

Package ‘curatedMetagenomicData’

April 1, 2025

Title Curated Metagenomic Data of the Human Microbiome

Description The curatedMetagenomicData package provides standardized, curated human microbiome data for novel analyses. It includes gene families, marker abundance, marker presence, pathway abundance, pathway coverage, and relative abundance for samples collected from different body sites. The bacterial, fungal, and archaeal taxonomic abundances for each sample were calculated with MetaPhlAn3, and metabolic functional potential was calculated with HUMAnN3. The manually curated sample metadata and standardized metagenomic data are available as (Tree)SummarizedExperiment objects.

biocViews ExperimentHub, Homo_sapiens_Data, MicrobiomeData, ReproducibleResearch

Version 3.14.0

License Artistic-2.0

Depends R (>= 4.1.0), SummarizedExperiment, TreeSummarizedExperiment

Imports AnnotationHub, ExperimentHub, S4Vectors, dplyr, magrittr, mia, purrr, rlang, stringr, tibble, tidyr, tidyselect

Suggests BiocStyle, DT, knitr, readr, rmarkdown, scater, testthat, utils, uwot, vegan

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

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

Encoding UTF-8

LazyData true

Roxygen list(markdown = TRUE)

RoxygenNote 7.2.3

VignetteBuilder knitr

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

git_branch RELEASE_3_20

git_last_commit 80d4eb6

git_last_commit_date 2024-10-29

Repository Bioconductor 3.20

Date/Publication 2025-04-01

Author Lucas schiffer [aut, cre] (<<https://orcid.org/0000-0003-3628-0326>>),
 Levi Waldron [aut],
 Edoardo Pasolli [ctb],
 Jennifer Wokaty [ctb],
 Sean Davis [ctb],
 Audrey Renson [ctb],
 Chloe Mirzayi [ctb],
 Paolo Manghi [ctb],
 Samuel Gamboa-Tuz [ctb],
 Marcel Ramos [ctb],
 Valerie Obenchain [ctb],
 Kelly Eckenrode [ctb],
 Nicola Segata [ctb]

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

Contents

curatedMetagenomicData	2
curatedMetagenomicData-defunct	3
mergeData	15
returnSamples	16
sampleMetadata	17

Index	18
--------------	-----------

curatedMetagenomicData

Access Curated Metagenomic Data

Description

To access curated metagenomic data users will use `curatedMetagenomicData()` after "shopping" the `sampleMetadata` data frame for resources they are interested in. The `dryrun` argument allows users to perfect a query prior to returning resources. When `dryrun = TRUE`, matched resources will be printed before they are returned invisibly as a character vector. When `dryrun = FALSE`, a list of resources containing `SummarizedExperiment` and/or `TreeSummarizedExperiment` objects, each with corresponding sample metadata, is returned. Multiple resources can be returned simultaneously and if there is more than one date corresponding to a resource, the most recent one is selected automatically. Finally, if a `relative_abundance` resource is requested and `counts = TRUE`, relative abundance proportions will be multiplied by read depth and rounded to the nearest integer.

Usage

```
curatedMetagenomicData(
  pattern,
  dryrun = TRUE,
  counts = FALSE,
  rownames = "long"
)
```

Arguments

pattern	regular expression pattern to look for in the titles of resources available in curatedMetagenomicData; "" will return all resources
dryrun	if TRUE (the default), a character vector of resource names is returned invisibly; if FALSE, a list of resources is returned
counts	if FALSE (the default), relative abundance proportions are returned; if TRUE, relative abundance proportions are multiplied by read depth and rounded to the nearest integer prior to being returned
rownames	the type of rownames to use for relative_abundance resources, one of: "long" (the default), "short" (species name), or "NCBI" (NCBI Taxonomy ID)

Details

Above "resources" refers to resources that exists in Bioconductor's ExperimentHub service. In the context of curatedMetagenomicData, these are study-level (sparse) matrix objects used to create [SummarizedExperiment](#) and/or [TreeSummarizedExperiment](#) objects that are ultimately returned as the list of resources. Only the gene_families data type (see [returnSamples](#)) is stored as a sparse matrix in ExperimentHub – this has no practical consequences for users and is done to optimize storage. When searching for "resources", users will use the study_name value from the [sampleMetadata](#) data frame.

Value

if dryrun = TRUE, a character vector of resource names is returned invisibly; if dryrun = FALSE, a list of resources is returned

See Also

[mergeData](#), [returnSamples](#), [sampleMetadata](#)

Examples

```
curatedMetagenomicData("AsnicarF_20.+")  
  
curatedMetagenomicData("AsnicarF_2017.relative_abundance", dryrun = FALSE)  
  
curatedMetagenomicData("AsnicarF_20.+relative_abundance", dryrun = FALSE, counts = TRUE)
```

curatedMetagenomicData-defunct

Defunct functions in package 'curatedMetagenomicData'

Description

These functions are defunct and no longer available.

Details

The following functions (methods) are defunct:

- cmdValidVersions()
- getMetaphlanTree()
- ExpressionSet2MRExperiment()
- ExpressionSet2phyloseq()

The following functions (accessors) are defunct:

- AsnicarF_2017.genefamilies_relab.milk()
- AsnicarF_2017.genefamilies_relab.stool()
- AsnicarF_2017.marker_abundance.milk()
- AsnicarF_2017.marker_abundance.stool()
- AsnicarF_2017.marker_presence.milk()
- AsnicarF_2017.marker_presence.stool()
- AsnicarF_2017.metaphlan_bugs_list.milk()
- AsnicarF_2017.metaphlan_bugs_list.stool()
- AsnicarF_2017.pathabundance_relab.milk()
- AsnicarF_2017.pathabundance_relab.stool()
- AsnicarF_2017.pathcoverage.milk()
- AsnicarF_2017.pathcoverage.stool()
- BackhedF_2015.genefamilies_relab.stool()
- BackhedF_2015.marker_abundance.stool()
- BackhedF_2015.marker_presence.stool()
- BackhedF_2015.metaphlan_bugs_list.stool()
- BackhedF_2015.pathabundance_relab.stool()
- BackhedF_2015.pathcoverage.stool()
- Bengtsson-PalmeJ_2015.genefamilies_relab.stool()
- Bengtsson-PalmeJ_2015.marker_abundance.stool()
- Bengtsson-PalmeJ_2015.marker_presence.stool()
- Bengtsson-PalmeJ_2015.metaphlan_bugs_list.stool()
- Bengtsson-PalmeJ_2015.pathabundance_relab.stool()
- Bengtsson-PalmeJ_2015.pathcoverage.stool()
- BritoIL_2016.genefamilies_relab.oralcavity()
- BritoIL_2016.genefamilies_relab.stool()
- BritoIL_2016.marker_abundance.oralcavity()
- BritoIL_2016.marker_abundance.stool()
- BritoIL_2016.marker_presence.oralcavity()
- BritoIL_2016.marker_presence.stool()
- BritoIL_2016.metaphlan_bugs_list.oralcavity()
- BritoIL_2016.metaphlan_bugs_list.stool()

- BritoIL_2016.pathabundance_relab.oralcavity()
- BritoIL_2016.pathabundance_relab.stool()
- BritoIL_2016.pathcoverage.oralcavity()
- BritoIL_2016.pathcoverage.stool()
- Castro_NallarE_2015.genefamilies_relab.oralcavity()
- Castro_NallarE_2015.marker_abundance.oralcavity()
- Castro_NallarE_2015.marker_presence.oralcavity()
- Castro_NallarE_2015.metaphlan_bugs_list.oralcavity()
- Castro_NallarE_2015.pathabundance_relab.oralcavity()
- Castro_NallarE_2015.pathcoverage.oralcavity()
- Castro-NallarE_2015.genefamilies_relab.oralcavity()
- Castro-NallarE_2015.marker_abundance.oralcavity()
- Castro-NallarE_2015.marker_presence.oralcavity()
- Castro-NallarE_2015.metaphlan_bugs_list.oralcavity()
- Castro-NallarE_2015.pathabundance_relab.oralcavity()
- Castro-NallarE_2015.pathcoverage.oralcavity()
- ChengpingW_2017.genefamilies_relab.stool()
- ChengpingW_2017.marker_abundance.stool()
- ChengpingW_2017.marker_presence.stool()
- ChengpingW_2017.metaphlan_bugs_list.stool()
- ChengpingW_2017.pathabundance_relab.stool()
- ChengpingW_2017.pathcoverage.stool()
- ChngKR_2016.genefamilies_relab.skin()
- ChngKR_2016.marker_abundance.skin()
- ChngKR_2016.marker_presence.skin()
- ChngKR_2016.metaphlan_bugs_list.skin()
- ChngKR_2016.pathabundance_relab.skin()
- ChngKR_2016.pathcoverage.skin()
- CosteaPI_2017.genefamilies_relab.stool()
- CosteaPI_2017.marker_abundance.stool()
- CosteaPI_2017.marker_presence.stool()
- CosteaPI_2017.metaphlan_bugs_list.stool()
- CosteaPI_2017.pathabundance_relab.stool()
- CosteaPI_2017.pathcoverage.stool()
- DavidLA_2015.genefamilies_relab.stool()
- DavidLA_2015.marker_abundance.stool()
- DavidLA_2015.marker_presence.stool()
- DavidLA_2015.metaphlan_bugs_list.stool()
- DavidLA_2015.pathabundance_relab.stool()
- DavidLA_2015.pathcoverage.stool()

- DhakanDB_2019.genefamilies_relab.stool()
- DhakanDB_2019.marker_abundance.stool()
- DhakanDB_2019.marker_presence.stool()
- DhakanDB_2019.metaphlan_bugs_list.stool()
- DhakanDB_2019.pathabundance_relab.stool()
- DhakanDB_2019.pathcoverage.stool()
- FengQ_2015.genefamilies_relab.stool()
- FengQ_2015.marker_abundance.stool()
- FengQ_2015.marker_presence.stool()
- FengQ_2015.metaphlan_bugs_list.stool()
- FengQ_2015.pathabundance_relab.stool()
- FengQ_2015.pathcoverage.stool()
- FerrettiP_2018.genefamilies_relab.oralcavity()
- FerrettiP_2018.genefamilies_relab.skin()
- FerrettiP_2018.genefamilies_relab.stool()
- FerrettiP_2018.genefamilies_relab.vagina()
- FerrettiP_2018.marker_abundance.oralcavity()
- FerrettiP_2018.marker_abundance.skin()
- FerrettiP_2018.marker_abundance.stool()
- FerrettiP_2018.marker_abundance.vagina()
- FerrettiP_2018.marker_presence.oralcavity()
- FerrettiP_2018.marker_presence.skin()
- FerrettiP_2018.marker_presence.stool()
- FerrettiP_2018.marker_presence.vagina()
- FerrettiP_2018.metaphlan_bugs_list.oralcavity()
- FerrettiP_2018.metaphlan_bugs_list.skin()
- FerrettiP_2018.metaphlan_bugs_list.stool()
- FerrettiP_2018.metaphlan_bugs_list.vagina()
- FerrettiP_2018.pathabundance_relab.oralcavity()
- FerrettiP_2018.pathabundance_relab.skin()
- FerrettiP_2018.pathabundance_relab.stool()
- FerrettiP_2018.pathabundance_relab.vagina()
- FerrettiP_2018.pathcoverage.oralcavity()
- FerrettiP_2018.pathcoverage.skin()
- FerrettiP_2018.pathcoverage.stool()
- FerrettiP_2018.pathcoverage.vagina()
- GopalakrishnanV_2018.genefamilies_relab.stool()
- GopalakrishnanV_2018.marker_abundance.stool()
- GopalakrishnanV_2018.marker_presence.stool()
- GopalakrishnanV_2018.metaphlan_bugs_list.stool()

- GopalakrishnanV_2018.pathabundance_relab.stool()
- GopalakrishnanV_2018.pathcoverage.stool()
- HanniganGD_2017.genefamilies_relab.stool()
- HanniganGD_2017.marker_abundance.stool()
- HanniganGD_2017.marker_presence.stool()
- HanniganGD_2017.metaphlan_bugs_list.stool()
- HanniganGD_2017.pathabundance_relab.stool()
- HanniganGD_2017.pathcoverage.stool()
- HansenLBS_2018.genefamilies_relab.stool()
- HansenLBS_2018.marker_abundance.stool()
- HansenLBS_2018.marker_presence.stool()
- HansenLBS_2018.metaphlan_bugs_list.stool()
- HansenLBS_2018.pathabundance_relab.stool()
- HansenLBS_2018.pathcoverage.stool()
- Heitz_BuschartA_2016.genefamilies_relab.stool()
- Heitz_BuschartA_2016.marker_abundance.stool()
- Heitz_BuschartA_2016.marker_presence.stool()
- Heitz_BuschartA_2016.metaphlan_bugs_list.stool()
- Heitz_BuschartA_2016.pathabundance_relab.stool()
- Heitz_BuschartA_2016.pathcoverage.stool()
- Heitz-BuschartA_2016.genefamilies_relab.stool()
- Heitz-BuschartA_2016.marker_abundance.stool()
- Heitz-BuschartA_2016.marker_presence.stool()
- Heitz-BuschartA_2016.metaphlan_bugs_list.stool()
- Heitz-BuschartA_2016.pathabundance_relab.stool()
- Heitz-BuschartA_2016.pathcoverage.stool()
- HMP_2012.genefamilies_relab.nasalcavity()
- HMP_2012.genefamilies_relab.oralcavity()
- HMP_2012.genefamilies_relab.skin()
- HMP_2012.genefamilies_relab.stool()
- HMP_2012.genefamilies_relab.vagina()
- HMP_2012.marker_abundance.nasalcavity()
- HMP_2012.marker_abundance.oralcavity()
- HMP_2012.marker_abundance.skin()
- HMP_2012.marker_abundance.stool()
- HMP_2012.marker_abundance.vagina()
- HMP_2012.marker_presence.nasalcavity()
- HMP_2012.marker_presence.oralcavity()
- HMP_2012.marker_presence.skin()
- HMP_2012.marker_presence.stool()

- HMP_2012.marker_presence.vagina()
- HMP_2012.metaphlan_bugs_list.nasalcavity()
- HMP_2012.metaphlan_bugs_list.oralcavity()
- HMP_2012.metaphlan_bugs_list.skin()
- HMP_2012.metaphlan_bugs_list.stool()
- HMP_2012.metaphlan_bugs_list.vagina()
- HMP_2012.pathabundance_relab.nasalcavity()
- HMP_2012.pathabundance_relab.oralcavity()
- HMP_2012.pathabundance_relab.skin()
- HMP_2012.pathabundance_relab.stool()
- HMP_2012.pathabundance_relab.vagina()
- HMP_2012.pathcoverage.nasalcavity()
- HMP_2012.pathcoverage.oralcavity()
- HMP_2012.pathcoverage.skin()
- HMP_2012.pathcoverage.stool()
- HMP_2012.pathcoverage.vagina()
- JieZ_2017.genefamilies_relab.stool()
- JieZ_2017.marker_abundance.stool()
- JieZ_2017.marker_presence.stool()
- JieZ_2017.metaphlan_bugs_list.stool()
- JieZ_2017.pathabundance_relab.stool()
- JieZ_2017.pathcoverage.stool()
- KarlssonFH_2013.genefamilies_relab.stool()
- KarlssonFH_2013.marker_abundance.stool()
- KarlssonFH_2013.marker_presence.stool()
- KarlssonFH_2013.metaphlan_bugs_list.stool()
- KarlssonFH_2013.pathabundance_relab.stool()
- KarlssonFH_2013.pathcoverage.stool()
- KieserS_2018.genefamilies_relab.stool()
- KieserS_2018.marker_abundance.stool()
- KieserS_2018.marker_presence.stool()
- KieserS_2018.metaphlan_bugs_list.stool()
- KieserS_2018.pathabundance_relab.stool()
- KieserS_2018.pathcoverage.stool()
- KosticAD_2015.genefamilies_relab.stool()
- KosticAD_2015.marker_abundance.stool()
- KosticAD_2015.marker_presence.stool()
- KosticAD_2015.metaphlan_bugs_list.stool()
- KosticAD_2015.pathabundance_relab.stool()
- KosticAD_2015.pathcoverage.stool()

- LeChatelierE_2013.genefamilies_relab.stool()
- LeChatelierE_2013.marker_abundance.stool()
- LeChatelierE_2013.marker_presence.stool()
- LeChatelierE_2013.metaphlan_bugs_list.stool()
- LeChatelierE_2013.pathabundance_relab.stool()
- LeChatelierE_2013.pathcoverage.stool()
- LiJ_2014.genefamilies_relab.stool()
- LiJ_2014.marker_abundance.stool()
- LiJ_2014.marker_presence.stool()
- LiJ_2014.metaphlan_bugs_list.stool()
- LiJ_2014.pathabundance_relab.stool()
- LiJ_2014.pathcoverage.stool()
- LiJ_2017.genefamilies_relab.stool()
- LiJ_2017.marker_abundance.stool()
- LiJ_2017.marker_presence.stool()
- LiJ_2017.metaphlan_bugs_list.stool()
- LiJ_2017.pathabundance_relab.stool()
- LiJ_2017.pathcoverage.stool()
- LiSS_2016.genefamilies_relab.stool()
- LiSS_2016.marker_abundance.stool()
- LiSS_2016.marker_presence.stool()
- LiSS_2016.metaphlan_bugs_list.stool()
- LiSS_2016.pathabundance_relab.stool()
- LiSS_2016.pathcoverage.stool()
- LiuW_2016.genefamilies_relab.stool()
- LiuW_2016.marker_abundance.stool()
- LiuW_2016.marker_presence.stool()
- LiuW_2016.metaphlan_bugs_list.stool()
- LiuW_2016.pathabundance_relab.stool()
- LiuW_2016.pathcoverage.stool()
- LomanNJ_2013.genefamilies_relab.stool()
- LomanNJ_2013.marker_abundance.stool()
- LomanNJ_2013.marker_presence.stool()
- LomanNJ_2013.metaphlan_bugs_list.stool()
- LomanNJ_2013.pathabundance_relab.stool()
- LomanNJ_2013.pathcoverage.stool()
- LoombaR_2017.genefamilies_relab.stool()
- LoombaR_2017.marker_abundance.stool()
- LoombaR_2017.marker_presence.stool()
- LoombaR_2017.metaphlan_bugs_list.stool()

- LoombaR_2017.pathabundance_relab.stool()
- LoombaR_2017.pathcoverage.stool()
- LouisS_2016.genefamilies_relab.stool()
- LouisS_2016.marker_abundance.stool()
- LouisS_2016.marker_presence.stool()
- LouisS_2016.metaphlan_bugs_list.stool()
- LouisS_2016.pathabundance_relab.stool()
- LouisS_2016.pathcoverage.stool()
- MatsonV_2018.genefamilies_relab.stool()
- MatsonV_2018.marker_abundance.stool()
- MatsonV_2018.marker_presence.stool()
- MatsonV_2018.metaphlan_bugs_list.stool()
- MatsonV_2018.pathabundance_relab.stool()
- MatsonV_2018.pathcoverage.stool()
- NielsenHB_2014.genefamilies_relab.stool()
- NielsenHB_2014.marker_abundance.stool()
- NielsenHB_2014.marker_presence.stool()
- NielsenHB_2014.metaphlan_bugs_list.stool()
- NielsenHB_2014.pathabundance_relab.stool()
- NielsenHB_2014.pathcoverage.stool()
- Obregon-TitoAJ_2015.genefamilies_relab.stool()
- Obregon-TitoAJ_2015.marker_abundance.stool()
- Obregon-TitoAJ_2015.marker_presence.stool()
- Obregon-TitoAJ_2015.metaphlan_bugs_list.stool()
- Obregon-TitoAJ_2015.pathabundance_relab.stool()
- Obregon-TitoAJ_2015.pathcoverage.stool()
- Obregon-TitoAJ_2015.genefamilies_relab.stool()
- Obregon-TitoAJ_2015.marker_abundance.stool()
- Obregon-TitoAJ_2015.marker_presence.stool()
- Obregon-TitoAJ_2015.metaphlan_bugs_list.stool()
- Obregon-TitoAJ_2015.pathabundance_relab.stool()
- Obregon-TitoAJ_2015.pathcoverage.stool()
- OhJ_2014.genefamilies_relab.skin()
- OhJ_2014.marker_abundance.skin()
- OhJ_2014.marker_presence.skin()
- OhJ_2014.metaphlan_bugs_list.skin()
- OhJ_2014.pathabundance_relab.skin()
- OhJ_2014.pathcoverage.skin()
- OlmMR_2017.genefamilies_relab.oralcavity()
- OlmMR_2017.genefamilies_relab.skin()

- `OlmMR_2017.genefamilies_relab.stool()`
- `OlmMR_2017.marker_abundance.oralcavity()`
- `OlmMR_2017.marker_abundance.skin()`
- `OlmMR_2017.marker_abundance.stool()`
- `OlmMR_2017.marker_presence.oralcavity()`
- `OlmMR_2017.marker_presence.skin()`
- `OlmMR_2017.marker_presence.stool()`
- `OlmMR_2017.metaphlan_bugs_list.oralcavity()`
- `OlmMR_2017.metaphlan_bugs_list.skin()`
- `OlmMR_2017.metaphlan_bugs_list.stool()`
- `OlmMR_2017.pathabundance_relab.oralcavity()`
- `OlmMR_2017.pathabundance_relab.skin()`
- `OlmMR_2017.pathabundance_relab.stool()`
- `OlmMR_2017.pathcoverage.oralcavity()`
- `OlmMR_2017.pathcoverage.skin()`
- `OlmMR_2017.pathcoverage.stool()`
- `PasolliE_2018.genefamilies_relab.stool()`
- `PasolliE_2018.marker_abundance.stool()`
- `PasolliE_2018.marker_presence.stool()`
- `PasolliE_2018.metaphlan_bugs_list.stool()`
- `PasolliE_2018.pathabundance_relab.stool()`
- `PasolliE_2018.pathcoverage.stool()`
- `PehrssonE_2016.genefamilies_relab.stool()`
- `PehrssonE_2016.marker_abundance.stool()`
- `PehrssonE_2016.marker_presence.stool()`
- `PehrssonE_2016.metaphlan_bugs_list.stool()`
- `PehrssonE_2016.pathabundance_relab.stool()`
- `PehrssonE_2016.pathcoverage.stool()`
- `QinJ_2012.genefamilies_relab.stool()`
- `QinJ_2012.marker_abundance.stool()`
- `QinJ_2012.marker_presence.stool()`
- `QinJ_2012.metaphlan_bugs_list.stool()`
- `QinJ_2012.pathabundance_relab.stool()`
- `QinJ_2012.pathcoverage.stool()`
- `QinN_2014.genefamilies_relab.stool()`
- `QinN_2014.marker_abundance.stool()`
- `QinN_2014.marker_presence.stool()`
- `QinN_2014.metaphlan_bugs_list.stool()`
- `QinN_2014.pathabundance_relab.stool()`
- `QinN_2014.pathcoverage.stool()`

- RampelliS_2015.genefamilies_relab.stool()
- RampelliS_2015.marker_abundance.stool()
- RampelliS_2015.marker_presence.stool()
- RampelliS_2015.metaphlan_bugs_list.stool()
- RampelliS_2015.pathabundance_relab.stool()
- RampelliS_2015.pathcoverage.stool()
- RaymondF_2016.genefamilies_relab.stool()
- RaymondF_2016.marker_abundance.stool()
- RaymondF_2016.marker_presence.stool()
- RaymondF_2016.metaphlan_bugs_list.stool()
- RaymondF_2016.pathabundance_relab.stool()
- RaymondF_2016.pathcoverage.stool()
- SchirmerM_2016.genefamilies_relab.stool()
- SchirmerM_2016.marker_abundance.stool()
- SchirmerM_2016.marker_presence.stool()
- SchirmerM_2016.metaphlan_bugs_list.stool()
- SchirmerM_2016.pathabundance_relab.stool()
- SchirmerM_2016.pathcoverage.stool()
- ShiB_2015.genefamilies_relab.oralcavity()
- ShiB_2015.marker_abundance.oralcavity()
- ShiB_2015.marker_presence.oralcavity()
- ShiB_2015.metaphlan_bugs_list.oralcavity()
- ShiB_2015.pathabundance_relab.oralcavity()
- ShiB_2015.pathcoverage.oralcavity()
- SmitsSA_2017.genefamilies_relab.stool()
- SmitsSA_2017.marker_abundance.stool()
- SmitsSA_2017.marker_presence.stool()
- SmitsSA_2017.metaphlan_bugs_list.stool()
- SmitsSA_2017.pathabundance_relab.stool()
- SmitsSA_2017.pathcoverage.stool()
- TettAJ_2016.genefamilies_relab.skin()
- TettAJ_2016.marker_abundance.skin()
- TettAJ_2016.marker_presence.skin()
- TettAJ_2016.metaphlan_bugs_list.skin()
- TettAJ_2016.pathabundance_relab.skin()
- TettAJ_2016.pathcoverage.skin()
- TettAJ_2019_a.genefamilies_relab.stool()
- TettAJ_2019_a.marker_abundance.stool()
- TettAJ_2019_a.marker_presence.stool()
- TettAJ_2019_a.metaphlan_bugs_list.stool()

- TettAJ_2019_a.pathabundance_relab.stool()
- TettAJ_2019_a.pathcoverage.stool()
- TettAJ_2019_b.genefamilies_relab.stool()
- TettAJ_2019_b.marker_abundance.stool()
- TettAJ_2019_b.marker_presence.stool()
- TettAJ_2019_b.metaphlan_bugs_list.stool()
- TettAJ_2019_b.pathabundance_relab.stool()
- TettAJ_2019_b.pathcoverage.stool()
- TettAJ_2019_c.genefamilies_relab.stool()
- TettAJ_2019_c.marker_abundance.stool()
- TettAJ_2019_c.marker_presence.stool()
- TettAJ_2019_c.metaphlan_bugs_list.stool()
- TettAJ_2019_c.pathabundance_relab.stool()
- TettAJ_2019_c.pathcoverage.stool()
- ThomasAM_2018a.genefamilies_relab.stool()
- ThomasAM_2018a.marker_abundance.stool()
- ThomasAM_2018a.marker_presence.stool()
- ThomasAM_2018a.metaphlan_bugs_list.stool()
- ThomasAM_2018a.pathabundance_relab.stool()
- ThomasAM_2018a.pathcoverage.stool()
- ThomasAM_2018b.genefamilies_relab.stool()
- ThomasAM_2018b.marker_abundance.stool()
- ThomasAM_2018b.marker_presence.stool()
- ThomasAM_2018b.metaphlan_bugs_list.stool()
- ThomasAM_2018b.pathabundance_relab.stool()
- ThomasAM_2018b.pathcoverage.stool()
- VatanenT_2016.genefamilies_relab.stool()
- VatanenT_2016.marker_abundance.stool()
- VatanenT_2016.marker_presence.stool()
- VatanenT_2016.metaphlan_bugs_list.stool()
- VatanenT_2016.pathabundance_relab.stool()
- VatanenT_2016.pathcoverage.stool()
- VincentC_2016.genefamilies_relab.stool()
- VincentC_2016.marker_abundance.stool()
- VincentC_2016.marker_presence.stool()
- VincentC_2016.metaphlan_bugs_list.stool()
- VincentC_2016.pathabundance_relab.stool()
- VincentC_2016.pathcoverage.stool()
- VogtmannE_2016.genefamilies_relab.stool()
- VogtmannE_2016.marker_abundance.stool()

- VogtmannE_2016.marker_presence.stool()
- VogtmannE_2016.metaphlan_bugs_list.stool()
- VogtmannE_2016.pathabundance_relab.stool()
- VogtmannE_2016.pathcoverage.stool()
- XieH_2016.genefamilies_relab.stool()
- XieH_2016.marker_abundance.stool()
- XieH_2016.marker_presence.stool()
- XieH_2016.metaphlan_bugs_list.stool()
- XieH_2016.pathabundance_relab.stool()
- XieH_2016.pathcoverage.stool()
- YeZ_2018.genefamilies_relab.stool()
- YeZ_2018.marker_abundance.stool()
- YeZ_2018.marker_presence.stool()
- YeZ_2018.metaphlan_bugs_list.stool()
- YeZ_2018.pathabundance_relab.stool()
- YeZ_2018.pathcoverage.stool()
- YuJ_2015.genefamilies_relab.stool()
- YuJ_2015.marker_abundance.stool()
- YuJ_2015.marker_presence.stool()
- YuJ_2015.metaphlan_bugs_list.stool()
- YuJ_2015.pathabundance_relab.stool()
- YuJ_2015.pathcoverage.stool()
- ZeeviD_2015.genefamilies_relab.stool()
- ZeeviD_2015.marker_abundance.stool()
- ZeeviD_2015.marker_presence.stool()
- ZeeviD_2015.metaphlan_bugs_list.stool()
- ZeeviD_2015.pathabundance_relab.stool()
- ZeeviD_2015.pathcoverage.stool()
- ZellerG_2014.genefamilies_relab.stool()
- ZellerG_2014.marker_abundance.stool()
- ZellerG_2014.marker_presence.stool()
- ZellerG_2014.metaphlan_bugs_list.stool()
- ZellerG_2014.pathabundance_relab.stool()
- ZellerG_2014.pathcoverage.stool()

`mergeData`*Merge curatedMetagenomicData List*

Description

To merge the list elements returned from `curatedMetagenomicData` into a single `SummarizedExperiment` or `TreeSummarizedExperiment` object, users will use `mergeData()` provided elements are the same `dataType` (see `returnSamples`). This is useful for analysis across entire studies (e.g. meta-analysis); however, when doing analysis across individual samples (e.g. mega-analysis) `returnSamples` is preferable.

Usage

```
mergeData(mergeList)
```

Arguments

`mergeList` a list returned from `curatedMetagenomicData` where all of the elements are of the same `dataType` (see `returnSamples`)

Details

Internally, `mergeData()` must full join assays and `rowData` slots of each `SummarizedExperiment` or `TreeSummarizedExperiment` object (`colData` is merged slightly more efficiently by row binding). While `dplyr` methods are used for maximum efficiency, users should be aware that memory requirements can be large when merging many list elements.

Value

when `mergeList` elements are of `dataType` (see `returnSamples`) `relative_abundance`, a `TreeSummarizedExperiment` object is returned; otherwise, a `SummarizedExperiment` object is returned

See Also

[curatedMetagenomicData](#), [returnSamples](#)

Examples

```
curatedMetagenomicData("LiJ_20.+marker_abundance", dryrun = FALSE) |>
  mergeData()

curatedMetagenomicData("LiJ_20.+pathway_abundance", dryrun = FALSE) |>
  mergeData()

curatedMetagenomicData("LiJ_20.+relative_abundance", dryrun = FALSE) |>
  mergeData()
```

returnSamples	<i>Return Samples Across Studies</i>
---------------	--------------------------------------

Description

To return samples across studies, users will use `returnSamples()` along with the `sampleMetadata` `data.frame` subset to include only desired samples and metadata. The subset `sampleMetadata` `data.frame` will be used to get the desired resources, `mergeData` will be used to merge them, and the subset `sampleMetadata` `data.frame` will be used again to subset the `SummarizedExperiment` or `TreeSummarizedExperiment` object to include only desired samples and metadata.

Usage

```
returnSamples(sampleMetadata, dataType, counts = FALSE, rownames = "long")
```

Arguments

<code>sampleMetadata</code>	the <code>sampleMetadata</code> <code>data.frame</code> subset to include only desired samples and metadata
<code>dataType</code>	the data type to be returned; one of the following: <ul style="list-style-type: none"> "gene_families" "marker_abundance" "marker_presence" "pathway_abundance" "pathway_coverage" "relative_abundance"
<code>counts</code>	if FALSE (the default), relative abundance proportions are returned; if TRUE, relative abundance proportions are multiplied by read depth and rounded to the nearest integer prior to being returned
<code>rownames</code>	the type of rownames to use for <code>relative_abundance</code> resources, one of: "long" (the default), "short" (species name), or "NCBI" (NCBI Taxonomy ID)

Details

At present, `curatedMetagenomicData` resources exists only as entire studies which requires potentially getting many resources for a limited number of samples. Furthermore, because it is necessary to use `mergeData` internally, the same caveats detailed under **Details** in `mergeData` apply here.

Value

when `dataType = "relative_abundance"`, a `TreeSummarizedExperiment` object is returned; otherwise, a `SummarizedExperiment` object is returned

Examples

```
sampleMetadata |>
  dplyr::filter(age >= 18) |>
  dplyr::filter(!base::is.na(alcohol)) |>
  dplyr::filter(body_site == "stool") |>
  dplyr::select(where(~ !base::all(base::is.na(.x)))) |>
```

```
returnSamples("relative_abundance")
```

sampleMetadata	<i>Manually Curated Sample Metadata</i>
----------------	---

Description

Manually curated sample metadata for all samples in curatedMetagenomicData.

Usage

```
sampleMetadata
```

Format

An object of class `data.frame` with 22588 rows and 141 columns.

Index

* datasets

sampleMetadata, 17

* internal

curatedMetagenomicData-defunct, 3

AsnicarF_2017.genefamilies_relab.milk
(curatedMetagenomicData-defunct),
3

AsnicarF_2017.genefamilies_relab.stool
(curatedMetagenomicData-defunct),
3

AsnicarF_2017.marker_abundance.milk
(curatedMetagenomicData-defunct),
3

AsnicarF_2017.marker_abundance.stool
(curatedMetagenomicData-defunct),
3

AsnicarF_2017.marker_presence.milk
(curatedMetagenomicData-defunct),
3

AsnicarF_2017.marker_presence.stool
(curatedMetagenomicData-defunct),
3

AsnicarF_2017.metaphlan_bugs_list.milk
(curatedMetagenomicData-defunct),
3

AsnicarF_2017.metaphlan_bugs_list.stool
(curatedMetagenomicData-defunct),
3

AsnicarF_2017.pathabundance_relab.milk
(curatedMetagenomicData-defunct),
3

AsnicarF_2017.pathabundance_relab.stool
(curatedMetagenomicData-defunct),
3

AsnicarF_2017.pathcoverage.milk
(curatedMetagenomicData-defunct),
3

AsnicarF_2017.pathcoverage.stool
(curatedMetagenomicData-defunct),
3

BackhedF_2015.genefamilies_relab.stool
(curatedMetagenomicData-defunct),
3

BackhedF_2015.marker_abundance.stool
(curatedMetagenomicData-defunct),
3

BackhedF_2015.marker_presence.stool
(curatedMetagenomicData-defunct),
3

BackhedF_2015.metaphlan_bugs_list.stool
(curatedMetagenomicData-defunct),
3

BackhedF_2015.pathabundance_relab.stool
(curatedMetagenomicData-defunct),
3

BackhedF_2015.pathcoverage.stool
(curatedMetagenomicData-defunct),
3

Bengtsson-PalmeJ_2015.genefamilies_relab.stool
(curatedMetagenomicData-defunct),
3

Bengtsson-PalmeJ_2015.marker_abundance.stool
(curatedMetagenomicData-defunct),
3

Bengtsson-PalmeJ_2015.marker_presence.stool
(curatedMetagenomicData-defunct),
3

Bengtsson-PalmeJ_2015.metaphlan_bugs_list.stool
(curatedMetagenomicData-defunct),
3

Bengtsson-PalmeJ_2015.pathabundance_relab.stool
(curatedMetagenomicData-defunct),
3

Bengtsson-PalmeJ_2015.pathcoverage.stool
(curatedMetagenomicData-defunct),
3

BritoIL_2016.genefamilies_relab.oralcavity
(curatedMetagenomicData-defunct),
3

BritoIL_2016.genefamilies_relab.stool
(curatedMetagenomicData-defunct),
3

BritoIL_2016.marker_abundance.oralcavity
(curatedMetagenomicData-defunct),
3

- BritoIL_2016.marker_abundance.stool
 (curatedMetagenomicData-defunct),
 3
- BritoIL_2016.marker_presence.oralcavity
 (curatedMetagenomicData-defunct),
 3
- BritoIL_2016.marker_presence.stool
 (curatedMetagenomicData-defunct),
 3
- BritoIL_2016.metaphlan_bugs_list.oralcavity
 (curatedMetagenomicData-defunct),
 3
- BritoIL_2016.metaphlan_bugs_list.stool
 (curatedMetagenomicData-defunct),
 3
- BritoIL_2016.pathabundance_relab.oralcavity
 (curatedMetagenomicData-defunct),
 3
- BritoIL_2016.pathabundance_relab.stool
 (curatedMetagenomicData-defunct),
 3
- BritoIL_2016.pathcoverage.oralcavity
 (curatedMetagenomicData-defunct),
 3
- BritoIL_2016.pathcoverage.stool
 (curatedMetagenomicData-defunct),
 3
- Castro-NallarE_2015.genefamilies_relab.oralcavity
 (curatedMetagenomicData-defunct),
 3
- Castro-NallarE_2015.marker_abundance.oralcavity
 (curatedMetagenomicData-defunct),
 3
- Castro-NallarE_2015.marker_presence.oralcavity
 (curatedMetagenomicData-defunct),
 3
- Castro-NallarE_2015.metaphlan_bugs_list.oralcavity
 (curatedMetagenomicData-defunct),
 3
- Castro-NallarE_2015.pathabundance_relab.oralcavity
 (curatedMetagenomicData-defunct),
 3
- Castro-NallarE_2015.pathcoverage.oralcavity
 (curatedMetagenomicData-defunct),
 3
- Castro_NallarE_2015.genefamilies_relab.oralcavity
 (curatedMetagenomicData-defunct),
 3
- Castro_NallarE_2015.marker_abundance.oralcavity
 (curatedMetagenomicData-defunct),
 3
- Castro_NallarE_2015.marker_presence.oralcavity
 (curatedMetagenomicData-defunct),
 3
- (curatedMetagenomicData-defunct),
 3
- Castro_NallarE_2015.metaphlan_bugs_list.oralcavity
 (curatedMetagenomicData-defunct),
 3
- Castro_NallarE_2015.pathabundance_relab.oralcavity
 (curatedMetagenomicData-defunct),
 3
- Castro_NallarE_2015.pathcoverage.oralcavity
 (curatedMetagenomicData-defunct),
 3
- Castro_NallarE_2015.pathcoverage.stool
 (curatedMetagenomicData-defunct),
 3
- ChngKR_2016.genefamilies_relab.skin
 (curatedMetagenomicData-defunct),
 3
- ChngKR_2016.marker_abundance.skin
 (curatedMetagenomicData-defunct),
 3
- ChngKR_2016.marker_presence.skin
 (curatedMetagenomicData-defunct),
 3
- ChngKR_2016.metaphlan_bugs_list.skin
 (curatedMetagenomicData-defunct),
 3
- ChngKR_2016.pathabundance_relab.skin
 (curatedMetagenomicData-defunct),
 3
- ChngKR_2016.pathcoverage.skin
 (curatedMetagenomicData-defunct),
 3
- cmdValidVersions
- CosteaPI_2017.genefamilies_relab.stool
 (curatedMetagenomicData-defunct),
 3

- 3
- CosteaPI_2017.marker_abundance.stool
(curatedMetagenomicData-defunct),
3
- CosteaPI_2017.marker_presence.stool
(curatedMetagenomicData-defunct),
3
- CosteaPI_2017.metaphlan_bugs_list.stool
(curatedMetagenomicData-defunct),
3
- CosteaPI_2017.pathabundance_relab.stool
(curatedMetagenomicData-defunct),
3
- CosteaPI_2017.pathcoverage.stool
(curatedMetagenomicData-defunct),
3
- curatedMetagenomicData, 2, 15
- curatedMetagenomicData-defunct, 3
- DavidLA_2015.genefamilies_relab.stool
(curatedMetagenomicData-defunct),
3
- DavidLA_2015.marker_abundance.stool
(curatedMetagenomicData-defunct),
3
- DavidLA_2015.marker_presence.stool
(curatedMetagenomicData-defunct),
3
- DavidLA_2015.metaphlan_bugs_list.stool
(curatedMetagenomicData-defunct),
3
- DavidLA_2015.pathabundance_relab.stool
(curatedMetagenomicData-defunct),
3
- DavidLA_2015.pathcoverage.stool
(curatedMetagenomicData-defunct),
3
- DhakanDB_2019.genefamilies_relab.stool
(curatedMetagenomicData-defunct),
3
- DhakanDB_2019.marker_abundance.stool
(curatedMetagenomicData-defunct),
3
- DhakanDB_2019.marker_presence.stool
(curatedMetagenomicData-defunct),
3
- DhakanDB_2019.metaphlan_bugs_list.stool
(curatedMetagenomicData-defunct),
3
- DhakanDB_2019.pathabundance_relab.stool
(curatedMetagenomicData-defunct),
3
- DhakanDB_2019.pathcoverage.stool
(curatedMetagenomicData-defunct),
3
- ExpressionSet2MRExperiment
(curatedMetagenomicData-defunct),
3
- ExpressionSet2phyloseq
(curatedMetagenomicData-defunct),
3
- FengQ_2015.genefamilies_relab.stool
(curatedMetagenomicData-defunct),
3
- FengQ_2015.marker_abundance.stool
(curatedMetagenomicData-defunct),
3
- FengQ_2015.marker_presence.stool
(curatedMetagenomicData-defunct),
3
- FengQ_2015.metaphlan_bugs_list.stool
(curatedMetagenomicData-defunct),
3
- FengQ_2015.pathabundance_relab.stool
(curatedMetagenomicData-defunct),
3
- FengQ_2015.pathcoverage.stool
(curatedMetagenomicData-defunct),
3
- FerrettiP_2018.genefamilies_relab.oralcavity
(curatedMetagenomicData-defunct),
3
- FerrettiP_2018.genefamilies_relab.skin
(curatedMetagenomicData-defunct),
3
- FerrettiP_2018.genefamilies_relab.stool
(curatedMetagenomicData-defunct),
3
- FerrettiP_2018.genefamilies_relab.vagina
(curatedMetagenomicData-defunct),
3
- FerrettiP_2018.marker_abundance.oralcavity
(curatedMetagenomicData-defunct),
3
- FerrettiP_2018.marker_abundance.skin
(curatedMetagenomicData-defunct),
3
- FerrettiP_2018.marker_abundance.stool
(curatedMetagenomicData-defunct),
3
- FerrettiP_2018.marker_abundance.vagina
(curatedMetagenomicData-defunct),
3

- FerrettiP_2018.marker_presence.oralcavity
(curatedMetagenomicData-defunct),
3
- FerrettiP_2018.marker_presence.skin
(curatedMetagenomicData-defunct),
3
- FerrettiP_2018.marker_presence.stool
(curatedMetagenomicData-defunct),
3
- FerrettiP_2018.marker_presence.vagina
(curatedMetagenomicData-defunct),
3
- FerrettiP_2018.metaphlan_bugs_list.oralcavity
(curatedMetagenomicData-defunct),
3
- FerrettiP_2018.metaphlan_bugs_list.skin
(curatedMetagenomicData-defunct),
3
- FerrettiP_2018.metaphlan_bugs_list.stool
(curatedMetagenomicData-defunct),
3
- FerrettiP_2018.metaphlan_bugs_list.vagina
(curatedMetagenomicData-defunct),
3
- FerrettiP_2018.pathabundance_relab.oralcavity
(curatedMetagenomicData-defunct),
3
- FerrettiP_2018.pathabundance_relab.skin
(curatedMetagenomicData-defunct),
3
- FerrettiP_2018.pathabundance_relab.stool
(curatedMetagenomicData-defunct),
3
- FerrettiP_2018.pathabundance_relab.vagina
(curatedMetagenomicData-defunct),
3
- FerrettiP_2018.pathcoverage.oralcavity
(curatedMetagenomicData-defunct),
3
- FerrettiP_2018.pathcoverage.skin
(curatedMetagenomicData-defunct),
3
- FerrettiP_2018.pathcoverage.stool
(curatedMetagenomicData-defunct),
3
- FerrettiP_2018.pathcoverage.vagina
(curatedMetagenomicData-defunct),
3
- getMetaphlanTree
(curatedMetagenomicData-defunct),
3
- GopalakrishnanV_2018.genefamilies_relab.stool
(curatedMetagenomicData-defunct),
3
- GopalakrishnanV_2018.marker_abundance.stool
(curatedMetagenomicData-defunct),
3
- GopalakrishnanV_2018.marker_presence.stool
(curatedMetagenomicData-defunct),
3
- GopalakrishnanV_2018.metaphlan_bugs_list.stool
(curatedMetagenomicData-defunct),
3
- GopalakrishnanV_2018.pathabundance_relab.stool
(curatedMetagenomicData-defunct),
3
- GopalakrishnanV_2018.pathcoverage.stool
(curatedMetagenomicData-defunct),
3
- HanniganGD_2017.genefamilies_relab.stool
(curatedMetagenomicData-defunct),
3
- HanniganGD_2017.marker_abundance.stool
(curatedMetagenomicData-defunct),
3
- HanniganGD_2017.marker_presence.stool
(curatedMetagenomicData-defunct),
3
- HanniganGD_2017.metaphlan_bugs_list.stool
(curatedMetagenomicData-defunct),
3
- HanniganGD_2017.pathabundance_relab.stool
(curatedMetagenomicData-defunct),
3
- HanniganGD_2017.pathcoverage.stool
(curatedMetagenomicData-defunct),
3
- HansenLBS_2018.genefamilies_relab.stool
(curatedMetagenomicData-defunct),
3
- HansenLBS_2018.marker_abundance.stool
(curatedMetagenomicData-defunct),
3
- HansenLBS_2018.marker_presence.stool
(curatedMetagenomicData-defunct),
3
- HansenLBS_2018.metaphlan_bugs_list.stool
(curatedMetagenomicData-defunct),
3
- HansenLBS_2018.pathabundance_relab.stool
(curatedMetagenomicData-defunct),
3
- HansenLBS_2018.pathcoverage.stool
(curatedMetagenomicData-defunct),
3

- 3
- Heitz-BuschartA_2016.genefamilies_relab.stool (curatedMetagenomicData-defunct), 3
- Heitz-BuschartA_2016.marker_abundance.stool (curatedMetagenomicData-defunct), 3
- Heitz-BuschartA_2016.marker_presence.stool (curatedMetagenomicData-defunct), 3
- Heitz-BuschartA_2016.metaphlan_bugs_list.stool (curatedMetagenomicData-defunct), 3
- Heitz-BuschartA_2016.pathabundance_relab.stool (curatedMetagenomicData-defunct), 3
- Heitz-BuschartA_2016.pathcoverage.stool (curatedMetagenomicData-defunct), 3
- Heitz_BuschartA_2016.genefamilies_relab.stool (curatedMetagenomicData-defunct), 3
- Heitz_BuschartA_2016.marker_abundance.stool (curatedMetagenomicData-defunct), 3
- Heitz_BuschartA_2016.marker_presence.stool (curatedMetagenomicData-defunct), 3
- Heitz_BuschartA_2016.metaphlan_bugs_list.stool (curatedMetagenomicData-defunct), 3
- Heitz_BuschartA_2016.pathabundance_relab.stool (curatedMetagenomicData-defunct), 3
- Heitz_BuschartA_2016.pathcoverage.stool (curatedMetagenomicData-defunct), 3
- HMP_2012.genefamilies_relab.nasalcavity (curatedMetagenomicData-defunct), 3
- HMP_2012.genefamilies_relab.oralcavity (curatedMetagenomicData-defunct), 3
- HMP_2012.genefamilies_relab.skin (curatedMetagenomicData-defunct), 3
- HMP_2012.genefamilies_relab.stool (curatedMetagenomicData-defunct), 3
- HMP_2012.genefamilies_relab.vagina (curatedMetagenomicData-defunct), 3
- HMP_2012.marker_abundance.nasalcavity (curatedMetagenomicData-defunct), 3
- HMP_2012.marker_abundance.oralcavity (curatedMetagenomicData-defunct), 3
- HMP_2012.marker_abundance.skin (curatedMetagenomicData-defunct), 3
- HMP_2012.marker_abundance.stool (curatedMetagenomicData-defunct), 3
- HMP_2012.marker_abundance.vagina (curatedMetagenomicData-defunct), 3
- HMP_2012.marker_presence.nasalcavity (curatedMetagenomicData-defunct), 3
- HMP_2012.marker_presence.oralcavity (curatedMetagenomicData-defunct), 3
- HMP_2012.marker_presence.skin (curatedMetagenomicData-defunct), 3
- HMP_2012.marker_presence.stool (curatedMetagenomicData-defunct), 3
- HMP_2012.marker_presence.vagina (curatedMetagenomicData-defunct), 3
- HMP_2012.metaphlan_bugs_list.nasalcavity (curatedMetagenomicData-defunct), 3
- HMP_2012.metaphlan_bugs_list.oralcavity (curatedMetagenomicData-defunct), 3
- HMP_2012.metaphlan_bugs_list.skin (curatedMetagenomicData-defunct), 3
- HMP_2012.metaphlan_bugs_list.stool (curatedMetagenomicData-defunct), 3
- HMP_2012.metaphlan_bugs_list.vagina (curatedMetagenomicData-defunct), 3
- HMP_2012.pathabundance_relab.nasalcavity (curatedMetagenomicData-defunct), 3
- HMP_2012.pathabundance_relab.oralcavity (curatedMetagenomicData-defunct), 3
- HMP_2012.pathabundance_relab.skin

- (curatedMetagenomicData-defunct),
3
- HMP_2012.pathabundance_relab.stool
(curatedMetagenomicData-defunct),
3
- HMP_2012.pathabundance_relab.vagina
(curatedMetagenomicData-defunct),
3
- HMP_2012.pathcoverage.nasalcavity
(curatedMetagenomicData-defunct),
3
- HMP_2012.pathcoverage.oralcavity
(curatedMetagenomicData-defunct),
3
- HMP_2012.pathcoverage.skin
(curatedMetagenomicData-defunct),
3
- HMP_2012.pathcoverage.stool
(curatedMetagenomicData-defunct),
3
- HMP_2012.pathcoverage.vagina
(curatedMetagenomicData-defunct),
3

- JieZ_2017.genefamilies_relab.stool
(curatedMetagenomicData-defunct),
3
- JieZ_2017.marker_abundance.stool
(curatedMetagenomicData-defunct),
3
- JieZ_2017.marker_presence.stool
(curatedMetagenomicData-defunct),
3
- JieZ_2017.metaphlan_bugs_list.stool
(curatedMetagenomicData-defunct),
3
- JieZ_2017.pathabundance_relab.stool
(curatedMetagenomicData-defunct),
3
- JieZ_2017.pathcoverage.stool
(curatedMetagenomicData-defunct),
3

- KarlssonFH_2013.genefamilies_relab.stool
(curatedMetagenomicData-defunct),
3
- KarlssonFH_2013.marker_abundance.stool
(curatedMetagenomicData-defunct),
3
- KarlssonFH_2013.marker_presence.stool
(curatedMetagenomicData-defunct),
3

- KarlssonFH_2013.metaphlan_bugs_list.stool
(curatedMetagenomicData-defunct),
3
- KarlssonFH_2013.pathabundance_relab.stool
(curatedMetagenomicData-defunct),
3
- KarlssonFH_2013.pathcoverage.stool
(curatedMetagenomicData-defunct),
3
- KieserS_2018.genefamilies_relab.stool
(curatedMetagenomicData-defunct),
3
- KieserS_2018.marker_abundance.stool
(curatedMetagenomicData-defunct),
3
- KieserS_2018.marker_presence.stool
(curatedMetagenomicData-defunct),
3
- KieserS_2018.metaphlan_bugs_list.stool
(curatedMetagenomicData-defunct),
3
- KieserS_2018.pathabundance_relab.stool
(curatedMetagenomicData-defunct),
3
- KieserS_2018.pathcoverage.stool
(curatedMetagenomicData-defunct),
3
- KosticAD_2015.genefamilies_relab.stool
(curatedMetagenomicData-defunct),
3
- KosticAD_2015.marker_abundance.stool
(curatedMetagenomicData-defunct),
3
- KosticAD_2015.marker_presence.stool
(curatedMetagenomicData-defunct),
3
- KosticAD_2015.metaphlan_bugs_list.stool
(curatedMetagenomicData-defunct),
3
- KosticAD_2015.pathabundance_relab.stool
(curatedMetagenomicData-defunct),
3
- KosticAD_2015.pathcoverage.stool
(curatedMetagenomicData-defunct),
3

- LeChatelierE_2013.genefamilies_relab.stool
(curatedMetagenomicData-defunct),
3
- LeChatelierE_2013.marker_abundance.stool
(curatedMetagenomicData-defunct),
3
- LeChatelierE_2013.marker_presence.stool

- (curatedMetagenomicData-defunct),
3
- LeChatelierE_2013.metaphlan_bugs_list.stool
(curatedMetagenomicData-defunct),
3
- LeChatelierE_2013.pathabundance_relab.stool
(curatedMetagenomicData-defunct),
3
- LeChatelierE_2013.pathcoverage.stool
(curatedMetagenomicData-defunct),
3
- LiJ_2014.genefamilies_relab.stool
(curatedMetagenomicData-defunct),
3
- LiJ_2014.marker_abundance.stool
(curatedMetagenomicData-defunct),
3
- LiJ_2014.marker_presence.stool
(curatedMetagenomicData-defunct),
3
- LiJ_2014.metaphlan_bugs_list.stool
(curatedMetagenomicData-defunct),
3
- LiJ_2014.pathabundance_relab.stool
(curatedMetagenomicData-defunct),
3
- LiJ_2014.pathcoverage.stool
(curatedMetagenomicData-defunct),
3
- LiJ_2017.genefamilies_relab.stool
(curatedMetagenomicData-defunct),
3
- LiJ_2017.marker_abundance.stool
(curatedMetagenomicData-defunct),
3
- LiJ_2017.marker_presence.stool
(curatedMetagenomicData-defunct),
3
- LiJ_2017.metaphlan_bugs_list.stool
(curatedMetagenomicData-defunct),
3
- LiJ_2017.pathabundance_relab.stool
(curatedMetagenomicData-defunct),
3
- LiJ_2017.pathcoverage.stool
(curatedMetagenomicData-defunct),
3
- LiSS_2016.genefamilies_relab.stool
(curatedMetagenomicData-defunct),
3
- LiSS_2016.marker_abundance.stool
(curatedMetagenomicData-defunct),
3
- LiSS_2016.marker_presence.stool
(curatedMetagenomicData-defunct),
3
- LiSS_2016.metaphlan_bugs_list.stool
(curatedMetagenomicData-defunct),
3
- LiSS_2016.pathabundance_relab.stool
(curatedMetagenomicData-defunct),
3
- LiSS_2016.pathcoverage.stool
(curatedMetagenomicData-defunct),
3
- LiuW_2016.genefamilies_relab.stool
(curatedMetagenomicData-defunct),
3
- LiuW_2016.marker_abundance.stool
(curatedMetagenomicData-defunct),
3
- LiuW_2016.marker_presence.stool
(curatedMetagenomicData-defunct),
3
- LiuW_2016.metaphlan_bugs_list.stool
(curatedMetagenomicData-defunct),
3
- LiuW_2016.pathabundance_relab.stool
(curatedMetagenomicData-defunct),
3
- LiuW_2016.pathcoverage.stool
(curatedMetagenomicData-defunct),
3
- LomanNJ_2013.genefamilies_relab.stool
(curatedMetagenomicData-defunct),
3
- LomanNJ_2013.marker_abundance.stool
(curatedMetagenomicData-defunct),
3
- LomanNJ_2013.marker_presence.stool
(curatedMetagenomicData-defunct),
3
- LomanNJ_2013.metaphlan_bugs_list.stool
(curatedMetagenomicData-defunct),
3
- LomanNJ_2013.pathabundance_relab.stool
(curatedMetagenomicData-defunct),
3
- LomanNJ_2013.pathcoverage.stool
(curatedMetagenomicData-defunct),
3
- LombaR_2017.genefamilies_relab.stool
(curatedMetagenomicData-defunct),
3

- LoombaR_2017.marker_abundance.stool
 (curatedMetagenomicData-defunct),
[3](#)
- LoombaR_2017.marker_presence.stool
 (curatedMetagenomicData-defunct),
[3](#)
- LoombaR_2017.metaphlan_bugs_list.stool
 (curatedMetagenomicData-defunct),
[3](#)
- LoombaR_2017.pathabundance_relab.stool
 (curatedMetagenomicData-defunct),
[3](#)
- LoombaR_2017.pathcoverage.stool
 (curatedMetagenomicData-defunct),
[3](#)
- LouisS_2016.genefamilies_relab.stool
 (curatedMetagenomicData-defunct),
[3](#)
- LouisS_2016.marker_abundance.stool
 (curatedMetagenomicData-defunct),
[3](#)
- LouisS_2016.marker_presence.stool
 (curatedMetagenomicData-defunct),
[3](#)
- LouisS_2016.metaphlan_bugs_list.stool
 (curatedMetagenomicData-defunct),
[3](#)
- LouisS_2016.pathabundance_relab.stool
 (curatedMetagenomicData-defunct),
[3](#)
- LouisS_2016.pathcoverage.stool
 (curatedMetagenomicData-defunct),
[3](#)
- MatsonV_2018.genefamilies_relab.stool
 (curatedMetagenomicData-defunct),
[3](#)
- MatsonV_2018.marker_abundance.stool
 (curatedMetagenomicData-defunct),
[3](#)
- MatsonV_2018.marker_presence.stool
 (curatedMetagenomicData-defunct),
[3](#)
- MatsonV_2018.metaphlan_bugs_list.stool
 (curatedMetagenomicData-defunct),
[3](#)
- MatsonV_2018.pathabundance_relab.stool
 (curatedMetagenomicData-defunct),
[3](#)
- MatsonV_2018.pathcoverage.stool
 (curatedMetagenomicData-defunct),
[3](#)
- mergeData, [3](#), [15](#), [16](#)
- NielsenHB_2014.genefamilies_relab.stool
 (curatedMetagenomicData-defunct),
[3](#)
- NielsenHB_2014.marker_abundance.stool
 (curatedMetagenomicData-defunct),
[3](#)
- NielsenHB_2014.marker_presence.stool
 (curatedMetagenomicData-defunct),
[3](#)
- NielsenHB_2014.metaphlan_bugs_list.stool
 (curatedMetagenomicData-defunct),
[3](#)
- NielsenHB_2014.pathabundance_relab.stool
 (curatedMetagenomicData-defunct),
[3](#)
- NielsenHB_2014.pathcoverage.stool
 (curatedMetagenomicData-defunct),
[3](#)
- Obregon-TitoAJ_2015.genefamilies_relab.stool
 (curatedMetagenomicData-defunct),
[3](#)
- Obregon-TitoAJ_2015.marker_abundance.stool
 (curatedMetagenomicData-defunct),
[3](#)
- Obregon-TitoAJ_2015.marker_presence.stool
 (curatedMetagenomicData-defunct),
[3](#)
- Obregon-TitoAJ_2015.metaphlan_bugs_list.stool
 (curatedMetagenomicData-defunct),
[3](#)
- Obregon-TitoAJ_2015.pathabundance_relab.stool
 (curatedMetagenomicData-defunct),
[3](#)
- Obregon-TitoAJ_2015.pathcoverage.stool
 (curatedMetagenomicData-defunct),
[3](#)
- Obregon_TitoAJ_2015.genefamilies_relab.stool
 (curatedMetagenomicData-defunct),
[3](#)
- Obregon_TitoAJ_2015.marker_abundance.stool
 (curatedMetagenomicData-defunct),
[3](#)
- Obregon_TitoAJ_2015.marker_presence.stool
 (curatedMetagenomicData-defunct),
[3](#)
- Obregon_TitoAJ_2015.metaphlan_bugs_list.stool
 (curatedMetagenomicData-defunct),
[3](#)
- Obregon_TitoAJ_2015.pathabundance_relab.stool
 (curatedMetagenomicData-defunct),
[3](#)
- Obregon_TitoAJ_2015.pathcoverage.stool

- (curatedMetagenomicData-defunct),
3
- OhJ_2014.genefamilies_relab.skin
(curatedMetagenomicData-defunct),
3
- OhJ_2014.marker_abundance.skin
(curatedMetagenomicData-defunct),
3
- OhJ_2014.marker_presence.skin
(curatedMetagenomicData-defunct),
3
- OhJ_2014.metaphlan_bugs_list.skin
(curatedMetagenomicData-defunct),
3
- OhJ_2014.pathabundance_relab.skin
(curatedMetagenomicData-defunct),
3
- OhJ_2014.pathcoverage.skin
(curatedMetagenomicData-defunct),
3
- OlmMR_2017.genefamilies_relab.oralcavity
(curatedMetagenomicData-defunct),
3
- OlmMR_2017.genefamilies_relab.skin
(curatedMetagenomicData-defunct),
3
- OlmMR_2017.genefamilies_relab.stool
(curatedMetagenomicData-defunct),
3
- OlmMR_2017.marker_abundance.oralcavity
(curatedMetagenomicData-defunct),
3
- OlmMR_2017.marker_abundance.skin
(curatedMetagenomicData-defunct),
3
- OlmMR_2017.marker_abundance.stool
(curatedMetagenomicData-defunct),
3
- OlmMR_2017.marker_presence.oralcavity
(curatedMetagenomicData-defunct),
3
- OlmMR_2017.marker_presence.skin
(curatedMetagenomicData-defunct),
3
- OlmMR_2017.marker_presence.stool
(curatedMetagenomicData-defunct),
3
- OlmMR_2017.metaphlan_bugs_list.oralcavity
(curatedMetagenomicData-defunct),
3
- OlmMR_2017.metaphlan_bugs_list.skin
(curatedMetagenomicData-defunct),
3
- OlmMR_2017.metaphlan_bugs_list.stool
(curatedMetagenomicData-defunct),
3
- OlmMR_2017.pathabundance_relab.oralcavity
(curatedMetagenomicData-defunct),
3
- OlmMR_2017.pathabundance_relab.skin
(curatedMetagenomicData-defunct),
3
- OlmMR_2017.pathabundance_relab.stool
(curatedMetagenomicData-defunct),
3
- OlmMR_2017.pathcoverage.oralcavity
(curatedMetagenomicData-defunct),
3
- OlmMR_2017.pathcoverage.skin
(curatedMetagenomicData-defunct),
3
- OlmMR_2017.pathcoverage.stool
(curatedMetagenomicData-defunct),
3
- PasolliE_2018.genefamilies_relab.stool
(curatedMetagenomicData-defunct),
3
- PasolliE_2018.marker_abundance.stool
(curatedMetagenomicData-defunct),
3
- PasolliE_2018.marker_presence.stool
(curatedMetagenomicData-defunct),
3
- PasolliE_2018.metaphlan_bugs_list.stool
(curatedMetagenomicData-defunct),
3
- PasolliE_2018.pathabundance_relab.stool
(curatedMetagenomicData-defunct),
3
- PasolliE_2018.pathcoverage.stool
(curatedMetagenomicData-defunct),
3
- PehrssonE_2016.genefamilies_relab.stool
(curatedMetagenomicData-defunct),
3
- PehrssonE_2016.marker_abundance.stool
(curatedMetagenomicData-defunct),
3
- PehrssonE_2016.marker_presence.stool
(curatedMetagenomicData-defunct),
3
- PehrssonE_2016.metaphlan_bugs_list.stool
(curatedMetagenomicData-defunct),
3

- PehrssonE_2016.pathabundance_relab.stool
(curatedMetagenomicData-defunct),
3
- PehrssonE_2016.pathcoverage.stool
(curatedMetagenomicData-defunct),
3
- QinJ_2012.genefamilies_relab.stool
(curatedMetagenomicData-defunct),
3
- QinJ_2012.marker_abundance.stool
(curatedMetagenomicData-defunct),
3
- QinJ_2012.marker_presence.stool
(curatedMetagenomicData-defunct),
3
- QinJ_2012.metaphlan_bugs_list.stool
(curatedMetagenomicData-defunct),
3
- QinJ_2012.pathabundance_relab.stool
(curatedMetagenomicData-defunct),
3
- QinJ_2012.pathcoverage.stool
(curatedMetagenomicData-defunct),
3
- QinN_2014.genefamilies_relab.stool
(curatedMetagenomicData-defunct),
3
- QinN_2014.marker_abundance.stool
(curatedMetagenomicData-defunct),
3
- QinN_2014.marker_presence.stool
(curatedMetagenomicData-defunct),
3
- QinN_2014.metaphlan_bugs_list.stool
(curatedMetagenomicData-defunct),
3
- QinN_2014.pathabundance_relab.stool
(curatedMetagenomicData-defunct),
3
- QinN_2014.pathcoverage.stool
(curatedMetagenomicData-defunct),
3
- RampelliS_2015.genefamilies_relab.stool
(curatedMetagenomicData-defunct),
3
- RampelliS_2015.marker_abundance.stool
(curatedMetagenomicData-defunct),
3
- RampelliS_2015.marker_presence.stool
(curatedMetagenomicData-defunct),
3
- RampelliS_2015.metaphlan_bugs_list.stool
(curatedMetagenomicData-defunct),
3
- RampelliS_2015.pathabundance_relab.stool
(curatedMetagenomicData-defunct),
3
- RampelliS_2015.pathcoverage.stool
(curatedMetagenomicData-defunct),
3
- RaymondF_2016.genefamilies_relab.stool
(curatedMetagenomicData-defunct),
3
- RaymondF_2016.marker_abundance.stool
(curatedMetagenomicData-defunct),
3
- RaymondF_2016.marker_presence.stool
(curatedMetagenomicData-defunct),
3
- RaymondF_2016.metaphlan_bugs_list.stool
(curatedMetagenomicData-defunct),
3
- RaymondF_2016.pathabundance_relab.stool
(curatedMetagenomicData-defunct),
3
- RaymondF_2016.pathcoverage.stool
(curatedMetagenomicData-defunct),
3
- returnSamples, 3, 15, 16
- sampleMetadata, 2, 3, 16, 17
- SchirmerM_2016.genefamilies_relab.stool
(curatedMetagenomicData-defunct),
3
- SchirmerM_2016.marker_abundance.stool
(curatedMetagenomicData-defunct),
3
- SchirmerM_2016.marker_presence.stool
(curatedMetagenomicData-defunct),
3
- SchirmerM_2016.metaphlan_bugs_list.stool
(curatedMetagenomicData-defunct),
3
- SchirmerM_2016.pathabundance_relab.stool
(curatedMetagenomicData-defunct),
3
- SchirmerM_2016.pathcoverage.stool
(curatedMetagenomicData-defunct),
3
- ShiB_2015.genefamilies_relab.oralcavity
(curatedMetagenomicData-defunct),
3
- ShiB_2015.marker_abundance.oralcavity
(curatedMetagenomicData-defunct),

- 3
- ShiB_2015.marker_presence.oralcavity
(curatedMetagenomicData-defunct),
3
- ShiB_2015.metaphlan_bugs_list.oralcavity
(curatedMetagenomicData-defunct),
3
- ShiB_2015.pathabundance_relab.oralcavity
(curatedMetagenomicData-defunct),
3
- ShiB_2015.pathcoverage.oralcavity
(curatedMetagenomicData-defunct),
3
- SmitsSA_2017.genefamilies_relab.stool
(curatedMetagenomicData-defunct),
3
- SmitsSA_2017.marker_abundance.stool
(curatedMetagenomicData-defunct),
3
- SmitsSA_2017.marker_presence.stool
(curatedMetagenomicData-defunct),
3
- SmitsSA_2017.metaphlan_bugs_list.stool
(curatedMetagenomicData-defunct),
3
- SmitsSA_2017.pathabundance_relab.stool
(curatedMetagenomicData-defunct),
3
- SmitsSA_2017.pathcoverage.stool
(curatedMetagenomicData-defunct),
3
- SummarizedExperiment, [2](#), [3](#), [15](#), [16](#)
- TettAJ_2016.genefamilies_relab.skin
(curatedMetagenomicData-defunct),
3
- TettAJ_2016.marker_abundance.skin
(curatedMetagenomicData-defunct),
3
- TettAJ_2016.marker_presence.skin
(curatedMetagenomicData-defunct),
3
- TettAJ_2016.metaphlan_bugs_list.skin
(curatedMetagenomicData-defunct),
3
- TettAJ_2016.pathabundance_relab.skin
(curatedMetagenomicData-defunct),
3
- TettAJ_2016.pathcoverage.skin
(curatedMetagenomicData-defunct),
3
- TettAJ_2019_a.genefamilies_relab.stool
(curatedMetagenomicData-defunct),
3
- TettAJ_2019_a.marker_abundance.stool
(curatedMetagenomicData-defunct),
3
- TettAJ_2019_a.marker_presence.stool
(curatedMetagenomicData-defunct),
3
- TettAJ_2019_a.metaphlan_bugs_list.stool
(curatedMetagenomicData-defunct),
3
- TettAJ_2019_a.pathabundance_relab.stool
(curatedMetagenomicData-defunct),
3
- TettAJ_2019_a.pathcoverage.stool
(curatedMetagenomicData-defunct),
3
- TettAJ_2019_b.genefamilies_relab.stool
(curatedMetagenomicData-defunct),
3
- TettAJ_2019_b.marker_abundance.stool
(curatedMetagenomicData-defunct),
3
- TettAJ_2019_b.marker_presence.stool
(curatedMetagenomicData-defunct),
3
- TettAJ_2019_b.metaphlan_bugs_list.stool
(curatedMetagenomicData-defunct),
3
- TettAJ_2019_b.pathabundance_relab.stool
(curatedMetagenomicData-defunct),
3
- TettAJ_2019_b.pathcoverage.stool
(curatedMetagenomicData-defunct),
3
- TettAJ_2019_c.genefamilies_relab.stool
(curatedMetagenomicData-defunct),
3
- TettAJ_2019_c.marker_abundance.stool
(curatedMetagenomicData-defunct),
3
- TettAJ_2019_c.marker_presence.stool
(curatedMetagenomicData-defunct),
3
- TettAJ_2019_c.metaphlan_bugs_list.stool
(curatedMetagenomicData-defunct),
3
- TettAJ_2019_c.pathabundance_relab.stool
(curatedMetagenomicData-defunct),
3
- TettAJ_2019_c.pathcoverage.stool
(curatedMetagenomicData-defunct),
3

- ThomasAM_2018a.genefamilies_relab.stool
(curatedMetagenomicData-defunct),
3
- ThomasAM_2018a.marker_abundance.stool
(curatedMetagenomicData-defunct),
3
- ThomasAM_2018a.marker_presence.stool
(curatedMetagenomicData-defunct),
3
- ThomasAM_2018a.metaphlan_bugs_list.stool
(curatedMetagenomicData-defunct),
3
- ThomasAM_2018a.pathabundance_relab.stool
(curatedMetagenomicData-defunct),
3
- ThomasAM_2018a.pathcoverage.stool
(curatedMetagenomicData-defunct),
3
- ThomasAM_2018b.genefamilies_relab.stool
(curatedMetagenomicData-defunct),
3
- ThomasAM_2018b.marker_abundance.stool
(curatedMetagenomicData-defunct),
3
- ThomasAM_2018b.marker_presence.stool
(curatedMetagenomicData-defunct),
3
- ThomasAM_2018b.metaphlan_bugs_list.stool
(curatedMetagenomicData-defunct),
3
- ThomasAM_2018b.pathabundance_relab.stool
(curatedMetagenomicData-defunct),
3
- ThomasAM_2018b.pathcoverage.stool
(curatedMetagenomicData-defunct),
3
- TreeSummarizedExperiment, [2](#), [3](#), [15](#), [16](#)
- VatanenT_2016.genefamilies_relab.stool
(curatedMetagenomicData-defunct),
3
- VatanenT_2016.marker_abundance.stool
(curatedMetagenomicData-defunct),
3
- VatanenT_2016.marker_presence.stool
(curatedMetagenomicData-defunct),
3
- VatanenT_2016.metaphlan_bugs_list.stool
(curatedMetagenomicData-defunct),
3
- VatanenT_2016.pathabundance_relab.stool
(curatedMetagenomicData-defunct),
3
- VatanenT_2016.pathcoverage.stool
(curatedMetagenomicData-defunct),
3
- VincentC_2016.genefamilies_relab.stool
(curatedMetagenomicData-defunct),
3
- VincentC_2016.marker_abundance.stool
(curatedMetagenomicData-defunct),
3
- VincentC_2016.marker_presence.stool
(curatedMetagenomicData-defunct),
3
- VincentC_2016.metaphlan_bugs_list.stool
(curatedMetagenomicData-defunct),
3
- VincentC_2016.pathabundance_relab.stool
(curatedMetagenomicData-defunct),
3
- VincentC_2016.pathcoverage.stool
(curatedMetagenomicData-defunct),
3
- VogtmannE_2016.genefamilies_relab.stool
(curatedMetagenomicData-defunct),
3
- VogtmannE_2016.marker_abundance.stool
(curatedMetagenomicData-defunct),
3
- VogtmannE_2016.marker_presence.stool
(curatedMetagenomicData-defunct),
3
- VogtmannE_2016.metaphlan_bugs_list.stool
(curatedMetagenomicData-defunct),
3
- VogtmannE_2016.pathabundance_relab.stool
(curatedMetagenomicData-defunct),
3
- VogtmannE_2016.pathcoverage.stool
(curatedMetagenomicData-defunct),
3
- XieH_2016.genefamilies_relab.stool
(curatedMetagenomicData-defunct),
3
- XieH_2016.marker_abundance.stool
(curatedMetagenomicData-defunct),
3
- XieH_2016.marker_presence.stool
(curatedMetagenomicData-defunct),
3
- XieH_2016.metaphlan_bugs_list.stool
(curatedMetagenomicData-defunct),
3
- XieH_2016.pathabundance_relab.stool

- (curatedMetagenomicData-defunct),
3
- XieH_2016.pathcoverage.stool
(curatedMetagenomicData-defunct),
3
- YeZ_2018.genefamilies_relab.stool
(curatedMetagenomicData-defunct),
3
- YeZ_2018.marker_abundance.stool
(curatedMetagenomicData-defunct),
3
- YeZ_2018.marker_presence.stool
(curatedMetagenomicData-defunct),
3
- YeZ_2018.metaphlan_bugs_list.stool
(curatedMetagenomicData-defunct),
3
- YeZ_2018.pathabundance_relab.stool
(curatedMetagenomicData-defunct),
3
- YeZ_2018.pathcoverage.stool
(curatedMetagenomicData-defunct),
3
- YuJ_2015.genefamilies_relab.stool
(curatedMetagenomicData-defunct),
3
- YuJ_2015.marker_abundance.stool
(curatedMetagenomicData-defunct),
3
- YuJ_2015.marker_presence.stool
(curatedMetagenomicData-defunct),
3
- YuJ_2015.metaphlan_bugs_list.stool
(curatedMetagenomicData-defunct),
3
- YuJ_2015.pathabundance_relab.stool
(curatedMetagenomicData-defunct),
3
- YuJ_2015.pathcoverage.stool
(curatedMetagenomicData-defunct),
3
- ZeeviD_2015.genefamilies_relab.stool
(curatedMetagenomicData-defunct),
3
- ZeeviD_2015.marker_abundance.stool
(curatedMetagenomicData-defunct),
3
- ZeeviD_2015.marker_presence.stool
(curatedMetagenomicData-defunct),
3
- ZeeviD_2015.metaphlan_bugs_list.stool
(curatedMetagenomicData-defunct),
3
- ZeeviD_2015.pathabundance_relab.stool
(curatedMetagenomicData-defunct),
3
- ZeeviD_2015.pathcoverage.stool
(curatedMetagenomicData-defunct),
3
- ZellerG_2014.genefamilies_relab.stool
(curatedMetagenomicData-defunct),
3
- ZellerG_2014.marker_abundance.stool
(curatedMetagenomicData-defunct),
3
- ZellerG_2014.marker_presence.stool
(curatedMetagenomicData-defunct),
3
- ZellerG_2014.metaphlan_bugs_list.stool
(curatedMetagenomicData-defunct),
3
- ZellerG_2014.pathabundance_relab.stool
(curatedMetagenomicData-defunct),
3
- ZellerG_2014.pathcoverage.stool
(curatedMetagenomicData-defunct),
3