

# Package: AdaptiveBoxplot (via r-universe)

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**Title** FDR(BH) Boxplot and FWER(Holm) Boxplot

**Version** 0.1.1

**Description** Implements a framework for creating boxplots where the whisker lengths are determined by formal multiple testing procedures, making them adaptive to sample size and data characteristics. The function `bh_boxplot()` generates boxplots that control the False Discovery Rate (FDR) via the Benjamini-Hochberg procedure, and the function `holm_boxplot()` generates boxplots that control the Family-Wise Error Rate (FWER) via the Holm procedure. The methods are based on the framework in Gang, Lin, and Tong (2025)  [<doi:10.48550/arXiv.2510.20259>](https://doi.org/10.48550/arXiv.2510.20259).

**License** GPL (>= 3)

**Encoding** UTF-8

**Depends** R (>= 3.5.0)

**RoxygenNote** 7.3.3

**NeedsCompilation** no

**Author** Bowen Gang [aut, cre], Hongmei Lin [aut], Tiejun Tong [aut]

**Maintainer** Bowen Gang <gangbowen02@gmail.com>

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`bh_boxplot`*False Discovery Rate (FDR) Boxplot*

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### Description

Generates a boxplot where whisker lengths are determined by the Benjamini-Hochberg procedure to control the False Discovery Rate (FDR), making the outlier detection rule adaptive to sample size and data characteristics.

### Usage

```
bh_boxplot(data, alpha = 0.01, group_col = NULL, value_col = NULL, ...)
```

### Arguments

<code>data</code>	A numeric vector for a single boxplot, or a data frame for grouped boxplots.
<code>alpha</code>	The target FDR level. Defaults to 0.01.
<code>group_col</code>	A string specifying the name of the grouping column in 'data'.
<code>value_col</code>	A string specifying the name of the value column in 'data'.
<code>...</code>	Additional arguments passed to the base <code>boxplot</code> function.

### Details

This function is a graphical implementation of the p-value pipeline proposed by Gang, Lin, and Tong (2025). It uses robust estimators for the mean and standard deviation based on quartiles to calculate p-values for each observation, then applies the Benjamini-Hochberg (BH) procedure to determine an adaptive p-value threshold for outlier detection. Outliers are points falling beyond the fences defined by this threshold.

### Value

A plot is drawn on the current graphics device.

### References

Gang, B., Lin, H., & Tong, T. (2025). Unifying Boxplots: A Multiple Testing Perspective.

### See Also

[holm\\_boxplot](#)

## Examples

```
# Single group example
set.seed(123)
data_single <- c(rnorm(50), 10, 12)
bh_boxplot(data_single, alpha = 0.05, main = "FDR Boxplot (Single Group)")

# Grouped data example
data_grouped <- data.frame(
  Category = rep(c("A", "B"), each = 100),
  Value = c(rnorm(100), rnorm(100, mean = 2, sd = 1.5))
)
bh_boxplot(data_grouped, group_col = "Category", value_col = "Value")
```

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holm\_boxplot

*Family-Wise Error Rate (FWER) Boxplot*

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## Description

Generates a boxplot where whisker lengths are determined by the Holm procedure to control the Family-Wise Error Rate (FWER), providing a conservative yet principled approach to outlier detection.

## Usage

```
holm_boxplot(
  data,
  alpha = 0.05,
  kfwer = 1,
  group_col = NULL,
  value_col = NULL,
  ...
)
```

## Arguments

data	A numeric vector for a single boxplot, or a data frame for grouped boxplots.
alpha	The target FWER level. Defaults to 0.05.
kfwer	The "k" in k-FWER control. Defaults to 1 for standard FWER.
group_col	A string specifying the name of the grouping column in 'data'.
value_col	A string specifying the name of the value column in 'data'.
...	Additional arguments passed to the base <code>boxplot</code> function.

**Details**

This function is a graphical implementation of the p-value pipeline proposed by Gang, Lin, and Tong (2025). It uses robust estimators for the mean and standard deviation based on quartiles to calculate p-values for each observation, then applies the Holm procedure to determine a p-value threshold that controls the FWER. This method is generally more conservative than the FDR boxplot.

**Value**

A plot is drawn on the current graphics device.

**References**

Gang, B., Lin, H., & Tong, T. (2025). Unifying Boxplots: A Multiple Testing Perspective.

**See Also**

[bh\\_boxplot](#)

**Examples**

```
# Single group example
set.seed(123)
data_single <- c(rnorm(50), 10, 12)
holm_boxplot(data_single, alpha = 0.05, main = "FWER Boxplot (Single Group)")

# Grouped data example
data_grouped <- data.frame(
  Category = rep(c("A", "B"), each = 100),
  Value = c(rnorm(100), rnorm(100, mean = 2, sd = 1.5))
)
holm_boxplot(data_grouped, group_col = "Category", value_col = "Value")
```

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