

# Package: missr (via r-universe)

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**Title** Classify Missing Data as MCAR, MAR, or MNAR

**Version** 1.0.1.9000

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**Description** Classify missing data as missing completely at random (MCAR), missing at random (MAR), or missing not at random (MNAR). This step is required before handling missing data (e.g. mean imputation) so that bias is not introduced. See Little (1988) <doi:10.1080/01621459.1988.10478722> for the statistical rationale for the methods used.

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**URL** <https://github.com/NoahHellen/missr>,  
<https://noahhellen.github.io/missr/>

**BugReports** <https://github.com/NoahHellen/missr/issues>

**Depends** R (>= 3.5)

**Imports** norm, tibble, lifecycle

**Suggests** knitr, rmarkdown, testthat (>= 3.0.0)

**VignetteBuilder** knitr

**Config/testthat/edition** 3

**Encoding** UTF-8

**Language** en-GB

**LazyData** true

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.3.2

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

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animalhealth	<i>Simulated animal health data (MCAR)</i>
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### Description

A toy dataset with heart rate data for various animals.

### Usage

animalhealth

### Format

A 200 x 2 data frame:

**animal** The animal of interest

**hear\_rate** The corresponding heart rate of the animal (bpm)

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companydata	<i>Simulated company data (MNAR)</i>
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### Description

A toy dataset with typical company metrics across various firms.

### Usage

companydata

**Format**

A 500 x 5 data frame:

- sales** Sales in the last fiscal year (USD, million)
- marketing\_spend** Marketing spend in last fiscal year (USD, million)
- product\_rating** Average rating across all products
- employees** Total employee count in last fiscal year
- gross\_profit** Gross profit in last fiscal year (USD, million)

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healthcheck	<i>Simulated health check data (MAR)</i>
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**Description**

A toy dataset with typical health check-up metrics for various individuals.

**Usage**

```
healthcheck
```

**Format**

A 200 x 5 data frame:

- bone\_mass** Bone mass of individual (kg)
- body\_fat** Body fat percentage of individual
- height** Height of individual (cm)
- age** Age of individual
- rbc** Red blood cell count of individual (million/mm<sup>3</sup>)

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mar	<i>Missing at random (MAR) test</i>
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**Description**

**[Stable]** `mar()` performs multiple logistic regressions to test for MAR. The null hypothesis for each is that the data are not MAR.

**Usage**

```
mar(data, debug = FALSE)
```

**Arguments**

data	A data frame.
debug	A logical value used only for unit testing.

**Details**

In the following, each column of  $M$  with missing data is regressed on  $D_{\text{obs}}$ . Each regression produces a vector of p-values (one for each variable in  $D_{\text{obs}}$ ). The smallest p-value is the most important. This is because missing data need only be dependent on one observed variable for the data to be MAR. If each reported smallest p-value is significant, the data is MAR. See `vignette("background")` for definitions of  $M$  and  $D_{\text{obs}}$ .

**Value**

A `tibble::tibble()`:

missing	Column of $M$ with missing data
p_value	Smallest p-value of the logistic regressions
explanatory	Variable corresponding to p_value
p_values	The p-values of the logistic regressions
variables	Variables corresponding to p_values
combined	Paired p_values and variables for easier interpretation

**Examples**

```
mar(healthcheck)
```

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mcar

*Little's missing completely at random (MCAR) test*


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**Description**

**[Stable]** `mcar()` performs Little's MCAR test to test for MCAR. The null hypothesis is that the data is MCAR.

**Usage**

```
mcar(data, debug = FALSE)
```

**Arguments**

data	A data frame.
debug	A logical value used only for unit testing.

**Details**

This function reproduces the  $d^2$  statistic in equation (5) from [1]. This statistic is used to test for MCAR. Comments reference variables from `vignette("background")` (in brackets) to improve readability and traceability.

**Value**

A `tibble::tibble()`:

<code>statistic</code>	The $d^2$ statistic
<code>degrees_freedom</code>	Degrees of freedom of chi-squared distribution
<code>p_val</code>	P-value of the test
<code>missing_patterns</code>	Number of missing patterns

**Note**

Code is adapted from `mcar_test()` from the `naniar` package using base R instead of the tidyverse.

**References**

[1] Little RJA. A Test of Missing Completely at Random for Multivariate Data with Missing Values. *Journal of the American Statistical Association*. 1988;83(404):1198-202.

**Examples**

```
mcar(pollutionlevels)
```

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mnar

*Missing not at random (MNAR) classification*

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**Description**

**[Stable]** `mnar()` presents the statistics from `mar()` and `mcar()`. If at least one p-value in `mar()` is not significant, and the p-value in `mcar()` is significant then the data is MNAR.

**Usage**

```
mnar(data)
```

**Arguments**

<code>data</code>	A data frame
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**Details**

There exists no formal test for MNAR data. This function therefore presents the statistics for the tests in `mar()` and `mcAR()`. If the results suggest the data is neither MAR nor MCAR, one can use process of elimination to deduce that the data is MNAR.

**Value**

A list:

<code>mcAR</code>	Results of Little's MCAR test
<code>mar</code>	Results of MAR test

**Examples**

```
mnar(companydata)
```

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<code>pollutionlevels</code>	<i>Simulated pollution level data (MCAR)</i>
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**Description**

A toy dataset with typical pollution level metrics for various settlements.

**Usage**

```
pollutionlevels
```

**Format**

A 200 x 4 data frame:

**light** Light pollution of settlement (mag/arcsec<sup>2</sup>)

**visual** Visual pollution of settlement (VPI)

**noise** Noise pollution of settlement (dB)

**air** Air pollution of settlement (AQI)

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`testscores`*Simulated test scores data*

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**Description**

A toy dataset with test scores of various students.

**Usage**

```
testscores
```

**Format**

A 200 x 2 data frame:

**id** The ID of the student

**score** The student's score in the test

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