

# Package: meddra.read (via r-universe)

March 26, 2025

**Title** Load and Merge MedDRA Data for Clinical Trials

**Version** 0.0.0.9000

**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.

**License** MIT + file LICENSE

**Suggests** spelling, testthat (>= 3.0.0)

**Config/testthat/edition** 3

**Encoding** UTF-8

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.3.2

**Imports** dplyr

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

**Language** en-US

**Repository** <https://humanpred.r-universe.dev>

**RemoteUrl** <https://github.com/humanpred/meddra.read>

**RemoteRef** HEAD

**RemoteSha** 64a2d81209d71eb418ab14a29c8b2d10d8615c62

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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()

**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"

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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

**Value**

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

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