

Package ‘LFDR.MLE’

October 2, 2019

Type Package

Title Estimation of the Local False Discovery Rates by Type II Maximum Likelihood Estimation

Version 1.0.1

Date 2015-07-30

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Description Suite of R functions for the estimation of the local false discovery rate (LFDR) using Type II maximum likelihood estimation (MLE).

License GPL-3

Depends stats, methods

URL <http://www.cran.r-project.org>, <http://www.statomics.com>

NeedsCompilation no

Repository CRAN

Date/Publication 2019-10-02 15:53:57 UTC

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LFDR.MLE-package	<i>Estimation of the Local False Discovery Rate using Type II Maximum Likelihood Estimation.</i>
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Description

Suite of R functions for the estimation of the local false discovery rate (LFDR) using Type II maximum likelihood estimation (MLE).

Details

Package:	LFDR.MLE
Type:	Package
Version:	1.0
Date:	2015-07-30
License:	GPL-3
Depends:	R (>= 2.14.0), stats, methods
URL:	http://www.cran.r-project.org , http://www.statomics.com

Author(s)

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References

Yang, Y., & Bickel, D. R. (2010). Minimum description length and empirical Bayes methods of identifying SNPs associated with disease. Technical Report, Ottawa Institute of Systems Biology, COBRA Preprint Series, Article 74, available at biostats.bepress.com/cobra/ps/art74.

Bickel, D. R. (2010). Minimum description length methods of medium-scale simultaneous inference. arXiv preprint [arXiv:1009.5981](https://arxiv.org/abs/1009.5981).

Padilla, M., & Bickel, D. R. (2012). Estimators of the local false discovery rate designed for small numbers of tests. *Statistical Applications in Genetics and Molecular Biology*, 11(5), art. 4.

Examples

```
dFUN<-dabsTd; dfx <- 4
n.alternative <- 3; n.null <- 4; true.ncp <- 7

#NOTE: arguments for dFUN are x, df, ncp. If dFUN has other arguments,
#please adapt them. For example:
#dFUN<-function(x,df,ncp){dnorm(x=x,mean=ncp,sd=df)};attr(dFUN,'name')<-'dnorm'
```

```

#In the examples, W is the result of the absolute value of the t.test statistics
#on the data

W<-abs(c(rt(n=n.alternative,ncp=true.ncp,df=dfx),rt(n=n.null,ncp=0,df=dfx)))
W[c(1,3,5)]<-NA

z1<-lfdr.mle(x=W,dfUN=dfUN, df=dfx)
z2<-lfdr.mle(x=W,dfUN=dfUN, df=dfx, fixed.p0=0.4, fixed.ncp=4)
z3<-lfdr.mdl(x=W,df=dfx,dfUN=dfUN)
z4<-lfdr.llo(x=W,df=dfx,dfUN=dfUN)
z5<-lfdr.lho(x=W,df=dfx,dfUN=dfUN, fixed.ncp=5)
z6<-lfdr.lo(x=W,v=1/3,df=dfx,dfUN=dfUN)
z7<-lfdr.mdlo(x=W,v=1/3,df=dfx,dfUN=dfUN)

```

dabsTd

Density of the absolute Student t Distribution.

Description

Density of the absolute t distribution with df degrees of freedom and non-centrality parameter ncp.

Usage

```
dabsTd(x, df, ncp = 0, ...)
```

Arguments

x	vector of quantiles.
df	degrees of freedom (>0).
ncp	noncentrality parameter.
...	arguments to pass to functions dt from basic R.

Value

numeric of length equal to the length of x.

Author(s)

Code: David R. Bickel,
Documentation: Alaa Ali, Kyle Leckett, Marta Padilla.

See Also

Function [dt](#) from basic R.

Examples

```
z1<-dabsTd(x = c(1:4), df = 3, ncp = 3)
```

lfdr.lho, lfdr.llo	<i>Leave-one-out (LIO) and leave-half-out (LHO) method for LFDR estimation.</i>
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Description

Estimate the local false discovery rate using the leave-one-out method (LIO) or the leave-half-out method (LHO).

Usage

```
lfdr.llo(x, dFUN = dabsTd, lower.ncp = 0.001, upper.ncp = 20, lower.p0 = 0,
         upper.p0 = 1, fixed.p0 = NULL, fixed.ncp = NULL, d0 = 0, ...)
```

```
lfdr.lho(x, dFUN = dabsTd, lower.ncp = 0.001, upper.ncp = 20, lower.p0 = 0,
         upper.p0 = 1, fixed.p0 = NULL, fixed.ncp = NULL, d0 = 0, ...)
```

```
lfdr.lo(x, dFUN = dabsTd, lower.ncp = 0.001, upper.ncp = 20, lower.p0 = 0,
        upper.p0 = 1, fixed.p0 = NULL, fixed.ncp = NULL, v = 0, d0 = 0, ...)
```

Arguments

x	Input numeric vector of statistics.
dFUN	Density function; default dabsTd (from absolute value of the Student t distribution)
lower.ncp	The lowerbound of the location parameter of dFUN (noncentrality parameter for default dFUN=dabsTd); default value is 0.001
upper.ncp	The upperbound of the location parameter of dFUN (noncentrality parameter for default dFUN=dabsTd); default value is 20
lower.p0	The lowerbound of p0 (proportion of unaffected features (null hypothesis)); default value is 0
upper.p0	The upperbound of p0 (proportion of unaffected features (null hypothesis)); default value is 1
fixed.p0	A fixed value of p0 (proportion of unaffected features (null hypothesis)); default value is NULL
fixed.ncp	A fixed value of the location parameter of dFUN (noncentrality parameter for default dFUN=dabsTd); default value is NULL
v	v in [0,1], portion of one feature that is considered in turn to estimate the LFDR; default value is v=0 (for lfdr.llo (LIO)) and v=1/2 (for lfdr.lho (LHO)). For other values of v, use lfdr.lo.
d0	the numeric value of the null hypothesis for dFUN, default value is 0.
...	Other parameters to pass to dFUN (see notes and examples).

Value

A list with:

LFDR.hat	estimates of the LFDR
p0.hat	estimate of the proportion of unaffected features p0 (true null hypothesis).
ncp.hat	estimate of the location parameter of the distribution dFUN (ncp: noncentrality parameter of dFUN=dabsTd by default).
info	method name and information about computation failure.

Note

- Requires `fixed.p0=NULL`.
- The probability density function (dFUN) can be set to any other distribution, adapted so that the location parameter corresponds to ncp, other parameter to df and any other can be passed to dFUN by the dots (see examples in [lfd.r.mle](#)).
- If computation fails for all features, p0.hat is set to NA and so is LFDR.hat, which is a vector of NA with length equal to the number of features. If it fails for a given feature, only the resulting LFDR for that feature is set to NA. Error messages are not suppressed.

Author(s)

Code: Marta Padilla
 Documentation: Alaa Ali, Kyle Leckett, Marta Padilla.

References

Padilla, M., & Bickel, D. R. (2012). Estimators of the local false discovery rate designed for small numbers of tests. *Statistical Applications in Genetics and Molecular Biology*, 11(5), art. 4.

See Also

[lfd.r.mle](#), [lfd.r.mdl](#).

Examples

```
dfx <- 4;n.alt <- 1;n.null <- 4>true.ncp <- 7
#numeric input data: statistics of the data with missing values (removed internally)
#(result of a absolute t.test statistics on the data)
W<-abs(c(rt(n=n.alt,ncp=true.ncp,df=dfx),rt(n=n.null,ncp=0,df=dfx)))
W[3]<-NA

z1<-lfd.r.llo(x=W,df=dfx)
z2<-lfd.r.lho(x=W,df=dfx,fixed.ncp=10)
z3<-lfd.r.lo(x=W,df=dfx,v=1/3,fixed.p0=0.3)
```

lfdr.mdl

*Minimum description length (MDL) method for estimation of LFDR.***Description**

Estimate the local false discovery rate using the minimum description length (MDL) method.

Usage

```
lfdr.mdl(x, dFUN = dabsTd, lower.ncp = 0.001, upper.ncp = 20, lower.p0 = 0,
         upper.p0 = 1, fixed.p0 = NULL, fixed.ncp = NULL, d0 = 0, ...)
```

```
lfdr.mdlo(x, v = 0, dFUN = dabsTd, lower.ncp = 0.001, upper.ncp = 20,
          lower.p0 = 0, upper.p0 = 1, fixed.p0 = NULL, fixed.ncp = NULL,
          d0 = 0, ...)
```

Arguments

x	Input numeric vector of statistics.
dFUN	Density function; default dabsTd (from absolute value of the Student t distribution)
v	v in [0,1], portion of one feature that is considered in turn to estimate the LFDR; default value is v=0 (for lfdr.l1o (L1O)) and v=1/2 (for lfdr.lho (LHO)). For other values of v, use lfdr.lo.
lower.ncp	The lowerbound of the location parameter of dFUN (noncentrality parameter for default dFUN=dabsTd); default value is 0.001
upper.ncp	The upperbound of the location parameter of dFUN (noncentrality parameter for default dFUN=dabsTd); default value is 20
lower.p0	The lowerbound of p0 (proportion of unaffected features (null hypothesis)); default value is 0
upper.p0	The upperbound of p0 (proportion of unaffected features (null hypothesis)); default value is 1
fixed.p0	A fixed value of p0 (proportion of unaffected features (null hypothesis)); default value is NULL
fixed.ncp	A fixed value of the location parameter of dFUN (noncentrality parameter for default dFUN=dabsTd); default value is NULL
d0	the numeric value of the null hypothesis for dFUN, default value is 0.
...	Other parameters to pass to dFUN (see notes and examples).

Value

A list with:

LFDR.hat	estimates of the LFDR
p_0 .hat	estimate of the proportion of unaffected features p_0 (true null hypothesis).
ncp.hat	estimate of the location parameter of the distribution dFUN (ncp: noncentrality parameter of dFUN=dabsTd by default).
info	method name and information about computation failure.

Note

- The probability density function (dFUN) can be set to any other distribution, adapted so that the location parameter corresponds to ncp, other parameter to df and any other can be passed to dFUN by the dots (see examples in [lfdr.mle](#)).

- If computation fails for all features, p_0 .hat is set to NA and so is LFDR.hat, which is a vector of NA with length equal to the number of features. If it fails for a given feature, only the resulting LFDR for that feature is set to NA. Error messages are not suppressed.

Author(s)

Code: Marta Padilla

Documentation: Alaa Ali, Kyle Leckett, Marta Padilla.

References

Bickel, D. R. (2010). Minimum description length methods of medium-scale simultaneous inference. arXiv preprint arXiv:1009.5981.

Padilla, M., & Bickel, D. R. (2012). Estimators of the local false discovery rate designed for small numbers of tests. *Statistical Applications in Genetics and Molecular Biology*, 11(5), art. 4.

See Also

[lfdr.mle](#), [lfdr.l1o](#).

Examples

```
dfx <- 4;n.alt <- 1;n.null <- 4>true.ncp <- 7
#numeric imput data: statistics of the data with missing values (removed internally)
#(result of a absolute t.test statistics on the data)
W<-abs(c(rt(n=n.alt,ncp=true.ncp,df=dfx),rt(n=n.null,ncp=0,df=dfx)))
W[3]<-NA

z1<-lfdr.mdl(x=W,df=dfx)
z2<-lfdr.mdl(x=W,df=dfx,fixed.ncp=10)
z3<-lfdr.mdlo(x=W,df=dfx,v=1/3,fixed.p0=0.3)
```

lfdR.mle

*Type II Maximum likelihood estimate of LFDR (LFDR-MLE).***Description**

Estimates the local false discovery rate by the Type II maximum likelihood estimates (MLE).

Usage

```
lfdR.mle(x, dFUN = dabsTd, lower.ncp = 0.001, upper.ncp = 20, lower.p0 = 0, upper.p0 = 1,
        fixed.p0 = NULL, fixed.ncp = NULL, d0 = 0, ...)
```

Arguments

x	Input numeric vector of statistics.
dFUN	Density function; default dabsTd (from absolute value of the Student t distribution)
lower.ncp	The lowerbound of the location parameter of dFUN (noncentrality parameter for default dFUN=dabsTd); default value is 0.001
upper.ncp	The upperbound of the location parameter of dFUN (noncentrality parameter for default dFUN=dabsTd); default value is 20
lower.p0	The lowerbound of p0 (proportion of unaffected features (null hypothesis)); default value is 0
upper.p0	The upperbound of p0 (proportion of unaffected features (null hypothesis)); default value is 1
fixed.p0	A fixed value of p0 (proportion of unaffected features (null hypothesis)); default value is NULL
fixed.ncp	A fixed value of the location parameter of dFUN (noncentrality parameter for default dFUN=dabsTd); default value is NULL
d0	the numeric value of the null hypothesis for dFUN, default value is 0.
...	Other parameters to pass to dFUN (see notes and examples).

Value

A list with:

LFDR.hat	estimates of the LFDR
p0.hat	estimate of the proportion of unaffected features p0 (true null hypothesis).
ncp.hat	estimate of the location parameter of the distribution dFUN (ncp: noncentrality parameter of dFUN=dabsTd by default).
info	method name and information about computation failure.

Note

- The probability density function (dFUN) can be set to any other distribution, adapted so that the location parameter corresponds to ncp, other parameter to df and any other can be passed to dFUN by the dots (see examples in [lfdR.mle](#)).
- If computation fails for all features, $p\hat{0}$ is set to NA and so is LFDR.hat, which is a vector of NA with length equal to the number of features. If it fails for a given feature, only the resulting LFDR for that feature is set to NA. Error messages are not suppressed.

Author(s)

Code: Ye Yang, Marta Padilla, Zhenyu Yang, Zuoqing Li, Corey M. Yanofsky
 Documentation: Alaa Ali, Kyle Leckett, Marta Padilla.

References

Yang, Y., & Bickel, D. R. (2010). Minimum description length and empirical Bayes methods of identifying SNPs associated with disease. Technical Report, Ottawa Institute of Systems Biology, COBRA Preprint Series, Article 74, available at biostats.bepress.com/cobra/ps/art74.

Bickel, D. R. (2010). Minimum description length methods of medium-scale simultaneous inference. arXiv preprint [arXiv:1009.5981](https://arxiv.org/abs/1009.5981).

Padilla, M., & Bickel, D. R. (2012). Estimators of the local false discovery rate designed for small numbers of tests. *Statistical Applications in Genetics and Molecular Biology*, 11(5), art. 4.

See Also

[lfdR.mdl](#), [lfdR.l1o](#), [lfdR.lho](#).

Examples

```
#numeric input data: statistics of the data with missing values (removed internally)
#(result of a absolute t.test statistics on the data)
dfx <- 4;n.alt <- 1;n.null <- 4>true.ncp <- 7
W<-abs(c(rt(n=n.alt,ncp=true.ncp,df=dfx),rt(n=n.null,ncp=0,df=dfx)))
W[3]<-NA

z1<-lfdR.mle(x=W,dFUN=dabsTd, df=dfx)
z2<-lfdR.mle(x=W,dFUN=dabsTd, df=dfx, fixed.p0=0.4, fixed.ncp=4)

#other dFUN -----
#NOTE: arguments for dFUN are x, df, ncp. If dFUN has other arguments,
#please adapt them. For example:

new.df<-function(x,df,ncp,...){df(x=x,ncp=ncp,df1=df,...)}
z3<-lfdR.mle(x=W,df=dfx,dFUN=new.df,df2=5)
```

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