

Package ‘mbend’

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Title Matrix Bending

Version 1.2.4

Description Bending non-positive-definite (symmetric) matrices to positive-definite, using weighted and unweighted methods.

Jorjani, H., et al. (2003) <doi:10.3168/jds.S0022-0302(03)73646-7>.

Schaeffer, L. R. (2010) <<http://animalbiosciences.uoguelph.ca/~lrs/piksLRS/PDforce.pdf>>.

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LazyData true

URL <https://github.com/nilforooshan/mbend>

BugReports <https://github.com/nilforooshan/mbend/issues>

RoxygenNote 7.0.2

Encoding UTF-8

Repository GitHub

Suggests knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

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Description

(Co)variance or correlation matrices are required in multivariate mixed models. For example, in multi-trait animal models, genetic and residual (co)variance matrices are required, involving the traits of interest. These matrices need to be positive definite (PD), mainly because those need to be inverted and non-PD matrices are not invertible. Variance component estimation is computationally expensive, especially for big data and many variables. As a result, the full (co)variance matrix may be assembled by combining smaller (co)variance matrices from variance component estimation analyses on subsets of variables. Possible missing covariances are filled with values from the literature or the best possible guess. Consequently, the assembled matrix may not be PD, and it needs to be bended to a PD matrix before being used in the model.

Details

A method for weighted bending of (co)variance matrices was developed by Jorjani et al. (2003), in which the matrix of interest is decomposed to matrices of eigenvectors and eigenvalues. Iteratively, eigenvalues smaller than a small positive value (close to 0) are replaced with that small positive value and the matrix is rebuilt, until the convergence is met (i.e., all eigenvalues being positive). Because there are different amount of data and certainty associated with different elements of the matrix, weighting factors should be involved, which are introduced through a symmetric matrix. Certainty associated with the elements of the matrix and the corresponding weights are inversely related. For example, the reciprocal of the number of common data points (i.e., data points in common between pairs of variables) can be used as weighting factors. Alternatively, number of data points can be used directly by setting the argument `reciprocal = TRUE`. To keep specific elements of the matrix unchanged during the bending process, set corresponding weights to 0. Providing no weight matrix is equivalent to unweighted bending. Another method implemented in this package is from Schaeffer (2010), which can be defined by using the argument `method = "lrs"`. If no method is defined, the default method = "hj" (Jorjani et al., 2003) is used. As a development to the method of Schaeffer (2010), a weight matrix can be used for weighted bending. Any (co)variance matrix with all diagonal elements equal to 1 is considered as a correlation matrix by the program.

Author(s)

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References

- Jorjani, H., et al. (2003). A Simple Method for Weighted Bending of Genetic (Co)variance Matrices. *J. Dairy Sci.*, 86:677-679. <doi:10.3168/jds.S0022-0302(03)73646-7>
- Schaeffer, L. R. (2010). Modification of negative eigenvalues to create positive definite matrices and approximation of standard errors of correlation estimates. Available at: [Link](#)

bend	<i>Matrix bending to positive-definite</i>
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Description

Bending a non-positive-definite matrix to positive-definite, using weighted or unweighted methods.

Usage

```
bend(
  inmat,
  wtmatrix,
  reciprocal = FALSE,
  max.iter = 10000,
  small.positive = 1e-04,
  method = "hj"
)
```

Arguments

inmat	: The matrix to be bended.
wtmat	: The weight matrix for weighted bending. If no input is provided, the un-weighted method (default) is used.
reciprocal	: If TRUE, reciprocal of the weighting factors are used. If no input is provided, default = FALSE.
max.iter	: Maximum number of iterations. If no input is provided, default = 10000.
small.positive	: A small positive value replacing smaller eigenvalues. If no input is provided, default = 0.0001.
method	: "hj" (Jorjani et al., 2003) or "lrs" (Schaeffer, 2010), default = "hj"

Value

bended : The output bended matrix.

Examples

```
# Test data
V = matrix(nrow=5, ncol=5, c( # matrix to be bended
  100, 95, 80, 40, 40,
  95, 100, 95, 80, 40,
  80, 95, 100, 95, 80,
  40, 80, 95, 100, 95,
  40, 40, 80, 95, 100))
W = matrix(nrow=5, ncol=5, c( # matrix of weights
  1000, 500, 20, 50, 200,
  500, 1000, 500, 5, 50,
  20, 500, 1000, 20, 20,
```

```
50, 5, 20, 1000, 200,  
200, 50, 20, 200, 1000))
```

```
# Example 1: Unweighted bending
```

```
bend(V)
```

```
## The default method (Jojani et al. 2003) is used.
```

```
# Example 2: Weighted bending using reciprocal of the weighting factors
```

```
bend(inmat=V, wtmat=W, reciprocal=TRUE)
```

```
# Example 3: Bending with fixed elements
```

```
## Assume we want to keep V[1:2, 1:2] constant.
```

```
W2 = W; W2[1:2, 1:2] = 0
```

```
bend(inmat=V, wtmat=W2, reciprocal=TRUE)
```

```
# Example 4: Bending a correlation matrix
```

```
V2 = cov2cor(V)
```

```
bend(V2, W, reciprocal=TRUE)
```

```
# Example 5: Bending using the method of Schaeffer (2010)
```

```
bend(inmat=V, method="lrs")
```

```
# Example 6: Bending a correlation matrix using the method of Schaeffer (2010)
```

```
bend(V2, method="lrs")
```

```
# Example 7: Bending the same correlation matrix using a weighted development of Schaeffer (2010)
```

```
bend(V2, W, reciprocal=TRUE, method="lrs")
```

```
# Example 8: Bending a covariance matrix using a weighted development of Schaeffer (2010)
```

```
bend(V, W, reciprocal=TRUE, method="lrs")
```

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