

# Package ‘boxTest’

May 8, 2026

**Type** Package

**Title** Boxplot and Significance Test for Two Groups

**Version** 0.1.0

**Description** Provides functions to create side-by-side boxplots for a continuous variable grouped by a two-level categorical variable, check normality assumptions using the Shapiro-Wilk test (Shapiro and Wilk (1965) <[doi:10.2307/2333709](https://doi.org/10.2307/2333709)>), and perform appropriate statistical tests such as the independent two-sample t-test (Student (1908) <[doi:10.1093/biomet/6.1.1](https://doi.org/10.1093/biomet/6.1.1)>) or the Mann–Whitney U test (Mann–Whitney (1947) <[doi:10.1214/aoms/117773](https://doi.org/10.1214/aoms/117773)>). It turns a publication-ready plot and test statistics including test statistic, degrees of freedom, and p-value.

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**Encoding** UTF-8

**Depends** R (>= 4.1.0)

**Imports** ggplot2, dplyr, stats, rlang

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

**VignetteBuilder** knitr

**RoxygenNote** 7.3.3

**Config/testthat/edition** 3

**NeedsCompilation** no

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**Repository** CRAN

**Date/Publication** 2025-10-01 07:00:16 UTC

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compare\_two\_groups      *Compare Two Groups with Boxplot and Significance Test*

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### Description

Generates side-by-side boxplots and runs Shapiro-Wilk tests by group to check for normality. If both groups are normally distributed, an independent two-sample t-test is applied. Otherwise, a Mann-Whitney U test (Wilcoxon rank-sum test) is performed. Returns a structured list with plots and a clear test summary.

### Usage

```
compare_two_groups(data, continuous, group)
```

### Arguments

data	A data.frame containing the variables.
continuous	Name of continuous variable (string).
group	Name of categorical variable with exactly 2 levels (string).

### Value

A list containing:

**plot** A ggplot object of the boxplot with jittered points.

**normality** A data.frame showing Shapiro-Wilk test results by group.

**test\_summary** A data.frame summarizing the statistical test used, statistic, df (if applicable), and p-value.

### Examples

```
res <- compare_two_groups(mtcars, "mpg", "am")
res$plot
res$normality
res$test_summary
```

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