Package ‘MeasurementError.cor’

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Title Measurement Error model estimate for correlation coefficient
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Description Two-stage measurement error model for correlation estimation with smaller bias than the usual sample correlation
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cor.me.matrix  A function to calculate measurement error estimates for all pairs of genes given by the matrix

Description

Given a matrix (p x n) for observed values of p variables and a corresponding matrix for their standard errors, the all pairwise measurement error estimates for true correlations are returned

Usage

   cor.me.matrix(exp, se)

Arguments

   exp observed value matrix
   se  standard error matrix
Value

The final estimates for true correlation (i.e. \texttt{cor.true}) from the measurement error model.

Note

The function involves using quasi-newton for linear optimization, "BFGS" is the only implemented method now. Refer to \texttt{cor.me.vector} for more details.

Author(s)

Beiying Ding

References


See Also

cor.me.vector

Examples

\begin{verbatim}
exp <- matrix(abs(rnorm(200,1000,20)),ncol=10)
se <- matrix(abs(rnorm(200,50,5)),ncol=10)
cor.me.matrix(exp,se)
\end{verbatim}
Value

- **Value**
  - **estimate**
    - Vecotr containing the estimates from the measurement error model, i.e. `cor.me`, `cor.true`, `mu1`, `mu2`, `s1`, `s2` which are correlation for the measurement error distribution of the two variables, true correlation between the two variables, and true mean and standard deviation estimates for the two variables respectively.
  - **count**
    - number of function and gradient evaluation
  - **convergence**
    - 0 if converged. See `optim()` for details.

Note

- Most applicable for microarray expression data where standard errors are readily estimated by most low level analysis softwares. Hence variables can be thought of as genes. One also need to differentiate between `cor.me` and `cor.true`: the first one being the correlation between the measurement error distributions of the two genes whereas the second one is the quantity of interest, i.e true correlation between the two gene expression profiles.
- The function involves using quasi-newton for linear optimization, "BFGS" is the only implemented method now.

Author(s)

- Beiying Ding

References


See Also

- `cor.me.matrix`

Examples

```r
exp <- matrix(abs(rnorm(200,1000,20)),ncol=10)
se <- matrix(abs(rnorm(200,50,5)),ncol=10)
cor.me.vector(exp[1,],se[1,],exp[2,],se[2,])
```
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