Package 'DoReMiTra'

October 27, 2026

Title Orchestrating Blood Radiation Transcriptomic Data

Version 1.2.0

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

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.3

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

git_url https://git.bioconductor.org/packages/DoReMiTra

git_branch RELEASE_3_23

git_last_commit ab6e436

git_last_commit_date 2026-04-28

Repository Bioconductor 3.23

Date/Publication 2026-10-27

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`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", "Tissue")
)
```

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

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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

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Description

Returns a metadata dataframe of all datasets available in the DoReMiTra collection, including details such as title, organism, radiation type, experimental setting, author, 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()
```

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list_DoReMiTra_metadata_fields

List available metadata fields and their values in DoReMiTra

Description

This function displays the available metadata fields across all DoReMiTra datasets along with the unique values observed for each field. It facilitates intuitive dataset discovery and filtering.

Usage

```
list_DoReMiTra_metadata_fields()
```

Value

Invisibly returns a named list of metadata fields and their values.

Examples

```
list_DoReMiTra_metadata_fields()
```

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,
  author = 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").
author	Character string (optional). Filter by the author name

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*

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)
```

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