

Package ‘MMRcaseselection’

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Type Package

Title Case Classification and Selection Based on Regression Results

Version 0.1.0

Depends R (>= 2.10)

Description Researchers doing a mixed-methods analysis (nested analysis as developed by Lieberman (2005) <doi:10.1017/S0003055405051762>) can use the package for the classification of cases and case selection using results of a linear regression. One can designate cases as typical, deviant, extreme and pathway case and use different case selection strategies for the choice of a case belonging to one of these types.

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Encoding UTF-8

LazyData true

Imports stats, ggplot2

RoxygenNote 7.1.0

URL <https://github.com/ingorohlfing/MMRcaseselection>

BugReports <https://github.com/ingorohlfing/MMRcaseselection>

Suggests knitr, rmarkdown

VignetteBuilder knitr

Language en-US

NeedsCompilation no

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extreme_on_x	<i>Extremeness of cases on an independent variable</i>
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Description

Extremeness of a case is calculated by the difference between a case's value on the independent variable and the variable's mean value.

Usage

```
extreme_on_x(lmobject = NULL, ind_var = NULL)
```

Arguments

lmobject	Object generated with <code>lm</code>
ind_var	Independent variable for which extremeness values should be calculated. Has to be entered as a character.

Details

Calculating the absolute value of the difference between the cases' values and the variable's mean value is proposed by Seawright, Jason (2016): The Case for Selecting Cases That Are Deviant or Extreme on the Independent Variable. *Sociological Methods & Research* 45 (3): 493-525. (<https://doi.org/10.1177/0049124116643556>)

Value

A dataframe with

- all variables in the linear model,
- absolute extremeness (absolute value of difference between variable score and mean value of variable),
- extremeness (difference between variable score and mean value of variable), which can be useful when the direction of extremeness is relevant.

The rows are ordered in decreasing order of the absolute extreme values.

Examples

```
df <- lm(mpg ~ disp + wt, data = mtcars)
extreme_on_x(df, "wt")
```

extreme_on_y

Extremeness of cases on the dependent variable

Description

Extremeness of a case is calculated by the difference between a case's value on the dependent variable and the variable's mean value.

Usage

```
extreme_on_y(lmobject)
```

Arguments

lmobject Object generated with `lm`

Details

Calculating the absolute value of the difference between the cases' values and the variable's mean value is proposed by Seawright, Jason (2016): The Case for Selecting Cases That Are Deviant or Extreme on the Independent Variable. *Sociological Methods & Research* 45 (3): 493-525. (<https://doi.org/10.1177/0049124116643556>)

Value

A dataframe with

- all variables in the linear model,
- absolute extremeness (absolute value of difference between variable score and mean value of variable),
- extremeness (difference between variable score and mean value of variable), which can be useful when the direction of extremeness is relevant.

The rows are ordered in decreasing order of the absolute extreme values.

Examples

```
df <- lm(mpg ~ disp + wt, data = mtcars)
extreme_on_y(df)
```

most_deviant

Identification of the most deviant case

Description

Identification of the most deviant case (= worst predicted case), based on regression estimates.

Usage

```
most_deviant(lmobject)
```

Arguments

lmobject Object generated with `lm`

Details

Proposed by Seawright, Jason and John Gerring (2008): Case Selection Techniques in Case Study Research: A Menu of Qualitative and Quantitative Options. *Political Research Quarterly* 61 (2): 294-308. (<https://journals.sagepub.com/doi/pdf/10.1177/1065912907313077>)

Value

The most deviant case with the largest absolute residual of all cases.

Examples

```
df <- lm(mpg ~ disp + wt, data = mtcars)
most_deviant(df)
```

most_overpredicted	<i>Identification of the most overpredicted case</i>
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Description

The case with the largest negative difference between the observed value and the predicted value on the outcome. Depending on the research question, there might be a specific interest in the case for which the model performs worst and yields a larger predicted value.

Usage

```
most_overpredicted(lmobject)
```

Arguments

lmobject Object generated with `lm`

Value

The most overpredicted case with the largest negative residual (the most negative residual).

Examples

```
df <- lm(mpg ~ disp + wt, data = mtcars)
most_overpredicted(df)
```

most_typical	<i>Identification of the most typical case</i>
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Description

The most typical case (= best predicted case) based on regression estimates.

Usage

```
most_typical(lmobject)
```

Arguments

lmobject Object generated with `lm`

Details

Proposed by Seawright, Jason and John Gerring (2008): Case Selection Techniques in Case Study Research: A Menu of Qualitative and Quantitative Options. *Political Research Quarterly* 61 (2): 294-308. (<https://journals.sagepub.com/doi/pdf/10.1177/1065912907313077>)

Value

The most typical case having the smallest absolute residual of all cases.

Examples

```
df <- lm(mpg ~ disp + wt, data = mtcars)
most_typical(df)
```

most_underpredicted *Identification of the most underpredicted case*

Description

The case with the largest positive difference between the observed value and the predicted value on the outcome. Depending on the research question, there might be a specific interest in the case for which the model performs worst and yields a smaller predicted value.

Usage

```
most_underpredicted(lmobject)
```

Arguments

lmobject Object generated with [lm](#)

Value

The most underpredicted case with the largest positive residual (the most positive residual).

Examples

```
df <- lm(mpg ~ disp + wt, data = mtcars)
most_underpredicted(df)
```

pathway	<i>Pathway case</i>
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Description

Calculation of pathway values, defined as the difference between residuals of full model and reduced model lacking the pathway variable. The larger the difference, the more a case qualifies as a pathway case suitable for the analysis of mechanisms.

Usage

```
pathway(full_model, reduced_model)
```

Arguments

full_model Full model including covariate of interest (= pathway variable)
reduced_model Reduced model excluding covariate of interest

Details

The difference between the absolute residuals of the full and reduced model follows the approach developed by Weller and Barnes (2014): *Finding Pathways: Mixed-Method Research for Studying Causal Mechanisms*. Cambridge: Cambridge University Press. <https://doi.org/10.1017/CB09781139644501>).

The calculation of the absolute difference between the full-model and reduced-model residuals, given a case's reduced-model residual is larger than its full-model residual, follows the proposal by Gerring (2007): Is There a (Viable) Crucial-Case Method? *Comparative Political Studies* 40 (3): 231-253. <https://journals.sagepub.com/doi/10.1177/0010414006290784>)

Value

A dataframe with

- all full model variables,
- full model residuals (full_resid),
- reduced model residuals (reduced_resid),
- pathway values following Weller/Barnes (pathway_wb),
- pathway values following Gerring (pathway_gvalue),
- variable showing whether Gerring's criterion for a pathway case is met (pathway_gstatus)

Examples

```
df_full <- lm(mpg ~ disp + wt, data = mtcars)
df_reduced <- lm(mpg ~ wt, data = mtcars)
pathway(df_full, df_reduced)
```

pathway_xvr	<i>Plot of residuals against pathway variable</i>
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Description

Plot of residuals against pathway variable

Usage

```
pathway_xvr(full_model, reduced_model, pathway_type)
```

Arguments

full_model	Full model including covariate of interest (= pathway variable)
reduced_model	Reduced model excluding covariate of interest
pathway_type	Type of pathway values. pathway_wb are pathway values proposed by Weller and Barnes. pathway_gvalue are values as calculated by Gerring.

Value

A plot of the chosen type of pathway values against the pathway variable created with [ggplot2](#).

Examples

```
df_full <- lm(mpg ~ disp + wt, data = mtcars)
df_reduced <- lm(mpg ~ wt, data = mtcars)
pathway_xvr(df_full, df_reduced, pathway_type = "pathway_wb")
```

predint	<i>Classification of cases as typical and deviant using a prediction interval.</i>
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Description

Cases are designated as typical (= well predicted) and deviant (= badly predicted) based on the prediction interval. The x% prediction interval represents the range that we expect to include x% of outcome values in repeated samples. For example, a 95% prediction interval ranging from 0-5 conveys that 95% of future outcome values will be in the range of 0-5. If the observed outcome is inside the prediction interval, the case is classified (or designated) as typical and as deviant otherwise.

Usage

```
predint(lmobject, piwidth = 0.95)
```


Arguments

lmodel Object generated with `lm`
piwidth Width of the prediction interval (default is 0.95).

Details

Proposed by Rohlfing, Ingo and Peter Starke (2013): Building on Solid Ground: Robust Case Selection in Multi-Method Research. *Swiss Political Science Review* 19 (4): 492-512. (<https://doi.org/10.1111/spsr.12052>)

Value

A dataframe with the observed outcome, fitted outcome, upper and lower bound of the % prediction interval and classification of cases as typical or deviant.

Examples

```
df <- lm(mpg ~ disp + wt, data = mtcars)
predint(df, piwidth = 0.9)
```

predint_plot *Plot of typical and deviant cases with prediction intervals*

Description

Presented in Rohlfing, Ingo and Peter Starke (2013): Building on Solid Ground: Robust Case Selection in Multi-Method Research. *Swiss Political Science Review* 19 (4): 492-512. (<https://doi.org/10.1111/spsr.12052>)

Usage

```
predint_plot(pred_df)
```

Arguments

pred_df A dataframe created with `predint`.

Value

A plot of the observed outcome against the fitted outcome with prediction intervals and case classifications. Created with `ggplot2`.

Examples

```
df <- lm(mpg ~ disp + wt, data = mtcars)
predint_status <- predint(df, piwidth = 0.9)
predint_plot(predint_status)
```

residstd	<i>Classification of cases as typical and deviant using the standard deviation of the residuals.</i>
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Description

The share of the standard deviation of the residuals is used to designate cases as typical or deviant.

Usage

```
residstd(lmobject, stdshare = 1)
```

Arguments

lmobject	Object generated with <code>lm</code>
stdshare	Share of standard deviation of residuals distinguishing between typical and deviant cases (default is 1).

Details

Proposed by Lieberman, Evan S. (2005): Nested Analysis as a Mixed-Method Strategy for Comparative Research. *American Political Science Review* 99 (3): 435-452. <https://doi.org/10.1017/S0003055405051762>.

Value

A dataframe with the observed outcome, fitted outcome, residual standard deviation and classification of cases as typical or deviant.

Examples

```
df <- lm(mpg ~ disp + wt, data = mtcars)
residstd(df, stdshare = 1)
```

residstd_plot	<i>Plot of typical and deviant cases based on residuals' standard deviation</i>
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Description

Plot of typical and deviant cases based on residuals' standard deviation

Usage

```
residstd_plot(resid_df)
```

Arguments

`resid_df` A dataframe created with `residstd`.

Value

A plot of the observed outcome against the fitted outcome with interval and case classifications.
Created with `ggplot2`.

Examples

```
df <- lm(mpg ~ disp + wt, data = mtcars)
residstd_status <- residstd(df, stdshare = 1)
residstd_plot(residstd_status)
```

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