

# Package ‘tensorMam’

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**Type** Package

**Title** tensorMam

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**Description** A tensor Estimation approach to multivariate additive models. The B-splines are used to approximate unknown function. The number of predictors can be diverged as sample size increases, in which the penalty LASSO, MCP or SCAD can be used.

**License** GPL (>= 2)

**Imports** splines, Rcpp (>= 0.11.15), RcppEigen (>= 0.3.2.3.0)

**LinkingTo** Rcpp, RcppEigen

**RoxygenNote** 6.0.1

**NeedsCompilation** yes

**Repository** github

**URL** <https://github.com/xliusufe/tensorMam>

**Encoding** UTF-8

## R topics documented:

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tensorMam-package	<i>A tensor estimation approach to multivariate additive models</i>
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## Description

For a high-dimensional multivariate additive model (MAM) using B-splines, with or without aparsity assumptions, treating the coefficients as a third-order tensor and borrowing Tucker decomposition to reduce the number of parameters. The multivariate sparse group lasso (mcp or scad) and the coordinate descent algorithm are used to estimate functions for sparsity situation.

## Details

This section should provide a more detailed overview of how to use the package, including the most important functions.

## Author(s)

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## References

A tensor estimation approach to multivariate additive models.

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breastData	<i>Breast cancer gene expression and DNA copy number dataset</i>
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## Description

The breast cancer dataset includes gene expressions and comparative genomic hybridization measurements for 89 subjects, which is from Chin et al. (2006). This dataset has been considered by Witten et al. (2009) and Chen et al. (2013). In our paper, we selected chromosome 21, including  $q = 44$  variables for copy-number variations and  $p = 227$  variables for gene expression. As in Chen et al. (2013), we consider copy-number variations as the responses and gene expressions as the predictors.

## Usage

```
data(breastData)
```

## Details

The "breastData" is formatted as a list with elements:

dna:	the CGH spots , a matrix with size $2149 \times 89$ and the sample size 89
rna:	genes, a matrix with size $19672 \times 89$ and the sample size 89
chrom:	chromosomal location of each CGH spot, a 2149-vector
nuc:	nucleotide position of each CGH spot, a 2149-vector
gene:	an accession number for each gene, a 19672-vector
genenames:	gene name, a 19672-vector

genechr: chromosomal location of each gene, a 19672-vector  
 genedesc: description of each gene, a 19672-vector  
 genepos: nucleotide position of each gene, a 19672-vector

## References

Chin, K., DeVries, S., Fridlyand, J., Spellman, P., Roydasgupta, R., Kuo, W.-L., Lapuk, A., Neve, R., Qian, Z., Ryder, T., Chen, F., Feiler, H., Tokuyasu, T., Kingsley, C., Dairkee, S., Meng, Z., Chew, K., Pinkel, D., Jain, A., Ljung, B., Esserman, L., Albertson, D., Waldman, F. & Gray, J. (2006). Genomic and transcriptional aberrations linked to breast cancer pathophysiologies. *Cancer cell* **10** (6), 429-541.

Witten, D. M., Tibshirani, R. and Hastie, T. (2009). A penalized matrix decomposition, with applications to sparse principal components and canonical correlation analysis. *Biostatistics* **10** (3), 515-534.

Chen, K., Dong, H., and Chan, K. S. (2013). Reduced rank regression via adaptive nuclear norm penalization. *Biometrika*, **100** (4), 901-920.

## Examples

```
data(breastData)
attach(breastData)
Y = t(dna[chrom==21,])
Xt = t(rna[which(genechr==21),])
n = nrow(Y)

minX = apply(Xt,2,min)
maxX = apply(Xt,2,max)
X = (Xt - matrix(rep(minX,each = n),n))/matrix(rep(maxX-minX,each = n),n)
Y = scale(Y)
fit <- mam_sparse_dr(Y[,1:5], X[,1:10])
D3hat <- fit$Dnew
opt <- fit$rk_opt
detach(breastData)
```

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generateData	<i>Generate data from MAM model.</i>
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## Description

Generate data for a high-dimensional multivariate additive model, with or without aparsity assumptions.

## Usage

```
generateData(n, q, p, s, D2, sigma2=NULL, indexF=NULL, seed_id=NULL)
```

**Arguments**

n	Sample size.
q	The number of responses, $q \geq 1$ .
p	The number of covariates, $p \geq 1$ .
s	The true covariates associating to response, $s \geq 1$ .
D2	The mode of unfolding $D_{(2)}$ .
sigma2	err variance. Default is 0.1.
indexF	A $q \times s$ matrix. The index of significant predictors corresponding to response $y_i$ . Default is the matrix with each row being $(1, 2, \dots, s)$ .
seed_id	A positive integer, the seed for generating the random numbers.

**Details**

This function gives pq functional coefficients' estimators of MAM. The singular value matrix of tensor is a  $r_1 \times r_2 \times r_3$ -tensor. We choose  $r_1$ ,  $r_2$  and  $r_3$  by BIC or CV.

**Value**

Y	Response, a $n \times q$ -matrix.
X	Design matrix, a $n \times p$ -matrix.
f0	True functions.

**References**

A tensor estimation approach to multivariate additive models.

**See Also**

mam\_sparse

**Examples**

```
# Example 1

D2 <- matrix(runif(30, 0.7, 1), 2, 15)
mydata <- generateData(200, 3, 5, 5, D2)

Y <- mydata$Y
X <- mydata$X

# Example 2
n <- 500
p <- 10
q <- 10
s <- 10
K <- 6
s0 <- s
r10=r20=r30=2
S3 <- matrix(runif(r10*r20*r30,3,7),nrow = r30)
T1 <- matrix(rnorm(s0*r10),nrow = s0)
U1 <- qr.Q(qr(T1))
```

```

T1 <- matrix(rnorm(K*r20),nrow = K)
U2 <- qr.Q(qr(T1))
T1 <- matrix(rnorm(q*r30),nrow = q)
U3 <- qr.Q(qr(T1))
D3 <- U3%*%S3%*%t(kronecker(U2,U1))
D2 <- TransferModalUnfoldings(D3,3,2,s0,K,q)
mydata <- generateData(n,q,p,s0,D2)

```

mam

*Fit MAM without sparsity assumption and with fixed ranks.*

## Description

Fit a low-dimensional multivariate additive model using B-splines, without aparsity assumptions, and given ranks given ranks  $r_1, r_2, r_3$ .

## Usage

```

mam(Y, X, K = 6, r1 = NULL, r2 = NULL, r3 = NULL, SABC = NULL,
     intercept = TRUE, mu = NULL, degr = 3, eps = 1e-4, max_step = 20)

```

## Arguments

Y	A $n \times q$ numeric matrix of responses.
X	A $n \times p$ numeric design matrix for the model.
K	The number of B-spline base function, that is the plus of both degrees of base functioin and the number of knots. Default is 6.
degr	the number of knots of B-spline base function. Default is 3.
r1	The first dimension of single value matrix of the tensor. Default is 2.
r2	The second dimension of single value matrix of the tensor. Default is 2.
r3	The third dimension of single value matrix of the tensor. Default is 2.
SABC	A user-specified list of initial coefficient matrix of $S, A, B, C$ . By default, initial matrices are provided by random.
intercept	Should intercept(s) be fitted (default=TRUE) or set to zero (FALSE)?
mu	A user-specified initial of intercept(s), a $q$ -vector. Default is 0.
eps	Convergence threshold. The algorithm iterates until the relative change in any coefficient is less than eps. Default is 1e-4.
max_step	Maximum number of iterations. Default is 20.

## Details

This function gives pq functional coefficients' estimators of MAM. The singular value matrix of tensor is a  $r_1 \times r_2 \times r_3$ -tensor. We choose  $r_1, r_2$  and  $r_3$  by BIC or CV.

**Value**

Dnew	Estimator of $D_{(3)}$ .
mu	Estimator of intercept $\mu$ .
rss	Residual sum of squares (RSS).
Y	Response $Y$ .
X	Design matrix $X$ .
Z	Design matrix of Bspline approximation.

**References**

A tensor estimation approach to multivariate additive models.

**See Also**

mam\_sparse

**Examples**

```
D2 <- matrix(runif(50, 0.7, 1), 2, 25) # tensor with size 5*2*5
mydata <- generateData(200, 5, 5, 5, D2)

fit <- mam(mydata$Y, mydata$X)
D3hat <- fit$Dnew
D2hat <- TransferModalUnfoldings(D3hat,3,2,5,2,5)
```

---

mam_dr	<i>Fit MAM without sparsity assumption, and with ranks selected by BIC or CV.</i>
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**Description**

Fit a low-dimensional multivariate additive model using B-splines, without sparsity assumptions, and with ranks  $r_1, r_2, r_3$  selected by BIC or CV.

**Usage**

```
mam_dr(Y, X, method = "BIC", ncv = 10, K_index = NULL, r1_index = NULL,
        r2_index = NULL, r3_index = NULL, SABC = NULL, intercept = TRUE, mu = NULL,
        degr = 3, eps = 1e-4, max_step = 20)
```

**Arguments**

Y	A $n \times q$ numeric matrix of responses.
X	A $n \times p$ numeric design matrix for the model.
method	The method to be applied to select parameters. Either "BIC" (the default), or "CV".
ncv	The number of cross-validation folds. Default is 10. If method is "BIC", ncv is useless.

K_index	A user-specified sequence of $K$ values, where $K$ is the number of B-spline base function. Default is k_index=6.
r1_index	A user-specified sequence of $r_1$ values, where $r_1$ is the first dimension of single value matrix of the tensor. Default is r1_index= $1, \dots, \min(\log(n), p)$ .
r2_index	A user-specified sequence of $r_2$ values, where $r_2$ is the second dimension of single value matrix of the tensor. Default is r2_index= $1, \dots, \max\{K\_index\}$ .
r3_index	A user-specified sequence of $r_3$ values, where $r_3$ is the third dimension of single value matrix of the tensor. Default is r3_index= $1, \dots, \min(\log(n), q)$ .
SABC	A user-specified list of initial coefficient matrix of $S, A, B, C$ , which is a list with values $S, A, B, C$ . By default, initial matrices are provided by random.
intercept	Should intercept(s) be fitted (default=TRUE) or set to zero (FALSE)?
mu	A user-specified initial of intercept(s), a $q$ -vector. Default is $\emptyset$ .
degr	the number of knots of B-spline base function. Default is 3.
eps	Convergence threshold. The algorithm iterates until the relative change in any coefficient is less than eps. Default is $1e-4$ .
max_step	Maximum number of iterations. Default is 20.

## Details

This function gives pq functional coefficients' estimators of MAM. The singular value matrix of tensor is a  $r_1 \times r_2 \times r_3$ -tensor. We choose  $r_1, r_2$  and  $r_3$  by BIC or CV.

## Value

Dnew	Estimator of $D_{(3)}$ .
mu	Estimator of intercept $\mu$ .
rss	Residual sum of squares (RSS).
rk_opt	The optimal parameters that selected by BIC or CV. It is a vector with length 4, which are selected $r_1, r_2, r_3$ , and $K$ .
selected	Which $\lambda$ is selection.
Y	Response $Y$ .
X	Design matrix $X$ .
Z	Design matrix of Bspline approximation.

## References

A tensor estimation approach to multivariate additive models.

## See Also

mam, mam\_sparse\_dr

## Examples

```
D2 <- matrix(runif(50, 0.7, 1), 2, 25) # tensor with size 5*2*5
mydata <- generateData(200, 5, 5, 5, D2)

fit <- mam_dr(mydata$Y, mydata$X)
D3hat <- fit$Dnew
D2hat <- TransferModalUnfoldings(D3hat,3,2,5,2,5)
opt <- fit$rk_opt
```

---

mam\_sparse

*Fit MAM with sparsity assumption and fixed ranks.*


---

## Description

Fit a high-dimensional multivariate additive model using B-splines, with or without sparsity assumptions, and given ranks  $r_1, r_2, r_3$ . The multivariate sparse group lasso (mcp or scad) and the coordinate descent algorithm are used to estimate functions for sparsity situation.

## Usage

```
mam_sparse(Y, X, K = 6, r1 = NULL, r2 = NULL, r3 = NULL, method="BIC", ncv=10,
  penalty="LASSO", isPenColumn=TRUE, lambda = NULL, SABC = NULL, intercept = TRUE,
  mu = NULL, degr = 3, nlam = 20, lam_min = 1e-3, eps1 = 1e-4, maxstep1 = 20,
  eps2 = 1e-4, maxstep2 = 20, gamma = 2, dfmax = NULL, alpha = 1)
```

## Arguments

Y	A $n \times q$ numeric matrix of responses.
X	A $n \times q$ numeric design matrix for the model.
K	The number of B-spline base function, that is the plus of both degrees of base function and the number of knots. Default is 7.
degr	The number of knots of B-spline base function. Default is 3.
r1	The first dimension of single value matrix of the tensor. Default is 2.
r2	The second dimension of single value matrix of the tensor. Default is 2.
r3	The third dimension of single value matrix of the tensor. Default is 2.
method	The method to be applied to select parameters. Either "BIC" (the default), or "CV".
ncv	The number of cross-validation folds. Default is 10. If method is BIC, ncv is useless.
penalty	The penalty to be applied to the model. Either "LASSO" (the default), "SCAD", or "MCP".
isPenColumn	A logical value indicating whether the coefficients associating with $X_j$ that affects whole response $y$ is penalized. Default is TRUE. If isPenColumn is TRUE, the coefficients associating with $X_j$ that affects simultaneously whole response $y$ is penalized for each $j \in \{1, \dots, p\}$ . If isPenColumn is FALSE, the coefficients associating with $X_j$ that affects single response $y_l$ is penalized for each $j \in \{1, \dots, p\}$ , where $l \in \{1, \dots, q\}$ .



lambda	A user-specified sequence of lambda values. By default, a sequence of values of length nlam is computed, equally spaced on the log scale.
SABC	A user-specified list of initial coefficient matrix of $S$ , $A$ , $B$ , $C$ . By default, initial matrices are provided by random.
intercept	Should intercept(s) be fitted (default=TRUE) or set to zero (FALSE)?
mu	A user-specified initial of intercept(s), a $q$ -vector. Default is 0.
nlam	The number of lambda values. Default is 20.
lam_min	The smallest value for lambda, as a fraction of lambda.max. Default is 1e-3.
eps1	Convergence threshold. The algorithm iterates until the relative change in any coefficient is less than eps1. Default is 1e-4.
maxstep1	Maximum number of iterations. Default is 20.
eps2	Convergence threshold. The Coordinate descent method algorithm iterates until the relative change in any coefficient is less than eps2. Default is 1e-4.
maxstep2	The maximum iterates number of coordinate descent method. Default is 20.
gamma	The tuning parameter of the MCP/SCAD penalty (see details).
dfmax	Upper bound for the number of nonzero coefficients. Default is no upper bound. However, for large data sets, computational burden may be heavy for models with a large number of nonzero coefficients.
alpha	Tuning parameter for the Mnet estimator which controls the relative contributions from the LASSO, MCP/SCAD penalty and the ridge, or L2 penalty. alpha=1 is equivalent to LASSO, MCP/SCAD penalty, while alpha=0 would be equivalent to ridge regression. However, alpha=0 is not supported; alpha may be arbitrarily small, but not exactly 0.

## Details

This function gives pq functional coefficients' estimators of MAM. The singular value matrix of tensor is a  $r_1 \times r_2 \times r_3$ -tensor.  $r_1$ ,  $r_2$  and  $r_3$  are fixed.

## Value

betapath	Solution path of $\beta$ .
rss	Residual sum of squares (RSS).
df	Degrees of freedom.
lambda	The sequence of regularization parameter values in the path.
lambda_opt	The value of lambda with the minimum BIC value.
selectedID	The index of lambda corresponding to lambda_opt.
activeA	The active set.
Dnew	Estimator of $D_{(3)}$ .
mu	Estimator of intercept $\mu$ .
Y	Response $Y$ .
X	Design matrix $X$ .
Z	Design matrix of Bspline approximation $\lambda$ .

## References

A tensor estimation approach to multivariate additive models.

**See Also**

mam, mam\_sparse\_dr

**Examples**

```
D2 <- matrix(runif(50, 0.7, 1), 2, 25) # tensor with size 5*2*5
mydata <- generateData(200, 5, 10, 5, D2)

fit <- mam_sparse(mydata$Y, mydata$X)
D3hat <- fit$Dnew
D2hat <- TransferModalUnfoldings(D3hat,3,2,5,2,5)
```

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mam\_sparse\_dr

---

*Fit MAM with sparsity assumption and ranks selected by BIC or CV.*


---

**Description**

Fit a high-dimensional multivariate additive model using B-splines, with or with aparsity assumptions and ranks selected by BIC or CV. The multivariate sparse group lasso (mcp or scad) and the coordinate descent algorithm are used to estimate functions for sparsity situation. The tuning parameter is selected by BIC or CV, which matches the method of rank selection.

**Usage**

```
mam_sparse_dr(Y, X, method = "BIC", ncv = 10, penalty = "LASSO", isPenColumn=TRUE,
  K_index = NULL, r1_index = NULL, r2_index = NULL, r3_index = NULL,
  lambda = NULL, SABC = NULL, intercept = TRUE, mu = NULL, nlam = 50,
  degr = 3, lam_min = 0.01, eps1 = 1e-4, maxstep1 = 20, eps2 = 1e-4,
  maxstep2 = 20, gamma = 2, dfmax = NULL, alpha = 1)
```

**Arguments**

Y	A $n \times q$ numeric matrix of responses.
X	A $n \times q$ numeric design matrix for the model.
method	The method to be applied to select parameters. Either "BIC" (the default), or "CV".
ncv	The number of cross-validation folds. Default is 10. If method is BIC, ncv is useless.
penalty	The penalty to be applied to the model. Either "LASSO" (the default), "SCAD", or "MCP".
isPenColumn	A logical value indicating whether the coefficients associating with $X_j$ that affects whole response $y$ is penalized. Default is TRUE. If isPenColumn is TRUE, the coefficients associating with $X_j$ that affects simultaneously whole response $y$ is penalized for each $j \in \{1, \dots, p\}$ . If isPenColumn is FALSE, the coefficients associating with $X_j$ that affects single response $y_l$ is penalized for each $j \in \{1, \dots, p\}$ , where $l \in \{1, \dots, q\}$ .
K_index	A user-specified sequence of K values, where K is the number of B-spline base function. Default is k_index=6.

r1_index	A user-specified sequence of $r_1$ values, where $r_1$ is the first dimension of single value matrix of the tensor. Default is $r1\_index = 1, \dots, \min(\lceil \log(n) \rceil, p)$ .
r2_index	A user-specified sequence of $r_2$ values, where $r_2$ is the second dimension of single value matrix of the tensor. Default is $r2\_index = 1, \dots, \max\{K\_index\}$ .
r3_index	A user-specified sequence of $r_3$ values, where $r_3$ is the third dimension of single value matrix of the tensor. Default is $r3\_index = 1, \dots, \min(\lceil \log(n) \rceil, q)$ .
lambda	A user-specified sequence of lambda values. By default, a sequence of values of length nlam is computed, equally spaced on the log scale.
SABC	A user-specified list of initial coefficient matrix of $S, A, B, C$ . By default, initial matrices are provided by random.
intercept	Should intercept(s) be fitted (default=TRUE) or set to zero (FALSE)?
mu	A user-specified initial of intercept(s), a $q$ -vector. Default is $\emptyset$ .
nlam	The number of lambda values. Default is 50.
degr	The number of knots of B-spline base function. Default is $degr = 3$ .
lam_min	The smallest value for lambda, as a fraction of lambda.max. Default is $1e-2$ .
eps1	Convergence threshold. The algorithm iterates until the relative change in any coefficient is less than eps1. Default is $1e-4$ .
maxstep1	Maximum number of iterations. Default is 20.
eps2	Convergence threshold. The Coordinate descent method algorithm iterates until the relative change in any coefficient is less than eps2. Default is $1e-4$ .
maxstep2	The maximum iterates number of coordinate descent method. Default is 20.
gamma	The tuning parameter of the MCP/SCAD penalty (see details).
dfmax	Upper bound for the number of nonzero coefficients. Default is no upper bound. However, for large data sets, computational burden may be heavy for models with a large number of nonzero coefficients.
alpha	Tuning parameter for the Mnet estimator which controls the relative contributions from the LASSO, MCP/SCAD penalty and the ridge, or L2 penalty. $\alpha=1$ is equivalent to LASSO, MCP/SCAD penalty, while $\alpha=0$ would be equivalent to ridge regression. However, $\alpha=0$ is not supported; alpha may be arbitrarily small, but not exactly 0.

## Details

This function gives pq functional coefficients' estimators of MAM. The singular value matrix of tensor is a  $r_1 \times r_2 \times r_3$ -tensor. We choose  $r_1, r_2$  and  $r_3$  by BIC or CV.

## Value

Dnew	Estimator of $D_{(3)}$ .
mu	Estimator of intercept $\mu$ .
rss	Residual sum of squares (RSS).
df	Degrees of freedom.
activeA	The active set.
lambda	The sequence of regularization parameter values in the path.
selectedID	The index of lambda corresponding to lambda_opt.
lambda_opt	The value of lambda with the minimum BIC or CV value.

RSS	The values of BIC or CV, which is a vector.
rk_opt	The optimal parameters that selected by BIC or CV. It is a vector with length 4, which are selected $r_1$ , $r_2$ , $r_3$ , and $K$ .
Y	Response $Y$ .
X	Design matrix $X$ .
Z	Design matrix of Bspline approximation.

## References

A tensor estimation approach to multivariate additive models.

## See Also

mam\_dr, mam\_sparse

## Examples

```
#Example 1

D2 <- matrix(runif(50, 0.7, 1), 2, 25) # tensor with size 5*2*5
mydata <- generateData(200, 5, 10, 5, D2)

fit <- mam_sparse_dr(mydata$Y, mydata$X)
D3hat <- fit$Dnew
D2hat <- TransferModalUnfoldings(D3hat,3,2,5,2,5)
opt <- fit$rk_opt

#Example 2

data(breastData)
attach(breastData)
Y = t(dna[chrom==21,])
Xt = t(rna[which(genechr==21),])
n = nrow(Y)

minX = apply(Xt,2,min)
maxX = apply(Xt,2,max)
X = (Xt - matrix(rep(minX,each = n),n))/matrix(rep(maxX-minX,each = n),n)
Y = scale(Y)
fit <- mam_sparse_dr(Y[,1:5], X[,1:10])
D3hat <- fit$Dnew
opt <- fit$rk_opt
detach(breastData)
```

---

plotfuns

*Plot the estimated curves from tensorMam.*

---

## Description

Plot the curves fitted by mam, mam\_dr, mam\_sparse, and mam\_sparse\_dr

**Usage**

```
plotfuns(fit, funTrueID, true.curve=FALSE)
```

**Arguments**

<code>fit</code>	Object outputting from <code>mam</code> , <code>mam_dr</code> , <code>mam_sparse</code> or <code>mam_sparse_dr</code> .
<code>funTrueID</code>	Which function to be plotted. It is a 2-vector. In MAM models, there are $s_0 \times q$ true functions. Thus, the first argument must be smaller than $s_0$ , and the second argument must be smaller than $q$ .
<code>true.curve</code>	A Logical flag. Plot both true and estimated curves if <code>true.curve=TRUE</code> . Plot estimated curve only if <code>true.curve=FALSE</code> . Default is <code>FALSE</code> .

**Details**

This function gives pq functional coefficients' estimators of MAM. The singular value matrix of tensor is a  $r_1 \times r_2 \times r_3$ -tensor. We choose  $r_1$ ,  $r_2$  and  $r_3$  by BIC or CV.

**References**

A tensor estimation approach to multivariate additive models.

**See Also**

`mam`, `mam_dr`, `mam_sparse`, `mam_sparse_dr`

**Examples**

```
n <- 200
p <- 10
q <- 10
s <- 10
K <- 6
s0 <- s
r10=r20=r30=2
S3 <- matrix(runif(r10*r20*r30,3,7),nrow = r30)
T1 <- matrix(rnorm(s0*r10),nrow = s0)
U1 <- qr.Q(qr(T1))
T1 <- matrix(rnorm(K*r20),nrow = K)
U2 <- qr.Q(qr(T1))
T1 <- matrix(rnorm(q*r30),nrow = q)
U3 <- qr.Q(qr(T1))
D3 <- U3%*%S3%*%t(kronecker(U2,U1))
D2 <- TransferModalUnfoldings(D3,3,2,s0,K,q)
mydata <- generateData(n, q, p, s0, D2)
fit <- mam(mydata$Y, mydata$X)
fit$D2 <- D2
fit$s0 <- s0
fit$X0 <- matrix(runif(100*p),100,p)
plotfuns(fit, c(1,1))
```

---

TransferModalUnfoldings

*Transfer a tensor's modal unfoldings to another.*


---

### Description

Transfer a tensor's modal unfoldings to another.

### Usage

```
TransferModalUnfoldings(S, d1, d2 , r1, r2, r3)
```

### Arguments

S	A mode-d1-unfolding of a tensor with size $r_1 \times r_2 \times r_3$ , input unfolding
d1	An integer, the mode of unfolding $S_{(d_1)}$
d2	An integer, the mode of output unfolding $S_{(d_2)}$
r1	The first dimension of tensor
r2	The second dimension of tensor
r3	The third dimension of tensor

### Details

This function transfers an input mode-d1-unfolding  $S_{(d_1)}$  to mode-d2-unfolding  $S_{(d_2)}$

### Value

D the output mode-d2-unfolding,  $S_{(d_2)}$

### References

A tensor estimation approach to multivariate additive models.

### Examples

```
D1 <- matrix(1:24,nrow = 4) # A tensor unfolding with size 4*6
D2 <- TransferModalUnfoldings(D1,1,2,4,3,2)
```

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