

# Package: multilevelmod (via r-universe)

July 2, 2024

**Title** Model Wrappers for Multi-Level Models

**Version** 1.0.0.9000

**Description** Bindings for hierarchical regression models for use with the 'parsnip' package. Models include longitudinal generalized linear models (Liang and Zeger, 1986) <[doi:10.1093/biomet/73.1.13](https://doi.org/10.1093/biomet/73.1.13)>, and mixed-effect models (Pinheiro and Bates) <[doi:10.1007/978-1-4419-0318-1\\_1](https://doi.org/10.1007/978-1-4419-0318-1_1)>.

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**URL** <https://github.com/tidymodels/multilevelmod>,  
<http://multilevelmod.tidymodels.org/>

**Depends** parsnip (>= 1.0.0), R (>= 3.5)

**Imports** dplyr, lme4, purrr, rlang, tibble, withr

**Suggests** covr, gee, ggplot2, knitr, nlme, rmarkdown, spelling, testthat (>= 3.0.0), tidymodels

**VignetteBuilder** knitr

**Config/Needs/website** tidymodels/tidymodels, tidyverse/tidytemplate

**Encoding** UTF-8

**Language** en-US

**LazyData** true

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.2.3

**Config/testthat/edition** 3

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

**RemoteUrl** <https://github.com/tidymodels/multilevelmod>

**RemoteRef** HEAD

**RemoteSha** 255bf73aa5bab3f6f8af34490e914c49544456fb

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longitudinal_counts	<i>Simulated longitudinal Poisson counts</i>
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### Description

Simulated longitudinal Poisson counts

### Details

These are simulated data of 100 subjects each with 10 time points and an additional numeric covariate. The linear predictor has a random standard normal intercept per subject, a time coefficient of 1.50, and a covariate coefficient of 0.25.

### Value

longitudinal\_counts  
a tibble

### Examples

```
data(longitudinal_counts)
str(longitudinal_counts)
```

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msa_data	<i>Measurement systems analysis data</i>
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### Description

Measurement systems analysis data

### Details

A biological assay (i.e. a lab test) was run on 56 separate samples twice. The goal is to measure what percentage of the total variation in the results is related to the measurement system and how much is attributable to the true systematic difference (sample-to-sample).

### Value

msa\_data a tibble

**Examples**

```
data(msa_data)
str(msa_data)
```

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riesby	<i>Imipramine longitudinal data</i>
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**Description**

Imipramine longitudinal data

**Details**

These data are from a longitudinal clinical trial for depression. The outcome is the change in depression scores week-to-week. The endogenous column is an indicator for whether the subject fit the WHO Depression Scale classification of endogenous. The imipramine and desipramine columns are measurements of plasma levels for both substances.

**Value**

riesby            a tibble

**Source**

Reisby, N., Gram, L.F., Bech, P. et al. Imipramine: Clinical effects and pharmacokinetic variability. *Psychopharmacology* 54, 263-272 (1977).

**Examples**

```
data(riesby)
str(riesby)
```

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