

# MeasurementError.cor

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<code>cor.me.matrix</code>	<i>A function to calculate measurement error estimates for all pairs of genes given by the matrix</i>
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## Description

Given a matrix ( $p \times n$ ) 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

<code>exp</code>	observed value matrix
<code>se</code>	standard error matrix

## Value

The final estimates for true correlation (i.e. `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 `cor.me.vector` for more details.

## Author(s)

Beiyong Ding

## References

Ding, B. Y. and Gentleman, R.(2003) Measurement error model for correlation coefficient estimation and its application in microarray analysis

## See Also

`cor.me.vector`

**Examples**

```
exp <- matrix(abs(rnorm(200,1000,20)),ncol=10)
se <- matrix(abs(rnorm(200,50,5)),ncol=10)
cor.me.matrix(exp,se)
```

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cor.me.vector	<i>A function to calculate measurement error model estimates for correlation coefficient between two variables</i>
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**Description**

Given the observed value of two variables and their respective standard error, the measurement error estimate for their correlation coefficient is returned

**Usage**

```
cor.me.vector(exp1, se1, exp2, se2)
```

**Arguments**

exp1	observed value for vector 1
se1	estimated standard error for vector 1
exp2	observed value for vector 2
se2	estimated standard error for vector 2

**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	numer 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)**

Beiyong Ding

**References**

Ding, B.Y. and Gentleman, R. (2003) Measurement Error Model for correlation coefficient estimation and its application in microarray analysis

**See Also**

`cor.me.matrix`

**Examples**

```
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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