

Package ‘MedZlsc’

August 28, 2026

Type Package

Title Statistical Framework for Co-Mediators of Zero-Inflated
Single-Cell Data

Version 0.0.5

Description A causal mediation framework for single-cell data that incorporates two key features ('MedZlsc', pronounced Magics): (1) zero-inflation using beta regression and (2) overdispersed expression counts using negative binomial regression. This approach also includes a screening step based on penalized and marginal models to handle high-dimensionality. Full methodological details are available in our recent preprint by Ahn S et al. (2025) <[doi:10.48550/arXiv.2507.06113](https://doi.org/10.48550/arXiv.2507.06113)>.

License GPL-3

Encoding UTF-8

RoxygenNote 7.3.2

Depends R (>= 3.5.0)

Imports MASS, betareg, glmnet

Suggests knitr, rmarkdown, testthat (>= 3.0.0)

LazyData true

Config/testthat/edition 3

NeedsCompilation no

Author Seungjun Ahn [cre, aut] (ORCID:
<<https://orcid.org/0000-0002-4816-8924>>),
Zhigang Li [ctb]

Maintainer Seungjun Ahn <seungjun.ahn@mountsinai.org>

Repository CRAN

Date/Publication 2026-08-28 09:50:43 UTC

Contents

adjust_Fg	2
compute_M	2
Magics	3
simulated_data	4

adjust_Fg	<i>adjust_Fg</i>
-----------	------------------

Description

A function that adjusts zero proportion values to meet the requirements of beta regression by bounding values of 0 and 1 to 0.001 and 0.999.

Usage

adjust_Fg(Fg)

Arguments

Fg

A numeric vector of length n, where each element represents the proportion of zero counts for a given gene g across cells for subject i.

Value

A vector of adjusted zero proportions, with values constrained between 0.001 and 0.999.

compute_M	<i>Compute M Mediator</i>
-----------	---------------------------

Description

Computes the sample-level expression mediator used for `Magics()`.

Usage

compute_M(counts, sample_id, M_type = c("overall", "nonzero"))

Arguments

counts

A matrix or data.frame of cell-level gene expression counts, with cells in rows and genes in columns.

sample_id

A vector indicating the sample corresponding to each cell. Its length must equal the number of rows in counts.

M_type

A character string specifying how the expression mediator is calculated. "overall" calculates M_g as the mean expression across all cells within each sample, while "nonzero" calculates M_g^* as the mean expression among cells with nonzero expression. Default is "overall".

Value

A data.frame with one row per sample and one M variable per gene. For `M_type = "nonzero"`, the M value is set to 0 when a gene has zero expression in all cells within a sample.

Magics

Magics

Description

A main function for conducting causal mediation analysis with co-mediators derived from zero-inflated single-cell data.

Usage

```
Magics(data.name, n_genes, covariate.names)
```

Arguments

<code>data.name</code>	A data.frame or matrix with $N \times (2G + k)$, where N is the number of samples, G is the number of genes, and K is the number of covariates. For each gene, the input includes <code>M_g</code> and <code>F_g</code> , where <code>M_g</code> represents the sample-level expression mediator and <code>F_g</code> represents the proportion of cells with nonzero expression.
<code>n_genes</code>	An integer value. The number of genes (G) represented in the data.
<code>covariate.names</code>	A character vector to specify the column name of covariates.

Value

A list containing the following elements: (1) estimated coefficients from the outcome and two mediation models (M and F models in methodology paper); (2) standard errors corresponding to (1); (3) logical vector indicating whether each gene's mediator component (M model) is statistically significant; (4) logical vector indicating whether each gene's zero-inflation component (F model) is statistically significant; (5) Adjusted p-values for M and F model (joint significance test).

References

Ahn S, Li Z. A Statistical Framework for Co-Mediators of Zero-Inflated Single-Cell RNA-Seq Data. ArXiv. 2025 July 8:arXiv:2507.06113v1. Available at: <https://arxiv.org/pdf/2507.06113>

Examples

```
data("simulated_data")
n_genes = ncol(simulated_data[, grep("^M_", colnames(simulated_data))])
Magics(data.name = simulated_data, n_genes = n_genes, covariate.names = c("Z1", "Z2", "Z3"))
```

simulated_data	<i>Simulated Mediation Dataset</i>
----------------	------------------------------------

Description

A simulated dataset created for zero-inflated single-cell mediation analysis.

Usage

```
simulated_data
```

Format

An object of class `data.frame` with 400 rows and 405 columns.

Details

A simulated dataset used to evaluate mediation methods for zero-inflated single-cell data. The dataset includes 300 samples with a continuous outcome (Y), a binary exposure (X), three co-variates (Z1–Z3), 200 aggregated gene expression values (M_1–M_200), and corresponding zero proportions (F_1–F_200).

Source

Simulated using code in `inst/scripts/simulate_example_data.R`

Index

* **datasets**

simulated_data, [4](#)

adjust_Fg, [2](#)

compute_M, [2](#)

Magics, [3](#)

simulated_data, [4](#)