Package 'SpaMTPData'

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Type Package

Title Experiment Data Resources for SpaMTP Workflows

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Description Provides lightweight, version-aware access to spatial metabolomics and multi-omics experiment data used in SpaMTP workflows. Resources cover mouse brain, mouse urinary bladder, simulated single-cell multi-omics, annotation-refinement, and human brain examples. Large files are retrieved through ExperimentHub or verified source-URL caches rather than stored in the package repository. A small deterministic synthetic SpatialExperiment with a paired transcriptome supports offline examples and interoperability tests. Native SpatialExperiment datasets are available in a separate resource release; historical archival objects retain their original representations. Conversion and analysis are handled by the SpaMTP software package. Native experimental files share a Zenodo version family with SpaMTPdb without coupling the packages at runtime.

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Depends R (>= 4.6.0)

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`SpaMTPData-package` *SpaMTPData: ExperimentHub data for SpaMTP*

Description

`SpaMTPData` provides discoverable, cached access to the experiment data used in SpaMTP examples, tests and vignettes.

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See Also

Useful links:

- https://github.com/BCRL-tylu/SpaMTPData
- Report bugs at https://github.com/BCRL-tylu/SpaMTPData/issues

spaMTPData *Retrieve a SpaMTP experiment resource*

Description

Returns the representation actually stored in the published file; no implicit conversion is performed. Release `1.1.0`, selected by default, supplies seven native SpatialExperiment datasets. Use `version = "1.0.0"` to request a historical release explicitly. Registry entries with `requires_conversion = TRUE` are historical Seurat objects. Convert these explicitly at the SpaMTP workflow boundary, or use `spaMTPExampleData()` for a small native example that needs neither Seurat nor network access. Local files and a verified download cache are checked before any Hub query. Existing immutable files retain their original classes and checksums. Loaded native experiments additionally carry `metadata(x)$SpaMTPData` with registry provenance and species, enabling analysis packages to check annotation compatibility. Assays, row names and coordinates are preserved. Provenance is also carried by nested `altExp()` experiments so that species checks survive extracting a paired transcriptome. Explicit species metadata already declared by a child experiment is retained rather than relabelled.

Usage

```
spaMTPData(
  resource,
  version = "latest",
  local_dir = NULL,
  hub = NULL,
  metadata = FALSE,
  offline = FALSE,
  fallback_url = TRUE,
  cache_dir = NULL,
  timeout = 1800,
  retries = 3L,
  verify = TRUE
)
```

Arguments

`resource`	Resource name; see `spaMTPDataResources()`.
`version`	Data release version or `"latest"`.
`local_dir`	Optional directory containing downloaded source files.
`hub`	Optional pre-created `ExperimentHub` object.
`metadata`	Return only the registry row.
`offline`	If `TRUE`, use local files or a verified cache only; never query ExperimentHub or the source URL.
`fallback_url`	If `TRUE`, use the immutable source URL when the resource has not yet been ingested into ExperimentHub.
`cache_dir`	Cache directory for source-URL downloads. Defaults to the platform-specific user cache returned by `tools::R_user_dir()`.
`timeout`	Download timeout in seconds for the source-URL fallback.

retries	Number of verified download attempts.
verify	Verify local files against the published size and checksum. Set to FALSE only for intentional development fixtures. Downloaded and cached files are always verified; loaded object classes are always checked.

Value

The requested experiment object or local file path. With metadata = TRUE, returns one registry row.

Examples

```
spaMTPData("mouse_brain_dhb_striatum", metadata = TRUE)
```

---

spaMTPDataResource *Alias for explicit SpaMTPData resource retrieval*

Description

Alias for explicit SpaMTPData resource retrieval

Usage

```
spaMTPDataResource(
  resource,
  version = "latest",
  local_dir = NULL,
  hub = NULL,
  metadata = FALSE,
  offline = FALSE,
  fallback_url = TRUE,
  cache_dir = NULL,
  timeout = 1800,
  retries = 3L,
  verify = TRUE
)
```

Arguments

resource	Resource name; see spaMTPDataResources().
version	Data release version or "latest".
local_dir	Optional directory containing downloaded source files.
hub	Optional pre-created ExperimentHub object.
metadata	Return only the registry row.
offline	If TRUE, use local files or a verified cache only; never query ExperimentHub or the source URL.
fallback_url	If TRUE, use the immutable source URL when the resource has not yet been ingested into ExperimentHub.
cache_dir	Cache directory for source-URL downloads. Defaults to the platform-specific user cache returned by tools::R_user_dir().

timeout	Download timeout in seconds for the source-URL fallback.
retries	Number of verified download attempts.
verify	Verify local files against the published size and checksum. Set to FALSE only for intentional development fixtures. Downloaded and cached files are always verified; loaded object classes are always checked.

Value

The value returned by spaMTPData().

Examples

```
spaMTPDataResource("mouse_brain_dhb_striatum", metadata = TRUE)
```

---

spaMTPDataResources *List SpaMTP experiment resources*

Description

List SpaMTP experiment resources

Usage

```
spaMTPDataResources(version = NULL, category = NULL)
```

Arguments

version	Data release version. NULL returns all versions.
category	Optional resource category.

Value

A data frame describing the registered resources.

Examples

```
spaMTPDataResources()
```

spaMTPDataVersion *Report the available SpaMTPData releases*

Description

Report the available SpaMTPData releases

Usage

```
spaMTPDataVersion()
```

Value

A character vector of data releases, newest first.

Examples

```
spaMTPDataVersion()
```

spaMTPExampleData *Construct a small native spatial multi-omics example*

Description

A deterministic, synthetic example for tutorials and interoperability tests. This is not a biological dataset or a downloaded ExperimentHub resource. The primary experiment contains six m/z features measured at twelve pixels; an optional paired transcriptome has five genes at the same pixels. All data use existing Bioconductor containers and public accessors. Neither SpaMTP nor Seurat is required to construct or inspect the example.

Usage

```
spaMTPExampleData(paired = TRUE)
```

Arguments

paired	Include a transcriptome in `altExp(x, "transcriptome")`.

Value

A `SpatialExperiment` with intensities in `assay(x, "counts")`, m/z values in `rowData(x)`, regions in `colData(x)`, pixel x/y coordinates in `spatialCoords(x)` and synthetic-data provenance in `metadata(x)`.

Examples

```
spe <- spaMTPExampleData()
SummarizedExperiment::assayNames(spe)
SummarizedExperiment::rowData(spe)$mz
SpatialExperiment::spatialCoords(spe)
SingleCellExperiment::altExpNames(spe)
```

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