Package ‘psycModel’

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Type Package

Title Integrated Toolkit for Psychological Analysis and Modeling in R

Version 0.4.0

Description A beginner-friendly R package for modeling in psychology or related field. It allows fitting models, plotting, checking goodness of fit, and model assumption violations all in one place. It also produces beautiful and easy-to-read output.

License GPL (>= 3)

URL `https://jasonmoy28.github.io/psycModel/`

Depends R (>= 3.2)

Imports dplyr, ggplot2, glue, insight, lavaan, lifecycle, lme4, lmerTest, parameters, patchwork, performance, psych, rlang (>= 0.1.2), stringr, tibble, tidyr, utils

Suggests correlation, covr, cowplot, fansi, ggrepel, GPArotation, gridExtra, interactions, knitr, nFactors, nlme, pagedown, qqplotr, rmarkdown, roxygen2, sandwich, see, semPlot, spelling, testthat (>= 3.0.0), tidyselect

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R topics documented:

`anova_plot` *ANOVA Plot*

Description

[Experimental]
Plot categorical variable with barplot. Continuous moderator are plotted at ± 1 SD from the mean.

Usage

```
anova_plot(model, predictor = NULL, graph_label_name = NULL)
```

Arguments

`model`	fitted model (usually `lm` or `aov` object)
`predictor`	predictor variable. Must specified for non-interaction plot and must not specify for interaction plot.
`graph_label_name`	vector or function. Vector should be passed in the form of `c(response_var, predict_var1, predict_var2, ...)`. Function should be passed as a switch function that return the label based on the name passed (e.g., a switch function)

Value

plot object

Examples

```
fit = iris %>% lm(data = ., Sepal.Length ~ Species)
anova_plot(fit,predictor = Species)
```

`cfa_groupwise` *Confirmatory Factor Analysis (groupwise)*

Description

[Stable]
This function will run N number of CFA where N = `length(group)`, and report the fit measures of CFA in each group. The function is intended to help you get a better understanding of which group has abnormal fit indicator

Usage

```
cfa_groupwise(data, ..., group, model = NULL, ordered = FALSE)
```

Arguments

`data`	data frame
`...`	CFA items. Support `dplyr::select()` syntax.
`group`	character. group variable. Support `dplyr::select()` syntax.
`model`	explicit `lavaan` model. Must be specify with `model = lavaan_model_syntax`. **[Experimental]**
`ordered`	logical. default is `FALSE`. If it is set to `TRUE`, lavaan will treat it as a ordinal variable and use `DWLS` instead of `ML`

Details

All argument must be explicitly specified. If not, all arguments will be treated as CFA items

Value

a `data.frame` with group-wise CFA result

Examples

```
# The example is used as the illustration of the function output only.
# It does not imply the data is appropriate for the analysis.
cfa_groupwise(
  data = lavaan::HolzingerSwineford1939,
  group = "school",
  x1:x3,
  x4:x6,
  x7:x9
)
```

`cfa_summary` *Confirmatory Factor Analysis*

Description

[Stable]
The function fits a CFA model using the `lavaan::cfa()`. Users can fit single and multiple factors CFA, and it also supports multilevel CFA (by specifying the group). Users can fit the model by passing the items using `dplyr::select()` syntax or an explicit lavaan model for more versatile usage. All arguments (except the CFA items) must be explicitly named (e.g., model = your-model; see example for inappropriate behavior).

Usage

```
cfa_summary(
  data,
  ...,
  model = NULL,
  group = NULL,
  ordered = FALSE,
  digits = 3,
  model_covariance = TRUE,
  model_variance = TRUE,
  plot = TRUE,
  group_partial = NULL,
  streamline = FALSE,
  quite = FALSE,
  return_result = FALSE
)
```

Arguments

`data`	data frame
`...`	CFA items. Multi-factor CFA items should be separated by comma (as different argument). See below for examples. Support `dplyr::select()` syntax.
`model`	explicit `lavaan` model. Must be specify with `model = lavaan_model_syntax`. **[Experimental]**
`group`	optional character. used for multi-level CFA. the nested variable for multilevel dataset (e.g., Country). Support `dplyr::select()` syntax.
`ordered`	Default is `FALSE`. If it is set to `TRUE`, `lavaan` will treat it as a ordinal variable and use `DWLS` instead of `ML`
`digits`	number of digits to round to
`model_covariance`	print model covariance. Default is `TRUE`
`model_variance`	print model variance. Default is `TRUE`
`plot`	print a path diagram. Default is `TRUE`
`group_partial`	Items for partial equivalence. The form should be c('DV =~ item1', 'DV =~ item2').
`streamline`	print streamlined output
`quite`	suppress printing output
`return_result`	If it is set to `TRUE`, it will return the `lavaan` model

Details

First, just like researchers have argued against p value of 0.05 is not a good cut-of, researchers have also argue against that fit indicies (more importantly, the cut-off criteria) are not completely representative of the goodness of fit. Nonetheless, you are required to report them if you are publishing an article anyway. I will summarize the general recommended cut-off criteria for CFA model below. Researchers consider models with CFI (Bentler, 1990) that is > 0.95 to be excellent fit (Hu & Bentler, 1999), and > 0.9 to be acceptable fit. Researchers considered a model is excellent fit if CFI > 0.95 (Hu & Bentler, 1999), RMSEA < 0.06 (Hu & Bentler, 1999), TLI > 0.95, SRMR < 0.08. The model is considered an acceptable fit if CFI > 0.9 and RMSEA < 0.08. I need some time to find all the relevant references, but this should be the general consensus.

Value

a `lavaan` object if return_result is `TRUE`

References

Hu, L., & Bentler, P. M. (1999). Cutoff criteria for fit indexes in covariance structure analysis: Conventional criteria versus new alternatives. Structural Equation Modeling, 6, 1–55. https://doi.org/10.1080/1070551990954011

Examples

```
# REMEMBER, YOU MUST NAMED ALL ARGUMENT EXCEPT THE CFA ITEMS ARGUMENT
# Fitting a multilevel single factor CFA model
fit <- cfa_summary(
  data = lavaan::HolzingerSwineford1939,
  x1:x3,
  x4:x6,
  x7:x9,
  group = "sex",
  model_variance = FALSE, # do not print the model_variance
  model_covariance = FALSE # do not print the model_covariance
)


# Fitting a CFA model by passing explicit lavaan model (equivalent to the above model)
# Note in the below function how I added `model = ` in front of the lavaan model.
# Similarly, the same rule apply for all arguments (e.g., `ordered = FALSE` instead of just `FALSE`)

fit <- cfa_summary(
  model = "visual  =~ x1 + x2 + x3",
  data = lavaan::HolzingerSwineford1939,
  quite = TRUE # silence all output
)

## Not run:
# This will fail because I did not add `model = ` in front of the lavaan model.
# Therefore,you must add the tag in front of all arguments
# For example, `return_result = 'model'` instaed of `model`
cfa_summary("visual  =~ x1 + x2 + x3
             textual =~ x4 + x5 + x6
             speed   =~ x7 + x8 + x9 ",
  data = lavaan::HolzingerSwineford1939
)

## End(Not run)
```

---

compare_fit *Comparison of Model Fit*

Description

[Stable]
Compare the fit indices of models (see below for model support)

Usage

```
compare_fit(
  ...,
  digits = 3,
```

```
  quite = FALSE,
  streamline = FALSE,
  return_result = FALSE
)
```

Arguments

`...`	model. If it is a `lavaan` object, it will try to compute the measurement invariance. Other model types will be passed to `performance::compare_performance()`.
`digits`	number of digits to round to
`quite`	suppress printing output
`streamline`	print streamlined output
`return_result`	If it is set to `TRUE`, it will return the the compare fit data frame.

Value

a `dataframe` with fit indices and change in fit indices

Examples

```
# lme model

fit1 <- lm_model(
  data = popular,
  response_variable = popular,
  predictor_var = c(sex, extrav)
)

fit2 <- lm_model(
  data = popular,
  response_variable = popular,
  predictor_var = c(sex, extrav),
  two_way_interaction_factor = c(sex, extrav)
)

compare_fit(fit1, fit2)

# see ?measurement_invariance for measurement invariance example
```

`cor_test` *Correlation table*

Description

[Stable]
This function uses the `correlation::correlation()` to generate the correlation table.

Usage

```
cor_test(
  data,
  cols,
  ...,
  digits = 3,
  method = "pearson",
  p_adjust = "holm",
  streamline = FALSE,
  quite = FALSE,
  return_result = FALSE
)
```

Arguments

`data`	data frame
`cols`	correlation items. Support `dplyr::select()` syntax.
`...`	additional arguments passed to correlation::correlation(). See ?correlation::correlation. Note that the return data.frame from correlation::correlation() must contains `r` and `p` (e.g., passing `baysesian = TRUE` will not work)
`digits`	number of digits to round to
`method`	Default is "pearson". Options are "kendall", "spearman","biserial", "polychoric", "tetrachoric", "biweight", "distance", "percentage", "blomqvist", "hoeffding", "gamma", "gaussian","shepherd", or "auto". See ?correlation::correlation for detail
`p_adjust`	Default is "holm". Options are "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "somers" or "none". See ?stats::p.adjust for more detail
`streamline`	print streamlined output.
`quite`	suppress printing output
`return_result`	If it is set to `TRUE`, it will return the data frame of the correlation table

Value

a `data.frame` of the correlation table

Examples

```
cor_test(iris, where(is.numeric))
```

`cronbach_alpha` *Cronbach alpha* **[Stable]**

Description

Computing the Cronbach alphas for multiple factors.

Usage

```
cronbach_alpha(..., data, var_name, return_result = FALSE, group = NULL)
```

Arguments

`...`	Items. Group each latent factors using c() with when computing Cronbach alpha for 2+ factors (see example below)
`data`	`data.frame`. Must specify
`var_name`	character or a vector of characters. The order of `var_name` must be same as the order of the `...`
`return_result`	If it is set to `TRUE`, it will return a `dataframe` object
`group`	optional character. Specify this argument for computing Cronbach alpha for group separetely

Value

a `data.frame` object if return_result is `TRUE`

Examples

```
cronbach_alpha(
  data = lavaan::HolzingerSwineford1939,
  var_name = c('Visual','Textual','Speed'),
  c(x1,x2,x3), # one way to pass the items of a factor is by wrapping it with c()
  x4:x6, # another way to pass the items is use tidyselect syntax
  x7:x9)
```

`descriptive_table` *Descriptive Statistics Table*

Description

[Stable]
This function generates a table of descriptive statistics (mainly using `psych::describe()`) and or a correlation table. User can export this to a csv file (optionally, using the file_path argument). Users can open the csv file with MS Excel then copy and paste the table into MS Word table.

Usage

```
descriptive_table(
  data,
  cols,
  ...,
  digits = 3,
  descriptive_indicator = c("mean", "sd", "cor"),
  file_path = NULL,
  streamline = FALSE,
  quite = FALSE,
  return_result = FALSE
)
```

Arguments

`data`	`data.frame`
`cols`	column(s) need to be included in the table. Support `dplyr::select()` syntax.
`...`	additional arguments passed to cor_test. See ?cor_test.
`digits`	number of digit for the descriptive table
`descriptive_indicator`	Default is mean, sd, cor. Options are missing (missing value count), non_missing (non-missing value count), cor (correlation table), n, mean, sd, median, trimmed (trimmed mean), median, mad (median absolute deviation from the median), min, max, range, skew, kurtosis, se (standard error)
`file_path`	file path for export. The function will implicitly pass this argument to the write.csv(file = file_path)
`streamline`	print streamlined output
`quite`	suppress printing output
`return_result`	If it is set to `TRUE`, it will return the data frame of the descriptive table

Value

a `data.frame` of the descriptive table

Examples

```
descriptive_table(iris, cols = where(is.numeric)) # all numeric columns

descriptive_table(iris,
  cols = where(is.numeric),
  # get missing count, non-missing count, and mean & sd & correlation table
  descriptive_indicator = c("missing", "non_missing", "mean", "sd", "cor")
)
```

`efa_summary` *Exploratory Factor Analysis*

Description

[Stable]
The function is used to fit a exploratory factor analysis model. It will first find the optimal number of factors using parameters::n_factors. Once the optimal number of factor is determined, the function will fit the model using `psych::fa()`. Optionally, you can request a post-hoc CFA model based on the EFA model which gives you more fit indexes (e.g., CFI, RMSEA, TLI)

Usage

```
efa_summary(
  data,
  cols,
  rotation = "varimax",
  optimal_factor_method = FALSE,
  efa_plot = TRUE,
  digits = 3,
  n_factor = NULL,
  post_hoc_cfa = FALSE,
  quite = FALSE,
  streamline = FALSE,
  return_result = FALSE
)
```

Arguments

`data`	`data.frame`
`cols`	columns. Support `dplyr::select()` syntax.
`rotation`	the rotation to use in estimation. Default is 'oblimin'. Options are 'none', 'varimax', 'quartimax', 'promax', 'oblimin', or 'simplimax'
`optimal_factor_method`	Show a summary of the number of factors by optimization method (e.g., BIC, VSS complexity, Velicer's MAP)
`efa_plot`	show explained variance by number of factor plot. default is `TRUE`.
`digits`	number of digits to round to
`n_factor`	number of factors for EFA. It will bypass the initial optimization algorithm, and fit the EFA model using this specified number of factor
`post_hoc_cfa`	a CFA model based on the extracted factor
`quite`	suppress printing output
`streamline`	print streamlined output
`return_result`	If it is set to `TRUE` (default is `FALSE`), it will return a `fa` object from `psych`

Value

a `fa` object from `psych`

Examples

```
efa_summary(lavaan::HolzingerSwineford1939, starts_with("x"), post_hoc_cfa = TRUE)
```

`get_interaction_term` *get interaction term*

Description

get interaction term

Usage

```
get_interaction_term(model)
```

Arguments

`model`	model

Value

a list with predict vars names

`get_predict_df` *get factor df to combine with mean_df*

Description

get factor df to combine with mean_df

Usage

```
get_predict_df(data)
```

Arguments

`data`	data

Value

factor_df

`glme_model` *Generalized Linear Mixed Effect Model*

Description

[Experimental]
Fit a generalized linear mixed effect model using `lme4::glmer()`. This function is still in early development stage.

Usage

```
glme_model(
  data,
  model = NULL,
  response_variable,
  random_effect_factors = NULL,
  non_random_effect_factors = NULL,
  family,
  two_way_interaction_factor = NULL,
  three_way_interaction_factor = NULL,
  id,
  estimation_method = "REML",
  opt_control = "bobyqa",
  na.action = stats::na.omit,
  quite = FALSE
)
```

Arguments

`data`	`data.frame`
`model`	`lme4` model syntax. Support more complicated model. Note that model_summary will only return fixed effect estimates. This is not tested. **[Experimental]**
`response_variable`	DV (i.e., outcome variable / response variable). Length of 1. Support `dplyr::select()` syntax.
`random_effect_factors`	random effect factors (level-1 variable for HLM people) Factors that need to estimate fixed effect and random effect (i.e., random slope / varying slope based on the id). Support `dplyr::select()` syntax.
`non_random_effect_factors`	non-random effect factors (level-2 variable for HLM people). Factors only need to estimate fixed effect. Support `dplyr::select()` syntax.
`family`	a GLM family. It will passed to the family argument in glmer. See `?glmer` for possible options.

`two_way_interaction_factor`	two-way interaction factors. You need to pass 2+ factor. Support `dplyr::select()` syntax.
`three_way_interaction_factor`	three-way interaction factor. You need to pass exactly 3 factors. Specifying three-way interaction factors automatically included all two-way interactions, so please do not specify the two_way_interaction_factor argument. Support `dplyr::select()` syntax.
`id`	the nesting variable (e.g. group, time). Length of 1. Support `dplyr::select()` syntax.
`estimation_method`	character. `ML` or `REML` default to `REML`.
`opt_control`	character. default is bobyqa. See `?lme4::glmerControl` for more options.
`na.action`	default is `stats::na.omit`. Another common option is `na.exclude`
`quite`	suppress printing output

Value

An object of class `glmerMod` representing the linear mixed-effects model fit.

---

glm_model *Generalized Linear Regression*

Description

[Experimental]
Fit a generalized linear regression using `glm()`. This function is still in early development stage.

Usage

```
glm_model(
  data,
  response_variable,
  predictor_variable,
  two_way_interaction_factor = NULL,
  three_way_interaction_factor = NULL,
  family,
  quite = FALSE
)
```

Arguments

`data`	`data.frame`
`response_variable`	response variable. Support `dplyr::select()` syntax.

`predictor_variable`	predictor variable. Support `dplyr::select()` syntax.
`two_way_interaction_factor`	two-way interaction factors. You need to pass 2+ factor. Support `dplyr::select()` syntax.
`three_way_interaction_factor`	three-way interaction factor. You need to pass exactly 3 factors. Specifying three-way interaction factors automatically included all two-way interactions, so please do not specify the two_way_interaction_factor argument. Support `dplyr::select()` syntax.
`family`	a GLM family. It will passed to the family argument in glmer. See `?glmer` for possible options.
`quite`	suppress printing output

Value

an object class of `glm` representing the linear regression fit

Examples

```
fit <- glm_model(
  response_variable = incidence,
  predictor_variable = period,
  family = "poisson", # or you can enter as poisson(link = 'log'),
  data = lme4::cbpp
)
```

`html_to_pdf` *Convert HTML to PDF*

Description

[Experimental]
This is a helper function for knitting Rmd. Due to technological limitation, the output cannot knit to PDF in Rmd directly (the problem is with the latex engine printing unicode character). Therefore, to bypass this problem, you will first need to knit to html file first, then use this function to convert it to a PDF file.

Usage

```
html_to_pdf(file_path = NULL, dir = NULL, scale = 1, render_exist = FALSE)
```

Arguments

`file_path`	file path to the HTML file (can be relative if you are in a R project)
`dir`	file path to the directory of all HTML files (can be relative if you are in a R project)
`scale`	the scale of the PDF
`render_exist`	overwrite exist PDF. Default is `FALSE`

Value

no return value

Examples

```
## Not run:
html_to_pdf(file_path = "html_name.html")
# all HTML files in the my_html_folder will be converted
html_to_pdf(dir = "Users/Desktop/my_html_folder")

## End(Not run)
```

`interaction_plot` *Interaction plot* **[Stable]** *The function creates a two-way or three-way interaction plot. It will creates a plot with ± 1 SD from the mean of the independent variable. See below for supported model. I recommend using concurrently with* `lm_model()`, `lme_model()`.

Description

Interaction plot **[Stable]**
The function creates a two-way or three-way interaction plot. It will creates a plot with ± 1 SD from the mean of the independent variable. See below for supported model. I recommend using concurrently with `lm_model()`, `lme_model()`.

Usage

```
interaction_plot(
  model,
  data = NULL,
  graph_label_name = NULL,
  cateogrical_var = NULL,
  y_lim = NULL,
  plot_color = FALSE
)
```

Arguments

`model`	object from `lme`, `lme4`, `lmerTest` object.
`data`	data frame. If the function is unable to extract data frame from the object, then you may need to pass it directly
`graph_label_name`	vector of length 4 or a switch function (see ?two_way_interaction_plot example). Vector should be passed in the form of c(response_var, predict_var1, predict_var2, predict_var3).

`cateogrical_var`	list. Specify the upper bound and lower bound directly instead of using ± 1 SD from the mean. Passed in the form of `list(var_name1 = c(upper_bound1, lower_bound1),var_name2 = c(upper_bound2, lower_bound2))`
`y_lim`	the plot's upper and lower limit for the y-axis. Length of 2. Example: `c(lower_limit, upper_limit)`
`plot_color`	default if `FALSE`. Set to `TRUE` if you want to plot in color

Value

a `ggplot` object

Examples

```
lm_fit_2 <- lm(Sepal.Length ~ Sepal.Width + Petal.Length +
  Sepal.Width*Petal.Length, data = iris)

interaction_plot(lm_fit_2)

lm_fit_3 <- lm(Sepal.Length ~ Sepal.Width + Petal.Length + Petal.Width +
  Sepal.Width*Petal.Length:Petal.Width, data = iris)

interaction_plot(lm_fit_3)
```

`knit_to_Rmd` *Knit Rmd Files Instruction*

Description

This is a helper function that instruct users of the package how to knit a R Markdown (Rmd) files

Usage

```
knit_to_Rmd()
```

Value

no return value

Examples

```
knit_to_Rmd()
```

`label_name` *get label name*

Description

get label name

Usage

```
label_name(
  graph_label_name,
  response_var_name,
  predict_var1_name,
  predict_var2_name,
  predict_var3_name
)
```

Arguments

`graph_label_name`	label name
`response_var_name`	outcome variable name
`predict_var1_name`	predictor 1 name
`predict_var2_name`	predictor 2 name
`predict_var3_name`	predictor 3 name

Value

vector of var name

`lme_model` *Linear Mixed Effect Model*

Description

[Stable]
Fit a linear mixed effect model (i.e., hierarchical linear model, multilevel linear model) using the `nlme::lme()` or the `lmerTest::lmer()` function. Linear mixed effect model is used to explore the effect of continuous / categorical variables in predicting a normally distributed continuous variable.

Usage

```
lme_model(
  data,
  model = NULL,
  response_variable,
  random_effect_factors = NULL,
  non_random_effect_factors = NULL,
  two_way_interaction_factor = NULL,
  three_way_interaction_factor = NULL,
  id,
  estimation_method = "REML",
  opt_control = "bobyqa",
  na.action = stats::na.omit,
  use_package = "lmerTest",
  quite = FALSE
)
```

Arguments

`data`	`data.frame`
`model`	`lme4` model syntax. Support more complicated model. Note that model_summary will only return fixed effect estimates.
`response_variable`	DV (i.e., outcome variable / response variable). Length of 1. Support `dplyr::select()` syntax.
`random_effect_factors`	random effect factors (level-1 variable for HLM people) Factors that need to estimate fixed effect and random effect (i.e., random slope / varying slope based on the id). Support `dplyr::select()` syntax.
`non_random_effect_factors`	non-random effect factors (level-2 variable for HLM people). Factors only need to estimate fixed effect. Support `dplyr::select()` syntax.
`two_way_interaction_factor`	two-way interaction factors. You need to pass 2+ factor. Support `dplyr::select()` syntax.
`three_way_interaction_factor`	three-way interaction factor. You need to pass exactly 3 factors. Specifying three-way interaction factors automatically included all two-way interactions, so please do not specify the two_way_interaction_factor argument. Support `dplyr::select()` syntax.
`id`	the nesting variable (e.g. group, time). Length of 1. Support `dplyr::select()` syntax.
`estimation_method`	character. `ML` or `REML` default to `REML`.
`opt_control`	default is `optim` for `lme` and `bobyqa` for `lmerTest`
`na.action`	default is `stats::na.omit`. Another common option is `na.exclude`

`use_package`	Default is `lmerTest`. Only available for linear mixed effect model. Options are `nlme`, `lmerTest`, or `lme4('lme4` return similar result as `lmerTest` except the return model)
`quite`	suppress printing output

Details

Here is a little tip. If you are using generic selecting syntax (e.g., contains() or start_with()), you don’t need to remove the response variable and the id from the factors. It will be automatically remove. For example, if you have x1:x9 as your factors. You want to regress x2:x8 on x1. Your probably pass something like response_variable = x1, random_effect_factors = c(contains(’x’),-x1) to the function. However, you don’t need to do that, you can just pass random_effect_factors = c(contains(’x’)) to the function since it will automatically remove the response variable from selection.

Value

an object representing the linear mixed-effects model fit (it maybe an object from `lme` or `lmer` depending of the package you use)

Examples

```
# two-level model with level-1 and level-2 variable with random intercept and random slope
fit1 <- lme_model(
  data = popular,
  response_variable = popular,
  random_effect_factors = c(extrav, sex),
  non_random_effect_factors = texp,
  id = class
)


# added two-way interaction factor
fit2 <- lme_model(
  data = popular,
  response_variable = popular,
  random_effect_factors = c(extrav, sex),
  non_random_effect_factors = texp,
  two_way_interaction_factor = c(extrav, texp),
  id = class
)

# pass a explicit lme model (I don't why you want to do that, but you can)
lme_fit <- lme_model(
  model = "popular ~ extrav*texp + (1 + extrav | class)",
  data = popular
)
```

`lme_multilevel_model_summary`

Model Summary for Mixed Effect Model

Description

[Stable]
An integrated function for fitting a multilevel linear regression (also known as hierarchical linear regression).

Usage

```
lme_multilevel_model_summary(
  data,
  model = NULL,
  response_variable = NULL,
  random_effect_factors = NULL,
  non_random_effect_factors = NULL,
  two_way_interaction_factor = NULL,
  three_way_interaction_factor = NULL,
  family = NULL,
  cateogrical_var = NULL,
  id = NULL,
  graph_label_name = NULL,
  estimation_method = "REML",
  opt_control = "bobyqa",
  na.action = stats::na.omit,
  model_summary = TRUE,
  interaction_plot = TRUE,
  y_lim = NULL,
  plot_color = FALSE,
  digits = 3,
  use_package = "lmerTest",
  simple_slope = FALSE,
  assumption_plot = FALSE,
  quite = FALSE,
  streamline = FALSE,
  return_result = FALSE
)
```

Arguments

`data`	`data.frame`
`model`	`lme4` model syntax. Support more complicated model structure from `lme4`. It is not well-tested to ensure accuracy **[Experimental]**

`response_variable`	DV (i.e., outcome variable / response variable). Length of 1. Support `dplyr::select()` syntax.
`random_effect_factors`	random effect factors (level-1 variable for HLM from a HLM perspective) Factors that need to estimate fixed effect and random effect (i.e., random slope / varying slope based on the id). Support `dplyr::select()` syntax.
`non_random_effect_factors`	non-random effect factors (level-2 variable from a HLM perspective). Factors only need to estimate fixed effect. Support `dplyr::select()` syntax.
`two_way_interaction_factor`	two-way interaction factors. You need to pass 2+ factor. Support `dplyr::select()` syntax.
`three_way_interaction_factor`	three-way interaction factor. You need to pass exactly 3 factors. Specifying three-way interaction factors automatically included all two-way interactions, so please do not specify the two_way_interaction_factor argument. Support `dplyr::select()` syntax.
`family`	a GLM family. It will passed to the family argument in glmer. See ?`glmer` for possible options. **[Experimental]**
`cateogrical_var`	list. Specify the upper bound and lower bound directly instead of using ± 1 SD from the mean. Passed in the form of `list(var_name1 = c(upper_bound1, lower_bound1),var_name2 = c(upper_bound2, lower_bound2))`
`id`	the nesting variable (e.g. group, time). Length of 1. Support `dplyr::select()` syntax.
`graph_label_name`	optional vector or function. vector of length 2 for two-way interaction graph. vector of length 3 for three-way interaction graph. Vector should be passed in the form of c(response_var, predict_var1, predict_var2, ...). Function should be passed as a switch function (see ?two_way_interaction_plot for an example)
`estimation_method`	character. `ML` or `REML` default is `REML`.
`opt_control`	default is `optim` for `lme` and `bobyqa` for `lmerTest`.
`na.action`	default is `stats::na.omit`. Another common option is `na.exclude`
`model_summary`	print model summary. Required to be `TRUE` if you want `assumption_plot`.
`interaction_plot`	generate interaction plot. Default is `TRUE`
`y_lim`	the plot's upper and lower limit for the y-axis. Length of 2. Example: `c(lower_limit, upper_limit)`
`plot_color`	If it is set to `TRUE` (default is `FALSE`), the interaction plot will plot with color.
`digits`	number of digits to round to
`use_package`	Default is `lmerTest`. Only available for linear mixed effect model. Options are `nlme`, `lmerTest`, or `lme4`(`'lme4` return similar result as `lmerTest` except the return model)

`simple_slope`	Slope estimate at ± 1 SD and the mean of the moderator. Uses `interactions::sim_slope()` in the background.
`assumption_plot`	Generate an panel of plots that check major assumptions. It is usually recommended to inspect model assumption violation visually. In the background, it calls `performance::check_model()`.
`quite`	suppress printing output
`streamline`	print streamlined output.
`return_result`	If it is set to `TRUE` (default is `FALSE`), it will return the `model`, `model_summary`, and `plot` (`plot` if the interaction term is included)

Value

a list of all requested items in the order of model, model_summary, interaction_plot, simple_slope

Examples

```
fit <- lme_multilevel_model_summary(
  data = popular,
  response_variable = popular,
  random_effect_factors = NULL, # you can add random effect predictors here
  non_random_effect_factors = c(extrav,texp),
  two_way_interaction_factor = NULL, # you can add two-way interaction plot here
  graph_label_name = NULL, #you can also change graph lable name here
  id = class,
  simple_slope = FALSE, # you can also request simple slope estimate
  assumption_plot = FALSE, # you can also request assumption plot
  plot_color = FALSE, # you can also request the plot in color
  streamline = FALSE # you can change this to get the least amount of info
)
```

`lm_model` *Linear Regressions / ANOVA / ANCOVA*

Description

[Stable]
Fit a linear regression using `lm()`. Linear regression is used to explore the effect of continuous variables / categorical variables in predicting a normally-distributed continuous variables.

Usage

```
lm_model(
  data,
  response_variable,
  predictor_variable,
```

```
  two_way_interaction_factor = NULL,
  three_way_interaction_factor = NULL,
  quite = FALSE
)
```

Arguments

`data`	`data.frame`
`response_variable`	response variable. Support `dplyr::select()` syntax.
`predictor_variable`	predictor variable. Support `dplyr::select()` syntax. It will automatically remove the response variable from predictor variable, so you can use `contains()` or `start_with()` safely.
`two_way_interaction_factor`	two-way interaction factors. You need to pass 2+ factor. Support `dplyr::select()` syntax.
`three_way_interaction_factor`	three-way interaction factor. You need to pass exactly 3 factors. Specifying three-way interaction factors automatically included all two-way interactions, so please do not specify the two_way_interaction_factor argument. Support `dplyr::select()` syntax.
`quite`	suppress printing output

Value

an object class of `lm` representing the linear regression fit

Examples

```
fit <- lm_model(
  data = iris,
  response_variable = "Sepal.Length",
  predictor_variable = tidyselect::everything(),
  two_way_interaction_factor = c(Sepal.Width, Species)
)
```

`lm_model_summary` *Model Summary for Linear Regression*

Description

[Stable]
An integrated function for fitting a linear regression model.

Usage

```
lm_model_summary(
  data,
  response_variable = NULL,
  predictor_variable = NULL,
  two_way_interaction_factor = NULL,
  three_way_interaction_factor = NULL,
  family = NULL,
  cateogrical_var = NULL,
  graph_label_name = NULL,
  model_summary = TRUE,
  interaction_plot = TRUE,
  y_lim = NULL,
  plot_color = FALSE,
  digits = 3,
  simple_slope = FALSE,
  assumption_plot = FALSE,
  quite = FALSE,
  streamline = FALSE,
  return_result = FALSE
)
```

Arguments

`data`	`data.frame`
`response_variable`	DV (i.e., outcome variable / response variable). Length of 1. Support `dplyr::select()` syntax.
`predictor_variable`	IV. Support `dplyr::select()` syntax.
`two_way_interaction_factor`	two-way interaction factors. You need to pass 2+ factor. Support `dplyr::select()` syntax.
`three_way_interaction_factor`	three-way interaction factor. You need to pass exactly 3 factors. Specifying three-way interaction factors automatically included all two-way interactions, so please do not specify the two_way_interaction_factor argument. Support `dplyr::select()` syntax.
`family`	a GLM family. It will passed to the family argument in glm. See `?glm` for possible options. **[Experimental]**
`cateogrical_var`	list. Specify the upper bound and lower bound directly instead of using ± 1 SD from the mean. Passed in the form of `list(var_name1 = c(upper_bound1, lower_bound1),var_name2 = c(upper_bound2, lower_bound2))`
`graph_label_name`	optional vector or function. vector of length 2 for two-way interaction graph. vector of length 3 for three-way interaction graph. Vector should be passed in

	the form of c(response_var, predict_var1, predict_var2, ...). Function should be passed as a switch function (see ?two_way_interaction_plot for an example)
`model_summary`	print model summary. Required to be `TRUE` if you want `assumption_plot`.
`interaction_plot`	generate the interaction plot. Default is `TRUE`
`y_lim`	the plot's upper and lower limit for the y-axis. Length of 2. Example: `c(lower_limit, upper_limit)`
`plot_color`	If it is set to `TRUE` (default is `FALSE`), the interaction plot will plot with color.
`digits`	number of digits to round to
`simple_slope`	Slope estimate at +1/-1 SD and the mean of the moderator. Uses `interactions::sim_slope()` in the background.
`assumption_plot`	Generate an panel of plots that check major assumptions. It is usually recommended to inspect model assumption violation visually. In the background, it calls `performance::check_model()`
`quite`	suppress printing output
`streamline`	print streamlined output
`return_result`	If it is set to `TRUE` (default is `FALSE`), it will return the `model`, `model_summary`, and `plot` (if the interaction term is included)

Value

a list of all requested items in the order of model, model_summary, interaction_plot, simple_slope

Examples

```
fit <- lm_model_summary(
  data = iris,
  response_variable = "Sepal.Length",
  predictor_variable = tidyselect::everything(),
  two_way_interaction_factor = c(Sepal.Width, Species),
  interaction_plot = FALSE, # you can also request the interaction plot
  simple_slope = FALSE, # you can also request simple slope estimate
  assumption_plot = FALSE, # you can also request assumption plot
  streamline = FALSE #you can change this to get the least amount of info
)
```

`measurement_invariance` *Measurement Invariance*

Description

[Stable]
Compute the measurement invariance model (i.e., measurement equivalence model) using multi-group confirmatory factor analysis (MGCFA; Jöreskog, 1971). This function uses the lavaan::cfa() in the backend. Users can run the configural-metric or the configural-metric-scalar comparisons (see below for detail instruction). All arguments (except the CFA items) must be explicitly named (like model = your-model; see example for inappropriate behavior).

Usage

```
measurement_invariance(
  data,
  ...,
  model = NULL,
  group,
  ordered = FALSE,
  group_partial = NULL,
  invariance_level = "scalar",
  digits = 3,
  quite = FALSE,
  streamline = FALSE,
  return_result = FALSE
)
```

Arguments

`data`	`data.frame`
`...`	CFA items. Multi-factor CFA items should be separated by comma (as different argument). See below for examples. Support `dplyr::select()` syntax.
`model`	explicit `lavaan` model. Must be specify with `model = lavaan_model_syntax`. **[Experimental]**
`group`	the nested variable for multilevel dataset (e.g., Country). Support `dplyr::select()` syntax.
`ordered`	Default is `FALSE`. If it is set to `TRUE`, `lavaan` will treat it as a ordinal variable and use `DWLS` instead of `ML`
`group_partial`	items for partial equivalence. The form should be c('DV =~ item1', 'DV =~ item2'). See details for recommended practice.
`invariance_level`	"metric" or "scalar". Default is 'metric'. Set as 'metric' for configural-metric comparison, and set as 'scalar' for configural-metric-scalar comparison.
`digits`	number of digits to round to
`quite`	suppress printing output except the model summary.
`streamline`	print streamlined output
`return_result`	If it is set to `TRUE`, it will return a data frame of the fit measure summary

Details

Chen (2007) suggested that change in CFI <= |-0.010| supplemented by RMSEA <= 0.015 indicate non-invariance when sample sizes were equal across groups and larger than 300 in each group (Chen, 2007). And, Chen (2007) suggested that change in CFI <= |-0.005| and change in RMSEA <= 0.010 for unequal sample size with each group smaller than 300. For SRMR, Chen (2007) recommend change in SRMR < 0.030 for metric-invariance and change in SRMR < 0.015 for scalar-invariance. For large group size, Rutowski & Svetina (2014) recommended a more liberal cut-off for metric non-invariance for CFI (change in CFI <= |-0.020|) and RMSEA (RMSEA <= 0.030). However, this more liberal cut-off DOES NOT apply to testing scalar non-invariance. If measurement-invariance is not achieved, some researchers suggesting partial invariance is acceptable (by releasing the constraints on some factors). For example, Steenkamp and Baumgartner (1998) suggested that ideally more than half of items on a factor should be invariant. However, it is important to note that no empirical studies were cited to support the partial invariance guideline (Putnick & Bornstein, 2016).

Value

a `data.frame` of the fit measure summary

References

Chen, F. F. (2007). Sensitivity of Goodness of Fit Indexes to Lack of Measurement Invariance. Structural Equation Modeling: A Multidisciplinary Journal, 14(3), 464–504. https://doi.org/10.1080/10705510701301834

Jöreskog, K. G. (1971). Simultaneous factor analysis in several populations. Psychometrika, 36(4), 409-426.

Putnick, D. L., & Bornstein, M. H. (2016). Measurement Invariance Conventions and Reporting: The State of the Art and Future Directions for Psychological Research. Developmental Review: DR, 41, 71–90. https://doi.org/10.1016/j.dr.2016.06.004

Rutkowski, L., & Svetina, D. (2014). Assessing the Hypothesis of Measurement Invariance in the Context of Large-Scale International Surveys. Educational and Psychological Measurement, 74(1), 31–57. https://doi.org/10.1177/0013164413498257

Steenkamp, J.-B. E. M., & Baumgartner, H. (n.d.). Assessing Measurement Invariance in Cross-National Consumer Research. JOURNAL OF CONSUMER RESEARCH, 13.

Examples

```
# REMEMBER, YOU MUST NAMED ALL ARGUMENT EXCEPT THE CFA ITEMS ARGUMENT
# Fitting a multiple-factor measurement invariance model by passing items.
measurement_invariance(
  x1:x3,
  x4:x6,
  x7:x9,
  data = lavaan::HolzingerSwineford1939,
  group = "school",
  invariance_level = "scalar" # you can change this to metric
)

# Fitting measurement invariance model by passing explicit lavaan model
```

```
# I am also going to only test for metric invariance instead of the default scalar invariance

measurement_invariance(
  model = "visual  =~ x1 + x2 + x3;
           textual =~ x4 + x5 + x6;
           speed   =~ x7 + x8 + x9",
  data = lavaan::HolzingerSwineford1939,
  group = "school",
  invariance_level = "metric"
)


## Not run:
# This will fail because I did not add `model = ` in front of the lavaan model.
# Therefore,you must add the tag in front of all arguments
# For example, `return_result = 'model'` instaed of `model`
measurement_invariance(
  "visual  =~ x1 + x2 + x3;
             textual =~ x4 + x5 + x6;
             speed   =~ x7 + x8 + x9",
  data = lavaan::HolzingerSwineford1939
)

## End(Not run)
```

`mediation_summary` *Mediation Analysis*

Description

[Experimental]
It currently only support simple mediation analysis using the path analysis approach with the `lavaan` package. I am trying to implement multilevel mediation in `lavaan`. In the future, I will try supporting moderated mediation (through `lavaan` or `mediation`) and mediation with latent variable (through `lavaan`).

Usage

```
mediation_summary(
  data,
  response_variable,
  mediator,
  predictor_variable,
  control_variable = NULL,
  group = NULL,
  standardize = TRUE,
  digits = 3,
  quite = FALSE,
```

```
  streamline = FALSE,
  return_result = FALSE
)
```

Arguments

`data`	`data.frame`
`response_variable`	response variable. Support `dplyr::select()` syntax.
`mediator`	mediator. Support `dplyr::select()` syntax.
`predictor_variable`	predictor variable. Support `dplyr::select()` syntax.
`control_variable`	control variables / covariate. Support `dplyr::select()` syntax.
`group`	nesting variable for multilevel mediation. Not confident about the implementation method. **[Experimental]**
`standardize`	standardized coefficients. Default is `TRUE`
`digits`	number of digits to round to
`quite`	suppress printing output
`streamline`	print streamlined output
`return_result`	If it is set to `TRUE`, it will return the `lavaan` object

Value

an object from `lavaan`

Examples

```
mediation_summary(
  data = lmerTest::carrots,
  response_variable = Preference,
  mediator = Sweetness,
  predictor_variable = Crisp
)
```

`model_summary` *Model Summary for Regression Models*

Description

[Stable]
The function will extract the relevant coefficients from the regression models (see below for supported model).

Usage

```
model_summary(
  model,
  digits = 3,
  assumption_plot = FALSE,
  quite = FALSE,
  streamline = TRUE,
  return_result = FALSE,
  standardize = "basic"
)
```

Arguments

`model`	an model object. The following model are tested for accuracy: `lm`, `glm`, `lme`, `lmer`, `glmer`. Other model object may work if it work with parameters::model_parameters()
`digits`	number of digits to round to
`assumption_plot`	Generate an panel of plots that check major assumptions. It is usually recommended to inspect model assumption violation visually. In the background, it calls `performance::check_model()`.
`quite`	suppress printing output
`streamline`	print streamlined output. Only print model estimate and performance.
`return_result`	It set to `TRUE`, it return the model estimates data frame.
`standardize`	The method used for standardizing the parameters. Can be NULL (default; no standardization), "refit" (for re-fitting the model on standardized data) or one of "basic", "posthoc", "smart", "pseudo". See 'Details' in parameters::standardize_parameters()

Value

a list of model estimate data frame, model performance data frame, and the assumption plot (an `ggplot` object)

References

Nakagawa, S., & Schielzeth, H. (2013). A general and simple method for obtaining R2 from generalized linear mixed-effects models. Methods in Ecology and Evolution, 4(2), 133–142. https://doi.org/10.1111/j.2041-210x.2012.00261.x

Examples

```
# I am going to show the more generic usage of this function
# You can also use this package's built in function to fit the models
# I recommend using the integrated_multilevel_model_summary to get everything

# lme example
lme_fit <- lme4::lmer("popular ~ texp  + (1 | class)",
  data = popular
)
```

```
model_summary(lme_fit)

# lm example

lm_fit <- lm(Sepal.Length ~ Sepal.Width + Petal.Length + Petal.Width,
  data = iris
)

model_summary(lm_fit, assumption_plot = TRUE)
```

`polynomial_regression_plot`

Polynomial Regression Plot

Description

[Experimental]
The function create a simple regression plot (no interaction). Can be used to visualize polynomial regression.

Usage

```
polynomial_regression_plot(
  model,
  model_data = NULL,
  predictor,
  graph_label_name = NULL,
  x_lim = NULL,
  y_lim = NULL,
  plot_color = FALSE
)
```

Arguments

`model`	object from `lm`
`model_data`	optional dataframe (in case data cannot be retrieved from the model)
`predictor`	predictor variable name (must be character)
`graph_label_name`	vector of length 3 or function. Vector should be passed in the form of `c(response_var, predict_var1, predict_var2)`. Function should be passed as a switch function that return the label based on the name passed (e.g., a switch function)
`x_lim`	the plot's upper and lower limit for the x-axis. Length of 2. Example: `c(lower_limit, upper_limit)`
`y_lim`	the plot's upper and lower limit for the y-axis. Length of 2. Example: `c(lower_limit, upper_limit)`
`plot_color`	default if `FALSE`. Set to `TRUE` if you want to plot in color

Details

It appears that `predict` cannot handle categorical factors. All variables are converted to numeric before plotting.

Value

an object of class `ggplot`

`popular` *Popular dataset*

Description

Classic data-set from Chapter 2 of Joop Hox's Multilevel Analysis (2010). The popular dataset included student from different class (i.e., class is the nesting variable). The outcome variable is a self-rated popularity scale. Individual-level (i.e., level 1) predictors are sex, extroversion. Class level (i.e., level 2) predictor is teacher experience.

Usage

```
popular
```

Format

A data frame with 2000 rows and 6 variables:

pupil Subject ID

popular Self-rated popularity scale ranging from 1 to 10

class the class that students belong to (nesting variable)

extrav extraversion scale (individual-level)

sex gender of the student (individual-level)

texp teacher experience (class-level)

Source

`http://joophox.net/mlbook2/DataExchange.zip`

`reliability_summary` *Reliability Analysis*

Description

First, it will determine whether the data is uni-dimensional or multi-dimensional using `parameters::n_factors()`. If the data is uni-dimensional, then it will print a summary consists of alpha, G6, single-factor CFA, and descriptive statistics result. If it is multi-dimensional, it will print a summary consist of alpha, G6, omega result. You can bypass this by specifying the dimensionality argument.

Usage

```
reliability_summary(
  data,
  cols,
  dimensionality = NULL,
  digits = 3,
  descriptive_table = TRUE,
  quite = FALSE,
  streamline = FALSE,
  return_result = FALSE
)
```

Arguments

`data`	`data.frame`
`cols`	items for reliability analysis. Support `dplyr::select()` syntax.
`dimensionality`	Specify the dimensionality. Either `uni` (uni-dimensionality) or `multi` (multi-dimensionality). Default is `NULL` that determines the dimensionality using EFA.
`digits`	number of digits to round to
`descriptive_table`	Get descriptive statistics. Default is `TRUE`
`quite`	suppress printing output
`streamline`	print streamlined output
`return_result`	If it is set to `TRUE` (default is `FALSE`), it will return `psych::alpha` for uni-dimensional scale, and `psych::omega` for multidimensional scale.

Value

a `psych::alpha` object for unidimensional scale, and a `psych::omega` object for multidimensional scale.

Examples

```
fit <- reliability_summary(data = lavaan::HolzingerSwineford1939, cols = x1:x3)
fit <- reliability_summary(data = lavaan::HolzingerSwineford1939, cols = x1:x9)
```

`simple_slope` *Slope Estimate at Varying Level of Moderators*

Description

The function uses the `interaction::sim_slopes()` to calculate the slope estimate at varying level of moderators (+/- 1 SD and mean). Additionally, it will produce a Johnson-Newman plot that shows when the slope estimate is not significant

Usage

```
simple_slope(model, data = NULL)
```

Arguments

`model`	model object from `lm`, `lme`,`lmer`
`data`	`data.frame`

Value

a list with the slope estimate data frame and a Johnson-Newman plot.

Examples

```
fit <- lm_model(
  data = iris,
  response_variable = Sepal.Length,
  predictor_variable = tidyselect::everything(),
  three_way_interaction_factor = c(Sepal.Width, Petal.Width, Petal.Length)
)

simple_slope_fit <- simple_slope(
  model = fit,
)
```

`three_way_interaction_plot` *Three-way Interaction Plot*

Description

[Deprecated]
The function creates a two-way interaction plot. It will creates a plot with ± 1 SD from the mean of the independent variable. See below for supported model. I recommend using concurrently with `lm_model()`, `lme_model()`.

Usage

```
three_way_interaction_plot(
  model,
  data = NULL,
  cateogrical_var = NULL,
  graph_label_name = NULL,
  y_lim = NULL,
  plot_color = FALSE
)
```

Arguments

`model`	object from `lme`, `lme4`, `lmerTest` object.
`data`	`data.frame`. If the function is unable to extract data frame from the object, then you may need to pass it directly
`cateogrical_var`	list. Specify the upper bound and lower bound directly instead of using ± 1 SD from the mean. Passed in the form of `list(var_name1 = c(upper_bound1, lower_bound1),var_name2 = c(upper_bound2, lower_bound2))`
`graph_label_name`	vector of length 4 or a switch function (see ?two_way_interaction_plot example). Vector should be passed in the form of c(response_var, predict_var1, predict_var2, predict_var3).
`y_lim`	the plot's upper and lower limit for the y-axis. Length of 2. Example: `c(lower_limit, upper_limit)`
`plot_color`	default if `FALSE`. Set to `TRUE` if you want to plot in color

Details

It appears that “predict‘ cannot handle categorical factors. All variables are converted to numeric before plotting.

Value

a `ggplot` object

Examples

```
lm_fit <- lm(Sepal.Length ~ Sepal.Width + Petal.Length + Petal.Width +
  Sepal.Width:Petal.Length:Petal.Width, data = iris)

three_way_interaction_plot(lm_fit, data = iris)
```

`two_way_interaction_plot` *Two-way Interaction Plot*

Description

[Deprecated]
The function creates a two-way interaction plot. It will creates a plot with ± 1 SD from the mean of the independent variable. See supported model below. I recommend using concurrently with `lm_model` or `lme_model`.

Usage

```
two_way_interaction_plot(
  model,
  data = NULL,
  graph_label_name = NULL,
  cateogrical_var = NULL,
  y_lim = NULL,
  plot_color = FALSE
)
```

Arguments

`model`	object from `lm`, `nlme`, `lme4`, or `lmerTest`
`data`	`data.frame`. If the function is unable to extract data frame from the object, then you may need to pass it directly
`graph_label_name`	vector of length 3 or function. Vector should be passed in the form of `c(response_var, predict_var1, predict_var2)`. Function should be passed as a switch function that return the label based on the name passed (e.g., a switch function)
`cateogrical_var`	list. Specify the upper bound and lower bound directly instead of using ± 1 SD from the mean. Passed in the form of `list(var_name1 = c(upper_bound1, lower_bound1),var_name2 = c(upper_bound2, lower_bound2))`
`y_lim`	the plot's upper and lower limit for the y-axis. Length of 2. Example: `c(lower_limit, upper_limit)`
`plot_color`	default if `FALSE`. Set to `TRUE` if you want to plot in color

Details

It appears that "predict‘ cannot handle categorical factors. All variables are converted to numeric before plotting.

Value

an object of class `ggplot`

Examples

```
lm_fit <- lm(Sepal.Length ~ Sepal.Width * Petal.Width,
  data = iris
)
two_way_interaction_plot(lm_fit, data = iris)
```

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