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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`HuMMANet-package` *HuMMANet: Paired Human Microbiome-Metabolome Study Data*

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::MultiAssay` 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`, `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

studies	Optional character vector of studies to load. Defaults to all.
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

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

localHub	Logical scalar passed to 'ExperimentHub::ExperimentHub()'.
extdata_dir	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

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 study identifiers.

Examples

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

HuMMANet_study_index *Study Index for HuMMANet*

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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