Package: testflow (via r-universe)

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Title A Workflow for Statistical Testing, Interpretation, and 'ggplot2'-Based Visualization

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Description Provides a unified workflow for choosing, running, interpreting, and visualizing common statistical tests. The package combines assumption checks, test selection, effect sizes, formatted results, plain-language interpretation, and 'ggplot2'-based statistical visualizations. Implemented methods follow standard references including Casella and Berger (2002, ISBN:9780534243128), Hollander et al. (2013, ISBN:9781118553299), Agresti (2013, ISBN:9780470463635), and Cohen (1988, ISBN:9780805802832).

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Contents

`as_tibble` *Convert a testflow object to a one-row tibble*

Description

Convert a testflow object to a one-row tibble

Usage

```
as_tibble(x, ...)
```

Arguments

`x`	A testflow object.
`...`	Unused.

Value

A one-row tibble with the workflow name, design, variables, recommended test, null hypothesis, statistic, degrees of freedom when available, p-value, confidence interval when available, effect-size fields, and decision text.

`make_cardio_data` *Simulate a small cardiovascular teaching dataset*

Description

Simulate a small cardiovascular teaching dataset

Usage

```
make_cardio_data(n = 180, seed = 2026)
```

Arguments

`n`	Number of rows.
`seed`	Random seed.

Value

A tibble with example numeric and categorical variables.

`plot.testflow` *Plot a testflow object*

Description

Plot a testflow object

Usage

```
## S3 method for class 'testflow'
plot(x, title = NULL, subtitle = NULL, caption = NULL, ...)
```

Arguments

`x`	A testflow object.
`title`	Optional plot title override. Defaults to the stored title.
`subtitle`	Optional plot subtitle override. Defaults to the stored subtitle.
`caption`	Optional plot caption override. Defaults to the stored caption.
`...`	Unused.

Value

A `ggplot` object stored in the `testflow` object, with optional title, subtitle, and caption overrides applied. If the workflow was created with `plot = FALSE`, returns `NULL`.

`print.testflow` *Print a testflow object*

Description

Print a testflow object.

Usage

```
## S3 method for class 'testflow'
print(x, ...)
```

Arguments

`x`	A testflow object.
`...`	Unused.

Details

Console colors are enabled by default in interactive sessions. Use `options(testflow.cli_colors = FALSE)` to disable colors, or `options(testflow.cli_colors = TRUE)` to force colors in non-interactive output.

Value

The input `testflow` object, invisibly. Called for its side effect of printing a formatted workflow summary to the console.

`report` *Return a ready-to-use testflow report*

Description

Return a ready-to-use testflow report

Usage

```
report(x, ...)
```

Arguments

`x`	A testflow object.
`...`	Unused.

Value

A length-one character vector containing a plain-language summary of the workflow result, including the design, recommended test, p-value, effect size when reported, and null hypothesis when available.

`report_test` *Return a ready-to-use testflow report*

Description

Return a ready-to-use testflow report

Usage

```
report_test(x)
```

Arguments

`x`	A testflow object.

Value

A length-one character vector containing the same report text as `report()` for a `testflow` object.

`summary.testflow` *Summarize a testflow object*

Description

Summarize a testflow object.

Usage

```
## S3 method for class 'testflow'
summary(object, ...)
```

Arguments

`object`	A testflow object.
`...`	Unused.

Details

Console colors follow the same `testflow.cli_colors` option used by `print.testflow()`.

Value

A `summary.testflow` list containing the workflow metadata, descriptives, assumptions, recommended test, primary and alternative test results, post-hoc results when available, effect size, decision, and report text.

`sumtab` *Build a compact descriptive summary table*

Description

Builds a compact table of descriptive summaries using a formula interface. Numeric variables are summarized as mean (SD); median [Q1, Q3]; n. Categorical variables are summarized as n (percent).

Usage

```
sumtab(
  formula,
  data,
  p_value = FALSE,
  overall = TRUE,
  digits = 1,
  p_digits = 3,
  alpha = 0.05,
  fisher_threshold = 5,
  na.rm = TRUE
)
```

Arguments

`formula`	A one-sided formula such as `~ age + sex` or `~ age + sex | treatment`.
`data`	A data frame.
`p_value`	Logical; add a p-value column when a grouping variable is supplied.
`overall`	Logical; include an overall summary column.
`digits`	Number of digits for summary statistics.
`p_digits`	Number of digits for formatted p-values.
`alpha`	Significance level used by automatic test selection.
`fisher_threshold`	Expected-count threshold for Fisher's exact test.
`na.rm`	Logical; remove missing values before summaries and tests.

Details

When `p_value = TRUE` and a grouping variable is supplied, `sumtab()` chooses the p-value test automatically. Numeric variables use Student t-test, Welch t-test, or Wilcoxon rank-sum test for two groups, and one-way ANOVA, Welch ANOVA, or Kruskal-Wallis test for more than two groups. Categorical variables use a chi-square test unless expected counts fall below `fisher_threshold`, in which case Fisher's exact test is used.

Value

A tibble with one row per numeric variable and one row per categorical level.

Examples

```
dat <- make_cardio_data(80, seed = 1)
sumtab(~ age + sex | treatment, dat, p_value = TRUE)
```

`test_categorical` *Test association between two categorical variables*

Description

Test association between two categorical variables

Usage

```
test_categorical(
  formula,
  data,
  y = NULL,
  alpha = 0.05,
  fisher_threshold = 5,
  plot = TRUE,
  na.rm = TRUE
)
```

Arguments

`formula`	A formula such as `x ~ y`, or a data frame when using pipe/data-first style.
`data`	A data frame, or a first categorical column when using data-first style.
`y`	Second categorical column. Optional when using formula style.
`alpha`	Significance level.
`fisher_threshold`	Expected-count threshold for Fisher's exact test.
`plot`	Logical; include a ggplot object.
`na.rm`	Logical; remove missing values.

Value

A `testflow` object with class `testflow_categorical`. The object is a list containing the cleaned data, categorical descriptives, assumption checks, recommended association test, primary test result with null hypothesis, alternative chi-square and Fisher results, effect size, optional `ggplot`, original call, and report text.

References

Pearson, K. (1900). On the criterion that a given system of deviations from the probable in the case of a correlated system of variables is such that it can be reasonably supposed to have arisen from random sampling. *Philosophical Magazine*, 50(302), 157-175.

Fisher, R. A. (1922). On the interpretation of chi-square from contingency tables, and the calculation of P. *Journal of the Royal Statistical Society*, 85(1), 87-94.

Cramer, H. (1946). *Mathematical Methods of Statistics*. Princeton.

`test_correlation` *Test correlation between two numeric variables*

Description

Test correlation between two numeric variables

Usage

```
test_correlation(
  formula,
  data,
  y = NULL,
  method = c("auto", "pearson", "spearman", "kendall"),
  alpha = 0.05,
  plot = TRUE,
  na.rm = TRUE
)
```

Arguments

`formula`	A formula such as `y ~ x`, or a data frame when using pipe/data-first style.
`data`	A data frame, or a first numeric column when using data-first style.
`y`	Second numeric column. Optional when using formula style.
`method`	Correlation method or `"auto"`.
`alpha`	Significance level.
`plot`	Logical; include a ggplot object.
`na.rm`	Logical; remove missing values.

Value

A `testflow` object with class `testflow_correlation`. The object is a list containing the cleaned complete-case data, numeric descriptives, assumption checks, recommended correlation method, primary correlation test with null hypothesis, Pearson/Spearman/Kendall results, a correlation table, effect size, optional `ggplot`, original call, and report text.

References

Pearson, K. (1895). Notes on regression and inheritance in the case of two parents. *Proceedings of the Royal Society of London*, 58, 240-242.

Spearman, C. (1904). The proof and measurement of association between two things. *The American Journal of Psychology*, 15(1), 72-101.

Kendall, M. G. (1938). A new measure of rank correlation. *Biometrika*, 30(1/2), 81-93.

`test_correlation_matrix` *Test a correlation matrix*

Description

Test a correlation matrix

Usage

```
test_correlation_matrix(
  data,
  vars,
  method = c("spearman", "pearson", "kendall"),
  alpha = 0.05,
  plot = TRUE,
  na.rm = TRUE
)
```

Arguments

`data`	A data frame.
`vars`	Numeric columns.
`method`	Correlation method.
`alpha`	Significance level.
`plot`	Logical; include a ggplot object.
`na.rm`	Logical; remove missing values.

Value

A `testflow` object with class `testflow_correlation_matrix`. The object is a list containing the cleaned data, numeric descriptives, screening assumptions, selected correlation-matrix method, pairwise correlation matrix, pairwise p-value table, maximum absolute correlation as an effect-size summary, optional heatmap `ggplot`, original call, and report text.

`test_factorial` *Run a factorial ANOVA workflow*

Description

Run a factorial ANOVA workflow

Usage

```
test_factorial(
  formula,
  data,
  factors = NULL,
  alpha = 0.05,
  type = 2,
  plot = TRUE,
  na.rm = TRUE
)
```

Arguments

`formula`	A formula such as `outcome ~ factor1 * factor2`, or a data frame when using data-first style.
`data`	A data frame, or the outcome column when using data-first style.
`factors`	Factor columns selected with tidyselect syntax. Optional when using formula style.
`alpha`	Significance level.
`type`	ANOVA type placeholder for future car integration.
`plot`	Logical; include a ggplot object.
`na.rm`	Logical; remove missing values.

Value

A `testflow` object with class `testflow_factorial`. The object is a list containing the cleaned data, descriptive statistics, residual and variance assumption checks, recommended factorial ANOVA, primary ANOVA term result with null hypothesis, ANOVA table, effect size, optional `ggplot`, original call, and report text.

References

Fisher, R. A. (1925). *Statistical Methods for Research Workers*. Oliver and Boyd.

Cohen, J. (1988). *Statistical Power Analysis for the Behavioral Sciences* (2nd ed.). Lawrence Erlbaum.

`test_groups` *Compare a numeric outcome across more than two groups*

Description

Compare a numeric outcome across more than two groups

Usage

```
test_groups(
  formula,
  data,
  group = NULL,
  alpha = 0.05,
  posthoc = TRUE,
  plot = TRUE,
  na.rm = TRUE
)
```

Arguments

`formula`	A formula such as `outcome ~ group`, or a data frame when using pipe/data-first style.
`data`	A data frame, or an outcome column when using data-first style.
`group`	Grouping column. Optional when using formula style.
`alpha`	Significance level.
`posthoc`	Logical; compute post-hoc comparisons.
`plot`	Logical; include a ggplot object.
`na.rm`	Logical; remove missing values.

Value

A `testflow` object with class `testflow_groups`. The object is a list containing the cleaned data, grouped descriptive statistics, assumption checks, recommended omnibus test, primary test result with null hypothesis, alternative omnibus results, post-hoc comparisons when requested, effect size, optional `ggplot`, original call, and report text.

`test_multinomial` *Test multinomial goodness of fit*

Description

Test multinomial goodness of fit

Usage

```
test_multinomial(
  data,
  outcome,
  p = NULL,
  alpha = 0.05,
  plot = TRUE,
  na.rm = TRUE
)
```

Arguments

`data`	A data frame.
`outcome`	Categorical outcome column.
`p`	Expected probabilities, or `NULL` for equal probabilities.
`alpha`	Significance level.
`plot`	Logical; include a ggplot object.
`na.rm`	Logical; remove missing values.

Value

A `testflow` object with class `testflow_multinomial`. The object is a list containing the cleaned data, categorical descriptives, assumption checks, recommended goodness-of-fit test, primary chi-square result with null hypothesis, pairwise binomial checks, effect-size summary, optional `ggplot`, original call, and report text.

References

Pearson, K. (1900). On the criterion that a given system of deviations from the probable in the case of a correlated system of variables is such that it can be reasonably supposed to have arisen from random sampling. *Philosophical Magazine*, 50(302), 157-175.

`test_one_sample` *Test one numeric sample against a reference value*

Description

Test one numeric sample against a reference value

Usage

```
test_one_sample(
  data,
  outcome,
  mu = 0,
  alternative = c("two.sided", "less", "greater"),
  alpha = 0.05,
  plot = TRUE,
  na.rm = TRUE
)
```

Arguments

`data`	A data frame.
`outcome`	Numeric outcome column.
`mu`	Reference value.
`alternative`	Alternative hypothesis.
`alpha`	Significance level.
`plot`	Logical; include a ggplot object.
`na.rm`	Logical; remove missing values.

Value

A `testflow` object with class `testflow_one_sample`. The object is a list containing the cleaned data, descriptive statistics, assumption checks, recommended test, primary test result with null hypothesis, alternative test results, effect size, optional `ggplot`, original call, and report text.

References

Gosset, W. S. (1908). The probable error of a mean. *Biometrika*, 6(1), 1-25.

Wilcoxon, F. (1945). Individual comparisons by ranking methods. *Biometrics Bulletin*, 1(6), 80-83.

`test_outliers` *Detect numeric outliers*

Description

Detect numeric outliers

Usage

```
test_outliers(
  formula,
  data,
  group = NULL,
  method = c("iqr", "mahalanobis", "both"),
  plot = TRUE,
  na.rm = TRUE
)
```

Arguments

`formula`	Numeric columns to screen for outliers.
`data`	A data frame.
`group`	Optional grouping column.
`method`	Outlier method.
`plot`	Logical; include a ggplot object.
`na.rm`	Logical; remove missing values.

Value

A `testflow` object with class `testflow_outliers`. The object is a list containing the cleaned data, numeric descriptives, screening assumptions, selected outlier-screening method, flagged IQR and/or Mahalanobis rows, outlier-count summary, optional `ggplot`, original call, and report text. This is a screening workflow, not a single hypothesis test.

`test_paired` *Compare paired before and after numeric measurements*

Description

Compare paired before and after numeric measurements

Usage

```
test_paired(
  formula,
  data,
  after = NULL,
  alternative = c("two.sided", "less", "greater"),
  alpha = 0.05,
  plot = TRUE,
  na.rm = TRUE
)
```

Arguments

`formula`	A formula such as `after ~ before`, or a data frame when using data-first style.
`data`	A data frame, or the before column when using data-first style.
`after`	After column. Optional when using formula style.
`alternative`	Alternative hypothesis.
`alpha`	Significance level.
`plot`	Logical; include a ggplot object.
`na.rm`	Logical; remove missing values.

Value

A `testflow` object with class `testflow_paired`. The object is a list containing the cleaned paired data, paired difference, descriptive statistics, assumption checks, recommended paired test, primary test result with null hypothesis, alternative test results, effect size, optional `ggplot`, original call, and report text.

`test_paired_categorical`

Test paired categorical measurements

Description

Test paired categorical measurements

Usage

```
test_paired_categorical(
  data,
  before,
  after,
  alpha = 0.05,
  plot = TRUE,
  na.rm = TRUE
)
```

Arguments

`data`	A data frame.
`before`	Before categorical column.
`after`	After categorical column.
`alpha`	Significance level.
`plot`	Logical; include a ggplot object.
`na.rm`	Logical; remove missing values.

Value

A `testflow` object with class `testflow_paired_categorical`. The object is a list containing the cleaned paired categorical data, categorical descriptives, assumption checks, McNemar test result, discordant-pair table, optional `ggplot`, original call, and report text.

`test_proportion` *Test a one-sample proportion*

Description

Test a one-sample proportion

Usage

```
test_proportion(
  data,
  outcome,
  success,
  p = 0.5,
  alpha = 0.05,
  plot = TRUE,
  na.rm = TRUE
)
```

Arguments

`data`	A data frame.
`outcome`	Categorical outcome column.
`success`	Value counted as success.
`p`	Reference probability.
`alpha`	Significance level.
`plot`	Logical; include a ggplot object.
`na.rm`	Logical; remove missing values.

Value

A `testflow` object with class `testflow_proportion`. The object is a list containing the cleaned data, categorical descriptives, assumption checks, recommended exact or approximate one-sample proportion test, primary test result with null hypothesis, alternative exact and approximate results, observed proportion summary, optional `ggplot`, original call, and report text.

References

Clopper, C. J., & Pearson, E. S. (1934). The use of confidence or fiducial limits illustrated in the case of the binomial. *Biometrika*, 26(4), 404-413.

`test_repeated` *Run a repeated-measures workflow from wide data*

Description

Run a repeated-measures workflow from wide data

Usage

```
test_repeated(
  data,
  measures,
  id = NULL,
  between = NULL,
  alpha = 0.05,
  plot = TRUE,
  na.rm = TRUE
)
```

Arguments

`data`	A data frame.
`measures`	Repeated numeric columns selected with tidyselect syntax.
`id`	Optional subject identifier.
`between`	Optional between-subject factor.
`alpha`	Significance level.
`plot`	Logical; include a ggplot object.
`na.rm`	Logical; remove missing values.

Value

A `testflow` object with class `testflow_repeated`. The object is a list containing long-form repeated-measures data, numeric descriptives, assumption checks, recommended repeated-measures ANOVA or Friedman test, primary test result with null hypothesis, alternative repeated-measures results, post-hoc paired comparisons, effect size, optional `ggplot`, original call, and report text.

References

Fisher, R. A. (1925). *Statistical Methods for Research Workers*. Oliver and Boyd.

Friedman, M. (1937). The use of ranks to avoid the assumption of normality implicit in the analysis of variance. *Journal of the American Statistical Association*, 32(200), 675-701.

Wilcoxon, F. (1945). Individual comparisons by ranking methods. *Biometrics Bulletin*, 1(6), 80-83.

Girden, E. R. (1992). *ANOVA: Repeated Measures*. Sage.

`test_repeated_categorical`

Test repeated categorical measurements

Description

Test repeated categorical measurements

Usage

```
test_repeated_categorical(
  data,
  measures,
  id = NULL,
  alpha = 0.05,
  plot = TRUE,
  na.rm = TRUE
)
```

Arguments

`data`	A data frame.
`measures`	Repeated binary columns selected with tidyselect syntax.
`id`	Optional subject identifier.
`alpha`	Significance level.
`plot`	Logical; include a ggplot object.
`na.rm`	Logical; remove missing values.

Value

A `testflow` object with class `testflow_repeated_categorical`. The object is a list containing the cleaned repeated categorical data, descriptive counts, assumption checks, Cochran Q test result with null hypothesis, pairwise McNemar post-hoc comparisons, effect size, optional `ggplot`, original call, and report text.

References

Cochran, W. G. (1950). The comparison of percentages in matched samples. *Biometrika*, 37(3/4), 256-266.

McNemar, Q. (1947). Note on the sampling error of the difference between correlated proportions or percentages. *Psychometrika*, 12(2), 153-157.

`test_repeated_long` *Run a repeated-measures workflow from long data*

Description

Run a repeated-measures workflow from long data

Usage

```
test_repeated_long(
  data,
  outcome,
  within,
  id,
  between = NULL,
  alpha = 0.05,
  plot = TRUE,
  na.rm = TRUE
)
```

Arguments

`data`	A data frame.
`outcome`	Numeric outcome column.
`within`	Within-subject time/condition column.
`id`	Subject identifier column.
`between`	Optional between-subject factor.
`alpha`	Significance level.
`plot`	Logical; include a ggplot object.
`na.rm`	Logical; remove missing values.

Value

A `testflow` object with class `testflow_repeated`. The object is a list containing the cleaned long-format data, numeric descriptives, assumption checks, recommended repeated-measures ANOVA or Friedman test, primary test result with null hypothesis, alternative repeated-measures results, post-hoc paired comparisons, effect size, optional `ggplot`, original call, and report text.

`test_two_groups` *Compare a numeric outcome between two independent groups*

Description

Compare a numeric outcome between two independent groups

Usage

```
test_two_groups(
  formula,
  data,
  group = NULL,
  alternative = c("two.sided", "less", "greater"),
  alpha = 0.05,
  plot = TRUE,
  na.rm = TRUE
)
```

Arguments

`formula`	A formula such as `outcome ~ group`, or a data frame when using pipe/data-first style.
`data`	A data frame, or an outcome column when using data-first style.
`group`	Two-level grouping column. Optional when using formula style.
`alternative`	Alternative hypothesis.
`alpha`	Significance level.
`plot`	Logical; include a ggplot object.
`na.rm`	Logical; remove missing values.

Value

A `testflow` object with class `testflow_two_groups`. The object is a list containing the cleaned data, descriptive statistics by group, assumption checks, recommended test, primary test result with null hypothesis, alternative test results, effect size, optional `ggplot`, original call, and report text.

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