

Package ‘inferstat’

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Type Package

Title Publication-Ready Inferential Statistics and Visualization

Version 0.1.1

Description Provides publication-ready tools for inferential statistical analyses, assumption checking, effect size estimation, statistical visualizations, and standardized reporting. Methods for assessing normality follow Shapiro and Wilk (1965) [<doi:10.1093/biomet/52.3-4.591>](https://doi.org/10.1093/biomet/52.3-4.591), and guidance for standardized effect sizes is informed by Cohen (1988) [<doi:10.4324/9780203771587>](https://doi.org/10.4324/9780203771587).

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Imports car, dplyr, ggplot2, rlang

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

Config/testthat/edition 3

URL <https://github.com/vinodhpmd/inferstat>

BugReports <https://github.com/vinodhpmd/inferstat/issues>

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anova	<i>One-way Analysis of Variance</i>
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Description

Performs a one-way Analysis of Variance (ANOVA) to compare the means of two or more independent groups.

Usage

```
anova(  
  data,  
  response,  
  group,  
  alpha = 0.05,  
  conf.level = 0.95,  
  effect_size = c("eta", "omega", "none"),  
  posthoc = FALSE,  
  plot = TRUE,  
  theme = NULL,  
  na_action = c("fail", "omit")  
)
```

Arguments

data	A data frame.
response	Numeric response variable.
group	Grouping variable.
alpha	Significance level. Default is 0.05.
conf.level	Confidence level for Tukey HSD intervals.
effect_size	Effect size measure. One of "eta", "omega" or "none".
posthoc	Logical indicating whether Tukey HSD should be performed.
plot	Logical indicating whether a boxplot should be produced.
theme	Optional ggplot theme.
na_action	One of "fail" or "omit".

Details

The function returns an object of class "inferstat" containing the ANOVA table, effect size, optional Tukey HSD post hoc comparisons, interpretation, and publication-ready plot.

Value

An object of class "inferstat".

Examples

```
fit <- anova(  
  data = iris,  
  response = Sepal.Length,  
  group = Species  
)  
  
summary(fit)
```

check_assumptions	<i>Check Statistical Assumptions Performs a comprehensive assessment of statistical assumptions.</i>
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Description

Check Statistical Assumptions Performs a comprehensive assessment of statistical assumptions.

Usage

```
check_assumptions(  
  data,  
  response,  
  group = NULL,  
  normality = TRUE,  
  variance = TRUE,  
  outliers = TRUE,  
  alpha = 0.05,  
  plot = TRUE,  
  na_action = c("fail", "omit")  
)
```

Arguments

data	A data frame.
response	Numeric response variable supplied using tidy evaluation.
group	Optional grouping variable.
normality	Logical indicating whether the normality test is performed.

variance	Logical indicating whether homogeneity of variance is tested.
outliers	Logical indicating whether outlier detection is performed.
alpha	Significance level.
plot	Logical indicating whether diagnostic plots are produced.
na_action	One of "fail" or "omit".

Value

An object of class "inferstat" containing:

- result — individual assumption test results.
- table — combined summary table.
- assumptions — overall assumption status.
- figure — diagnostic plots.
- interpretation — overall interpretation.

Examples

```
fit <- check_assumptions(
  data = iris,
  response = Sepal.Length,
  group = Species
)

fit
summary(fit)
```

check_normality	<i>Check Normality</i>
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Description

Performs the Shapiro-Wilk normality test for a numeric variable.

Usage

```
check_normality(
  data,
  response,
  method = c("shapiro"),
  alpha = 0.05,
  plot = TRUE,
  plot_type = c("qq", "histogram"),
  type = NULL,
  na_action = c("fail", "omit")
)
```

Arguments

data	A data frame.
response	Numeric response variable.
method	Currently only "shapiro".
alpha	Significance level.
plot	Logical.
plot_type	Character string specifying the diagnostic plot. One of "qq" or "histogram".
type	Deprecated alias for plot_type.
na_action	One of "fail" or "omit".

Value

An object of class "inferstat" containing:

- result — Shapiro-Wilk test results.
- method — test name.
- figure — optional diagnostic plot.
- interpretation — interpretation of the test.

Examples

```
fit <- check_normality(
  data = iris,
  response = Sepal.Length
)

fit
summary(fit)
plot(fit)
```

check_outliers

Check Outliers

Description

Detects potential outliers in a numeric variable using one of several commonly used statistical methods.

Usage

```
check_outliers(
  data,
  response,
  method = c("iqr", "zscore", "modified_zscore", "mad"),
  threshold = NULL,
  plot = TRUE,
  na_action = c("fail", "omit")
)
```

Arguments

data	A data frame.
response	Numeric response variable supplied using tidy evaluation.
method	One of "iqr", "zscore", "modified_zscore" or "mad".
threshold	Numeric threshold. If NULL, the default is used.
plot	Logical indicating whether a boxplot should be produced.
na_action	One of "fail" or "omit".

Details

Supported methods include:

- IQR Rule (default)
- Z-score
- Modified Z-score
- MAD

Value

An object of class "inferstat" containing:

- result — summary table.
- n_outliers — number of detected outliers.
- outlier_index — indices of detected outliers.
- outlier_values — detected outlier values.
- figure — optional boxplot.
- interpretation — interpretation of the results.

check_variance	<i>Check Homogeneity of Variance</i>
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Description

Performs a test for homogeneity of variance across groups.

Usage

```
check_variance(
  data,
  response,
  group,
  method = c("levene", "bartlett", "fligner"),
  alpha = 0.05,
  plot = TRUE,
  na_action = c("fail", "omit")
)
```

Arguments

data	A data frame.
response	Numeric response variable supplied using tidy evaluation.
group	Grouping variable supplied using tidy evaluation.
method	One of "levene", "bartlett" or "fligner".
alpha	Significance level.
plot	Logical indicating whether a diagnostic plot should be produced.
na_action	One of "fail" or "omit".

Details

Supported methods:

- Levene's Test (default)
- Bartlett's Test
- Fligner-Killeen Test

Value

An object of class "inferstat" containing:

- result — homogeneity of variance test results.
- method — statistical method used.
- figure — optional boxplot.
- interpretation — interpretation of the test.

Examples

```
fit <- check_variance(  
  data = iris,  
  response = Sepal.Length,  
  group = Species  
)  
  
fit  
summary(fit)  
plot(fit)
```

`describe`*Descriptive Statistics*

Description

Computes publication-ready descriptive statistics.

Usage

```
describe(  
  data,  
  response,  
  group = NULL,  
  conf.level = 0.95,  
  plot = TRUE,  
  plot_type = c("histogram", "density", "boxplot", "violin", "qqplot"),  
  theme = NULL,  
  na_action = c("fail", "omit")  
)
```

Arguments

<code>data</code>	A data frame.
<code>response</code>	Numeric response variable supplied using tidy evaluation.
<code>group</code>	Optional grouping variable supplied using tidy evaluation.
<code>conf.level</code>	Confidence level.
<code>plot</code>	Logical indicating whether a figure should be produced.
<code>plot_type</code>	One of "histogram", "density", "boxplot", "violin" or "qqplot".
<code>theme</code>	Optional ggplot2 theme.
<code>na_action</code>	One of "fail" or "omit".

Value

An object of class "inferstat" containing:

- `result`: a data frame containing the computed descriptive statistics.
- `method`: a character string identifying the analysis method.
- `figure`: a ggplot object when plotting is requested, otherwise NULL.
- `interpretation`: a character string providing a summary interpretation of the descriptive analysis.

The `result` component summarizes the distribution, central tendency, variability, and confidence interval of the selected response variable, either overall or by the specified grouping variable.

Examples

```
fit <- describe(  
  data = iris,  
  response = Sepal.Length  
)  
  
fit  
summary(fit)  
plot(fit)
```

theme_publication	<i>Publication Theme for inferstat</i>
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Description

A clean, publication-quality ggplot2 theme designed for scientific manuscripts, journal articles, theses, and technical reports.

Usage

```
theme_publication(  
  base_size = 14,  
  base_family = "sans",  
  base_line_size = 0.6,  
  base_rect_size = 0.6  
)
```

Arguments

base_size	Base font size.
base_family	Base font family.
base_line_size	Base line width.
base_rect_size	Base rectangle line width.

Details

The theme is based on `ggplot2::theme_bw()` with modifications to improve readability and produce publication-ready graphics.

Features include:

- White background
- No panel grid
- Bold axis titles
- Black axis text

- Centered bold plot title
- Centered subtitle
- Bold legend title
- Right-positioned legend
- Styled facet strips

This is the default plotting theme used throughout the **inferstat** package.

Value

A ggplot2 theme.

See Also

`ggplot2::theme_bw()`

Examples

```
library(ggplot2)

ggplot(mtcars,
       aes(wt, mpg)) +
  geom_point() +
  theme_publication()
```

t_test	<i>Student's t-test</i>
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Description

Performs an independent, Welch's or paired Student's t-test.

Usage

```
t_test(
  data,
  response = NULL,
  group = NULL,
  x = NULL,
  y = NULL,
  paired = FALSE,
  var.equal = TRUE,
  alternative = c("two.sided", "less", "greater"),
  conf.level = 0.95,
  effect_size = c("cohen", "hedges", "glass", "none"),
  plot = TRUE,
  theme = NULL,
  na_action = c("fail", "omit")
)
```

Arguments

data	A data frame.
response	Numeric response variable.
group	Grouping variable for independent samples.
x	First paired variable.
y	Second paired variable.
paired	Logical indicating whether a paired t-test should be performed.
var.equal	Logical indicating equal variances.
alternative	Alternative hypothesis.
conf.level	Confidence level.
effect_size	Effect-size measure.
plot	Logical.
theme	Optional ggplot theme.
na_action	Missing-value handling.

Details

The function automatically returns publication-ready tables, effect sizes, confidence intervals and optional graphics.

Value

An object of class "inferstat".

Examples

```
iris2 <- subset(
  iris,
  Species != "virginica"
)

fit <- t_test(
  data = iris2,
  response = Sepal.Length,
  group = Species
)

print(fit)
summary(fit)
plot(fit)
```

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