

Package ‘missr’

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Title Classify Missing Data as MCAR, MAR, or MNAR

Version 1.0.1

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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](https://doi.org/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

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Contents

animalhealth	2
companydata	2
healthcheck	3
mar	3
mcar	4
mnar	5
pollutionlevels	6
testscores	7
Index	8

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)

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)

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/mm³)

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_obs*. Each regression produces a vector of p-values (one for each variable in *D_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_obs*.

Value

A `tibble::tibble()`:

missing	Column of <i>M</i> 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)
```

mcar	<i>Little's missing completely at random (MCAR) test</i>
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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 `nanian` 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)
```

mnar

Missing not at random (MNAR) classification

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)
```

<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/arcsec²)

visual Visual pollution of settlement (VPI)

noise Noise pollution of settlement (dB)

air Air pollution of settlement (AQI)

testscores	<i>Simulated test scores data</i>
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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

Index

* datasets

- animalhealth, [2](#)
- companydata, [2](#)
- healthcheck, [3](#)
- pollutionlevels, [6](#)
- testscores, [7](#)

animalhealth, [2](#)

companydata, [2](#)

healthcheck, [3](#)

mar, [3](#)

mar(), [5](#), [6](#)

mcar, [4](#)

mcar(), [5](#), [6](#)

mnar, [5](#)

pollutionlevels, [6](#)

testscores, [7](#)

tibble::tibble(), [4](#), [5](#)