

# Package ‘curatedMetagenomicData’

December 5, 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** 3.15.0

**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** devel

**git\_last\_commit** c2fbd63

**git\_last\_commit\_date** 2024-10-29

**Repository** Bioconductor 3.21

**Date/Publication** 2024-12-05

**Author** Lucas schiffer [aut, cre] (ORCID:  
<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 . . . . .	4
mergeData . . . . .	16
returnSamples . . . . .	17
sampleMetadata . . . . .	18
<b>Index</b>	<b>19</b>

---

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 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

```
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()
- VogtmanE\_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"> <li>"gene_families"</li> <li>"marker_abundance"</li> <li>"marker_presence"</li> <li>"pathway_abundance"</li> <li>"pathway_coverage"</li> <li>"relative_abundance"</li> </ul>
<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

* <b>datasets</b>	4
sampleMetadata, 18	
* <b>internal</b>	
curatedMetagenomicData-defunct, 4	
AsnicarF_2017.genefamilies_relab.milk (curatedMetagenomicData-defunct), 4	BackhedF_2015.genefamilies_relab.stool (curatedMetagenomicData-defunct), 4
AsnicarF_2017.genefamilies_relab.stool (curatedMetagenomicData-defunct), 4	BackhedF_2015.marker_abundance.stool (curatedMetagenomicData-defunct), 4
AsnicarF_2017.marker_abundance.milk (curatedMetagenomicData-defunct), 4	BackhedF_2015.marker_presence.stool (curatedMetagenomicData-defunct), 4
AsnicarF_2017.marker_abundance.stool (curatedMetagenomicData-defunct), 4	BackhedF_2015.metaphlan_bugs_list.stool (curatedMetagenomicData-defunct), 4
AsnicarF_2017.marker_presence.milk (curatedMetagenomicData-defunct), 4	BackhedF_2015.pathabundance_relab.stool (curatedMetagenomicData-defunct), 4
AsnicarF_2017.marker_presence.stool (curatedMetagenomicData-defunct), 4	BackhedF_2015.pathcoverage.stool (curatedMetagenomicData-defunct), 4
AsnicarF_2017.metaphlan_bugs_list.milk (curatedMetagenomicData-defunct), 4	Bengtsson-PalmeJ_2015.genefamilies_relab.stool (curatedMetagenomicData-defunct), 4
AsnicarF_2017.metaphlan_bugs_list.stool (curatedMetagenomicData-defunct), 4	Bengtsson-PalmeJ_2015.marker_abundance.stool (curatedMetagenomicData-defunct), 4
AsnicarF_2017.pathabundance_relab.milk (curatedMetagenomicData-defunct), 4	Bengtsson-PalmeJ_2015.marker_presence.stool (curatedMetagenomicData-defunct), 4
AsnicarF_2017.pathabundance_relab.stool (curatedMetagenomicData-defunct), 4	Bengtsson-PalmeJ_2015.metaphlan_bugs_list.stool (curatedMetagenomicData-defunct), 4
AsnicarF_2017.pathcoverage.milk (curatedMetagenomicData-defunct), 4	Bengtsson-PalmeJ_2015.pathabundance_relab.stool (curatedMetagenomicData-defunct), 4
AsnicarF_2017.pathcoverage.stool (curatedMetagenomicData-defunct),	Bengtsson-PalmeJ_2015.pathcoverage.stool (curatedMetagenomicData-defunct), 4
	BritoIL_2016.genefamilies_relab.oralcavity (curatedMetagenomicData-defunct),

- 4
- BritoIL\_2016.genefamilies\_relab.stool  
(curatedMetagenomicData-defunct),  
4
- BritoIL\_2016.marker\_abundance.oralcavity  
(curatedMetagenomicData-defunct),  
4
- BritoIL\_2016.marker\_abundance.stool  
(curatedMetagenomicData-defunct),  
4
- BritoIL\_2016.marker\_presence.oralcavity  
(curatedMetagenomicData-defunct),  
4
- BritoIL\_2016.marker\_presence.stool  
(curatedMetagenomicData-defunct),  
4
- BritoIL\_2016.metaphlan\_bugs\_list.oralcavity  
(curatedMetagenomicData-defunct),  
4
- BritoIL\_2016.metaphlan\_bugs\_list.stool  
(curatedMetagenomicData-defunct),  
4
- BritoIL\_2016.pathabundance\_relab.oralcavity  
(curatedMetagenomicData-defunct),  
4
- BritoIL\_2016.pathabundance\_relab.stool  
(curatedMetagenomicData-defunct),  
4
- BritoIL\_2016.pathcoverage.oralcavity  
(curatedMetagenomicData-defunct),  
4
- BritoIL\_2016.pathcoverage.stool  
(curatedMetagenomicData-defunct),  
4
- Castro-NallarE\_2015.genefamilies\_relab.oralcavity  
(curatedMetagenomicData-defunct),  
4
- Castro-NallarE\_2015.marker\_abundance.oralcavity  
(curatedMetagenomicData-defunct),  
4
- Castro-NallarE\_2015.marker\_presence.oralcavity  
(curatedMetagenomicData-defunct),  
4
- Castro-NallarE\_2015.metaphlan\_bugs\_list.oralcavity  
(curatedMetagenomicData-defunct),  
4
- Castro-NallarE\_2015.pathabundance\_relab.oralcavity  
(curatedMetagenomicData-defunct),  
4
- Castro-NallarE\_2015.pathcoverage.oralcavity  
(curatedMetagenomicData-defunct),  
4
- Castro-NallarE\_2015.pathcoverage.stool  
(curatedMetagenomicData-defunct),  
4
- ChengpingW\_2017.genefamilies\_relab.stool  
(curatedMetagenomicData-defunct),  
4
- ChengpingW\_2017.marker\_abundance.stool  
(curatedMetagenomicData-defunct),  
4
- ChengpingW\_2017.marker\_presence.stool  
(curatedMetagenomicData-defunct),  
4
- ChengpingW\_2017.metaphlan\_bugs\_list.stool  
(curatedMetagenomicData-defunct),  
4
- ChengpingW\_2017.pathabundance\_relab.stool  
(curatedMetagenomicData-defunct),  
4
- ChengpingW\_2017.pathcoverage.stool  
(curatedMetagenomicData-defunct),  
4
- ChngKR\_2016.genefamilies\_relab.skin  
(curatedMetagenomicData-defunct),  
4
- ChngKR\_2016.marker\_abundance.skin  
(curatedMetagenomicData-defunct),  
4
- ChngKR\_2016.marker\_presence.skin  
(curatedMetagenomicData-defunct),  
4

- 4
- ChngKR\_2016.metaphlan\_bugs\_list.skin  
(curatedMetagenomicData-defunct),  
4
- ChngKR\_2016.pathabundance\_relab.skin  
(curatedMetagenomicData-defunct),  
4
- ChngKR\_2016.pathcoverage.skin  
(curatedMetagenomicData-defunct),  
4
- cmdValidVersions  
(curatedMetagenomicData-defunct),  
4
- CosteaPI\_2017.genefamilies\_relab.stool  
(curatedMetagenomicData-defunct),  
4
- CosteaPI\_2017.marker\_abundance.stool  
(curatedMetagenomicData-defunct),  
4
- CosteaPI\_2017.marker\_presence.stool  
(curatedMetagenomicData-defunct),  
4
- CosteaPI\_2017.metaphlan\_bugs\_list.stool  
(curatedMetagenomicData-defunct),  
4
- CosteaPI\_2017.pathabundance\_relab.stool  
(curatedMetagenomicData-defunct),  
4
- CosteaPI\_2017.pathcoverage.stool  
(curatedMetagenomicData-defunct),  
4
- curatedMetagenomicData, [2](#), [16](#)  
curatedMetagenomicData-defunct, [4](#)
- DavidLA\_2015.genefamilies\_relab.stool  
(curatedMetagenomicData-defunct),  
4
- DavidLA\_2015.marker\_abundance.stool  
(curatedMetagenomicData-defunct),  
4
- DavidLA\_2015.marker\_presence.stool  
(curatedMetagenomicData-defunct),  
4
- DavidLA\_2015.metaphlan\_bugs\_list.stool  
(curatedMetagenomicData-defunct),  
4
- DavidLA\_2015.pathabundance\_relab.stool  
(curatedMetagenomicData-defunct),  
4
- DavidLA\_2015.pathcoverage.stool  
(curatedMetagenomicData-defunct),  
4
- DhakanDB\_2019.genefamilies\_relab.stool  
(curatedMetagenomicData-defunct),  
4
- DhakanDB\_2019.marker\_abundance.stool  
(curatedMetagenomicData-defunct),  
4
- DhakanDB\_2019.marker\_presence.stool  
(curatedMetagenomicData-defunct),  
4
- DhakanDB\_2019.metaphlan\_bugs\_list.stool  
(curatedMetagenomicData-defunct),  
4
- DhakanDB\_2019.pathabundance\_relab.stool  
(curatedMetagenomicData-defunct),  
4
- DhakanDB\_2019.pathcoverage.stool  
(curatedMetagenomicData-defunct),  
4
- ExpressionSet2MRExperiment  
(curatedMetagenomicData-defunct),  
4
- ExpressionSet2phyloseq  
(curatedMetagenomicData-defunct),  
4
- FengQ\_2015.genefamilies\_relab.stool  
(curatedMetagenomicData-defunct),  
4
- FengQ\_2015.marker\_abundance.stool  
(curatedMetagenomicData-defunct),  
4
- FengQ\_2015.marker\_presence.stool  
(curatedMetagenomicData-defunct),  
4
- FengQ\_2015.metaphlan\_bugs\_list.stool  
(curatedMetagenomicData-defunct),  
4
- FengQ\_2015.pathabundance\_relab.stool  
(curatedMetagenomicData-defunct),  
4
- FengQ\_2015.pathcoverage.stool  
(curatedMetagenomicData-defunct),  
4
- FerrettiP\_2018.genefamilies\_relab.oralcavity  
(curatedMetagenomicData-defunct),

- 4  
 FerrettiP\_2018.genefamilies\_relab.skin  
 (curatedMetagenomicData-defunct),  
 4  
 FerrettiP\_2018.genefamilies\_relab.stool  
 (curatedMetagenomicData-defunct),  
 4  
 FerrettiP\_2018.genefamilies\_relab.vagina  
 (curatedMetagenomicData-defunct),  
 4  
 FerrettiP\_2018.marker\_abundance.oralcavity  
 (curatedMetagenomicData-defunct),  
 4  
 FerrettiP\_2018.marker\_abundance.skin  
 (curatedMetagenomicData-defunct),  
 4  
 FerrettiP\_2018.marker\_abundance.stool  
 (curatedMetagenomicData-defunct),  
 4  
 FerrettiP\_2018.marker\_abundance.vagina  
 (curatedMetagenomicData-defunct),  
 4  
 FerrettiP\_2018.marker\_presence.oralcavity  
 (curatedMetagenomicData-defunct),  
 4  
 FerrettiP\_2018.marker\_presence.skin  
 (curatedMetagenomicData-defunct),  
 4  
 FerrettiP\_2018.marker\_presence.stool  
 (curatedMetagenomicData-defunct),  
 4  
 FerrettiP\_2018.marker\_presence.vagina  
 (curatedMetagenomicData-defunct),  
 4  
 FerrettiP\_2018.metaphlan\_bugs\_list.oralcavity  
 (curatedMetagenomicData-defunct),  
 4  
 FerrettiP\_2018.metaphlan\_bugs\_list.skin  
 (curatedMetagenomicData-defunct),  
 4  
 FerrettiP\_2018.metaphlan\_bugs\_list.stool  
 (curatedMetagenomicData-defunct),  
 4  
 FerrettiP\_2018.metaphlan\_bugs\_list.vagina  
 (curatedMetagenomicData-defunct),  
 4  
 FerrettiP\_2018.pathabundance\_relab.oralcavity  
 (curatedMetagenomicData-defunct),  
 4  
 FerrettiP\_2018.pathabundance\_relab.skin  
 (curatedMetagenomicData-defunct),  
 4  
 FerrettiP\_2018.pathabundance\_relab.stool  
 (curatedMetagenomicData-defunct),  
 4  
 FerrettiP\_2018.pathabundance\_relab.vagina  
 (curatedMetagenomicData-defunct),  
 4  
 FerrettiP\_2018.pathcoverage.oralcavity  
 (curatedMetagenomicData-defunct),  
 4  
 FerrettiP\_2018.pathcoverage.skin  
 (curatedMetagenomicData-defunct),  
 4  
 FerrettiP\_2018.pathcoverage.stool  
 (curatedMetagenomicData-defunct),  
 4  
 FerrettiP\_2018.pathcoverage.vagina  
 (curatedMetagenomicData-defunct),  
 4  
 getMetaphlanTree  
 (curatedMetagenomicData-defunct),  
 4  
 GopalakrishnanV\_2018.genefamilies\_relab.stool  
 (curatedMetagenomicData-defunct),  
 4  
 GopalakrishnanV\_2018.marker\_abundance.stool  
 (curatedMetagenomicData-defunct),  
 4  
 GopalakrishnanV\_2018.marker\_presence.stool  
 (curatedMetagenomicData-defunct),  
 4  
 GopalakrishnanV\_2018.metaphlan\_bugs\_list.stool  
 (curatedMetagenomicData-defunct),  
 4  
 GopalakrishnanV\_2018.pathabundance\_relab.stool  
 (curatedMetagenomicData-defunct),  
 4  
 GopalakrishnanV\_2018.pathcoverage.stool  
 (curatedMetagenomicData-defunct),  
 4  
 HanniganGD\_2017.genefamilies\_relab.stool  
 (curatedMetagenomicData-defunct),  
 4

- 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
- JieZ\_2017.genefamilies\_relab.stool  
(curatedMetagenomicData-defunct),  
4
- JieZ\_2017.marker\_abundance.stool  
(curatedMetagenomicData-defunct),  
4
- JieZ\_2017.marker\_presence.stool  
(curatedMetagenomicData-defunct),  
4
- JieZ\_2017.metaphlan\_bugs\_list.stool  
(curatedMetagenomicData-defunct),  
4
- JieZ\_2017.pathabundance\_relab.stool  
(curatedMetagenomicData-defunct),  
4
- JieZ\_2017.pathcoverage.stool  
(curatedMetagenomicData-defunct),  
4
- KarlssonFH\_2013.genefamilies\_relab.stool  
(curatedMetagenomicData-defunct),  
4
- KarlssonFH\_2013.marker\_abundance.stool  
(curatedMetagenomicData-defunct),  
4
- KarlssonFH\_2013.marker\_presence.stool  
(curatedMetagenomicData-defunct),  
4
- KarlssonFH\_2013.metaphlan\_bugs\_list.stool  
(curatedMetagenomicData-defunct),  
4
- KarlssonFH\_2013.pathabundance\_relab.stool  
(curatedMetagenomicData-defunct),  
4



- 4  
KarlssonFH\_2013.pathcoverage.stool  
(curatedMetagenomicData-defunct),  
4  
KieserS\_2018.genefamilies\_relab.stool  
(curatedMetagenomicData-defunct),  
4  
KieserS\_2018.marker\_abundance.stool  
(curatedMetagenomicData-defunct),  
4  
KieserS\_2018.marker\_presence.stool  
(curatedMetagenomicData-defunct),  
4  
KieserS\_2018.metaphlan\_bugs\_list.stool  
(curatedMetagenomicData-defunct),  
4  
KieserS\_2018.pathabundance\_relab.stool  
(curatedMetagenomicData-defunct),  
4  
KieserS\_2018.pathcoverage.stool  
(curatedMetagenomicData-defunct),  
4  
KosticAD\_2015.genefamilies\_relab.stool  
(curatedMetagenomicData-defunct),  
4  
KosticAD\_2015.marker\_abundance.stool  
(curatedMetagenomicData-defunct),  
4  
KosticAD\_2015.marker\_presence.stool  
(curatedMetagenomicData-defunct),  
4  
KosticAD\_2015.metaphlan\_bugs\_list.stool  
(curatedMetagenomicData-defunct),  
4  
KosticAD\_2015.pathabundance\_relab.stool  
(curatedMetagenomicData-defunct),  
4  
KosticAD\_2015.pathcoverage.stool  
(curatedMetagenomicData-defunct),  
4  
LeChatelierE\_2013.genefamilies\_relab.stool  
(curatedMetagenomicData-defunct),  
4  
LeChatelierE\_2013.marker\_abundance.stool  
(curatedMetagenomicData-defunct),  
4  
LeChatelierE\_2013.marker\_presence.stool  
(curatedMetagenomicData-defunct),  
4  
LeChatelierE\_2013.metaphlan\_bugs\_list.stool  
(curatedMetagenomicData-defunct),  
4  
LeChatelierE\_2013.pathabundance\_relab.stool  
(curatedMetagenomicData-defunct),  
4  
LeChatelierE\_2013.pathcoverage.stool  
(curatedMetagenomicData-defunct),  
4  
LiJ\_2014.genefamilies\_relab.stool  
(curatedMetagenomicData-defunct),  
4  
LiJ\_2014.marker\_abundance.stool  
(curatedMetagenomicData-defunct),  
4  
LiJ\_2014.marker\_presence.stool  
(curatedMetagenomicData-defunct),  
4  
LiJ\_2014.metaphlan\_bugs\_list.stool  
(curatedMetagenomicData-defunct),  
4  
LiJ\_2014.pathabundance\_relab.stool  
(curatedMetagenomicData-defunct),  
4  
LiJ\_2014.pathcoverage.stool  
(curatedMetagenomicData-defunct),  
4  
LiJ\_2017.genefamilies\_relab.stool  
(curatedMetagenomicData-defunct),  
4  
LiJ\_2017.marker\_abundance.stool  
(curatedMetagenomicData-defunct),  
4  
LiJ\_2017.marker\_presence.stool  
(curatedMetagenomicData-defunct),  
4  
LiJ\_2017.metaphlan\_bugs\_list.stool  
(curatedMetagenomicData-defunct),  
4  
LiJ\_2017.pathabundance\_relab.stool  
(curatedMetagenomicData-defunct),  
4  
LiJ\_2017.pathcoverage.stool  
(curatedMetagenomicData-defunct),  
4  
LiSS\_2016.genefamilies\_relab.stool  
(curatedMetagenomicData-defunct),  
4

- 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

- 4
- 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
- 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
- OhJ\_2014.pathabundance\_relab.skin  
(curatedMetagenomicData-defunct),  
4
- OhJ\_2014.pathcoverage.skin  
(curatedMetagenomicData-defunct),  
4
- OlmMR\_2017.genefamilies\_relab.oralcavity  
(curatedMetagenomicData-defunct),  
4
- OlmMR\_2017.genefamilies\_relab.skin  
(curatedMetagenomicData-defunct),  
4
- OlmMR\_2017.genefamilies\_relab.stool  
(curatedMetagenomicData-defunct),  
4
- OlmMR\_2017.marker\_abundance.oralcavity  
(curatedMetagenomicData-defunct),  
4

- 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.genefamilies\_relab.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
- PehrssonE\_2016.genefamilies\_relab.stool  
 (curatedMetagenomicData-defunct),  
 4
- PehrssonE\_2016.marker\_abundance.stool  
 (curatedMetagenomicData-defunct),  
 4
- PehrssonE\_2016.marker\_presence.stool  
 (curatedMetagenomicData-defunct),  
 4
- PehrssonE\_2016.metaphlan\_bugs\_list.stool  
 (curatedMetagenomicData-defunct),  
 4
- PehrssonE\_2016.pathabundance\_relab.stool  
 (curatedMetagenomicData-defunct),  
 4
- PehrssonE\_2016.pathcoverage.stool  
 (curatedMetagenomicData-defunct),  
 4
- QinJ\_2012.genefamilies\_relab.stool  
 (curatedMetagenomicData-defunct),  
 4
- QinJ\_2012.marker\_abundance.stool  
 (curatedMetagenomicData-defunct),  
 4
- QinJ\_2012.marker\_presence.stool  
 (curatedMetagenomicData-defunct),  
 4
- QinJ\_2012.metaphlan\_bugs\_list.stool  
 (curatedMetagenomicData-defunct),  
 4
- QinJ\_2012.pathabundance\_relab.stool  
 (curatedMetagenomicData-defunct),  
 4
- QinJ\_2012.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
- ShiB\_2015.pathabundance\_relab.oralcavity  
(curatedMetagenomicData-defunct),  
4
- ShiB\_2015.pathcoverage.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

- ThomasAM\_2018a.metaphlan\_bugs\_list.stool  
(curatedMetagenomicData-defunct),  
4
- ThomasAM\_2018a.pathabundance\_relab.stool  
(curatedMetagenomicData-defunct),  
4
- ThomasAM\_2018a.pathcoverage.stool  
(curatedMetagenomicData-defunct),  
4
- ThomasAM\_2018b.genefamilies\_relab.stool  
(curatedMetagenomicData-defunct),  
4
- ThomasAM\_2018b.marker\_abundance.stool  
(curatedMetagenomicData-defunct),  
4
- ThomasAM\_2018b.marker\_presence.stool  
(curatedMetagenomicData-defunct),  
4
- ThomasAM\_2018b.metaphlan\_bugs\_list.stool  
(curatedMetagenomicData-defunct),  
4
- ThomasAM\_2018b.pathabundance\_relab.stool  
(curatedMetagenomicData-defunct),  
4
- ThomasAM\_2018b.pathcoverage.stool  
(curatedMetagenomicData-defunct),  
4
- TreeSummarizedExperiment, [2](#), [3](#), [16](#), [17](#)
- VatanenT\_2016.genefamilies\_relab.stool  
(curatedMetagenomicData-defunct),  
4
- VatanenT\_2016.marker\_abundance.stool  
(curatedMetagenomicData-defunct),  
4
- VatanenT\_2016.marker\_presence.stool  
(curatedMetagenomicData-defunct),  
4
- VatanenT\_2016.metaphlan\_bugs\_list.stool  
(curatedMetagenomicData-defunct),  
4
- VatanenT\_2016.pathabundance\_relab.stool  
(curatedMetagenomicData-defunct),  
4
- VatanenT\_2016.pathcoverage.stool  
(curatedMetagenomicData-defunct),  
4
- VincentC\_2016.genefamilies\_relab.stool  
(curatedMetagenomicData-defunct),  
4
- VincentC\_2016.marker\_abundance.stool  
(curatedMetagenomicData-defunct),  
4
- VincentC\_2016.marker\_presence.stool  
(curatedMetagenomicData-defunct),  
4
- VincentC\_2016.metaphlan\_bugs\_list.stool  
(curatedMetagenomicData-defunct),  
4
- VincentC\_2016.pathabundance\_relab.stool  
(curatedMetagenomicData-defunct),  
4
- VincentC\_2016.pathcoverage.stool  
(curatedMetagenomicData-defunct),  
4
- VogtmannE\_2016.genefamilies\_relab.stool  
(curatedMetagenomicData-defunct),  
4
- VogtmannE\_2016.marker\_abundance.stool  
(curatedMetagenomicData-defunct),  
4
- VogtmannE\_2016.marker\_presence.stool  
(curatedMetagenomicData-defunct),  
4
- VogtmannE\_2016.metaphlan\_bugs\_list.stool  
(curatedMetagenomicData-defunct),  
4
- VogtmannE\_2016.pathabundance\_relab.stool  
(curatedMetagenomicData-defunct),  
4
- VogtmannE\_2016.pathcoverage.stool  
(curatedMetagenomicData-defunct),  
4
- XieH\_2016.genefamilies\_relab.stool  
(curatedMetagenomicData-defunct),  
4
- XieH\_2016.marker\_abundance.stool  
(curatedMetagenomicData-defunct),  
4
- XieH\_2016.marker\_presence.stool  
(curatedMetagenomicData-defunct),  
4
- XieH\_2016.metaphlan\_bugs\_list.stool  
(curatedMetagenomicData-defunct),  
4
- XieH\_2016.pathabundance\_relab.stool  
(curatedMetagenomicData-defunct),  
4

- 4  
XieH\_2016.pathcoverage.stool  
(curatedMetagenomicData-defunct),  
4
- YeZ\_2018.genefamilies\_relab.stool  
(curatedMetagenomicData-defunct),  
4
- YeZ\_2018.marker\_abundance.stool  
(curatedMetagenomicData-defunct),  
4
- YeZ\_2018.marker\_presence.stool  
(curatedMetagenomicData-defunct),  
4
- YeZ\_2018.metaphlan\_bugs\_list.stool  
(curatedMetagenomicData-defunct),  
4
- YeZ\_2018.pathabundance\_relab.stool  
(curatedMetagenomicData-defunct),  
4
- YeZ\_2018.pathcoverage.stool  
(curatedMetagenomicData-defunct),  
4
- YuJ\_2015.genefamilies\_relab.stool  
(curatedMetagenomicData-defunct),  
4
- YuJ\_2015.marker\_abundance.stool  
(curatedMetagenomicData-defunct),  
4
- YuJ\_2015.marker\_presence.stool  
(curatedMetagenomicData-defunct),  
4
- YuJ\_2015.metaphlan\_bugs\_list.stool  
(curatedMetagenomicData-defunct),  
4
- YuJ\_2015.pathabundance\_relab.stool  
(curatedMetagenomicData-defunct),  
4
- YuJ\_2015.pathcoverage.stool  
(curatedMetagenomicData-defunct),  
4
- ZeeviD\_2015.genefamilies\_relab.stool  
(curatedMetagenomicData-defunct),  
4
- ZeeviD\_2015.marker\_abundance.stool  
(curatedMetagenomicData-defunct),  
4
- ZeeviD\_2015.marker\_presence.stool  
(curatedMetagenomicData-defunct),  
4
- ZeeviD\_2015.metaphlan\_bugs\_list.stool  
(curatedMetagenomicData-defunct),  
4
- ZeeviD\_2015.pathabundance\_relab.stool  
(curatedMetagenomicData-defunct),  
4
- ZeeviD\_2015.pathcoverage.stool  
(curatedMetagenomicData-defunct),  
4
- ZellerG\_2014.genefamilies\_relab.stool  
(curatedMetagenomicData-defunct),  
4
- ZellerG\_2014.marker\_abundance.stool  
(curatedMetagenomicData-defunct),  
4
- ZellerG\_2014.marker\_presence.stool  
(curatedMetagenomicData-defunct),  
4
- ZellerG\_2014.metaphlan\_bugs\_list.stool  
(curatedMetagenomicData-defunct),  
4
- ZellerG\_2014.pathabundance\_relab.stool  
(curatedMetagenomicData-defunct),  
4
- ZellerG\_2014.pathcoverage.stool  
(curatedMetagenomicData-defunct),  
4