExpressionSet2phyloseq(eset, simplify = TRUE, relab = TRUE)
Arguments

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

Value

A phyloseq object

Examples

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

---

**HMP_2012.genefamilies_relab**

*Relabeled genefamilies data from the HMP_2012 dataset*

Description

Relabeled genefamilies data from the HMP_2012 dataset

Datasets

- **HMP_2012.genefamilies_relab.anterior_nares**: An ExpressionSet with 93 samples and 1,964,481 features specific to the anterior_nares bodysite
- **HMP_2012.genefamilies_relab.buccal_mucosa**: An ExpressionSet with 119 samples and 1,964,481 features specific to the buccal_mucosa bodysite
- **HMP_2012.genefamilies_relab.hard_palate**: An ExpressionSet with 1 sample and 1,964,481 features specific to the hard_palate bodysite
- **HMP_2012.genefamilies_relab.keratinized_gingiva**: An ExpressionSet with 6 samples and 1,964,481 features specific to the keratinized_gingiva bodysite
- **HMP_2012.genefamilies_relab.l_retroauricularcrease**: An ExpressionSet with 9 samples and 1,964,481 features specific to the l_retroauricularcrease bodysite
- **HMP_2012.genefamilies_relab.mid_vagina**: An ExpressionSet with 2 samples and 1,964,481 features specific to the mid_vagina bodysite
- **HMP_2012.genefamilies_relab.palatine_tonsils**: An ExpressionSet with 6 samples and 1,964,481 features specific to the palatine_tonsils bodysite
- **HMP_2012.genefamilies_relab.posterior_fornix**: An ExpressionSet with 62 samples and 1,964,481 features specific to the posterior_fornix bodysite
- **HMP_2012.genefamilies_relab.r_retroauricularcrease**: An ExpressionSet with 18 samples and 1,964,481 features specific to the r_retroauricularcrease bodysite
**HMP_2012.marker_abundance**

- **HMP_2012.genefamilies_relab.saliva**: An ExpressionSet with 5 samples and 1,964,481 features specific to the saliva bodysite
- **HMP_2012.genefamilies_relab.stool**: An ExpressionSet with 147 samples and 1,964,481 features specific to the stool bodysite
- **HMP_2012.genefamilies_relab.subgingival_plaque**: An ExpressionSet with 7 samples and 1,964,481 features specific to the subgingival_plaque bodysite
- **HMP_2012.genefamilies_relab.supragingival_plaque**: An ExpressionSet with 128 samples and 1,964,481 features specific to the supragingival_plaque bodysite
- **HMP_2012.genefamilies_relab.throat**: An ExpressionSet with 7 samples and 1,964,481 features specific to the throat bodysite
- **HMP_2012.genefamilies_relab.tongue_dorsum**: An ExpressionSet with 136 samples and 1,964,481 features specific to the tongue_dorsum bodysite
- **HMP_2012.genefamilies_relab.vaginal_introitus**: An ExpressionSet with 3 samples and 1,964,481 features specific to the vaginal_introitus bodysite

**Source**

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

**See Also**


**Examples**

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

---

**HMP_2012.marker_abundance**

*Marker abundance data from the HMP_2012 dataset*

**Description**

Marker abundance data from the HMP_2012 dataset

**Datasets**

- **HMP_2012.marker_abundance.anterior_nares**: An ExpressionSet with 93 samples and 162,108 features specific to the anterior_nares bodysite
- **HMP_2012.marker_abundance.buccal_mucosa**: An ExpressionSet with 119 samples and 162,108 features specific to the buccal_mucosa bodysite
- **HMP_2012.marker_abundance.hard_palate**: An ExpressionSet with 1 sample and 162,108 features specific to the hard_palate bodysite
HMP_2012.marker_abundance.keratinized_gingiva: An ExpressionSet with 6 samples and 162,108 features specific to the keratinized_gingiva bodysite

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

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

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

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

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

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

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

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

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

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

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

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

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

See Also

Examples
HMP_2012.marker_abundance.anterior_nares()
HMP_2012.marker_presence

Marker presence data from the HMP_2012 dataset

Description

Marker presence data from the HMP_2012 dataset

Datasets

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

**HMP_2012.marker_presence.vaginal_introitus**: An ExpressionSet with 3 samples and 158,646 features specific to the vaginal_introitus bodysite
Source
Department of Psychology, Abdul Haq Campus, Federal Urdu University for Arts, Science and Technology, Karachi, Pakistan. shahiq_psy@yahoo.com

See Also

Examples
HMP_2012.marker_presence.anterior_nares()

HMP_2012.metaphlan_bugs_list
Taxonomic abundance data from the HMP_2012 dataset

Description
Taxonomic abundance data from the HMP_2012 dataset

Datasets
HMP_2012.metaphlan_bugs_list.anterior_nares: An ExpressionSet with 93 samples and 1,988 features specific to the anterior_nares bodysite
HMP_2012.metaphlan_bugs_list.buccal_mucosa: An ExpressionSet with 119 samples and 1,988 features specific to the buccal_mucosa bodysite
HMP_2012.metaphlan_bugs_list.hard_palate: An ExpressionSet with 1 sample and 1,988 features specific to the hard_palate bodysite
HMP_2012.metaphlan_bugs_list.keratinized_gingiva: An ExpressionSet with 6 samples and 1,988 features specific to the keratinized_gingiva bodysite
HMP_2012.metaphlan_bugs_list.l_retroauricularcrease: An ExpressionSet with 9 samples and 1,988 features specific to the l_retroauricularcrease bodysite
HMP_2012.metaphlan_bugs_list.mid_vagina: An ExpressionSet with 2 samples and 1,988 features specific to the mid_vagina bodysite
HMP_2012.metaphlan_bugs_list.palatine_tonsils: An ExpressionSet with 6 samples and 1,988 features specific to the palatine_tonsils bodysite
HMP_2012.metaphlan_bugs_list.posterior_fornix: An ExpressionSet with 62 samples and 1,988 features specific to the posterior_fornix bodysite
HMP_2012.metaphlan_bugs_list.r_retroauricularcrease: An ExpressionSet with 18 samples and 1,988 features specific to the r_retroauricularcrease bodysite
HMP_2012.metaphlan_bugs_list.saliva: An ExpressionSet with 5 samples and 1,988 features specific to the saliva bodysite
HMP_2012.metaphlan_bugs_list.stool: An ExpressionSet with 147 samples and 1,988 features specific to the stool bodysite

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

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

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

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

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

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

See Also

Examples
HMP_2012.metaphlan_bugs_list.anterior_nares()
HMP_2012.pathabundance_relab.l_retroauricularcrease: An ExpressionSet with 9 samples and 23,271 features specific to the l_retroauricularcrease bodysite

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

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

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

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

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

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

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

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

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

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

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

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

See Also

Examples
HMP_2012.pathabundance_relab.anterior_nares()
Pathcoverage data from the HMP_2012 dataset

Description
Pathcoverage data from the HMP_2012 dataset

Datasets

**HMP\_2012.pathcoverage.anterior\_nares:** An ExpressionSet with 93 samples and 23,271 features specific to the anterior\_nares bodysite

**HMP\_2012.pathcoverage.buccal\_mucosa:** An ExpressionSet with 119 samples and 23,271 features specific to the buccal\_mucosa bodysite

**HMP\_2012.pathcoverage.hard\_palate:** An ExpressionSet with 1 sample and 23,271 features specific to the hard\_palate bodysite

**HMP\_2012.pathcoverage.keratinized\_gingiva:** An ExpressionSet with 6 samples and 23,271 features specific to the keratinized\_gingiva bodysite

**HMP\_2012.pathcoverage.l\_retroauricular\_crease:** An ExpressionSet with 9 samples and 23,271 features specific to the l\_retroauricular\_crease bodysite

**HMP\_2012.pathcoverage.mid\_vagina:** An ExpressionSet with 2 samples and 23,271 features specific to the mid\_vagina bodysite

**HMP\_2012.pathcoverage.palatine\_tonsils:** An ExpressionSet with 6 samples and 23,271 features specific to the palatine\_tonsils bodysite

**HMP\_2012.pathcoverage.posterior\_fornix:** An ExpressionSet with 62 samples and 23,271 features specific to the posterior\_fornix bodysite

**HMP\_2012.pathcoverage.r\_retroauricular\_crease:** An ExpressionSet with 18 samples and 23,271 features specific to the r\_retroauricular\_crease bodysite

**HMP\_2012.pathcoverage.saliva:** An ExpressionSet with 5 samples and 23,271 features specific to the saliva bodysite

**HMP\_2012.pathcoverage.stool:** An ExpressionSet with 147 samples and 23,271 features specific to the stool bodysite

**HMP\_2012.pathcoverage.subgingival\_plaque:** An ExpressionSet with 7 samples and 23,271 features specific to the subgingival\_plaque bodysite

**HMP\_2012.pathcoverage.supragingival\_plaque:** An ExpressionSet with 128 samples and 23,271 features specific to the supragingival\_plaque bodysite

**HMP\_2012.pathcoverage.throat:** An ExpressionSet with 7 samples and 23,271 features specific to the throat bodysite

**HMP\_2012.pathcoverage.tongue\_dorsum:** An ExpressionSet with 136 samples and 23,271 features specific to the tongue\_dorsum bodysite

**HMP\_2012.pathcoverage.vaginal\_introitus:** An ExpressionSet with 3 samples and 23,271 features specific to the vaginal\_introitus bodysite
KarlssonFH_2013.genefamilies_relab

Source

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

See Also


Examples

HMP_2012.pathcoverage.anterior_nares()

KarlssonFH_2013.genefamilies_relab

Relabeled genefamilies data from the KarlssonFH_2013 dataset

Description

Relabeled genefamilies data from the KarlssonFH_2013 dataset

Datasets

KarlssonFH_2013.genefamilies_relab.stool: An ExpressionSet with 145 samples and 1,415,610 features specific to the stool bodysite

Source

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

See Also


Examples

KarlssonFH_2013.genefamilies_relab.stool()
**KarlssonFH_2013.marker_abundance**

*Marker abundance data from the KarlssonFH_2013 dataset*

**Description**

Marker abundance data from the KarlssonFH_2013 dataset

**Datasets**

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

**Source**

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

**See Also**


**Examples**

KarlssonFH_2013.marker_abundance.stool()
**Examples**

KarlssonFH_2013.marker_presence.stool()

---

KarlssonFH_2013.metaphlan_bugs_list

*Taxonomic abundance data from the KarlssonFH_2013 dataset*

---

**Description**

Taxonomic abundance data from the KarlssonFH_2013 dataset

**Datasets**

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

**Source**

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

**See Also**


**Examples**

KarlssonFH_2013.metaphlan_bugs_list.stool()

---

KarlssonFH_2013.pathabundance_relab

*Relabeled pathabundance data from the KarlssonFH_2013 dataset*

---

**Description**

Relabeled pathabundance data from the KarlssonFH_2013 dataset

**Datasets**

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

**Source**

Department of Chemical and Biological Engineering, Chalmers University of Technology, SE-412 96 Gothenburg, Sweden.
KarlssonFH_2013.pathcoverage

See Also

Examples
KarlssonFH_2013.pathabundance_relab.stool()

KarlssonFH_2013.pathcoverage
Pathcoverage data from the KarlssonFH_2013 dataset

Description
Pathcoverage data from the KarlssonFH_2013 dataset

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

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

See Also

Examples
KarlssonFH_2013.pathcoverage.stool()

LeChatelierE_2013.genefamilies_relab
Relabeled genefamilies data from the LeChatelierE_2013 dataset

Description
Relabeled genefamilies data from the LeChatelierE_2013 dataset

Datasets
LeChatelierE_2013.genefamilies_relab.stool: An ExpressionSet with 292 samples and 1,519,376 features specific to the stool bodysite
Marker abundance data from the LeChatelierE_2013 dataset

Marker abundance data from the LeChatelierE_2013 dataset

Datasets

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

Source

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

See Also


Examples

LeChatelierE_2013.marker_abundance.stool()
Marker presence data from the LeChatelierE_2013 dataset

Datasets

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

Source

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

See Also


Taxonomic abundance data from the LeChatelierE_2013 dataset

Datasets

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

Source

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

See Also

Examples

LeChatelierE_2013.pathabundance_relab

Relabeled pathabundance data from the LeChatelierE_2013 dataset

Description

Relabeled pathabundance data from the LeChatelierE_2013 dataset

Datasets

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

Source

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

See Also


Examples

LeChatelierE_2013.pathabundance_relab.stool()

Pathcoverage data from the LeChatelierE_2013 dataset

Description

Pathcoverage data from the LeChatelierE_2013 dataset

Datasets

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

Source

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

Examples
LeChatelierE_2013.pathcoverage.stool()
Marker presence data from the LomanNJ_2013_Hi dataset

Marker presence data from the LomanNJ_2013_Hi dataset

LomanNJ_2013_Hi.marker_presence

Datasets

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

Source

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

See Also


Examples

LomanNJ_2013_Hi.marker_presence.stool()
LomanNJ_2013_Hi.metaphlan_bugs_list

*Taxonomic abundance data from the LomanNJ_2013_Hi dataset*

**Description**

Taxonomic abundance data from the LomanNJ_2013_Hi dataset

**Datasets**

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

**Source**

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

**See Also**


**Examples**

LomanNJ_2013_Hi.metaphlan_bugs_list.stool()

---

LomanNJ_2013_Hi.pathabundance_relab

*Relabeled pathabundance data from the LomanNJ_2013_Hi dataset*

**Description**

Relabeled pathabundance data from the LomanNJ_2013_Hi dataset

**Datasets**

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

**Source**

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

**See Also**


**Examples**

LomanNJ_2013_Hi.pathabundance_relab.stool()
LomanNJ_2013_Hi.pathcoverage

Pathcoverage data from the LomanNJ_2013_Hi dataset

Description
Pathcoverage data from the LomanNJ_2013_Hi dataset

Datasets

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

Source
Institute of Microbiology and Infection, University of Birmingham, Birmingham, England.

See Also

Examples
LomanNJ_2013_Hi.pathcoverage.stool()

LomanNJ_2013_Mi.genefamilies_relab

Relabeled genefamilies data from the LomanNJ_2013_Mi dataset

Description
Relabeled genefamilies data from the LomanNJ_2013_Mi dataset

Datasets

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

Source
Institute of Microbiology and Infection, University of Birmingham, Birmingham, England.

See Also

Examples
LomanNJ_2013_Mi.genefamilies_relab.stool()
**LomanNJ_2013_Mi.marker_abundance**

*Marker abundance data from the LomanNJ_2013_Mi dataset*

**Description**

Marker abundance data from the LomanNJ_2013_Mi dataset

**Datasets**

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

**Source**

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

**See Also**

*LomanNJ_2013_Mi.genefamilies_relab, LomanNJ_2013_Mi.marker_presence, LomanNJ_2013_Mi.metaphlan_bugs_list, LomanNJ_2013_Mi.pathabundance_relab, LomanNJ_2013_Mi.pathcoverage*

**Examples**

LomanNJ_2013_Mi.marker_abundance.stool()

---

**LomanNJ_2013_Mi.marker_presence**

*Marker presence data from the LomanNJ_2013_Mi dataset*

**Description**

Marker presence data from the LomanNJ_2013_Mi dataset

**Datasets**

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

**Source**

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

**See Also**

*LomanNJ_2013_Mi.genefamilies_relab, LomanNJ_2013_Mi.marker_abundance, LomanNJ_2013_Mi.metaphlan_bugs_list, LomanNJ_2013_Mi.pathabundance_relab, LomanNJ_2013_Mi.pathcoverage*

**Examples**

LomanNJ_2013_Mi.marker_presence.stool()
LomanNJ_2013_Mi.metaphlan_bugs_list

*Taxonomic abundance data from the LomanNJ_2013_Mi dataset*

**Description**

Taxonomic abundance data from the LomanNJ_2013_Mi dataset

**Datasets**

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

**Source**

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

**See Also**


**Examples**

LomanNJ_2013_Mi.metaphlan_bugs_list.stool()

---

LomanNJ_2013_Mi.pathabundance_relab

*Relabeled pathabundance data from the LomanNJ_2013_Mi dataset*

**Description**

Relabeled pathabundance data from the LomanNJ_2013_Mi dataset

**Datasets**

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

**Source**

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

**See Also**


**Examples**

LomanNJ_2013_Mi.pathabundance_relab.stool()
Pathcoverage data from the LomanNJ_2013_Mi dataset

Description
Pathcoverage data from the LomanNJ_2013_Mi dataset

Datasets

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

Source
Institute of Microbiology and Infection, University of Birmingham, Birmingham, England.

See Also

Examples
LomanNJ_2013_Mi.pathcoverage.stool()
Examples

NielsenHB_2014.marker_abundance

Marker abundance data from the NielsenHB_2014 dataset

Datasets

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

Source

[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].

See Also


Examples

NielsenHB_2014.marker_abundance.stool()

Description

Marker presence data from the NielsenHB_2014 dataset

Datasets

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

Source

[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].
See Also

NielsenHB_2014.pathabundance_relab, NielsenHB_2014.pathcoverage

Examples

NielsenHB_2014.marker_presence.stool()

NielsenHB_2014.metaphlan_bugs_list

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**Taxonomic abundance data from the NielsenHB_2014 dataset**

Description

Taxonomic abundance data from the NielsenHB_2014 dataset

Datasets

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

Source

[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].

See Also

NielsenHB_2014.pathabundance_relab, NielsenHB_2014.pathcoverage

Examples

NielsenHB_2014.metaphlan_bugs_list.stool()

NielsenHB_2014.pathabundance_relab

---

**Relabeled pathabundance data from the NielsenHB_2014 dataset**

Description

Relabeled pathabundance data from the NielsenHB_2014 dataset

Datasets

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

Source

[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].

See Also


Examples

NielsenHB_2014.pathabundance_relab.stool()


NielsenHB_2014.pathcoverage

Pathcoverage data from the NielsenHB_2014 dataset

Description

Pathcoverage data from the NielsenHB_2014 dataset

Datasets

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

Source

[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].

See Also


Examples

NielsenHB_2014.pathcoverage.stool()
Obregon_TitoAJ_2015.genefamilies_relab

Relabeled genefamilies data from the Obregon_TitoAJ_2015 dataset

Description

Relabeled genefamilies data from the Obregon_TitoAJ_2015 dataset

Datasets

Obregon_TitoAJ_2015.genefamilies_relab.stool: An ExpressionSet with 58 samples and 1,192,382 features specific to the stool bodysite

Source


See Also


Examples

Obregon_TitoAJ_2015.genefamilies_relab.stool()

Obregon_TitoAJ_2015.marker_abundance

Marker abundance data from the Obregon_TitoAJ_2015 dataset

Description

Marker abundance data from the Obregon_TitoAJ_2015 dataset

Datasets

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

Source

See Also

Obregon_TitoAJ_2015.pathabundance_relab, Obregon_TitoAJ_2015.pathcoverage

Examples

Obregon_TitoAJ_2015.marker_abundance.stool()

Obregon_TitoAJ_2015.marker_presence

Marker presence data from the Obregon_TitoAJ_2015 dataset

Description

Marker presence data from the Obregon_TitoAJ_2015 dataset

Datasets

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

Source


See Also

Obregon_TitoAJ_2015.pathabundance_relab, Obregon_TitoAJ_2015.pathcoverage

Examples

Obregon_TitoAJ_2015.marker_presence.stool()

Obregon_TitoAJ_2015.metaphlan_bugs_list

Taxonomic abundance data from the Obregon_TitoAJ_2015 dataset

Description

Taxonomic abundance data from the Obregon_TitoAJ_2015 dataset

Datasets

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


**See Also**


**Examples**

Obregon_TitoAJ_2015.metaphlan_bugs_list.stool()

---

**Obregon_TitoAJ_2015.pathabundance_relab**

*Relabeled pathabundance data from the Obregon_TitoAJ_2015 dataset*

**Description**

Relabeled pathabundance data from the Obregon_TitoAJ_2015 dataset

**Datasets**

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

**Source**


**See Also**


**Examples**

Obregon_TitoAJ_2015.pathabundance_relab.stool()
Obregon_TitoAJ_2015.pathcoverage

Pathcoverage data from the Obregon_TitoAJ_2015 dataset

Description

Pathcoverage data from the Obregon_TitoAJ_2015 dataset

Datasets

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

Source


See Also


Examples

Obregon_TitoAJ_2015.pathcoverage.stool()

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OhJ_2014.genefamilies_relab

Relabeled genefamilies data from the OhJ_2014 dataset

Description

Relabeled genefamilies data from the OhJ_2014 dataset

Datasets

OhJ_2014.genefamilies_relab.skin: An ExpressionSet with 291 samples and 3,956,473 features specific to the skin bodysite

Source

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

See Also

**OhJ_2014.marker_abundance**

**Examples**

OhJ_2014.marker_abundance

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**Description**

Marker abundance data from the OhJ_2014 dataset

**Datasets**

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

**Source**

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

**See Also**

OhJ_2014.marker_abundance

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**OhJ_2014.marker_presence**

**Marker presence data from the OhJ_2014 dataset**

**Description**

Marker presence data from the OhJ_2014 dataset

**Datasets**

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

**Source**

Translational and Functional Genomics Branch, National Human Genome Research Institute, NIH, Bethesda, Maryland 20892, USA.
**OhJ_2014.pathabundance_relab**

See Also


Examples

OhJ_2014.marker_presence.skin()

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**OhJ_2014.metaphlan_bugs_list**

*Taxonomic abundance data from the OhJ_2014 dataset*

**Description**

Taxonomic abundance data from the OhJ_2014 dataset

**Datasets**

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

**Source**

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

See Also


Examples

OhJ_2014.metaphlan_bugs_list.skin()

---

**OhJ_2014.pathabundance_relab**

*Relabeled pathabundance data from the OhJ_2014 dataset*

**Description**

Relabeled pathabundance data from the OhJ_2014 dataset

**Datasets**

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

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

**See Also**


**Examples**

OhJ_2014.pathabundance_relab.skin()

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**OhJ_2014.pathcoverage**  *Pathcoverage data from the OhJ_2014 dataset*

**Description**
Pathcoverage data from the OhJ_2014 dataset

**Datasets**

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

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

**See Also**


**Examples**

OhJ_2014.pathcoverage.skin()
QinJ_2012.marker_abundance

Marker abundance data from the QinJ_2012 dataset

Description

Marker abundance data from the QinJ_2012 dataset

Datasets

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

Source

BGI-Shenzhen, Shenzhen 518083, China.

See Also


Examples

QinJ_2012.marker_abundance.stool()

QinJ_2012.marker_presence

Relabeled genefamilies data from the QinJ_2012 dataset

Description

Relabeled genefamilies data from the QinJ_2012 dataset

Datasets

QinJ_2012.genefamilies_relab: An ExpressionSet with 363 samples and 1,690,774 features specific to the stool bodysite

Source

BGI-Shenzhen, Shenzhen 518083, China.

See Also


Examples

QinJ_2012.genefamilies_relab()
QinJ_2012.marker_presence

Marker presence data from the QinJ_2012 dataset

Description
Marker presence data from the QinJ_2012 dataset

Datasets

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

Source
BGI-Shenzhen, Shenzhen 518083, China.

See Also

Examples
QinJ_2012.marker_presence.stool()

QinJ_2012.metaphlan_bugs_list

Taxonomic abundance data from the QinJ_2012 dataset

Description
Taxonomic abundance data from the QinJ_2012 dataset

Datasets

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

Source
BGI-Shenzhen, Shenzhen 518083, China.

See Also

Examples
QinJ_2012.metaphlan_bugs_list.stool()
QinJ_2012.pathabundance_relab

Relabeled pathabundance data from the QinJ_2012 dataset

Description

Relabeled pathabundance data from the QinJ_2012 dataset

Datasets

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

Source

BGI-Shenzhen, Shenzhen 518083, China.

See Also


Examples

QinJ_2012.pathabundance_relab.stool()

QinJ_2012.pathcoverage

Pathcoverage data from the QinJ_2012 dataset

Description

Pathcoverage data from the QinJ_2012 dataset

Datasets

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

Source

BGI-Shenzhen, Shenzhen 518083, China.

See Also


Examples

QinJ_2012.pathcoverage.stool()
QinN_2014.genefamilies_relab

Relabeled genefamilies data from the QinN_2014 dataset

Description

Relabeled genefamilies data from the QinN_2014 dataset

Datasets

QinN_2014.genefamilies_relab.stool: An ExpressionSet with 237 samples and 1,747,534 features specific to the stool bodysite

Source

[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].

See Also


Examples

QinN_2014.genefamilies_relab.stool()

QinN_2014.marker_abundance

Marker abundance data from the QinN_2014 dataset

Description

Marker abundance data from the QinN_2014 dataset

Datasets

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

Source

[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].
QinN_2014.marker_presence

See Also


Examples

QinN_2014.marker_abundance.stool()

QinN_2014.marker_presence

Marker presence data from the QinN_2014 dataset

Description

Marker presence data from the QinN_2014 dataset

Datasets

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

Source

[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].

See Also


Examples

QinN_2014.marker_presence.stool()
QinN_2014.metaphlan_bugs_list

Taxonomic abundance data from the QinN_2014 dataset

Description
Taxonomic abundance data from the QinN_2014 dataset

Datasets

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

Source
[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].

See Also

Examples
QinN_2014.metaphlan_bugs_list.stool()

QinN_2014.pathabundance_relab

Relabeled pathabundance data from the QinN_2014 dataset

Description
Relabeled pathabundance data from the QinN_2014 dataset

Datasets

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

Source
[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].
See Also

QinN_2014.genefamilies_relab, QinN_2014.marker_abundance, QinN_2014.marker_presence,
QinN_2014.metaphlan_bugs_list, QinN_2014.pathcoverage

Examples

QinN_2014.pathabundance_relab.stool()
RampelliS_2015.genefamilies_relab

Relabeled genefamilies data from the RampelliS_2015 dataset

Description
Relabeled genefamilies data from the RampelliS_2015 dataset

Datasets

RampelliS_2015.genefamilies_relab.stool: An ExpressionSet with 38 samples and 788,641 features specific to the stool bodysite

Source
Department of Pharmacy and Biotechnology, University of Bologna, Bologna 40126, Italy.

See Also

Examples
RampelliS_2015.genefamilies_relab.stool()
RampelliS_2015.marker_presence

Marker presence data from the RampelliS_2015 dataset

Description

Marker presence data from the RampelliS_2015 dataset

Datasets

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

Source

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

See Also


Examples

RampelliS_2015.marker_presence.stool()

RampelliS_2015.metaphlan_bugs_list

Taxonomic abundance data from the RampelliS_2015 dataset

Description

Taxonomic abundance data from the RampelliS_2015 dataset

Datasets

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

Source

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

See Also


Examples

RampelliS_2015.metaphlan_bugs_list.stool()
RampelliS_2015.pathabundance_relab

Relabeled pathabundance data from the RampelliS_2015 dataset

Description

Relabeled pathabundance data from the RampelliS_2015 dataset

Datasets

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

Source

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

See Also


Examples

RampelliS_2015.pathabundance_relab.stool()

RampelliS_2015.pathcoverage

Pathcoverage data from the RampelliS_2015 dataset

Description

Pathcoverage data from the RampelliS_2015 dataset

Datasets

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

Source

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

See Also


Examples

RampelliS_2015.pathcoverage.stool()
**TettAJ_2016.genefamilies_relab**

*Relabeled genefamilies data from the TettAJ_2016 dataset*

**Description**

Relabeled genefamilies data from the TettAJ_2016 dataset

**Datasets**

- **TettAJ_2016.genefamilies_relab.left_ear:** An ExpressionSet with 22 samples and 1,183,854 features specific to the left_ear bodysite
- **TettAJ_2016.genefamilies_relab.left_elbow:** An ExpressionSet with 26 samples and 1,183,854 features specific to the left_elbow bodysite
- **TettAJ_2016.genefamilies_relab.right_ear:** An ExpressionSet with 26 samples and 1,183,854 features specific to the right_ear bodysite
- **TettAJ_2016.genefamilies_relab.right_elbow:** An ExpressionSet with 23 samples and 1,183,854 features specific to the right_elbow bodysite

**See Also**


**Examples**

- TettAJ_2016.genefamilies_relab.left_ear()

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**TettAJ_2016.marker_abundance**

*Marker abundance data from the TettAJ_2016 dataset*

**Description**

Marker abundance data from the TettAJ_2016 dataset

**Datasets**

- **TettAJ_2016.marker_abundance.left_ear:** An ExpressionSet with 22 samples and 64,040 features specific to the left_ear bodysite
- **TettAJ_2016.marker_abundance.left_elbow:** An ExpressionSet with 26 samples and 64,040 features specific to the left_elbow bodysite
- **TettAJ_2016.marker_abundance.right_ear:** An ExpressionSet with 26 samples and 64,040 features specific to the right_ear bodysite
- **TettAJ_2016.marker_abundance.right_elbow:** An ExpressionSet with 23 samples and 64,040 features specific to the right_elbow bodysite
Marker presence data from the TettAJ_2016 dataset

Datasets

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

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

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

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

See Also


Examples

TettAJ_2016.marker_presence.left_ear()
Description
Taxonomic abundance data from the TettAJ_2016 dataset

Datasets
- **TettAJ_2016.metaphlan_bugs_list.left_ear**: An ExpressionSet with 22 samples and 1,004 features specific to the left_ear bodysite
- **TettAJ_2016.metaphlan_bugs_list.left_elbow**: An ExpressionSet with 26 samples and 1,004 features specific to the left_elbow bodysite
- **TettAJ_2016.metaphlan_bugs_list.right_ear**: An ExpressionSet with 26 samples and 1,004 features specific to the right_ear bodysite
- **TettAJ_2016.metaphlan_bugs_list.right_elbow**: An ExpressionSet with 23 samples and 1,004 features specific to the right_elbow bodysite

See Also

Examples
- `TettAJ_2016.metaphlan_bugs_list.left_ear()`

Description
Relabeled pathabundance data from the TettAJ_2016 dataset

Datasets
- **TettAJ_2016.pathabundance_relab.left_ear**: An ExpressionSet with 22 samples and 21,899 features specific to the left_ear bodysite
- **TettAJ_2016.pathabundance_relab.left_elbow**: An ExpressionSet with 26 samples and 21,899 features specific to the left_elbow bodysite
- **TettAJ_2016.pathabundance_relab.right_ear**: An ExpressionSet with 26 samples and 21,899 features specific to the right_ear bodysite
- **TettAJ_2016.pathabundance_relab.right_elbow**: An ExpressionSet with 23 samples and 21,899 features specific to the right_elbow bodysite
**TettAJ_2016.pathcoverage**

**Description**

Pathcoverage data from the TettAJ_2016 dataset

**Datasets**

- **TettAJ_2016.pathcoverage.left_ear**: An ExpressionSet with 22 samples and 21,899 features specific to the left_ear bodysite
- **TettAJ_2016.pathcoverage.left_elbow**: An ExpressionSet with 26 samples and 21,899 features specific to the left_elbow bodysite
- **TettAJ_2016.pathcoverage.right_ear**: An ExpressionSet with 26 samples and 21,899 features specific to the right_ear bodysite
- **TettAJ_2016.pathcoverage.right_elbow**: An ExpressionSet with 23 samples and 21,899 features specific to the right_elbow bodysite

**See Also**


**Examples**

TettAJ_2016.pathabundance_relab.left_ear()
ZellerG_2014.geneFamilies_relab

Relabeled geneFamilies data from the ZellerG_2014 dataset

Description

Relabeled geneFamilies data from the ZellerG_2014 dataset

Datasets

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

Source

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

See Also


Examples

ZellerG_2014.geneFamilies_relab.stool()

ZellerG_2014.marker_abundance

Marker abundance data from the ZellerG_2014 dataset

Description

Marker abundance data from the ZellerG_2014 dataset

Datasets

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

Source

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

See Also

### ZellerG_2014.marker_presence

**Examples**

\[
\text{ZellerG\_2014.marker\_abundance.stool()}
\]

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**Description**

Marker presence data from the ZellerG_2014 dataset

**Datasets**

- **ZellerG\_2014.marker\_presence.stool**: An ExpressionSet with 156 samples and 126,622 features specific to the stool bodysite

**Source**

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

**See Also**


**Examples**

\[
\text{ZellerG\_2014.marker\_presence.stool()}
\]

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### ZellerG_2014.metaphlan_bugs_list

**Description**

Taxonomic abundance data from the ZellerG_2014 dataset

**Datasets**

- **ZellerG\_2014.metaphlan\_bugs\_list.stool**: An ExpressionSet with 156 samples and 1,505 features specific to the stool bodysite

**Source**

Structural and Computational Biology Unit, European Molecular Biology Laboratory, Heidelberg, Germany.
ZellerG_2014.pathcoverage

See Also

ZellerG_2014.path_abundance_relab, ZellerG_2014.pathcoverage

Examples

ZellerG_2014.metaphlan_bugs_list.stool()

ZellerG_2014.path_abundance_relab

Relabeled path abundance data from the ZellerG_2014 dataset

Description

Relabeled path abundance data from the ZellerG_2014 dataset

Datasets

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

Source

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

See Also


Examples

ZellerG_2014.path_abundance_relab.stool()

ZellerG_2014.pathcoverage

Path coverage data from the ZellerG_2014 dataset

Description

Path coverage data from the ZellerG_2014 dataset

Datasets

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

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

See Also


Examples

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