

# Package: LFDR.MME (via r-universe)

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**Type** Package

**Title** Estimating Local False Discovery Rates Using the Method of Moments

**Version** 1.0

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**Author** Ali Karimnezhad

**Maintainer** Ali Karimnezhad <ali.karimnezhad@gmail.com>

**Description** Estimation of the local false discovery rate using the method of moments.

**Depends** R(>= 2.14.2)

**Encoding** UTF-8

**biocViews** Bayesian, MathematicalBiology, MultipleComparison

**License** GPL-3

**RoxygenNote** 7.1.1

**NeedsCompilation** no

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

**RemoteUrl** <https://github.com/cran/LFDR.MME>

**RemoteRef** HEAD

**RemoteSha** b029ba29a7e5b4e9b9ade6355757591b42a6daec

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`LFDR.MM`*Performs a Multiple Hypothesis Testing Using the Method of Moments*

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**Description**

Based on a given vector of chi-square test statistics, provides estimates of local false discoveries.

**Usage**`LFDR.MM(x)`**Arguments**

`x` A vector of chi-square test statistics with one degree of freedom.

**Details**

For  $N$  given features (genes, proteins, SNPs, etc.), the function tests the null hypothesis  $H_{0i}$ ,  $i = 1, \dots, N$ , indicating that there is no association between feature  $i$  and a specific disease, versus its alternative hypothesis  $H_{1i}$ . For each unassociated feature  $i$ , it is supposed that the corresponding test statistic  $x_i$  follows a central chi-square distribution with one degree of freedom. For each associated feature  $i$ , it is assumed that the corresponding test statistic  $x_i$  follows a non-central chi-square distribution with one degree of freedom and non-centrality parameter  $\lambda$ . In this package, association is measured by estimating the local false discovery rate (LFDR), the posterior probability that the null hypothesis  $H_{0i}$  given the test statistic  $x_i$  is true. This package returns three components as mentioned in the **Value** section.

**Value**

Outputs three elements as seen below:

|                       |                                                                                                     |
|-----------------------|-----------------------------------------------------------------------------------------------------|
| <code>pi0.hat</code>  | estimate of proportion of unassociated features $\pi_0$ .                                           |
| <code>ncp.hat</code>  | estimate of the non-centrality parameter $\lambda$ of the chi-square model for associated features. |
| <code>lfdr.hat</code> | estimates of local false discovery rates.                                                           |

**Author(s)**

Code: Ali Karimnezhad.  
Documentation: Ali Karimnezhad.

**References**

Karimnezhad, A. (2020). A Simple Yet Efficient Parametric Method of Local False Discovery Rate Estimation Designed for Genome-Wide Association Data Analysis. Retrieved from <https://arxiv.org/abs/1909.13307>

**Examples**

```
# vector of test statistics for associated features
stat.assoc<- rchisq(n=1000,df=1, ncp = 3)

# vector of test statistics for unassociated features
stat.unassoc<- rchisq(n=9000,df=1, ncp = 0)

# vector of test statistics
stat<- c(stat.assoc,stat.unassoc)

output <- LFDR.MM(x=stat)

# Estimated  $\pi_0$ 
output$p0.hat

# Estimated non-centrality parameter
output$ncp.hat

# Estimated LFDRs
output$lfdr.hat
```

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