Package ‘curatedMetagenomicData’

July 24, 2025

Title Curated Metagenomic Data of the Human Microbiome

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

biocViews ExperimentHub, Homo_sapiens_Data, MicrobiomeData, ReproducibleResearch

Version 3.17.1

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 7.3.2

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`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()`
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- `ChengpingW_2017.marker_abundance.stool()`
- `ChengpingW_2017.marker_presence.stool()`
- `ChengpingW_2017.metaphlan_bugs_list.stool()`
- `ChengpingW_2017.pathabundance_relab.stool()`
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- `ChngKR_2016.genefamilies_relab.skin()`
- `ChngKR_2016.marker_abundance.skin()`
- `ChngKR_2016.marker_presence.skin()`
- `ChngKR_2016.metaphlan_bugs_list.skin()`
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- `CosteaPI_2017.marker_abundance.stool()`
- `CosteaPI_2017.marker_presence.stool()`
- `CosteaPI_2017.metaphlan_bugs_list.stool()`
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- `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()`
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- `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()`
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- `FerrettiP_2018.marker_presence.oralcavity()`
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- `HMP_2012.pathabundance_relab.vagina()`
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- `NielsenHB_2014.pathabundance_relab.stool()`
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- `Obregon_TitoAJ_2015.genefamilies_relab.stool()`
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- `Obregon_TitoAJ_2015.marker_presence.stool()`
- `Obregon_TitoAJ_2015.metaphlan_bugs_list.stool()`
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- `Obregon-TitoAJ_2015.marker_presence.stool()`
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- `Obregon-TitoAJ_2015.pathabundance_relab.stool()`
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- `OlmMR_2017.genefamilies_relab.oralcavity()`
- `OlmMR_2017.genefamilies_relab.skin()`

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- `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()`
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- `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()`
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- `PasolliE_2018.marker_abundance.stool()`
- `PasolliE_2018.marker_presence.stool()`
- `PasolliE_2018.metaphlan_bugs_list.stool()`
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- `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()`
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- `QinN_2014.pathabundance_relab.stool()`
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- `RampelliS_2015.genefamilies_relab.stool()`
- `RampelliS_2015.marker_abundance.stool()`
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`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` *Return Samples Across Studies*

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

`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

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` *Manually Curated Sample Metadata*

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.

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VincentC_2016.marker_presence.stool *(curatedMetagenomicData-defunct)*, 3
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