Package ‘curatedMetagenomicData’

May 2, 2024

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 3.12.0

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_19

git_last_commit c5711e9

git_last_commit_date 2024-04-30
curatedMetagenomicData

Repository  Bioconductor 3.19

Date/Publication  2024-05-02

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

<table>
<thead>
<tr>
<th>Function</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>curatedMetagenomicData</td>
<td>2</td>
</tr>
<tr>
<td>curatedMetagenomicData-defunct</td>
<td>4</td>
</tr>
<tr>
<td>mergeData</td>
<td>16</td>
</tr>
<tr>
<td>returnSamples</td>
<td>17</td>
</tr>
<tr>
<td>sampleMetadata</td>
<td>18</td>
</tr>
</tbody>
</table>

Index  19

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

```r
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 dataType (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

```r
curatedMetagenomicData("AsnicarF_20.+"")

curatedMetagenomicData("AsnicarF_2017.relative_abundance", dryrun = FALSE)

curatedMetagenomicData("AsnicarF_20.+relative_abundance", dryrun = FALSE, counts = TRUE)
```
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_abundance.stool()
• ChengpingW_2017.metaphlan_bugs_list.oralcavity()
• 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.gene_families_relab.stool()
• Heitz-BuschartA_2016.marker_abundance.stool()
• Heitz-BuschartA_2016.marker_presence.stool()
• Heitz-BuschartA_2016.metaphlan_bugs_list.stool()
• Heitz-BuschartA_2016.path_abundance_relab.stool()
• Heitz-BuschartA_2016.path_coverage.stool()
• HMP_2012.gene_families_relab.nasal_cavity()
• HMP_2012.gene_families_relab.oral_cavity()
• HMP_2012.gene_families_relab.skin()
• HMP_2012.gene_families_relab.stool()
• HMP_2012.gene_families_relab.vagina()
• HMP_2012.marker_abundance.nasal_cavity()
• HMP_2012.marker_abundance.oral_cavity()
• HMP_2012.marker_abundance.skin()
• HMP_2012.marker_abundance.stool()
• HMP_2012.marker_abundance.vagina()
• HMP_2012.marker_presence.nasal_cavity()
• HMP_2012.marker_presence.oral_cavity()
• HMP_2012.marker_presence.skin()
• HMP_2012.marker_presence.stool()
• HMP_2012.marker_presence.vagina()
• HMP_2012.metaphlan_bugs_list.nasal_cavity()
• HMP_2012.metaphlan_bugs_list.oral_cavity()
• HMP_2012.metaphlan_bugs_list.skin()
• HMP_2012.metaphlan_bugs_list.stool()
• HMP_2012.metaphlan_bugs_list.vagina()
• HMP_2012.path_abundance_relab.nasal_cavity()
• HMP_2012.path_abundance_relab.oral_cavity()
• HMP_2012.path_abundance_relab.skin()
• HMP_2012.path_abundance_relab.stool()
• HMP_2012.path_abundance_relab.vagina()
• HMP_2012.path_coverage.nasal_cavity()
• HMP_2012.path_coverage.oral_cavity()
• HMP_2012.path_coverage.skin()
• HMP_2012.path_coverage.stool()
• HMP_2012.path_coverage.vagina()
• JieZ_2017.gene_families_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()
curatedMetagenomicData-defunct

- 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()
curatedMetagenomicData-defunct

- 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()
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**

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

**Arguments**

- `sampleMetadata`: the `sampleMetadata` data.frame subset to include only desired samples and metadata
- `dataType`: the data type to be returned; one of the following:
  - "gene_families"
  - "marker_abundance"
  - "marker_presence"
  - "pathway_abundance"
  - "pathway_coverage"
  - "relative_abundance"
- `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**

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
sampleMetadata

Examples

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

<table>
<thead>
<tr>
<th>sampleMetadata</th>
<th>Manually Curated Sample Metadata</th>
</tr>
</thead>
</table>

Description

Manually curated sample metadata for all samples in curatedMetagenomicData.

Usage

```r
sampleMetadata
```

Format

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

* datasets
  sampleMetadata, 18

* internal
  curatedMetagenomicData-defunct, 4

  AsnicarF_2017.genefamilies_relab.milk (curatedMetagenomicData-defunct), 4
  AsnicarF_2017.genefamilies_relab.stool (curatedMetagenomicData-defunct), 4
  AsnicarF_2017.marker_abundance.milk (curatedMetagenomicData-defunct), 4
  AsnicarF_2017.marker_abundance.stool (curatedMetagenomicData-defunct), 4
  AsnicarF_2017.marker_presence.milk (curatedMetagenomicData-defunct), 4
  AsnicarF_2017.marker_presence.stool (curatedMetagenomicData-defunct), 4
  AsnicarF_2017.metaphlan_bugs_list.milk (curatedMetagenomicData-defunct), 4
  AsnicarF_2017.metaphlan_bugs_list.stool (curatedMetagenomicData-defunct), 4
  AsnicarF_2017.pathabundance_relab.milk (curatedMetagenomicData-defunct), 4
  AsnicarF_2017.pathabundance_relab.stool (curatedMetagenomicData-defunct), 4
  AsnicarF_2017.pathcoverage.milk (curatedMetagenomicData-defunct), 4
  AsnicarF_2017.pathcoverage.stool (curatedMetagenomicData-defunct), 4
  BackhedF_2015.genefamilies_relab.stool (curatedMetagenomicData-defunct), 4
  BackhedF_2015.marker_abundance.stool (curatedMetagenomicData-defunct), 4
  BackhedF_2015.marker_presence.stool (curatedMetagenomicData-defunct), 4
  BackhedF_2015.metaphlan_bugs_list.stool (curatedMetagenomicData-defunct), 4
  BackhedF_2015.pathabundance_relab.stool (curatedMetagenomicData-defunct), 4
  BackhedF_2015.pathcoverage.stool (curatedMetagenomicData-defunct), 4
  Bengtsson-PalmeJ_2015.genefamilies_relab.stool (curatedMetagenomicData-defunct), 4
  Bengtsson-PalmeJ_2015.marker_abundance.stool (curatedMetagenomicData-defunct), 4
  Bengtsson-PalmeJ_2015.marker_presence.stool (curatedMetagenomicData-defunct), 4
  Bengtsson-PalmeJ_2015.metaphlan_bugs_list.stool (curatedMetagenomicData-defunct), 4
  Bengtsson-PalmeJ_2015.pathabundance_relab.stool (curatedMetagenomicData-defunct), 4
  Bengtsson-PalmeJ_2015.pathcoverage.stool (curatedMetagenomicData-defunct), 4
  BritoIL_2016.genefamilies_relab.oralcavity (curatedMetagenomicData-defunct), 4
BritoIL_2016.genefamilies_relab.stool (curatedMetagenomicData-defunct),

BritoIL_2016.marker_abundance.oralcavity (curatedMetagenomicData-defunct),

BritoIL_2016.marker_abundance.stool (curatedMetagenomicData-defunct),

BritoIL_2016.marker_presence.oralcavity (curatedMetagenomicData-defunct),

BritoIL_2016.marker_presence.stool (curatedMetagenomicData-defunct),

BritoIL_2016.metaphlan_bugs_list.oralcavity (curatedMetagenomicData-defunct),

BritoIL_2016.metaphlan_bugs_list.stool (curatedMetagenomicData-defunct),

BritoIL_2016.pathabundance_relab.oralcavity (curatedMetagenomicData-defunct),

BritoIL_2016.pathabundance_relab.stool (curatedMetagenomicData-defunct),

BritoIL_2016.pathcoverage.oralcavity (curatedMetagenomicData-defunct),

BritoIL_2016.pathcoverage.stool (curatedMetagenomicData-defunct),

ChengpingW_2017.genefamilies_relab.stool (curatedMetagenomicData-defunct),

ChengpingW_2017.marker_abundance.stool (curatedMetagenomicData-defunct),

ChengpingW_2017.marker_presence.stool (curatedMetagenomicData-defunct),

ChengpingW_2017.metaphlan_bugs_list.stool (curatedMetagenomicData-defunct),

ChengpingW_2017.pathabundance_relab.stool (curatedMetagenomicData-defunct),

ChengpingW_2017.pathcoverage.stool (curatedMetagenomicData-defunct),

ChngKR_2016.genefamilies_relab.skin (curatedMetagenomicData-defunct),

ChngKR_2016.marker_abundance.skin (curatedMetagenomicData-defunct),

ChngKR_2016.marker_presence.skin (curatedMetagenomicData-defunct),

ChngKR_2016.metaphlan_bugs_list.oralcavity (curatedMetagenomicData-defunct),

ChngKR_2016.pathabundance_relab.oralcavity (curatedMetagenomicData-defunct),

ChngKR_2016.pathcoverage.oralcavity (curatedMetagenomicData-defunct),

Castro-NallarE_2015.genefamilies_relab.oralcavity (curatedMetagenomicData-defunct),

Castro-NallarE_2015.marker_abundance.oralcavity (curatedMetagenomicData-defunct),

Castro-NallarE_2015.marker_presence.oralcavity (curatedMetagenomicData-defunct),

Castro-NallarE_2015.metaphlan_bugs_list.oralcavity (curatedMetagenomicData-defunct),

Castro-NallarE_2015.pathabundance_relab.oralcavity (curatedMetagenomicData-defunct),

Castro-NallarE_2015.pathcoverage.oralcavity (curatedMetagenomicData-defunct),

Castro-NallarE_2015.marker_abundance.stool (curatedMetagenomicData-defunct),

Castro-NallarE_2015.marker_presence.stool (curatedMetagenomicData-defunct),

Castro-NallarE_2015.metaphlan_bugs_list.stool (curatedMetagenomicData-defunct),

Castro-NallarE_2015.pathabundance_relab.stool (curatedMetagenomicData-defunct),

Castro-NallarE_2015.pathcoverage.stool (curatedMetagenomicData-defunct),

Castro-NallarE_2015.marker_abundance.skin (curatedMetagenomicData-defunct),

Castro-NallarE_2015.marker_presence.skin (curatedMetagenomicData-defunct),
INDEX

FerrettiP_2018.genefamilies_relab.skin (curatedMetagenomicData-defunct),

FerrettiP_2018.genefamilies_relab.stool (curatedMetagenomicData-defunct),

FerrettiP_2018.genefamilies_relab.vagina (curatedMetagenomicData-defunct),

FerrettiP_2018.marker_abundance.oralcavity (curatedMetagenomicData-defunct),

FerrettiP_2018.marker_abundance.skin (curatedMetagenomicData-defunct),

FerrettiP_2018.marker_abundance.stool (curatedMetagenomicData-defunct),

FerrettiP_2018.marker_abundance.vagina (curatedMetagenomicData-defunct),

FerrettiP_2018.marker_presence.oralcavity (curatedMetagenomicData-defunct),

FerrettiP_2018.marker_presence.skin (curatedMetagenomicData-defunct),

FerrettiP_2018.marker_presence.stool (curatedMetagenomicData-defunct),

FerrettiP_2018.marker_presence.vagina (curatedMetagenomicData-defunct),

FerrettiP_2018.metaphlan_bugs_list.oralcavity (curatedMetagenomicData-defunct),

FerrettiP_2018.metaphlan_bugs_list.skin (curatedMetagenomicData-defunct),

FerrettiP_2018.metaphlan_bugs_list.stool (curatedMetagenomicData-defunct),

FerrettiP_2018.metaphlan_bugs_list.vagina (curatedMetagenomicData-defunct),

GopalakrishnanV_2018.genefamilies_relab.stool (curatedMetagenomicData-defunct),

GopalakrishnanV_2018.marker_abundance.stool (curatedMetagenomicData-defunct),

GopalakrishnanV_2018.marker_presence.stool (curatedMetagenomicData-defunct),

GopalakrishnanV_2018.metaphlan_bugs_list.stool (curatedMetagenomicData-defunct),

GopalakrishnanV_2018.pathabundance_relab.stool (curatedMetagenomicData-defunct),

GopalakrishnanV_2018.pathcoverage.stool (curatedMetagenomicData-defunct),

GopalakrishnanV_2018.pathcoverage.vagina (curatedMetagenomicData-defunct),

getMetaphlanTree (curatedMetagenomicData-defunct),

HanniganGD_2017.genefamilies_relab.stool (curatedMetagenomicData-defunct),

FerrettiP_2018.pathabundance_relab.oralcavity (curatedMetagenomicData-defunct),

FerrettiP_2018.pathabundance_relab.stool (curatedMetagenomicData-defunct),

FerrettiP_2018.pathabundance_relab.vagina (curatedMetagenomicData-defunct),

FerrettiP_2018.pathcoverage.oralcavity (curatedMetagenomicData-defunct),

FerrettiP_2018.pathcoverage.skin (curatedMetagenomicData-defunct),

FerrettiP_2018.pathcoverage.stool (curatedMetagenomicData-defunct),

FerrettiP_2018.pathcoverage.vagina (curatedMetagenomicData-defunct),

HanniganGD_2017.genefamilies_relab.stool (curatedMetagenomicData-defunct),

FerrettiP_2018.pathcoverage.oralcavity (curatedMetagenomicData-defunct),
INDEX

HanniganGD_2017.marker_abundance.stool (curatedMetagenomicData-defunct), 4
HanniganGD_2017.marker_presence.stool (curatedMetagenomicData-defunct), 4
HanniganGD_2017.metaphlan_bugs_list.stool (curatedMetagenomicData-defunct), 4
HanniganGD_2017.pathabundance_relab.stool (curatedMetagenomicData-defunct), 4
HanniganGD_2017.pathcoverage.stool (curatedMetagenomicData-defunct), 4
HansenLBS_2018.genefamilies_relab.stool (curatedMetagenomicData-defunct), 4
HansenLBS_2018.marker_abundance.stool (curatedMetagenomicData-defunct), 4
HansenLBS_2018.marker_presence.stool (curatedMetagenomicData-defunct), 4
HansenLBS_2018.metaphlan_bugs_list.stool (curatedMetagenomicData-defunct), 4
HansenLBS_2018.pathabundance_relab.stool (curatedMetagenomicData-defunct), 4
HansenLBS_2018.pathcoverage.stool (curatedMetagenomicData-defunct), 4
Heitz-BuschartA_2016.genefamilies_relab.stool (curatedMetagenomicData-defunct), 4
Heitz-BuschartA_2016.marker_abundance.stool (curatedMetagenomicData-defunct), 4
Heitz-BuschartA_2016.marker_presence.stool (curatedMetagenomicData-defunct), 4
Heitz-BuschartA_2016.metaphlan_bugs_list.stool (curatedMetagenomicData-defunct), 4
Heitz-BuschartA_2016.pathabundance_relab.stool (curatedMetagenomicData-defunct), 4
Heitz_BuschartA_2016.pathcoverage.stool (curatedMetagenomicData-defunct), 4
HMP_2012.genefamilies_relab.nasalcavity (curatedMetagenomicData-defunct), 4
HMP_2012.genefamilies_relab.oralcavity (curatedMetagenomicData-defunct), 4
HMP_2012.genefamilies_relab.skin (curatedMetagenomicData-defunct), 4
HMP_2012.genefamilies_relab.stool (curatedMetagenomicData-defunct), 4
HMP_2012.genefamilies_relab.vagina (curatedMetagenomicData-defunct), 4
HMP_2012.marker_abundance.nasalcavity (curatedMetagenomicData-defunct), 4
HMP_2012.marker_abundance.oralcavity (curatedMetagenomicData-defunct), 4
HMP_2012.marker_abundance.skin (curatedMetagenomicData-defunct), 4
HMP_2012.marker_abundance.stool (curatedMetagenomicData-defunct), 4
HMP_2012.marker_abundance.vagina (curatedMetagenomicData-defunct), 4
HMP_2012.marker_presence.nasalcavity (curatedMetagenomicData-defunct), 4
HMP_2012.marker_presence.oralcavity (curatedMetagenomicData-defunct), 4
HMP_2012.marker_presence.skin (curatedMetagenomicData-defunct), 4
HMP_2012.marker_presence.stool (curatedMetagenomicData-defunct), 4
HMP_2012.marker_presence.vagina (curatedMetagenomicData-defunct), 4
HMP_2012.metaphlan_bugs_list.nasalcavity (curatedMetagenomicData-defunct), 4
HMP_2012.metaphlan_bugs_list.oralcavity (curatedMetagenomicData-defunct), 4
HMP_2012.metaphlan_bugs_list.skin (curatedMetagenomicData-defunct), 4
HMP_2012.metaphlan_bugs_list.stool (curatedMetagenomicData-defunct), 4
HMP_2012.metaphlan_bugs_list.vagina (curatedMetagenomicData-defunct), 4
HMP_2012.pathabundance_relab.nasalcavity (curatedMetagenomicData-defunct), 4
HMP_2012.pathabundance_relab.oralcavity (curatedMetagenomicData-defunct), 4
HMP_2012.pathabundance_relab.skin (curatedMetagenomicData-defunct), 4
HMP_2012.pathabundance_relab.stool (curatedMetagenomicData-defunct), 4
HMP_2012.pathabundance_relab.vagina (curatedMetagenomicData-defunct), 4
HMP_2012.pathcoverage.nasalcavity (curatedMetagenomicData-defunct), 4
HMP_2012.pathcoverage.oralcavity (curatedMetagenomicData-defunct), 4
HMP_2012.pathcoverage.skin (curatedMetagenomicData-defunct), 4
HMP_2012.pathcoverage.stool (curatedMetagenomicData-defunct), 4
HMP_2012.pathcoverage.vagina (curatedMetagenomicData-defunct), 4
INDEX

4 KarlssonFH_2013.pathcoverage.stool (curatedMetagenomicData-defunct), 4
4 KieserS_2018.genefamilies_relab.stool (curatedMetagenomicData-defunct), 4
4 KieserS_2018.marker_abundance.stool (curatedMetagenomicData-defunct), 4
4 KieserS_2018.marker_presence.stool (curatedMetagenomicData-defunct), 4
4 KieserS_2018.metaphlan_bugs_list.stool (curatedMetagenomicData-defunct), 4
4 KieserS_2018.pathabundance_relab.stool (curatedMetagenomicData-defunct), 4
4 KieserS_2018.pathcoverage.stool (curatedMetagenomicData-defunct), 4
4 KosticAD_2015.genefamilies_relab.stool (curatedMetagenomicData-defunct), 4
4 KosticAD_2015.marker_abundance.stool (curatedMetagenomicData-defunct), 4
4 KosticAD_2015.marker_presence.stool (curatedMetagenomicData-defunct), 4
4 KosticAD_2015.metaphlan_bugs_list.stool (curatedMetagenomicData-defunct), 4
4 KosticAD_2015.pathabundance_relab.stool (curatedMetagenomicData-defunct), 4
4 KosticAD_2015.pathcoverage.stool (curatedMetagenomicData-defunct), 4
4 LeChatelierE_2013.metaphlan_bugs_list.stool (curatedMetagenomicData-defunct), 4
4 LeChatelierE_2013.pathabundance_relab.stool (curatedMetagenomicData-defunct), 4
4 LeChatelierE_2013.pathcoverage.stool (curatedMetagenomicData-defunct), 4
4 LiJ_2014.genefamilies_relab.stool (curatedMetagenomicData-defunct), 4
4 LiJ_2014.marker_abundance.stool (curatedMetagenomicData-defunct), 4
4 LiJ_2014.marker_presence.stool (curatedMetagenomicData-defunct), 4
4 LiJ_2014.pathabundance_relab.stool (curatedMetagenomicData-defunct), 4
4 LiJ_2014.pathcoverage.stool (curatedMetagenomicData-defunct), 4
4 LiJ_2017.genefamilies_relab.stool (curatedMetagenomicData-defunct), 4
4 LiJ_2017.marker_abundance.stool (curatedMetagenomicData-defunct), 4
4 LiJ_2017.marker_presence.stool (curatedMetagenomicData-defunct), 4
4 LiJ_2017.pathabundance_relab.stool (curatedMetagenomicData-defunct), 4
4 LiJ_2017.pathcoverage.stool (curatedMetagenomicData-defunct), 4
4 LiSS_2016.genefamilies_relab.stool (curatedMetagenomicData-defunct), 4


LiSS_2016.marker_abundance.stool (curatedMetagenomicData-defunct), 4
LiSS_2016.marker_presence.stool (curatedMetagenomicData-defunct), 4
LiSS_2016.metaphlan_bugs_list.stool (curatedMetagenomicData-defunct), 4
LiSS_2016.pathabundance_relab.stool (curatedMetagenomicData-defunct), 4
LiSS_2016.pathcoverage.stool (curatedMetagenomicData-defunct), 4
LiuW_2016.genefamilies_relab.stool (curatedMetagenomicData-defunct), 4
LiuW_2016.marker_abundance.stool (curatedMetagenomicData-defunct), 4
LiuW_2016.marker_presence.stool (curatedMetagenomicData-defunct), 4
LiuW_2016.metaphlan_bugs_list.stool (curatedMetagenomicData-defunct), 4
LiuW_2016.pathabundance_relab.stool (curatedMetagenomicData-defunct), 4
LiuW_2016.pathcoverage.stool (curatedMetagenomicData-defunct), 4
LomanNJ_2013.genefamilies_relab.stool (curatedMetagenomicData-defunct), 4
LomanNJ_2013.marker_abundance.stool (curatedMetagenomicData-defunct), 4
LomanNJ_2013.marker_presence.stool (curatedMetagenomicData-defunct), 4
LomanNJ_2013.metaphlan_bugs_list.stool (curatedMetagenomicData-defunct), 4
LomanNJ_2013.pathabundance_relab.stool (curatedMetagenomicData-defunct), 4
LomanNJ_2013.pathcoverage.stool (curatedMetagenomicData-defunct), 4
LoombaR_2017.genefamilies_relab.stool (curatedMetagenomicData-defunct), 4
LoombaR_2017.marker_abundance.stool (curatedMetagenomicData-defunct), 4
LoombaR_2017.marker_presence.stool (curatedMetagenomicData-defunct), 4
LoombaR_2017.metaphlan_bugs_list.stool (curatedMetagenomicData-defunct), 4
LoombaR_2017.pathabundance_relab.stool (curatedMetagenomicData-defunct), 4
LoombaR_2017.pathcoverage.stool (curatedMetagenomicData-defunct), 4
LouisS_2016.genefamilies_relab.stool (curatedMetagenomicData-defunct), 4
LouisS_2016.marker_abundance.stool (curatedMetagenomicData-defunct), 4
LouisS_2016.marker_presence.stool (curatedMetagenomicData-defunct), 4
LouisS_2016.metaphlan_bugs_list.stool (curatedMetagenomicData-defunct), 4
LouisS_2016.pathabundance_relab.stool (curatedMetagenomicData-defunct), 4
LouisS_2016.pathcoverage.stool (curatedMetagenomicData-defunct), 4
MatsonV_2018.genefamilies_relab.stool (curatedMetagenomicData-defunct), 4
MatsonV_2018.marker_abundance.stool (curatedMetagenomicData-defunct), 4
MatsonV_2018.marker_presence.stool (curatedMetagenomicData-defunct), 4
INDEX

MatsonV_2018.metaphlan_bugs_list.stool (curatedMetagenomicData-defunct), 4
MatsonV_2018.pathabundance_relab.stool (curatedMetagenomicData-defunct), 4
MatsonV_2018.pathcoverage.stool (curatedMetagenomicData-defunct), 4
mergeData, 3, 16, 17

NielsenHB_2014.genefamilies_relab.stool (curatedMetagenomicData-defunct), 4
NielsenHB_2014.marker_abundance.stool (curatedMetagenomicData-defunct), 4
NielsenHB_2014.marker_presence.stool (curatedMetagenomicData-defunct), 4
NielsenHB_2014.metaphlan_bugs_list.stool (curatedMetagenomicData-defunct), 4
NielsenHB_2014.pathabundance_relab.stool (curatedMetagenomicData-defunct), 4
NielsenHB_2014.pathcoverage.stool (curatedMetagenomicData-defunct), 4

Obregon_TitoAJ_2015.genefamilies_relab.stool (curatedMetagenomicData-defunct), 4
Obregon_TitoAJ_2015.marker_abundance.stool (curatedMetagenomicData-defunct), 4
Obregon_TitoAJ_2015.marker_presence.stool (curatedMetagenomicData-defunct), 4
Obregon_TitoAJ_2015.metaphlan_bugs_list.stool (curatedMetagenomicData-defunct), 4
Obregon_TitoAJ_2015.pathabundance_relab.stool (curatedMetagenomicData-defunct), 4
Obregon_TitoAJ_2015.pathcoverage.stool (curatedMetagenomicData-defunct), 4
OhJ_2014.genefamilies_relab.skin (curatedMetagenomicData-defunct), 4
OhJ_2014.marker_abundance.skin (curatedMetagenomicData-defunct), 4
OhJ_2014.marker_presence.skin (curatedMetagenomicData-defunct), 4
OhJ_2014.metaphlan_bugs_list.skin (curatedMetagenomicData-defunct), 4

OlmMR_2017.genefamilies_relab.oralcavity (curatedMetagenomicData-defunct), 4
OlmMR_2017.genefamilies_relab.skin (curatedMetagenomicData-defunct), 4
OlmMR_2017.marker_abundance.oralcavity (curatedMetagenomicData-defunct), 4
OlmMR_2017.marker_abundance.skin (curatedMetagenomicData-defunct), 4
INDEX

OlmMR_2017.marker_abundance.skin
(curatedMetagenomicData-defunct), 4

OlmMR_2017.marker_abundance.stool
(curatedMetagenomicData-defunct), 4

OlmMR_2017.marker_presence.oralcavity
(curatedMetagenomicData-defunct), 4

OlmMR_2017.marker_presence.skin
(curatedMetagenomicData-defunct), 4

OlmMR_2017.marker_presence.stool
(curatedMetagenomicData-defunct), 4

OlmMR_2017.metaphlan_bugs_list.oralcavity
(curatedMetagenomicData-defunct), 4

OlmMR_2017.metaphlan_bugs_list.skin
(curatedMetagenomicData-defunct), 4

OlmMR_2017.metaphlan_bugs_list.stool
(curatedMetagenomicData-defunct), 4

OlmMR_2017.pathabundance_relab.oralcavity
(curatedMetagenomicData-defunct), 4

OlmMR_2017.pathabundance_relab.skin
(curatedMetagenomicData-defunct), 4

OlmMR_2017.pathabundance_relab.stool
(curatedMetagenomicData-defunct), 4

OlmMR_2017.pathcoverage.oralcavity
(curatedMetagenomicData-defunct), 4

OlmMR_2017.pathcoverage.skin
(curatedMetagenomicData-defunct), 4

OlmMR_2017.pathcoverage.stool
(curatedMetagenomicData-defunct), 4

PasolliE_2018.marker_abundance.stool
(curatedMetagenomicData-defunct), 4

PasolliE_2018.marker_presence.stool
(curatedMetagenomicData-defunct), 4

PasolliE_2018.metaphlan_bugs_list.stool
(curatedMetagenomicData-defunct), 4

PasolliE_2018.pathabundance_relab.stool
(curatedMetagenomicData-defunct), 4

PasolliE_2018.pathcoverage.stool
(curatedMetagenomicData-defunct), 4

PasolliE_2018.marker_abundance.stool
(curatedMetagenomicData-defunct), 4

PasolliE_2018.marker_presence.stool
(curatedMetagenomicData-defunct), 4

PasolliE_2018.metaphlan_bugs_list.stool
(curatedMetagenomicData-defunct), 4

PasolliE_2018.pathabundance_relab.stool
(curatedMetagenomicData-defunct), 4

PasolliE_2018.pathcoverage.stool
(curatedMetagenomicData-defunct), 4

PasolliE_2018.marker_abundance.stool
(curatedMetagenomicData-defunct), 4

PasolliE_2018.marker_presence.stool
(curatedMetagenomicData-defunct), 4

PasolliE_2018.metaphlan_bugs_list.stool
(curatedMetagenomicData-defunct), 4

PasolliE_2018.pathabundance_relab.stool
(curatedMetagenomicData-defunct), 4

PasolliE_2018.pathcoverage.stool
(curatedMetagenomicData-defunct), 4

PasolliE_2018.marker_abundance.stool
(curatedMetagenomicData-defunct), 4

PasolliE_2018.marker_presence.stool
(curatedMetagenomicData-defunct), 4

PasolliE_2018.metaphlan_bugs_list.stool
(curatedMetagenomicData-defunct), 4

PasolliE_2018.pathabundance_relab.stool
(curatedMetagenomicData-defunct), 4

PasolliE_2018.pathcoverage.stool
(curatedMetagenomicData-defunct), 4
QinN_2014.genefamilies_relab.stool
(curatedMetagenomicData-defunct), 4
QinN_2014.marker_abundance.stool
(curatedMetagenomicData-defunct), 4
QinN_2014.marker_presence.stool
(curatedMetagenomicData-defunct), 4
QinN_2014.metaphlan_bugs_list.stool
(curatedMetagenomicData-defunct), 4
QinN_2014.pathabundance_relab.stool
(curatedMetagenomicData-defunct), 4
QinN_2014.pathcoverage.stool
(curatedMetagenomicData-defunct), 4
RampelliS_2015.genefamilies_relab.stool
(curatedMetagenomicData-defunct), 4
RampelliS_2015.marker_abundance.stool
(curatedMetagenomicData-defunct), 4
RampelliS_2015.marker_presence.stool
(curatedMetagenomicData-defunct), 4
RampelliS_2015.metaphlan_bugs_list.stool
(curatedMetagenomicData-defunct), 4
RampelliS_2015.pathabundance_relab.stool
(curatedMetagenomicData-defunct), 4
RampelliS_2015.pathcoverage.stool
(curatedMetagenomicData-defunct), 4
RaymondF_2016.genefamilies_relab.stool
(curatedMetagenomicData-defunct), 4
RaymondF_2016.marker_abundance.stool
(curatedMetagenomicData-defunct), 4
RaymondF_2016.marker_presence.stool
(curatedMetagenomicData-defunct), 4
RaymondF_2016.metaphlan_bugs_list.stool
(curatedMetagenomicData-defunct), 4
RaymondF_2016.pathabundance_relab.stool
(curatedMetagenomicData-defunct), 4
RaymondF_2016.pathcoverage.stool
(curatedMetagenomicData-defunct), 4
returnSamples.3, 16, 17
sampleMetadata.2, 3, 17, 18
SchirmerM_2016.genefamilies_relab.stool
(curatedMetagenomicData-defunct), 4
SchirmerM_2016.marker_abundance.stool
(curatedMetagenomicData-defunct), 4
SchirmerM_2016.marker_presence.stool
(curatedMetagenomicData-defunct), 4
SchirmerM_2016.metaphlan_bugs_list.stool
(curatedMetagenomicData-defunct), 4
SchirmerM_2016.pathabundance_relab.stool
(curatedMetagenomicData-defunct), 4
SchirmerM_2016.pathcoverage.stool
(curatedMetagenomicData-defunct), 4
ShiB_2015.genefamilies_relab.oralcavity
(curatedMetagenomicData-defunct), 4
ShiB_2015.marker_abundance.oralcavity
(curatedMetagenomicData-defunct), 4
ShiB_2015.marker_presence.oralcavity
(curatedMetagenomicData-defunct), 4
ShiB_2015.metaphlan_bugs_list.oralcavity
(curatedMetagenomicData-defunct), 4
SmitsSA_2017.genefamilies_relab.stool
(curatedMetagenomicData-defunct), 4
SmitsSA_2017.marker_abundance.stool
(curatedMetagenomicData-defunct), 4
SmitsSA_2017.marker_presence.stool (curatedMetagenomicData-defunct), 4
SmitsSA_2017.metaphlan_bugs_list.stool (curatedMetagenomicData-defunct), 4
SmitsSA_2017.pathabundance_relab.stool (curatedMetagenomicData-defunct), 4
SmitsSA_2017.pathcoverage.stool (curatedMetagenomicData-defunct), 4
SummarizedExperiment, 2, 3, 16, 17
TettAJ_2016.genefamilies_relab.skin (curatedMetagenomicData-defunct), 4
TettAJ_2016.marker_abundance.skin (curatedMetagenomicData-defunct), 4
TettAJ_2016.marker_presence.skin (curatedMetagenomicData-defunct), 4
TettAJ_2016.metaphlan_bugs_list.skin (curatedMetagenomicData-defunct), 4
TettAJ_2016.pathabundance_relab.skin (curatedMetagenomicData-defunct), 4
TettAJ_2016.pathcoverage.skin (curatedMetagenomicData-defunct), 4
TettAJ_2019_a.genefamilies_relab.stool (curatedMetagenomicData-defunct), 4
TettAJ_2019_a.marker_abundance.stool (curatedMetagenomicData-defunct), 4
TettAJ_2019_a.marker_presence.stool (curatedMetagenomicData-defunct), 4
TettAJ_2019_a.metaphlan_bugs_list.stool (curatedMetagenomicData-defunct), 4
TettAJ_2019_a.pathabundance_relab.stool (curatedMetagenomicData-defunct), 4
TettAJ_2019_a.pathcoverage.stool (curatedMetagenomicData-defunct), 4
TettAJ_2019_b.genefamilies_relab.stool (curatedMetagenomicData-defunct), 4
TettAJ_2019_b.marker_abundance.stool (curatedMetagenomicData-defunct), 4
TettAJ_2019_b.marker_presence.stool (curatedMetagenomicData-defunct), 4
TettAJ_2019_b.metaphlan_bugs_list.stool (curatedMetagenomicData-defunct), 4
TettAJ_2019_b.pathabundance_relab.stool (curatedMetagenomicData-defunct), 4
TettAJ_2019_b.pathcoverage.stool (curatedMetagenomicData-defunct), 4
TettAJ_2019_c.genefamilies_relab.stool (curatedMetagenomicData-defunct), 4
TettAJ_2019_c.marker_abundance.stool (curatedMetagenomicData-defunct), 4
TettAJ_2019_c.marker_presence.stool (curatedMetagenomicData-defunct), 4
TettAJ_2019_c.metaphlan_bugs_list.stool (curatedMetagenomicData-defunct), 4
TettAJ_2019_c.pathabundance_relab.stool (curatedMetagenomicData-defunct), 4
TettAJ_2019_c.pathcoverage.stool (curatedMetagenomicData-defunct), 4
ThomasAM_2018a.genefamilies_relab.stool (curatedMetagenomicData-defunct), 4
ThomasAM_2018a.marker_abundance.stool (curatedMetagenomicData-defunct), 4
ThomasAM_2018a.marker_presence.stool (curatedMetagenomicData-defunct), 4