

# Package: robustETM (via r-universe)

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**Type** Package

**Title** Robust Methods using Exponential Tilt Model

**Version** 1.0

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**Imports** stats

**Description** Testing homogeneity for generalized exponential tilt model. This package includes a collection of functions for (1) implementing methods for testing homogeneity for generalized exponential tilt model; and (2) implementing existing methods under comparison.

**Depends** R (>= 2.5.0)

**License** GPL (>= 2)

**LazyLoad** no

**NeedsCompilation** yes

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**Repository** <https://chuanhong.r-universe.dev>

**RemoteUrl** <https://github.com/cran/robustETM>

**RemoteRef** HEAD

**RemoteSha** 772fb620ac3fc5d4d3d70532307e313f5c26da1c

## Contents

robustETM-package . . . . .	2
sim . . . . .	3
<b>Index</b>	<b>5</b>

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robustETM-package

*Robust Exponential Tilt Mixture Model*

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## Description

The package **robustETM** consists of the functions to perform pseudolikelihood based EM test for homogeneity in generalized exponential tilt mixture models.

## Details

Package:	robustETM
Type:	robustETM
Version:	1.0
Date:	2016-03-27
License:	GPL>=2

## Testing for homogeneity in generalized exponential tilt mixture model

Motivated by analyses of DNA methylation data, we propose a semiparametric mixture model, namely the generalized exponential tilt mixture model, to account for heterogeneity between differentially methylated and non-differentially methylated subjects in the cancer group, and capture the differences in higher order moments (e.g. mean and variance) between subjects in cancer and normal groups. A pairwise pseudolikelihood is constructed to eliminate the unknown nuisance function. To circumvent boundary and non-identifiability problems as in parametric mixture models, we modify the pseudolikelihood by adding a penalty function. In addition, test with simple asymptotic distribution has computational advantages over permutational test for high-dimensional genetic and epigenetic data. We propose a pseudolikelihood based expectation-maximization test, and show the proposed test follows a simple chi-squared limiting distribution.

The methods contains in function sim are:

- **The proposed PLEMT test (pseudolikelihood based EM test)**
- **The t-test**
- **The modified empirical likelihood ratio test**
- **The empirical likelihood ratio test**
- **The logistic regression test**
- **The Wilcoxon test**
- **The F test**
- **The KS test**

**Author(s)**

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**References**

Hong, C., Chen Y., Ning Y., Wang S., Wu H. and Carroll R.J. (2016). PLEMT: A novel pseudolikelihood based EM test for homogeneity in generalized exponential tilt mixture model (in preparation).

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sim	<i>Tests under comparison for testing for homogeneity in generalized exponential tilt mixture models</i>
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**Description**

The function conducts the pseudolikelihood based EM test for homogeneity in generalized exponential tilt mixture models

**Usage**

```
sim(itr, K, cc, i.n, isetting, lambda, distn)
```

**Arguments**

itr	random seed
K	Number of grid values for proportion parameter lambda
cc	Tuning parameter C for penalty function
isetting	Type I error or power scenarios I II and III for simulation study
lambda	Proportion parameter lambda
i.n	Sample size setting
distn	Distribution

**Value**

mplrt_EM.TS	Test statistic for the proposed PLEMT test
qin.TS	Test statistic for empirical likelihood ratio test
liu.TS	Test statistic for modified empirical likelihood ratio test
t.TS	Test statistic for t-test
wilcox.p	p-value for wilcoxon test
logist.TS	Test statistic for logistic regression test

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**References**

Hong, C., Chen Y., Ning Y., Wang S., Wu H. and Carroll R.J. (2016). PLEMT: A novel pseudolikelihood based EM test for homogeneity in generalized exponential tilt mixture model (in preparation).

**Examples**

```
# not run
#myresult=sim(itr=1234, K=10, cc=20, i.n=2, isetting=1, lambda=0.3, distn="norm")
```

# Index

- \* **Conditional likelihood**

  - sim, [3](#)

- \* **Penalized likelihood**

  - sim, [3](#)

- \* **Semiparametric mixture model**

  - sim, [3](#)

- \* **package**

  - robustETM-package, [2](#)

robustETM (robustETM-package), [2](#)

robustETM-package, [2](#)

sim, [3](#)