

Package ‘HuMMANet’

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Type Package

Title Curated Paired Human Microbiome-Metabolome Study Data

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Description Provides access to curated paired human microbiome-metabolome study bundles available through Bioconductor ExperimentHub. The package organizes matched sample metadata, species abundance profiles, original and harmonized metabolite profiles, and study-specific annotation resources including metabolite identifier mappings, microbial producer annotations, disease associations, pathway annotations, and drug similarity matches. The resource is designed to support consistent and reproducible cross-study microbiome-metabolome analyses.

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URL <https://github.com/ShivangiV-IIITD/HuMMANet>

BugReports <https://github.com/ShivangiV-IIITD/HuMMANet/issues>

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Author Shivangi Verma [aut, fnd] (ORCID: <https://orcid.org/0009-0006-8505-0032>),
 Nalin Arora [aut, cre] (ORCID: <https://orcid.org/0009-0009-1340-688X>),
 Himel Mallick [aut] (ORCID: <https://orcid.org/0000-0003-4956-2429>),
 Tarini Shankar Ghosh [aut, fnd] (ORCID: <https://orcid.org/0000-0001-9570-0365>)

Maintainer Nalin Arora <naa4050@med.cornell.edu>

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HuMMANet-package	<i>HuMMANet: Paired Human Microbiome-Metabolome Study Data</i>
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Description

HuMMANet is a Bioconductor experiment data package that provides access to curated paired human microbiome-metabolome studies. The package organizes matched sample metadata, species abundance profiles, original and harmonized metabolite profiles, and study-specific annotation resources including metabolite identifier mappings, microbial producer annotations, disease associations, pathway annotations, and drug similarity matches through Bioconductor ExperimentHub.

Details

Study resources are designed to support reproducible access to paired species and metabolite data across studies through a consistent set of functions. Each study is represented as a `MultiAssayExperiment::MultiAssayExperiment` with matched sample metadata stored in `colData()`, assay-level species and metabolite profiles stored in `experiments()`, and long-form annotation tables attached in `metadata()`. HuMMANet data can be discovered and retrieved from Bioconductor ExperimentHub using convenience accessors such as `HuMMANetHub`, `HuMMANet_studies`, `HuMMANet_study_index`, `HuMMANet_load_modality`, and `HuMMANet_load_study`.

Value

This help page documents the HuMMANet package as a whole and does not return a value.

See Also

`HuMMANet`, `HuMMANetHub`, `HuMMANet_resource_table`, `HuMMANet_study_index`, `HuMMANet_load_modality`, and `HuMMANet_load_study`

HuMMANet*HuMMANet Accessor*

Description

Main convenience loader for HuMMANet data.

Usage

```
HuMMANet(  
  studies = NULL,  
  modalities = HuMMANet_public_modality_names(),  
  extdata_dir = NULL,  
  drop_missing = TRUE,  
  localHub = FALSE  
)
```

Arguments

<code>studies</code>	Optional character vector of studies to load. Defaults to all.
<code>modalities</code>	Character vector of modalities to load.
<code>extdata_dir</code>	Optional explicit path to a local development 'extdata' directory.
<code>drop_missing</code>	If 'TRUE', missing modalities are omitted from output.
<code>localHub</code>	Logical scalar passed to 'ExperimentHub::ExperimentHub()' when hub access is used.

Value

Named list keyed by study, where each element is a 'MultiAssayExperiment'.

Examples

```
extdata_dir <- system.file("extdata", package = "HuMMANet")  
if (dir.exists(file.path(extdata_dir, "studies"))) {  
  out <- HuMMANet(  
    studies = "WuY_2025",  
    modalities = c("MetadataProfile", "OriginalMetaboliteProfile"),  
    extdata_dir = extdata_dir  
  )  
  names(out)  
}
```

HuMMANetHub

HuMMANet ExperimentHub Records

Description

Return the ‘ExperimentHub’ subset associated with ‘HuMMANet’.

Usage

```
HuMMANetHub(localHub = FALSE)
```

Arguments

localHub Logical scalar passed to ‘ExperimentHub::ExperimentHub()’.

Value

An ‘ExperimentHub’ subset filtered to ‘package == "HuMMANet"’.

Examples

```
if (interactive()) {
  hub <- HuMMANetHub(localHub = TRUE)
  hub
}
```

HuMMANet_available_modalities

List Available Modalities for a Study

Description

List Available Modalities for a Study

Usage

```
HuMMANet_available_modalities(study, extdata_dir = NULL, localHub = FALSE)
```

Arguments

study Study identifier (for example “‘FranzosaE_2019’”).

extdata_dir Optional explicit path to a local development ‘extdata’ directory.

localHub Logical scalar passed to ‘ExperimentHub::ExperimentHub()’ when hub access is used.

Value

Character vector of public HuMMANet modality names.

Examples

```
extdata_dir <- system.file("extdata", package = "HuMMANet")
if (dir.exists(file.path(extdata_dir, "studies"))) {
  HuMMANet_available_modalities("WuY_2025", extdata_dir = extdata_dir)
}
```

HuMMANet_load_modality

Load a Single Modality for One Study

Description

Load a Single Modality for One Study

Usage

```
HuMMANet_load_modality(
  study,
  modality = HuMMANet_public_modality_names(),
  extdata_dir = NULL,
  allow_missing = FALSE,
  localHub = FALSE
)
```

Arguments

study	Study identifier.
modality	One public HuMMANet modality name.
extdata_dir	Optional explicit path to a local development ‘extdata’ directory.
allow_missing	If ‘TRUE’, return ‘NULL’ when modality is missing.
localHub	Logical scalar passed to ‘ExperimentHub::ExperimentHub()’ when hub access is used.

Value

A ‘DataFrame’, ‘SummarizedExperiment’, annotation ‘data.frame’, or ‘NULL’ if missing and ‘allow_missing = TRUE’.

Examples

```
extdata_dir <- system.file("extdata", package = "HuMMANet")
if (dir.exists(file.path(extdata_dir, "studies"))) {
  md <- HuMMANet_load_modality(
    "WuY_2025",
    "MetadataProfile",
    extdata_dir = extdata_dir
  )
  dim(md)
}
```

HuMMANet_load_study *Load Curated Data for One Study*

Description

Load one study from the HuMMANet ‘ExperimentHub’ resources. For local development you may pass ‘extdata_dir’ to read directly from csv files.

Usage

```
HuMMANet_load_study(
  study,
  modalities = HuMMANet_public_modality_names(),
  extdata_dir = NULL,
  drop_missing = TRUE,
  localHub = FALSE
)
```

Arguments

study	Study identifier.
modalities	Character vector of modalities to load.
extdata_dir	Optional explicit path to a local development ‘extdata’ directory.
drop_missing	If ‘TRUE’, missing modalities are omitted from output.
localHub	Logical scalar passed to ‘ExperimentHub::ExperimentHub()’ when hub access is used.

Value

A study-level ‘MultiAssayExperiment’.

Examples

```
extdata_dir <- system.file("extdata", package = "HuMMANet")
if (dir.exists(file.path(extdata_dir, "studies"))) {
  x <- HuMMANet_load_study(
    "WuY_2025",
    modalities = c("MetadataProfile", "harmonizedMetaboliteProfile"),
    extdata_dir = extdata_dir
  )
  class(x)
  names(MultiAssayExperiment::experiments(x))
}
```

`HuMMANet_resource_table`*HuMMANet Resource Table*

Description

Inspect the expected HuMMANet ExperimentHub resources.

Usage

```
HuMMANet_resource_table(localHub = FALSE, extdata_dir = NULL)
```

Arguments

<code>localHub</code>	Logical scalar passed to ‘ExperimentHub::ExperimentHub()’.
<code>extdata_dir</code>	Optional explicit path to a local development ‘extdata’ directory.

Value

A ‘data.frame’ describing the HuMMANet records.

Examples

```
extdata_dir <- system.file("extdata", package = "HuMMANet")
tbl <- HuMMANet_resource_table(extdata_dir = extdata_dir)
head(tbl[, c("title", "record_type")])
```

`HuMMANet_studies`*List Available Studies*

Description

List Available Studies

Usage

```
HuMMANet_studies(extdata_dir = NULL, localHub = FALSE)
```

Arguments

<code>extdata_dir</code>	Optional explicit path to a local development ‘extdata’ directory.
<code>localHub</code>	Logical scalar passed to ‘ExperimentHub::ExperimentHub()’ when hub access is used.

Value

Character vector of study identifiers.

Examples

```
extdata_dir <- system.file("extdata", package = "HuMMANet")
head(HuMMANet_studies(extdata_dir = extdata_dir))
```

HuMMANet_study_index	<i>Study Index for HuMMANet</i>
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Description

Read the HuMMANet study index. By default this uses the ‘ExperimentHub’ resource when available and falls back to the packaged ‘study_index.csv’.

Usage

```
HuMMANet_study_index(extdata_dir = NULL, localHub = FALSE)
```

Arguments

extdata_dir	Optional explicit path to a local development ‘extdata’ directory.
localHub	Logical scalar passed to ‘ExperimentHub::ExperimentHub()’ when hub access is used.

Value

A ‘data.frame’ with one row per study and modality file metadata.

Examples

```
extdata_dir <- system.file("extdata", package = "HuMMANet")
idx <- HuMMANet_study_index(extdata_dir = extdata_dir)
head(idx[, c("study", "study_slug")])
```

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