Package: CMGFM (via r-universe)

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Type Package

Title Covariate-Augumented Generalized Factor Model

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Author Wei Liu [aut, cre], Jiakun Jiang [aut], Dewei Xiang [aut], Xuancheng Zhou [aut]

Maintainer Wei Liu <LiuWeideng@gmail.com>

Description Covariate-augumented generalized factor model is designed to account for cross-modal heterogeneity, capture nonlinear dependencies among the data, incorporate additional information, and provide excellent interpretability while maintaining high computational efficiency.

BugReports https://github.com/feiyoung/CMGFM/issues

License GPL-3

Depends irlba, R (>= 3.5.0)

Imports MASS, stats, GFM, Rcpp (>= 1.0.10)

Suggests knitr, rmarkdown

LinkingTo Rcpp, RcppArmadillo

VignetteBuilder knitr

Encoding UTF-8

RoxygenNote 7.3.1

NeedsCompilation yes

Repository https://cran.r-universe.dev

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CMGFM *Fit the CMGFM model*

Description

Fit the covariate-augumented generalized factor model

Usage

```
CMGFM(
  XList,
  Z,
  types,
  numvarmat,
  q = 15,
  Alist = NULL,
  init = c("LFM", "GFM", "random"),
  maxIter = 30,
  epsELBO = 1e-08,
  verbose = TRUE,
  add_IC_iter = FALSE,
  seed = 1
)
```

Arguments

XList	a list consisting of multiple matrices in which each matrix has the same type of values, i.e., continuous, or count, or binomial/binary values.
Z	a matrix, the fixed-dimensional covariate matrix with control variables.
types	a string vector, specify the variable type in each matrix in XList;
numvarmat	a length(types)-by-d matrix, specify the number of variables in modalities that belong to the same type.
q	an optional string, specify the number of factors; default as 15.
Alist	an optional vector, the offset for each unit; default as full-zero vector.
init	an optional character, specify the method in initialization.
maxIter	the maximum iteration of the VEM algorithm. The default is 30.
epsELBO	an optional positive value, tolerance of relative variation rate of the evidence lower bound value, default as '1e-8'.

verbose	a logical value, whether output the information in iteration.
add_IC_iter	a logical value, add the identifiability condition in iterative algorithm or add it after algorithm converges; default as FALSE.
seed	an integer, set the random seed in initialization, default as 1;

Details

None

Value

return a list including the following components:

- betaf - the estimated regression coefficient vector for each modality;
- Bf - the estimated loading matrix for each modality;
- M - the estimated modality-shared factor matrix;
- Xif - the estimated modality-specified factor vector;
- S - the estimated covariance matrix of modality-shared latent factors;
- Om - the posterior variance of modality-specified latent factors;
- muf - the estimated intercept vector for each modality;
- Sigmam - the variance of modality-specified factors;
- invLambdaf - the inverse of the estimated variances of error for each modality.
- ELBO - the ELBO value when algorithm stops;
- ELBO_seq - the sequence of ELBO values.
- time_use - the running time in model fitting;

References

None

See Also

None

Examples

```
pveclist <- list('gaussian'=c(50, 150),'poisson'=c(50, 150),
   'binomial'=c(100,60))
q <- 6
sigmavec <- rep(1,3)
pvec <- unlist(pveclist)
datlist <- gendata_cmgfm(pveclist = pveclist, seed = 1, n = 300,d = 3,
                         q = q, rho = rep(1,length(pveclist)), rho_z=0.2,
                         sigmavec=sigmavec, sigma_eps=1)
XList <- datlist$XList
Z <- datlist$Z
numvarmat <- datlist$numvarmat
```

```
types <- datlist$types
rlist <- CMGFM(XList, Z, types=types, numvarmat, q=q)
str(rlist)
```

---

gendata_cmgfm *Generate simulated data*

Description

Generate simulated data from covariate-augumented generalized factor model

Usage

```
gendata_cmgfm(
  seed = 1,
  n = 300,
  pveclist = list(gaussian = c(50, 150), poisson = c(50), binomial = c(100, 60)),
  q = 6,
  d = 3,
  rho = rep(1, length(pveclist)),
  rho_z = 1,
  sigmavec = rep(0.5, length(pveclist)),
  n_bin = 1,
  sigma_eps = 1,
  seed.para = 1
)
```

Arguments

seed	a positive integer, the random seed for reproducibility of data generation process.
n	a positive integer, specify the sample size.
pveclist	a named list, specify the number of modalities for each variable type and dimension of variables in each modality.
q	a positive integer, specify the number of modality-shared factors.
d	a positive integer, specify the dimension of covariate matrix.
rho	a numeric vector with length `length(pveclist)` and positive elements, specify the signal strength of loading matrix for each modality with the same variable type.
rho_z	a positive real, specify the signal strength of covariates.
sigmavec	a positive vector with length `length(pveclist)`, the variance of modality-specified latent factors.
n_bin	a positive integer, specify the number of trails in Binomial distribution.
sigma_eps	a positive real, the variance of overdispersion error.
seed.para	a positive integer, the random seed for reproducibility of data generation process by fixing the regression coefficient vector and loading matrices.

Details

None

Value

return a list including the following components:

- `XList` - a list consisting of multiple matrices in which each matrix has the same type of values, i.e., continuous, or count, or binomial/binary values.
- `Z` - a matrix, the fixed-dimensional covariate matrix with control variables;
- `Alist` - the the offset vector for each modality;
- `B0list` - the true loading matrix for each modality;
- `mu0` - the true intercept vector for each modality;
- `U0` - the modality-specified factor vector;
- `F0` - the modality-shared factor matrix;
- `Uplist` - the true intercept-loading matrix for each modality;
- `beta` - the true regression coefficient vector for each modality;
- `sigma_eps` - the standard deviation of error term;
- `numvarmat` - a length(types)-by-d matrix, the number of variables in modalities that belong to the same type.

References

None

See Also

CMGFM

Examples

```
n <- 300;
pveclist = list('gaussian'=c(50, 150),'poisson'=c(50),'binomial'=c(100,60))
d <- 20; q <- 6;
datlist <- gendata_cmgfm(n=n, pveclist=pveclist, q=q, d=d)
str(datlist)
```

MSVR *Select the number of factors*

Description

Select the number of factors using maximum singular value ratio based method

Usage

```
MSVR(
  XList,
  Z,
  types,
  numvarmat,
  Alist = NULL,
  q_max = 20,
  threshold = 1e-05,
  ...
)
```

Arguments

XList	a list consisting of multiple matrices in which each matrix has the same type of values, i.e., continuous, or count, or binomial/binary values.
Z	a matrix, the fixed-dimensional covariate matrix with control variables.
types	a string vector, specify the variable type in each matrix in XList;
numvarmat	a length(types)-by-d matrix, specify the number of variables in modalities that belong to the same type.
Alist	an optional vector, the offset for each unit; default as full-zero vector.
q_max	an optional string, specify the maximum number of factors; default as 20.
threshold	an optional positive value, a cutoff to filter the singular values that are smaller than it.
...	other arguments passed to CMGFM

Details

None

Value

return the estimated number of factors.

References

None

See Also

None

Examples

```
pveclist <- list('gaussian'=c(50, 150),'poisson'=c(50, 150),
   'binomial'=c(100,60))
q <- 6
sigmavec <- rep(1,3)
pvec <- unlist(pveclist)
datlist <- gendata_cmgfm(pveclist = pveclist, seed = 1, n = 300,d = 3,
                         q = q, rho = rep(1,length(pveclist)), rho_z=0.2,
                         sigmavec=sigmavec, sigma_eps=1)
XList <- datlist$XList
Z <- datlist$Z
numvarmat <- datlist$numvarmat
types <- datlist$types
hq <- MSVR(XList, Z, types=types, numvarmat, q_max=20)

print(c(q_true=q, q_est=hq))
```

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