Package ‘DoReMiTra’

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Title Orchestrating Blood Radiation Transcriptomic Data

Version 1.0.0

Description DoReMiTra is an R data package providing access to curated transcriptomic datasets related to blood radiation, with a focus on neutron, x-ray, and gamma ray studies. It is designed to facilitate radiation biology research and support data exploration and reproducibility in radiation transcriptomics. All datasets are provided as SummarizedExperiment objects, allowing seamless integration with the Bioconductor ecosystem.

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Encoding UTF-8

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Depends R (>= 4.5.0)

Imports ExperimentHub, SummarizedExperiment, AnnotationHub, utils, glue, S4Vectors, scater

Suggests testthat (>= 3.0.0), knitr, rmarkdown, BiocStyle, DT

Config/testthat/edition 3

URL `https://github.com/AhmedSAHassan/DoReMiTra`

BugReports `https://github.com/AhmedSAHassan/DoReMiTra/issues`

VignetteBuilder knitr

biocViews ExperimentData, RNASeqData, ExperimentHub, ExpressionData, GEO, PackageTypeData

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Contents

`compare_DoReMiTra_datasets`

Compare two or more dataset from the DoReMiTra collection

Description

This function compares the essential metadata information of 2 or more SE objects including radiation type, dose, time point, etc.

Usage

```
compare_DoReMiTra_datasets(
  se_list,
  fields = c("Radiation_type", "Dose", "Sex", "Time_point", "Organism")
)
```

Arguments

`se_list`	names of the se objects to be compared
`fields`	a character vector of the main metadata info

Value

a dataframe comparing the metadata of the selected datasets

Examples

```
se1 <- get_DoReMiTra_data("SE_Paul_2010_InVivo_GSE23393_GPL6480")
se2 <- get_DoReMiTra_data("SE_Amundson_2011_InVivo_GSE20162_GPL6480")
se_list<- list(Amundson = se1, Paul= se2)
compare_DoReMiTra_datasets(se_list = se_list)
```

`DoReMiTra-pkg` `DoReMiTra`: *radiation DOse REsponse Measured In TRAnscriptomics*

Description

`DoReMiTra` is a Bioconductor package that provides curated and harmonized radiation transcriptomic datasets from publicly available radiation studies. It enables easy access to dose- and time-dependent gene expression data across various organisms, radiation types, and experimental settings.

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See Also

Useful links:

- `https://github.com/AhmedSAHassan/DoReMiTra`
- Report bugs at `https://github.com/AhmedSAHassan/DoReMiTra/issues`

`get_all_DoReMiTra_datasets`

Fetch all datasets from the DoReMiTra collection

Description

Retrieves all datasets available in the DoReMiTra package from ExperimentHub and returns them as a named list of `SummarizedExperiment` objects. This is useful for batch processing or exploring all curated radiation response datasets at once.

Usage

```
get_all_DoReMiTra_datasets(verbose = TRUE)
```

Arguments

`verbose`	Logical. Whether to print progress messages. Default is TRUE.

Value

A list storing all the SE objects

Examples

```
get_all_DoReMiTra_datasets()
```

`get_DoReMiTra_data` *Fetch a selected dataset from the DoReMiTra collection*

Description

This function fetches a `SummarizedExperiment` object from ExperimentHub corresponding to a dataset in the DoReMiTra package.

Usage

```
get_DoReMiTra_data(dataset_name, gene_symbol = FALSE)
```

Arguments

`dataset_name`	Character. The exact name of the dataset (e.g. "SE_Amundson_2008_ExVivo_GSE8917_GPL1708")
`gene_symbol`	Logical. default is FALSE. If TRUE, gene symbol will be assigned to rownames. If some gene symbols were found to be duplicated, gene symbol and the corresponding probe id will be appended together.

Value

A `SummarizedExperiment` object fetched from ExperimentHub.

Examples

```
get_DoReMiTra_data("SE_Amundson_2008_ExVivo_GSE8917_GPL1708")
```

`list_DoReMiTra_datasets` *List all available DoReMiTra datasets with associated key metadata information*

Description

Returns a metadata dataframe of all datasets available in the DoReMiTra collection, including details such as title, organism, radiation type, experimental setting, and accession numbers. Can optionally display extended metadata fields.

Usage

```
list_DoReMiTra_datasets(show_all_fields = FALSE)
```

Arguments

`show_all_fields`	Logical. If TRUE, it returns all the metadata information

Value

A data.frame with metadata for each dataset

Examples

```
list_DoReMiTra_datasets()
```

`search_DoReMiTra_datasets`

Search DoReMiTra datasets by metadata filters

Description

Filters the available DoReMiTra datasets using metadata fields such as radiation type, organism, or experimental setting. This function helps narrow down datasets of interest before fetching them.

Usage

```
search_DoReMiTra_datasets(
  radiation_type = NULL,
  organism = NULL,
  exp_setting = NULL
)
```

Arguments

`radiation_type`	Character string (optional). Filter datasets by radiation type (e.g., "x-ray", "neutron").
`organism`	Character string (optional). Filter by organism (e.g., "Homo sapiens").
`exp_setting`	Character string (optional). Filter by experimental setting (e.g., "in vivo", "ex vivo").

Value

a vector with the names of the se objects matching the inclusion criteria. If none match, returns an empty vector with a message.

Examples

```
search_DoReMiTra_datasets()
```

`summarize_DoReMiTra_se`

Summarize the metadata of a SummarizedExperiment object from the DoReMiTra collection

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Description

#' Provides a concise overview of a `SummarizedExperiment` object from the DoReMiTra collection. Displays information such as the number of samples, metadata content, and key experimental conditions like radiation type, organism, and platform.

Usage

```
summarize_DoReMiTra_se(se)
```

Arguments

`se`	The name of the SE object as defined by the user

Value

A character string containing a essential information about the dataset metadata

Examples

```
se <- get_DoReMiTra_data("SE_Ghandhi_2018_InVivo_GSE84898_GPL13497")
summarize_DoReMiTra_se(se)
```

Index