

Package ‘meddra.read’

May 8, 2026

Title Load and Use 'MedDRA' Data for Clinical Trials

Version 0.0.1

Description 'MedDRA' data is used for defining adverse events in clinical studies. You can load and merge the data for use in categorizing the adverse events using this package. The package requires the data licensed from 'MedDRA' <<https://www.meddra.org/>>.

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Imports dplyr

Suggests spelling, testthat (>= 3.0.0)

Config/testthat/edition 3

Encoding UTF-8

RoxygenNote 7.3.2

URL <https://humanpred.github.io/meddra.read/>

Language en-US

NeedsCompilation no

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Repository CRAN

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join_meddra	<i>Combine together all of the MedDRA terms into a single data.frame</i>
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Description

Combine together all of the MedDRA terms into a single data.frame

Usage

```
join_meddra(data)
```

Arguments

data	MedDRA source data from read_meddra()
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Value

A data.frame with the "soc_code", "soc_name", "soc_abbrev", "hlgt_code", "hlgt_name", "hlt_code", "hlt_name", "pt_code", "pt_name", "pt_soc_code", "lft_code", "lft_name", and "lft_currency"

Examples

```
## Not run:
meddra_raw <- read_meddra("/path/to/meddra/distribution")
meddra_df <- join_meddra(meddra_raw)

## End(Not run)
```

read_meddra	<i>Read MedDRA datasets from the source MedDRA datasets</i>
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Description

Read MedDRA datasets from the source MedDRA datasets

Usage

```
read_meddra(directory)
```

Arguments

directory	the directory containing the MedAscii and SeqAscii directories
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Value

A list of data.frames for each file in the MedDRA source distribution

Examples

```
## Not run:  
read_meddra("/path/to/meddra/distribution")  
  
## End(Not run)
```

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