

Package: robusttseq (via r-universe)

June 3, 2026

Title Robust Statistical Methods with Huber Estimators

Version 0.1.0

Author Nair Gonzalez Sotomayor [aut, cre], Aquiles Enrique Darghan Contreras [aut]

Maintainer Nair Gonzalez Sotomayor <njgonzalezs@unal.edu.co>

Description Provides robust statistical methods for analyzing numeric data, including robust estimation of location and scale using Huber M-estimators and a robust two-sample t-test. Methods are based on Huber (1981, ISBN:0471418056) ``Robust Statistics" and Smyth (2004) <doi:10.2202/1544-6115.1027>.

License MIT + file LICENSE

Encoding UTF-8

RoxygenNote 7.3.3

Imports limma, stats

NeedsCompilation no

Repository https://cran.r-universe.dev

Date/Publication 2026-06-03 17:24:31 UTC

RemoteUrl https://github.com/cran/robusttseq

RemoteRef HEAD

RemoteSha 5b10623019233834ccbda8f0f87f2d86fab95b29

Contents

huber_estimation	2
robust_huber_moderated	2
robust_t_test	3

Index	4
--------------	----------

huber_estimation *Huber M-estimator for location and scale*

Description

Computes robust estimates of mean (μ) and scale (σ) using Huber's M-estimator.

Usage

```
huber_estimation(x, c = 1.345, tol = 1e-06, max_iter = 100)
```

Arguments

x	Numeric vector of observations.
c	Tuning constant (default 1.345). Larger values make the estimator closer to the mean, smaller values make it more robust.
tol	Convergence tolerance (default 1e-6).
max_iter	Maximum number of iterations (default 100).

Value

A list with two elements:

mu Estimated robust mean

sigma Estimated robust scale (standard deviation)

Examples

```
set.seed(123)
x <- c(rnorm(100), 10) # outlier at 10
huber_estimation(x)
```

robust_huber_moderated

Robust Huber-Moderated t-Test for Gene Expression

Description

Performs a moderated two-sample t-test on count data using Huber M-estimators and empirical Bayes variance shrinkage (via `limma::squeezeVar`).

Usage

```
robust_huber_moderated(counts, group, c_huber = 1.345, robust_prior = TRUE)
```

Arguments

counts	Numeric matrix of counts (genes in rows, samples in columns).
group	Factor indicating group membership for each column/sample.
c_huber	Tuning constant for Huber estimator (default 1.345).
robust_prior	Logical; if TRUE, uses a robust empirical Bayes prior (default TRUE).

Value

Numeric vector of p-values, one per gene.

Examples

```
library(limma)
counts <- matrix(rpois(200, lambda = 10), nrow = 20)
group <- factor(rep(c("A", "B"), each = 5))
pvals <- robust_huber_moderated(counts, group)
```

robust_t_test	<i>Two-Sample Robust t-Test (Huber)</i>
---------------	---

Description

Performs a robust two-sample t-test using Huber M-estimators for location and scale.

Usage

```
robust_t_test(x, y, c = 1.345)
```

Arguments

x	Numeric vector of sample 1.
y	Numeric vector of sample 2.
c	Tuning constant for Huber estimator (default 1.345).

Value

An object of class "htest" similar to `t.test`.

Examples

```
set.seed(123)
x <- rnorm(30, mean = 5)
y <- rnorm(35, mean = 6)
robust_t_test(x, y)
```

Index

huber_estimation, 2

robust_huber_moderated, 2

robust_t_test, 3