

Package ‘SpaCOAP’

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Type Package

Title High-Dimensional Spatial Covariate-Augmented Overdispersed Poisson Factor Model

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Description A spatial covariate-augmented overdispersed Poisson factor model is proposed to perform efficient latent representation learning method for high-dimensional large-scale spatial count data with additional covariates.

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URL <https://github.com/feiyoung/SpaCOAP>

BugReports <https://github.com/feiyoung/SpaCOAP/issues>

Imports LaplacesDemon, stats, methods, Matrix, MASS, Rcpp (>= 1.0.10)

Depends irlba, R (>= 3.5.0)

Suggests knitr, rmarkdown

LinkingTo Rcpp, RcppArmadillo

VignetteBuilder knitr

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NeedsCompilation yes

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chooseParams	<i>Select the parameters in COAP models</i>
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Description

Select the number of factors and the rank of coefficient matrix in the covariate-augmented overdispersed Poisson factor model

Usage

```
chooseParams(
  X_count,
  Adj_sp,
  H,
  Z = matrix(1, nrow(X_count), 1),
  offset = rep(0, nrow(X_count)),
  q_max = 15,
  r_max = 24,
  threshold = c(0.1, 0.01),
  verbose = TRUE,
  ...
)
```

Arguments

X_count	a count matrix, the observed count matrix with shape n-by-p.
Adj_sp	a sparse matrix, the weighted adjacency matrix;
H	a n-by-d matrix, the covariate matrix with low-rank regression coefficient matrix;
Z	an optional matrix, the fixed-dimensional covariate matrix with control variables; default as a full-one column vector if there is no additional covariates.
offset	an optional vector, the offset for each unit; default as full-zero vector.
q_max	an optional string, specify the upper bound for the number of factors; default as 15.
r_max	an optional integer, specify the upper bound for the rank of the regression coefficient matrix; default as 24.
threshold	an optional 2-dimensional positive vector, specify the the thresholds that filters the singular values of beta and B, respectively.
verbose	a logical value, whether output the information in iteration.
...,	other arguments passed to the function SpaCOAP .

Details

The threshold is to filter the singular values with low signal, to assist the identification of underlying model structure.

Value

return a named vector with names ‘hr’ and ‘hq’, the estimated rank and number of factors.

References

None

See Also

[SpaCOAP](#)

Examples

```
width <- 20; height <- 15; p <- 300
d <- 20; k <- 3; q <- 6; r <- 3
datlist <- gendata_spacoap(width=width, height=height, p=p, d=d, k=k, q=q, rank0=r)
set.seed(1)
para_vec <- chooseParams(X_count=datlist$X, Adj_sp=datlist$Adj_sp,
                           H=datlist$H, Z = datlist$Z, r_max=6)
print(para_vec)
```

gendata_spacoap *Generate simulated data*

Description

Generate simulated data from spatial covariate-augmented Poisson factor models

Usage

```
gendata_spacoap(
  seed = 1,
  width = 20,
  height = 30,
  p = 500,
  d = 40,
  k = 3,
  q = 5,
  rank0 = 3,
  eta0 = 0.5,
  bandwidth = 1,
  rho = c(10, 1),
  sigma2_eps = 1,
  seed.beta = 1
)
```

Arguments

<code>seed</code>	a positive integer, the random seed for reproducibility of data generation process.
<code>width</code>	a positive integer, specify the width of the spatial grid.
<code>height</code>	a positive integer, specify the height of the spatial grid.
<code>p</code>	a positive integer, specify the dimension of count variables.
<code>d</code>	a positive integer, specify the dimension of covariate matrix with low-rank regression coefficient matrix.
<code>k</code>	a positive integer, specify the dimension of covariate matrix as control variables.
<code>q</code>	a positive integer, specify the number of factors.
<code>rank0</code>	a positive integer, specify the rank of the coefficient matrix.
<code>eta0</code>	a real between 0 and 1, specify the spatial autocorrelation parameter.
<code>bandwidth</code>	a real positive value, specify the bandwidth in calculating the weighted adjacency matrix.
<code>rho</code>	a numeric vector with length 2 and positive elements, specify the signal strength of loading matrix and regression coefficient, respectively.
<code>sigma2_eps</code>	a positive real, the variance of overdispersion error.
<code>seed.beta</code>	a positive integer, the random seed for reproducibility of data generation process by fixing the regression coefficient matrix beta.

Details

None

Value

return a list including the following components:

- `X` - the high-dimensional count matrix;
- `Z` - the low-dimensional covariate matrix with control variables.
- `H` - the high-dimensional covariate matrix;
- `Adj_sp` - the weighted adjacency matrix;
- `alpha0` - the regression coefficient matrix corresponding to `Z`;
- `bbeta0` - the low-rank large regression coefficient matrix corresponding to `H`;
- `B0` - the loading matrix;
- `F0` - the latent factor matrix;
- `rank0` - the true rank of `bbeta0`;
- `q` - the true number of factors;
- `eta0` - spatial autocorrelation parameter;
- `pos` - spatial coordinates for each observation.

References

None

See Also

[SpaCOAP](#)

Examples

```
width <- 20; height <- 15; p <- 100
d <- 20; k <- 3; q <- 6; r <- 3
datlist <- gendata_spacoap(width=width, height=height, p=p, d=d, k=k, q=q, rank0=r)
str(datlist)
```

SpaCOAP

Fit the SpaCOAP model

Description

Fit the spatial covariate-augmented overdispersed Poisson factor model

Usage

```
SpaCOAP(
  X_count,
  Adj_sp,
  H,
  Z = matrix(1, nrow(X_count), 1),
  offset = rep(0, nrow(X_count)),
  rank_use = 5,
  q = 15,
  epsELBO = 1e-08,
  maxIter = 30,
  verbose = TRUE,
  add_IC_inter = FALSE,
  seed = 1,
  algo = 1
)
```

Arguments

X_count	a count matrix, the observed count matrix with shape n-by-p.
Adj_sp	a sparse matrix, the weighted adjacency matrix;
H	a n-by-d matrix, the covariate matrix with low-rank regression coefficient matrix;
Z	an optional matrix, the fixed-dimensional covariate matrix with control variables; default as a full-one column vector if there is no additional covariates.
offset	an optional vector, the offset for each unit; default as full-zero vector.
rank_use	an optional integer, specify the rank of the regression coefficient matrix; default as 5.

<code>q</code>	an optional string, specify the number of factors; default as 15.
<code>epsELBO</code>	an optional positive value, tolerance of relative variation rate of the evidence lower bound value, default as '1e-8'.
<code>maxIter</code>	the maximum iteration of the VEM algorithm. The default is 30.
<code>verbose</code>	a logical value, whether output the information in iteration.
<code>add_IC_inter</code>	a logical value, add the identifiability condition in iterative algorithm or add it after algorithm converges; default as FALSE.
<code>seed</code>	an integer, set the random seed in initialization, default as 1;
<code>algo</code>	an optional integer taking value 1 Or 2, select the algorithm used, default as 1, representing variational EM algorithm.

Details

None

Value

return a list including the following components:

- `F` - the predicted factor matrix;
- `B` - the estimated loading matrix;
- `bbeta` - the estimated low-rank large coefficient matrix;
- `alpha0` - the estimated regression coefficient matrix corresponding to Z ;
- `invLambda` - the inverse of the estimated variances of error;
- `eta` - the estimated spatial autocorrelation parameter;
- `S` - the approximated posterior covariance for each row of `F`;
- `ELBO` - the ELBO value when algorithm stops;
- `ELBO_seq` - the sequence of ELBO values.
- `time_use` - the running time in model fitting of SpaCOAP;

References

Liu W, Zhong Q. High-dimensional covariate-augmented overdispersed poisson factor model. *Biometrics*. 2024 Jun;80(2):ujae031.

See Also

None

Examples

```
width <- 20; height <- 15; p <- 100
d <- 20; k <- 3; q <- 6; r <- 3
datlist <- gendata_spacoap(width=width, height=height, p=p, d=d, k=k, q=q, rank0=r)
fitlist <- SpaCOAP(X_count=datlist$X, Adj_sp = datlist$Adj_sp,
H= datlist$H, Z = datlist$Z, q=6, rank_use=3)
str(fitlist)
```

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