

# Package ‘DoReMiTra’

November 11, 2025

**Title** Orchestrating Blood Radiation Transcriptomic Data

**Version** 1.1.0

**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.

**License** MIT + file LICENSE

**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** devel

**git\_last\_commit** 6542a3e

**git\_last\_commit\_date** 2025-10-29

**Repository** Bioconductor 3.23

**Date/Publication** 2025-11-11

**Author** Ahmed Salah [aut, cre] (ORCID: <<https://orcid.org/0000-0001-7003-4466>>),  
Federico Marini [aut] (ORCID: <<https://orcid.org/0000-0003-3252-7758>>)

**Maintainer** Ahmed Salah <ahhassan@uni-mainz.de>

## Contents

|                                      |          |
|--------------------------------------|----------|
| compare_DoReMiTra_datasets . . . . . | 2        |
| DoReMiTra-pkg . . . . .              | 3        |
| get_all_DoReMiTra_datasets . . . . . | 3        |
| get_DoReMiTra_data . . . . .         | 4        |
| list_DoReMiTra_datasets . . . . .    | 4        |
| search_DoReMiTra_datasets . . . . .  | 5        |
| summarize_DoReMiTra_se . . . . .     | 6        |
| <b>Index</b>                         | <b>7</b> |

---

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-pkgDoReMiTra: *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.

## Author(s)

**Maintainer:** Ahmed Salah <ahhassan@uni-mainz.de> ([ORCID](#))

Authors:

- Federico Marini <marinif@uni-mainz.de> ([ORCID](#))

## 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 row-names. 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*

---

**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**

|                 |                                                  |
|-----------------|--------------------------------------------------|
| <code>se</code> | 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

## \* **internal**

DoReMiTra-pkg, [3](#)

compare\_DoReMiTra\_datasets, [2](#)

DoReMiTra (DoReMiTra-pkg), [3](#)

DoReMiTra-package (DoReMiTra-pkg), [3](#)

DoReMiTra-pkg, [3](#)

get\_all\_DoReMiTra\_datasets, [3](#)

get\_DoReMiTra\_data, [4](#)

list\_DoReMiTra\_datasets, [4](#)

search\_DoReMiTra\_datasets, [5](#)

summarize\_DoReMiTra\_se, [6](#)