

# Package ‘FARDEEP’

April 24, 2019

**Title** Fast and Robust Deconvolution of Tumor Infiltrating Lymphocyte  
from Expression Profiles using Least Trimmed Squares

**Version** 1.0.1

**Description** Using the idea of least trimmed square, it could automatically detects and removes outliers from data before estimating the coefficients. It is a robust machine learning tool which can be applied to gene-expression deconvolution technique. Yuning Hao, Ming Yan, Blake R. Heath, Yu L. Lei and Yuying Xie (2019) <doi:10.1101/358366>.

**Depends** R (>= 3.3.0)

**License** MIT + file LICENSE

**Imports** nnls(>= 1.4), stats, preprocessCore

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 6.1.1

**NeedsCompilation** no

**Author** Yuning Hao [aut],  
Ming Yan [aut],  
Blake R. Heath [aut],  
Yu L. Lei [aut],  
Yuying Xie [aut, cre]

**Maintainer** Yuying Xie <xyy@egr.msu.edu>

**Repository** CRAN

**Date/Publication** 2019-04-24 15:10:03 UTC

## R topics documented:

alts . . . . .	2
fardeep . . . . .	3
LM22 . . . . .	4
mixture . . . . .	5
sample.sim . . . . .	6
tuningBIC . . . . .	7

<b>Index</b>	<b>9</b>
--------------	----------

---

alts *Using the basic idea of least trimmed square to detect and remove outliers before estimating the coefficients. Adaptive least trimmed square.*

---

### Description

Using the basic idea of least trimmed square to detect and remove outliers before estimating the coefficients. Adaptive least trimmed square.

### Usage

```
alts(x, y, alpha1 = 0.1, alpha2 = 1.5, k = 6, nn = TRUE,
     intercept = TRUE)
```

### Arguments

x	input matrix of predictors with n rows and p columns.
y	input vector of dependent variable with length n.
alpha1	parameter used to adjust the upper bound of outliers. Take value from 0 to 1, default 0.1.
alpha2	parameter used to adjust the lower bound of outliers. Take value larger than 1, default 1.5.
k	parameter used to determine the boundary of outliers in the following step of algorithm. Take value from 1 to 10, default 6.
nn	whether coefficients are non-negative, default TRUE.
intercept	whether intercept is included in model, default TRUE.

### Value

beta: estimation of coefficients.  
 number\_outlier: number of outliers.  
 outlier\_detect: index of detected outliers.  
 X.new: good observed points for independent variables.  
 Y.new: good observed points for dependent variables.  
 k: modified k (if the input value is not appropriate).

### Author(s)

Yuning Hao, Ming Yan, Blake R. Heath, Yu L. Lei and Yuying Xie

### References

Yuning Hao, Ming Yan, Blake R. Heath, Yu L. Lei and Yuying Xie. Fast and Robust Deconvolution of Tumor Infiltrating Lymphocyte from Expression Profiles using Least Trimmed Squares. <doi:10.1101/358366>

**Examples**

```
library(FARDEEP)
samp = sample.sim(n = 500, p = 20, sig = 1, a1 = 0.1, a2 = 0.2, nn = TRUE, intercept = TRUE)
result = alts(samp$x, samp$y, alpha1 = 0.1, alpha2 = 1.5, k = 6, nn = TRUE, intercept = TRUE)
coef = result$beta
```

---

fardeep	<i>Using the idea of least trimmed square to detect and remove outliers before estimating the coefficients. A robust method for gene-expression deconvolution.</i>
---------	--

---

**Description**

Using the idea of least trimmed square to detect and remove outliers before estimating the coefficients. A robust method for gene-expression deconvolution.

**Usage**

```
fardeep(X, Y, alpha1 = 0.1, alpha2 = 1.5, up = 10, low = 1,
        nn = TRUE, intercept = TRUE, lognorm = TRUE, permn = 100,
        QN = FALSE)
```

**Arguments**

X	input matrix of predictors with n rows and p columns.
Y	input vector of dependent variable.
alpha1	parameter used to adjust the upper bound of outliers. Take value from 0 to 1, default 0.1.
alpha2	parameter used to adjust the lower bound of outliers. Take value larger than 1, default 1.5.
up	upper bound of parameter k in function alts, default 10.
low	lower bound of parameter k in function alts, default 1.
nn	whether coefficients are non-negative, default TRUE.
intercept	whether intercept is included in model, default TRUE.
lognorm	whether noise is log-normal distributed, default TRUE.
permn	the number of permutation to get the p-values, default TRUE.
QN	whether perform quantile normalization, default TRUE.

**Value**

abs.beta: estimation of absolute abundance of cells (TIL subset scores).  
 relative.beta: estimation of relative proportions by normalizing abs.beta to 1.  
 pval: statistical significance for the deconvolution result.  
 k.value: tuned parameter by modified BIC.

**Author(s)**

Yuning Hao, Ming Yan, Blake R. Heath, Yu L. Lei and Yuying Xie

**References**

Yuning Hao, Ming Yan, Blake R. Heath, Yu L. Lei and Yuying Xie. Fast and Robust Deconvolution of Tumor Infiltrating Lymphocyte from Expression Profiles using Least Trimmed Squares. <doi:10.1101/358366>

**Examples**

```
library(FARDEEP)
data(LM22)
data(mixture)
# toy examples
result = fardeep(LM22, mixture[, 1:2], permn = 0)

result = fardeep(LM22, mixture)
coef = result$abs.beta
```

---

LM22

*Signature matrix*

---

**Description**

A dataset containing 547 genes and 22 TILs.

**Usage**

LM22

**Format**

A data frame with 547 rows and 22 variables:

**B.cells.naive** naive B cells

**B.cells.memory** memory B cells

**Plasma.cells** Plasma cells

**T.cells.CD8** CD8 T cells

**T.cells.CD4.naive** naive CD4 T cells

**T.cells.CD4.memory.resting** resting memory CD4 T cells

**T.cells.CD4.memory.activated** activated memory CD4 T cells

**T.cells.follicular.helper** follicular helper T cells

**T.cells.regulatory.Tregs.** regulatory T cells

**T.cells.gamma.delta** gamma delta T cells  
**NK.cells.resting** resting natural killer cells  
**NK.cells.activated** activated natural killer cells  
**Monocytes** monocytes  
**Macrophages.M0** M0 macrophages  
**Macrophages.M1** M1 macrophages  
**Macrophages.M2** M2 macrophages  
**Dendritic.cells.resting** resting dendritic cells  
**Dendritic.cells.activated** activated dendritic cells  
**Mast.cells.resting** resting mast cells  
**Mast.cells.activated** activated mast cells  
**Eosinophils** eosinophils  
**Neutrophils** neutrophils

## References

Aaron M. Newman, Chih Long Liu, Michael R. Green, Andrew J. Gentles, Weiguo Feng, Yue Xu, Chuong D. Hoang, Maximilian Diehn and Ash A. Alizadeh. Robust enumeration of cell subsets from tissue expression profiles.

---

 mixture

*Gene-expression data from 14 follicular lymphoma patients*

---

## Description

This gene-expression dataset consists of surgical lymph node biopsies of 14 follicular lymphoma patients with 19416 genes. It is available on Gene Expression Omnibus (GEO) with accession number GSE65135. <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE65135>.

## Usage

mixture

## Format

A data frame with 19416 rows and 14 variables:

**GSM1587831** FL lymph node biopsy, untreated, 1063  
**GSM1587832** FL lymph node biopsy, untreated, 1080  
**GSM1587833** FL lymph node biopsy, untreated, 575  
**GSM1587834** FL lymph node biopsy, untreated, 581  
**GSM1587835** FL lymph node biopsy, untreated, 598

**GSM1587836** FL lymph node biopsy, untreated, 639  
**GSM1587837** FL lymph node biopsy, untreated, 664  
**GSM1587838** FL lymph node biopsy, untreated, 666  
**GSM1587839** FL lymph node biopsy, untreated, 695  
**GSM1587840** FL lymph node biopsy, untreated, 706  
**GSM1587841** FL lymph node biopsy, untreated, 726  
**GSM1587842** FL lymph node biopsy, untreated, 731  
**GSM1587843** FL lymph node biopsy, untreated, 944  
**GSM1587844** FL lymph node biopsy, untreated, 959

## References

Aaron M. Newman, Chih Long Liu, Michael R. Green, Andrew J. Gentles, Weiguo Feng, Yue Xu, Chuong D. Hoang, Maximilian Diehn and Ash A. Alizadeh. Robust enumeration of cell subsets from tissue expression profiles.

---

sample.sim	<i>Generate random sample with different proportion of outliers and leverage points</i>
------------	---

---

## Description

Generate random sample with different proportion of outliers and leverage points

## Usage

```
sample.sim(n, p, sig, a1, a2, nn = TRUE, intercept = FALSE)
```

## Arguments

n	number of observations.
p	number of independent variables (predictors).
sig	variance of dependent variable.
a1	proportion of outliers.
a2	proportion of leverage points in outliers.
nn	whether coefficients are non-negative, default TRUE.
intercept	whether intercept is included in model, default TRUE.

## Value

y: vector of dependent variable.  
 x: matrix of predictors with n rows and p columns.  
 loc: index of added outliers.  
 beta: vector of coefficients.

**Author(s)**

Yuning Hao, Ming Yan, Blake R. Heath, Yu L. Lei and Yuying Xie

**References**

Yuning Hao, Ming Yan, Blake R. Heath, Yu L. Lei and Yuying Xie. Fast and Robust Deconvolution of Tumor Infiltrating Lymphocyte from Expression Profiles using Least Trimmed Squares. <doi:10.1101/358366>

**Examples**

```
library(FARDEEP)
samp = sample.sim(n = 500, p = 20, sig = 1, a1 = 0.1, a2 = 0.2, nn = TRUE, intercept = TRUE)
```

---

tuningBIC	<i>Tuning parameter k in function alts using Bayesian Information Criterion (BIC) with some adjustment.</i>
-----------	---

---

**Description**

Tuning parameter k in function alts using Bayesian Information Criterion (BIC) with some adjustment.

**Usage**

```
tuningBIC(x, y, alpha1 = 0.1, alpha2 = 1.5, up = 10, low = 1,
          nn = TRUE, intercept = TRUE, lognorm = TRUE)
```

**Arguments**

x	input matrix of predictors with n rows and p columns.
y	input vector of dependent variable with length n.
alpha1	parameter used to adjust the upper bound of outliers. Take value from 0 to 1, default 0.1.
alpha2	parameter used to adjust the lower bound of outliers. Take value larger than 1, default 1.5.
up	upper bound of parameter k in function alts, default 10.
low	lower bound of parameter k in function alts, default 1.
nn	whether coefficients are non-negative, default TRUE.
intercept	whether intercept is included in model, default TRUE.
lognorm	whether noise is log-normal distributed, default TRUE.

**Value**

k: tuning result of parameter k for function alts.

**Author(s)**

Yuning Hao, Ming Yan, Blake R. Heath, Yu L. Lei and Yuying Xie

**References**

Yuning Hao, Ming Yan, Blake R. Heath, Yu L. Lei and Yuying Xie. Fast and Robust Deconvolution of Tumor Infiltrating Lymphocyte from Expression Profiles using Least Trimmed Squares. <doi:10.1101/358366>

**Examples**

```
library(FARDEEP)
samp = sample.sim(n = 500, p = 20, sig = 1, a1 = 0.1, a2 = 0.2, nn = TRUE, intercept = TRUE)
k = tuningBIC(samp$x, samp$y, lognorm = FALSE)
```



# Index

## \*Topic **datasets**

LM22, 4

mixture, 5

alts, 2

fardeep, 3

LM22, 4

mixture, 5

sample.sim, 6

tuningBIC, 7