Package 'ZINQL'

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Type Package

Title What the Package Does (Title Case)

Version 1.0

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Description More about what it does (maybe more than one line)
Use four spaces when indenting paragraphs within the Description.

License ???

Encoding UTF-8

LazyData true

Imports lme4, quantreg, Matrix, MASS, dplyr

RoxygenNote 7.2.3

Suggests knitr,
rmarkdown

VignetteBuilder knitr

R topics documented:

`ZINQL_fit` *ZINQL_fit*

Description

A Zero-Inflated Quantile Approach for Differential Abundance Analysis of Longitudinal Microbiome Data. The test combines both logistic mixed-effects model and longitudinal quantile regression model. The test is applied to individual taxon.

Usage

```
ZINQL_fit(y, formula, formula.logistics = NA,
  meta, C, taus = c(0.1, 0.25, 0.5, 0.75, 0.9),
  method = "both", n.positive.cut = 5,
  seed = 2024)
```

Arguments

`y`	The taxa read count. It should be numeric.
`formula`	The full model for ZINQ-L. By default, this is the formula for both logistics mixed-effects regression and longitudinal quantile regression. For example, y ~ X + Y + (1|ID), where y is zero-inflated.
`formula.logistics`	The model of logistics mixed-effects regression. By default the user does not need to input, and this will be the same as `formula`.
`meta`	A data.frame including all covariates of interest. All of them should be numeric. The user should transfer factor variables to binary or numeric values.
`C`	The name of clinical variable of interest. The final P-value will tell whether the abundance is associated with this variable.
`taus`	A grid of quantile levels, e.g., 0.5 for the median, 0.75 for the 3rd quartile; default is c(0.1, 0.25, 0.5, 0.75, 0.9).
`method`	Combination method, "MinP" for MinP combination, "Cauchy" for Truncated Cauchy combination, or 'Both' which will return results for both methods. The default is "Both".
`n.positive.cut`	Minimum number of positive values for y. If the condition is not satisfied, the test will not be conducted and NA P-values will be returned.
`seed`	A seed for any steps with randomness. The default is 2024.

Details

- ZINQ-L requires at least `n.positive.cut` of positive `y`. If this condition is not satisfied, the test will not be conducted and NA P-values will be returned.
- By default, the user does not need to input `formula.logistics`. This means that the formula of logistics mixed-effects regression is consistent with the longitudinal quantile regression. If the user wants the formula of them to be different, the user can input a different formula for logistics mixed-effects regression, and the `formula` will be the model for longitudinal quantile regression.
- ZINQ-L will automatically drop covariates with unique values. ZINQ-L will also drop variables that have unique values on positive part of `y` for longitudinal quantile regression.

Value

The function returns a list:

- Final_P_value - This is the Final P-value of ZINQ-L.
- model - This is a String variable suggesting the status of the test. If the test is successful conducted, this will be either 'ZINQL_MinP', 'ZINQL_Cauchy' or 'Both'. If the test fails, this will be String 'None'.
- Intermediate_P_value - These are intermediate P-values that are combined to form the final P-value by either Truncated Cauchy or MinP approach.

Author(s)

The package is developed by Shuai Li, Runzhe Li, Wodan Ling and Ni Zhao.

References

references

Examples

```
#generate example data
y = c(rep(0,5),1,2,5,6,7)
meta = data.frame(
  ID=c('1','1','1','2','2','2','3','4','3','4'),
  gender=c(0,0,0,1,1,1,0,1,0,1),
  x=c(0,0,0,1,1,1,1,0,1,0),
  age=c(1,2,3,2,3,4,1,2,2,3)
)

#run the function
result = ZINQL_fit(y=y, formula=y~x+age+gender+(1|ID),
  C='x', taus=c(0.1, 0.25, 0.5, 0.75, 0.9), seed=2024,
  meta=meta, method='Both')
print( result )
```

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