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Spatial regression with RE-ESF for very large samples

Description
Memory-free implementation of RE-ESF-based spatial regression for very large samples. This model estimates residual spatial dependence, constant coefficients, and non-spatially varying coefficients (NVC; coefficients varying with respect to explanatory variable value).

Usage
besf( y, x = NULL, nvc = FALSE, nvc_sel = TRUE, coords, s_id = NULL, covmodel="exp", enum = 200, method = "reml", penalty = "bic", nvc_num = 5, maxiter = 30, bsize = 4000, cl = NULL )

Arguments
- **y**: Vector of explained variables (N x 1)
- **x**: Matrix of explanatory variables (N x K)
- **nvc**: If TRUE, NVCs are assumed on x. Otherwise, constant coefficients are assumed. Default is FALSE
- **nvc_sel**: If TRUE, type of coefficients (NVC or constant) is selected through a BIC (default) or AIC minimization. If FALSE, NVCs are assumed across x. Alternatively, nvc_sel can be given by column number(s) of x. For example, if nvc_sel = 2, the coefficient on the second explanatory variable in x is NVC and the other coefficients are constants. The Default is TRUE
- **coords**: Matrix of spatial point coordinates (N x 2)
- **s_id**: Optional. ID specifying groups modeling spatially dependent process (N x 1). If it is specified, group-level spatial process is estimated. It is useful, e.g., for multilevel modeling (s_id is given by the group ID) and panel data modeling (s_id is given by individual location id). Default is NULL
- **covmodel**: Type of kernel to model spatial dependence. The currently available options are "exp" for the exponential kernel, "gau" for the Gaussian kernel, and "sph" for the spherical kernel
Number of Moran eigenvectors to be used for spatial process modeling (scalar). Default is 200

Estimation method. Restricted maximum likelihood method ("reml") and maximum likelihood method ("ml") are available. Default is "reml"

Penalty to select type of coefficients (NVC or constant) to stabilize the estimates. The current options are "bic" for the Baysian information criterion-type penalty (N x log(K)) and "aic" for the Akaike information criterion (2K) (see Muller et al., 2013). Default is "bic"

Number of basis functions used to model NVC. An intercept and nvc_num natural spline basis functions are used to model each NVC. Default is 5

Maximum number of iterations. Default is 30

Block/badge size. bsize x bsize elements are iteratively processed during the parallelized computation. Default is 4000

Number of cores used for the parallel computation. If cl = NULL, the number of available cores is detected. Default is NULL

Matrix with columns for the estimated coefficients on x, their standard errors, z-values, and p-values (K x 4). Effective if nvc =FALSE

Matrix of estimated NVCs on x (N x K). Effective if nvc =TRUE

Matrix of standard errors for the NVCs on x (N x K). Effective if nvc =TRUE

Matrix of t-values for the NVCs on x (N x K). Effective if nvc =TRUE

Matrix of p-values for the NVCs on x (N x K). Effective if nvc =TRUE

Vector of estimated variance parameters (2 x 1). The first and the second elements denote the standard error and the Moran’s I value of the estimated spatially dependent component, respectively. The Moran’s I value is scaled to take a value between 0 (no spatial dependence) and 1 (the maximum possible spatial dependence). Based on Griffith (2003), the scaled Moran’s I value is interpretable as follows: 0.25-0.50:weak; 0.50-0.70:moderate; 0.70-0.90:strong; 0.90-1.00:marked

Vector whose elements are residual standard error (resid_SE), adjusted conditional R2 (adjR2(cond)), restricted log-likelihood (rlogLik), Akaike information criterion (AIC), and Bayesian information criterion (BIC). When method = "ml", restricted log-likelihood (rlogLik) is replaced with log-likelihood (logLik)

List indicating whether NVC are removed or not during the BIC/AIC minimization. 1 indicates not removed whereas 0 indicates removed

Vector of estimated random coefficients on Moran’s eigenvectors (L x 1)

Vector of estimated spatial dependent component (N x 1)

Vector of predicted values (N x 1)

Vector of residuals (N x 1)

List of other outcomes, which are internally used
Author(s)

Daisuke Murakami

References


See Also

resf

Examples

```r
require(spdep)
data(boston)
y <- boston.c[, "CMEDV"]
x <- boston.c[,c("CRIM","ZN","INDUS","CHAS","NOX","RM","AGE",
                  "DIS","RAD","TAX","PRTATIO","B","STAT")]
xgroup <- boston.c[,"TOWN"]
coords <- boston.c[,c("LON","LAT")]

######## Regression considering spatially dependent residuals
#res <- besf(y = y, x = x, coords=coords)
#res

######## Regression considering spatially dependent residuals and NVC
######## (coefficients or NVC is selected)
#res2 <- besf(y = y, x = x, coords=coords, nvc = TRUE)

######## Regression considering spatially dependent residuals and NVC
######## (all the coefficients are NVCs)
#res3 <- besf(y = y, x = x, coords=coords, nvc = TRUE, nvc_sel=FALSE)
```

besf_vc

Spatially and non-spatially varying coefficient (SNVC) modeling for very large samples
**Description**

Memory-free implementation of SNVC modeling for very large samples. The model estimates residual spatial dependence, constant coefficients, spatially varying coefficients (SVCs), non-spatially varying coefficients (NVC; coefficients varying with respect to explanatory variable value), and SNVC (= SVC + NVC). Type of coefficients can be selected through BIC/AIC minimization. By default, it estimates a SVC model.

Note: SNVCs can be mapped just like SVCs. Unlike SVC models, SNVC model is robust against spurious correlation (multicollinearity), so, stable (see Murakami and Griffith, 2020).

**Usage**

```r
besf_vc( y, x, xconst = NULL, coords, s_id = NULL, x_nvc = FALSE, xconst_nvc = FALSE, 
        x_sel = TRUE, x_nvc_sel = TRUE, xconst_nvc_sel = TRUE, nvc_num=5, 
        method = "reml", penalty = "bic", maxiter = 30, 
        covmodel="exp", enum = 200, bsize = 4000, cl=NULL )
```

**Arguments**

- `y` Vector of explained variables (N x 1)
- `x` Matrix of explanatory variables with spatially varying coefficients (SVC) (N x K)
- `xconst` Matrix of explanatory variables with constant coefficients (N x K_c). Default is NULL
- `coords` Matrix of spatial point coordinates (N x 2)
- `s_id` Optional. ID specifying groups modeling spatially dependent process (N x 1). If it is specified, group-level spatial process is estimated. It is useful for multilevel modeling (s_id is given by the group ID) and panel data modeling (s_id is given by individual location id). Default is NULL
- `x_nvc` If TRUE, SNVCs are assumed on x. Otherwise, SVCs are assumed. Default is FALSE
- `xconst_nvc` If TRUE, NVCs are assumed on xconst. Otherwise, constant coefficients are assumed. Default is FALSE
- `x_sel` If TRUE, type of coefficient (SVC or constant) on x is selected through a BIC (default) or AIC minimization. If FALSE, SVCs are assumed across x. Alternatively, x_sel can be given by column number(s) of x. For example, if x_sel = 2, the coefficient on the second explanatory variable in x is SVC and the other coefficients are constants. The Default is TRUE
- `x_nvc_sel` If TRUE, type of coefficient (NVC or constant) on x is selected through the BIC (default) or AIC minimization. If FALSE, NVCs are assumed across x. Alternatively, x_nvc_sel can be given by column number(s) of x. For example, if x_nvc_sel = 2, the coefficient on the second explanatory variable in x is NVC and the other coefficients are constants. The Default is TRUE
- `xconst_nvc_sel` If TRUE, type of coefficient (NVC or constant) on xconst is selected through the BIC (default) or AIC minimization. If FALSE, NVCs are assumed across xconst. Alternatively, xconst_nvc_sel can be given by column number(s) of
xconst. For example, if xconst_nvc_sel = 2, the coefficient on the second explanatory variable in xconst is NVC and the other coefficients are constants. The Default is TRUE

**nvc_num**  Number of basis functions used to model NVC. An intercept and nvc_num natural spline basis functions are used to model each NVC. Default is 5

**method**  Estimation method. Restricted maximum likelihood method ("reml") and maximum likelihood method ("ml") are available. Default is "reml"

**penalty**  Penalty to select type of coefficients (SNVC, SVC, NVC, or constant) to stabilize the estimates. The current options are "bic" for the Baysian information criterion-type penalty (N x log(K)) and "aic" for the Akaike information criterion (2K) (see Muller et al., 2013). Default is "bic"

**maxiter**  Maximum number of iterations. Default is 30

**covmodel**  Type of kernel to model spatial dependence. The currently available options are "exp" for the exponential kernel, "gau" for the Gaussian kernel, and "sph" for the spherical kernel

**enum**  Number of Moran eigenvectors to be used for spatial process modeling (scalar). Default is 200

**bsize**  Block/badge size. bsize x bsize elements are iteratively processed during the parallelized computation. Default is 4000

**cl**  Number of cores used for the parallel computation. If cl = NULL, the number of available cores is detected. Default is NULL

**Value**

- **b_vc**  Matrix of estimated SNVC (= SVC + NVC) on x (N x K)
- **bse_vc**  Matrix of standard errors for the SNVCs on x (N x k)
- **z_vc**  Matrix of z-values for the SNVCs on x (N x K)
- **p_vc**  Matrix of p-values for the SNVCs on x (N x K)
- **B_vc_s**  List summarizing estimated SVCs (in SNVC) on x. The four elements are the SVCs (N x K), the standard errors (N x K), z-values (N x K), and p-values (N x K), respectively
- **B_vc_n**  List summarizing estimated NVCs (in SNVC) on x. The four elements are the NVCs (N x K), the standard errors (N x K), z-values (N x K), and p-values (N x K), respectively
- **c**  Matrix with columns for the estimated coefficients on xconst, their standard errors, z-values, and p-values (K_c x 4). Effective if xconst_nvc = FALSE
- **c_vc**  Matrix of estimated NVCs on xconst (N x K_c). Effective if xconst_nvc = TRUE
- **cse_vc**  Matrix of standard errors for the NVCs on xconst (N x k_c). Effective if xconst_nvc = TRUE
- **cz_vc**  Matrix of z-values for the NVCs on xconst (N x K_c). Effective if xconst_nvc = TRUE
- **cp_vc**  Matrix of p-values for the NVCs on xconst (N x K_c). Effective if xconst_nvc = TRUE
besf_vc

s  List of variance parameters in the SNVC (SVC + NVC) on x. The first element is a 2 x K matrix summarizing variance parameters for SVC. The (1, k)-th element is the standard error of the k-th SVC, while the (2, k)-th element is the Moran’s I value is scaled to take a value between 0 (no spatial dependence) and 1 (strongest spatial dependence). Based on Griffith (2003), the scaled Moran’s I value is interpretable as follows: 0.25-0.50:weak; 0.50-0.70:moderate; 0.70-0.90:strong; 0.90-1.00:marked. The second element of s is the vector of standard errors of the NVCs

s_c  Vector of standard errors of the NVCs on xconst

vc  List indicating whether SVC/NVC are removed or not during the BIC/AIC minimization. 1 indicates not removed (replaced with constant) whereas 0 indicates removed

e  Vector whose elements are residual standard error (resid_SE), adjusted conditional R2 (adjR2(cond)), restricted log-likelihood (rlogLik), Akaike information criterion (AIC), and Bayesian information criterion (BIC). When method = "ml", restricted log-likelihood (rlogLik) is replaced with log-likelihood (logLik)

pred  Vector of predicted values (N x 1)

resid  Vector of residuals (N x 1)

other  List of other outcomes, which are internally used

Author(s)
Daisuke Murakami

References


See Also
resf_vc

Examples
require(spdep)
data(boston)
y <- boston.c[, "CMEDV"]
x <- boston.c[,c("ZN", "INDUS","LSTAT")]
xconst <- boston.c[,c("CRIM", "NOX", "CHAS", "AGE", "DIS", "RAD", "TAX","PTRATIO","B","RM")]
coords <- boston.c[,c("LAT","LON")]

######## SVC model
# res <- besf_vc(y=y,x=x,xconst=xconst,coords=coords)

######## SNVC model
# res2 <- besf_vc(y=y,x=x,xconst=xconst,coords=coords,x_nvc=TRUE)

require(spdep)
data(boston)
y <- boston.c[, "CMEDV"]
x <- boston.c[,c("CRIM", "AGE")]
xconst <- boston.c[,c("ZN","DIS","RAD","NOX", "TAX","RM","PTRATIO","B")]
xgroup <- boston.c[,"TOWN"]
coords <- boston.c[,c("LON","LAT")]

################# SVC modeling1 #################
######## (SVC on x; Constant coefficients on xconst)
#res <- besf_vc(y=y,x=x,xconst=xconst,coords=coords, x_sel = FALSE )
# res
#plot_s(res,0) # Spatially varying intercept
#plot_s(res,1) # 1st SVC
#plot_s(res,2) # 2nd SVC

################# SVC modeling2 #################
######## (SVC or constant coefficients on x; Constant coefficients on xconst)
#res2 <- besf_vc(y=y,x=x,xconst=xconst,coords=coords )

################# SVC modeling3 #################
######## - Group-level SVC or constant coefficients on x
######## - Constant coefficients on xconst
#res3 <- besf_vc(y=y,x=x,xconst=xconst,coords=coords, s_id=xgroup)

################# SNVC modeling1 #################
######## - SNVC, SVC, NVC, or constant coefficients on x
######## - Constant coefficients on xconst
#res4 <- besf_vc(y=y,x=x,xconst=xconst,coords=coords, x_nvc =TRUE)

################# SNVC modeling2 #################
######## - SNVC, SVC, NVC, or constant coefficients on x
######## - NVC or Constant coefficients on xconst
#res5 <- besf_vc(y=y,x=x,xconst=xconst,coords=coords, x_nvc =TRUE, xconst_nvc=TRUE)
#plot_s(res5,0) # Spatially varying intercept
#plot_s(res5,1) # 1st SNVC
#plot_s(res5,1,snvc=FALSE)# SVC in the 1st SNVC
#plot_n(res5,1,xtype="x") # NVC in the 1st NVC
#plot_n(res5,6,xtype="xconst"
**esf**  
*Spatial regression with eigenvector spatial filtering*

**Description**
This function estimates the linear eigenvector spatial filtering (ESF) model. The eigenvectors are selected by a forward stepwise method.

**Usage**
esf( y, x = NULL, vif = NULL, meig, fn = "r2" )

**Arguments**
- **y**: Vector of explained variables (N x 1)
- **x**: Matrix of explanatory variables (N x K). Default is NULL
- **vif**: Maximum acceptable value of the variance inflation factor (VIF) (scalar). For example, if vif = 10, eigenvectors are selected so that the maximum VIF value among explanatory variables and eigenvectors is equal to or less than 10. Default is NULL
- **meig**: Moran eigenvectors and eigenvalues. Output from `meigen` or `meigen_f`
- **fn**: Objective function for the stepwise eigenvector selection. The adjusted R2 ("r2"), AIC ("aic"), or BIC ("bic") are available. Alternatively, all the eigenvectors in meig are use if fn = "all". This is acceptable for large samples (see Murakami and Griffith, 2019). Default is "r2"

**Value**
- **b**: Matrix with columns for the estimated coefficients on x, their standard errors, t-values, and p-values (K x 4)
- **s**: Vector of statistics for the estimated spatial component (2 x 1). The first element is the standard error and the second element is the Moran’s I value of the estimated spatially dependent component. The Moran’s I value is scaled to take a value between 0 (no spatial dependence) and 1 (the maximum possible spatial dependence). Based on Griffith (2003), the scaled Moran’s I value is interpretable as follows: 0.25-0.50:weak; 0.50-0.70:moderate; 0.70-0.90:strong; 0.90-1.00:marked
- **r**: Matrix with columns for the estimated coefficients on Moran’s eigenvectors, their standard errors, t-values, and p-values (L x 4)
- **vif**: Vector of variance inflation factors of the explanatory variables (N x 1)
- **e**: Vector whose elements are residual standard error (resid_SE), adjusted R2 (adjR2), log-likelihood (logLik), AIC, and BIC
**sf**  Vector of estimated spatial dependent component ($E_\gamma$) (N x 1)

**pred**  Vector of predicted values (N x 1)

**resid**  Vector of residuals (N x 1)

**other**  List of other outcomes, which are internally used

**Author(s)**

Daisuke Murakami

**References**


**See Also**

`resf`

**Examples**

```r
require(spdep)
data(boston)
y <- boston.c[, "CMEDV"

x <- boston.c[,c("CRIM","ZN","INDUS", "CHAS", "NOX","RM", "AGE")]
coords <- boston.c[,c("LON", "LAT")]

#########Distance-based ESF
meig <- meigen(coords=coords)
esfD <- esf(y=y, x=x, meig=meig, vif=5)
esfD

#########Fast approximation
meig_f <- meigen_f(coords=coords)
esfD <- esf(y=y, x=x, meig=meig_f, vif=10, fn="all")
esfD

##########################################################################

#########Not run

#####Topology-based ESF (it is commonly used in regional science)

# #cknn <- knearnearth(coordinates(coords), k=4) #4-nearest neighbors
#cmat <- nb2mat(knn2nb(cknn), style="B")
#meig <- meigen(cmat=cmat, threshold=0.25)
#esfT <- esf(y=y, x=x, meig=meig)
esfT
```
**Description**

This function estimates the low rank spatial error model.

**Usage**

```r
lsem( y, x, weig, method = "reml" )
```

**Arguments**

- `y`: Vector of explained variables (N x 1)
- `x`: Matrix of explanatory variables (N x K)
- `weig`: Eigenvectors and eigenvalues of a spatial weight matrix. Output from `weigen`
- `method`: Estimation method. Restricted maximum likelihood method ("reml") and maximum likelihood method ("ml") are available. Default is "reml"

**Value**

- `b`: Matrix with columns for the estimated coefficients on x, their standard errors, t-values, and p-values (K x 4)
- `s`: Vector of estimated variance parameters (2 x 1). The first and the second elements denote the estimated rho parameter (sp_lambda) quantifying the scale of spatial dependent process, and the standard error of the process (sp_SE), respectively.
- `e`: Vector whose elements are residual standard error (resid_SE), adjusted conditional R2 (adjR2(cond)), restricted log-likelihood (rlogLik), Akaike information criterion (AIC), and Bayesian information criterion (BIC). When method = "ml", restricted log-likelihood (rlogLik) is replaced with log-likelihood (logLik)
- `r`: Vector of estimated random coefficients on the spatial eigenvectors (L x 1)
- `pred`: Vector of predicted values (N x 1)
- `resid`: Vector of residuals (N x 1)

**Author(s)**

Daisuke Murakami

**References**


**See Also**

`meigen, meigen_f`
Examples

```r
require(spdep)
data(boston)
y <- boston.c[, "CMEDV"]
coords <- boston.c[,c("LON", "LAT")]
weig <- weigen(coords)
res <- lsem(y=y, x=x, weig=weig)
res
```

**lslm**  
*Low rank spatial lag model (LSLM) estimation*

### Description

This function estimates the low rank spatial lag model.

### Usage

```r
lslm( y, x, weig, method = "reml", boot = FALSE, iter = 200 )
```

### Arguments

- **y**: Vector of explained variables (N x 1)
- **x**: Matrix of explanatory variables (N x K)
- **weig**: Eigenvectors and eigenvalues of a spatial weight matrix. Output from `weigen`
- **method**: Estimation method. Restricted maximum likelihood method ("reml") and maximum likelihood method ("ml") are available. Default is "reml"
- **boot**: If it is TRUE, confidence intervals for the spatial dependence parameters (s), the mean direct effects (de), and the mean indirect effects (ie), are estimated through a parametric bootstrapping. Default is FALSE
- **iter**: The number of bootstrap replicates. Default is 200

### Value

- **b**: Matrix with columns for the estimated coefficients on x, their standard errors, t-values, and p-values (K x 4)
- **s**: Vector of estimated shrinkage parameters (2 x 1). The first and the second elements denote the estimated rho parameter (sp_rho) quantifying the scale of spatial dependence, and the standard error of the spatial dependent component (sp_SE), respectively. If boot = TRUE, their 95 percent confidence intervals and the resulting p-values are also provided
meigen

Vector whose elements are residual standard error (resid_SE), adjusted conditional R2 (adjR2(cond)), restricted log-likelihood (rlogLik), Akaike information criterion (AIC), and Bayesian information criterion (BIC). When method = "ml", restricted log-likelihood (rlogLik) is replaced with log-likelihood (logLik)

de
Matrix with columns for the estimated mean direct effects on x. If boot = TRUE, their 95 percent confidence intervals and the resulting p-values are also provided

ie
Matrix with columns for the estimated mean indirect effects on x. If boot = TRUE, their 95 percent confidence intervals and the resulting p-values are also provided

r
Vector of estimated random coefficients on the spatial eigenvectors (L x 1)
pred
Vector of predicted values (N x 1)
resid
Vector of residuals (N x 1)

Author(s)
Daisuke Murakami

References

See Also
weigen, lsem

Examples

```r
require(spdep)
data(boston)
y <- boston.c[, "CMEDV"]
coords <- boston.c[, c("LON", "LAT")]
weig <- weigen(coords)
res <- lslm(y=y,x=x,weig=weig)
## res <- lslm(y=y,x=x,weig=weig, boot=TRUE)
res
```

meigen

Extraction of Moran's eigenvectors

Description
This function calculates Moran eigenvectors and eigenvalues.
Usage
meigen( coords, model = "exp", threshold = 0, enum = NULL, cmat = NULL, s_id = NULL )

Arguments

coords  Matrix of spatial point coordinates (N x 2)
model   Type of kernel to model spatial dependence. The currently available options are "exp" for the exponential kernel, "gau" for the Gaussian kernel, and "sph" for the spherical kernel. Default is "exp"
threshold Threshold for the eigenvalues (scalar). Suppose that lambda_1 is the maximum eigenvalue, this function extracts eigenvectors whose corresponding eigenvalue is equal or greater than (threshold x lambda_1). threshold must be a value between 0 and 1. Default is zero (see Details)
enum    Optional. The maximum acceptable number of eigenvectors to be extracted (scalar)
cmat    Optional. A user-specified spatial connectivity matrix (N x N). It must be provided when the user wants to use a spatial connectivity matrix other than the default matrices
s_id    Optional. ID specifying groups modeling spatial effects (N x 1). If specified, Moran eigenvectors are extracted by groups. It is useful e.g. for multilevel modeling (s_id is the groups) and panel data modeling (s_id is given by individual location id). Default is NULL

Details
If cmat is not provided and model = "exp" (default), this function extracts Moran eigenvectors from MCM, where M = I - 11'/N is a centering operator. C is a N x N connectivity matrix whose (i, j)-th element equals exp(-d(i,j)/h), where d(i,j) is the Euclidean distance between the sample sites i and j, and h is given by the maximum length of the minimum spanning tree connecting sample sites (see Dray et al., 2006). If cmat is provided, this function performs the same calculation after C is replaced with cmat.
If threshold is not provided (default), all the eigenvectors corresponding to positive eigenvalue, explaining positive spatial dependence, are extracted to model positive spatial dependence. threshold = 0.00 or 0.25 are standard assumptions (see Griffith, 2003; Murakami and Griffith, 2015).

Value
sf       Matrix of the first L eigenvectors (N x L)
ev       Vector of the first L eigenvalues (L x 1)
ev_full  Vector of all eigenvalues (N x 1)
other    List of other outcomes, which are internally used

Author(s)
Daisuke Murakami
References


See Also

meigen_f for fast eigen-decomposition

Description

This function estimates Moran eigenvectors at unobserved sites using the Nystrom extension.

Usage

meigen0( meig, coords0, s_id0 = NULL )

Arguments

coords0 Matrix of spatial point coordinates of unobserved sites (N_0 x 2)
meig Moran eigenvectors and eigenvalues. Output from meigen or meigen_f
s_id0 Optional. ID specifying groups modeling spatial effects (N_0 x 1). If specified, Moran eigenvectors are extracted by groups. It is useful e.g. for multilevel modeling (s_id is the groups) and panel data modeling (s_id is given by individual location id). Default is NULL

Value

sf Matrix of the first L eigenvectors at unobserved sites (N_0 x L)
ev Vector of the first L eigenvalues (L x 1)
ev_full Vector of all eigenvalues (N x 1)

Author(s)

Daisuke Murakami

References

**meigen_f**

**Fast approximation of Moran eigenvectors**

**Description**

This function performs a fast approximation of Moran eigenvectors and eigenvalues.

**Usage**

```r
meigen_f( coords, model = "exp", enum = 200, s_id = NULL )
```

**Arguments**

- `coords`: Matrix of spatial point coordinates (N x 2)
- `model`: Type of kernel to model spatial dependence. The currently available options are "exp" for the exponential kernel, "gau" for the Gaussian kernel, and "sph" for the spherical kernel. Default is "exp"
- `enum`: Number of eigenvectors and eigenvalues to be extracted (scalar). Default is 200
- `s_id`: Optional. ID specifying groups modeling spatial effects (N x 1). If specified, Moran eigenvectors are extracted by groups. It is useful e.g. for multilevel modeling (s_id is the groups) and panel data modeling (s_id is given by individual location id). Default is NULL

**Details**

This function extracts approximated Moran eigenvectors from MCM. \( M = I - 11'/N \) is a centering operator, and \( C \) is a spatial connectivity matrix whose \( (i, j) \)-th element is given by \( \exp(-d(i,j)/h) \), where \( d(i,j) \) is the Euclidean distance between the sample sites \( i \) and \( j \), and \( h \) is a range parameter given by the maximum length of the minimum spanning tree connecting sample sites (see Dray et al., 2006).

Following a simulation result that 200 eigenvectors are sufficient for accurate approximation of ESF models (Murakami and Griffith, 2019), this function approximates the 200 eigenvectors corresponding to the 200 largest eigenvalues by default (i.e., \( \text{enum} = 200 \)). If \( \text{enum} \) is given by a smaller value like 100, the computation time will be shorter, but with greater approximation error. Eigenvectors corresponding to negative eigenvalues are omitted from the \( \text{enum} \) eigenvectors.

**Value**

- `sf`: Matrix of the first \( L \) approximated eigenvectors (N x L)
- `ev`: Vector of the first \( L \) approximated eigenvalues (L x 1)
- `ev_full`: Vector of all approximated eigenvalues (enum x 1)
- `other`: List of other outcomes, which are internally used

**See Also**

- `meigen`, `meigen_f`
Author(s)
Daisuke Murakami

References

See Also
meigen

plot_n

Plot non-spatially varying coefficients (NVCs)

Description
This function plots non-spatially varying coefficients (NVCs; coefficients varying with respect to explanatory variable value) and their 95 percent confidence intervals

Usage
plot_n( mod, xnum = 1, xtype = "x", cex.lab = 20, cex.axis = 15, lwd = 1.5, ylim = NULL, nmax = 20000 )

Arguments
mod
Output from resf, besf, resf_vc, or besf_vc function
xnum
The NVC on the xnum-th explanatory variable is plotted. Default is 1
xtype
Effective for resf_vc and besf_vc. If "x", the num-th NVC in the spatially and non-spatially varying coefficients on x is plotted. If "xconst", the num-th NVC on xconst is plotted. Default is "x"
cex.lab
The size of the x and y axis labels
cex.axis
The size of the tick label numbers
lwd
The width of the line drawing the coefficient estimates
ylim
The limints of the y-axis
nmax
If sample size exceeds nmax, nmax samples are randomly selected and plotted. Default is 20,000

See Also
resf, besf, resf_vc, besf_vc
plot_qr  

Plot quantile regression coefficients estimated from SF-UQR

Description

This function plots regression coefficients estimated from the spatial filter unconditional quantile regression (SF-UQR) model.

Usage

plot_qr( mod, pnum = 1, par = "b", cex.main = 20, cex.lab = 18, cex.axis = 15, lwd = 1.5 )

Arguments

mod  

Output from the resf_qr function

pnum  

A number specifying the parameter being plotted. If par = "b", the coefficients on the pnum-th explanatory variable are plotted (intercepts are plotted if pnum = 1). If par = "s" and pnum = 1, the estimated standard errors for the residual spatial process are plotted. If par = "s" and pnum = 2, the Moran's I values of the residual spatial process are plotted. The Moran's I value is scaled to take a value between 0 (no spatial dependence) and 1 (the maximum possible spatial dependence). Based on Griffith (2003), the scaled Moran's I value is interpretable as follows: 0.25-0.50:weak; 0.50-0.70:moderate; 0.70-0.90:strong; 0.90-1.00:marked

par  

If it is "b", regression coefficients are plotted. If it is "s", shrinkage (variance) parameters for the residual spatial process are plotted. Default is "b"

cex.main  

Graphical parameter specifying the size of the main title

cex.lab  

Graphical parameter specifying the size of the x and y axis labels

cex.axis  

Graphical parameter specifying the size of the tick label numbers

lwd  

Graphical parameters specifying the width of the line drawing the coefficient estimates

Note

See par for the graphical parameters

See Also

resf_qr
plot_s

Mapping spatially (and non-spatially) varying coefficients (SVCs or SNVC)

Description

This function plots spatially and non-spatially varying coefficients (SNVC) or spatially varying coefficients (SVC). Note that SNVC = SVC + NVC (NVC is a coefficient varying with respect to explanatory variable value)

Usage

plot_s( mod, xnum = 0, btype = "snvc", xtype = "x", pmax = NULL, ncol = 8, col = NULL, inv = FALSE, brks = "regular", cex = 1, nmax = 20000)

Arguments

mod Output from resf, besf, resf_vc, or besf_vc function
xnum For resf_vc and besf_vc, xnum-th S(N)VC on x is plotted. If num = 0, spatially varying intercept is plotted. For resf and besf, estimated spatially dependent component in the residuals is plotted irrespective of the xnum value. Default is 0
btype Effective for resf_vc and besf_vc. If "snvc" (default), SNVC (= SVC + NVC) is plotted. If "svc", SVC is plotted. If "nvc", NVC is plotted
xtype If "x" (default), coefficients on x is plotted. If "xconst", those on xconst is plotted
pmax The maximum p-value for the S(N)VC to be displayed. For example, if pmax = 0.05, only coefficients that are statistically significant at the 5 percent level are plotted. If NULL, all the coefficients are plotted. Default is NULL
ncol Number of colors in the color palette. Default is 8
col Color palette used for the mapping. If NULL, the blue-pink-yellow color scheme is used. Palettes in the RColorBrewer package are available. Default is NULL
inv If TRUE, the color palette is inverted. Default is FALSE
brks If "regular", color is changed at regular intervals. If "quantile", color is changed for each quartile
cex Size of the dots representing sample sites
nmax If sample size exceeds nmax, nmax samples are randomly selected and plotted. Default is 20,000

See Also

resf, besf, resf_vc, besf_vc
predict0

**Spatial prediction using eigenvector spatial filtering (ESF) or random effects ESF**

**Description**

This function predicts explained variables using eigenvector spatial filtering (ESF) or random effects ESF. The Nystrom extension is used to perform a prediction minimizing the expected prediction error.

**Usage**

```r
predict0( mod, meig0, x0 = NULL, xgroup0 = NULL )
```

**Arguments**

- `mod`: ESF or RE-ESF model estimates. Output from `esf` or `resf`.
- `meig0`: Moran eigenvectors at predicted sites. Output from `meigen0`.
- `x0`: Matrix of explanatory variables at predicted sites (N_0 x K). Default is NULL.
- `xgroup0`: Matrix of group IDs that may be group IDs (integers) or group names (N_0 x K_group). Default is NULL.

**Value**

- `pred`: Matrix with the first column for the predicted values (pred). The second and the third columns are the predicted trend component (xb) and the residual spatial process (sf_residual). If `xgroup0` is specified, the fourth column is the predicted group effects (group).
- `c_vc`: Matrix of estimated non-spatially varying coefficients (NVCs) on x0 (N x K). Effective if `nvc =TRUE` in `resf`.
- `cse_vc`: Matrix of standard errors for the NVCs on x0 (N x K). Effective if `nvc =TRUE` in `resf`.
- `ct_vc`: Matrix of t-values for the NVCs on x0 (N x K). Effective if `nvc =TRUE` in `resf`.
- `cp_vc`: Matrix of p-values for the NVCs on x0 (N x K). Effective if `nvc =TRUE` in `resf`.

**References**


**See Also**

`meigen0`, `predict0_vc`
Examples

```r
require(spdep)
data(boston)
samp <- sample(dim(boston.c)[1], 400)

d <- boston.c[samp,]  ## Data at observed sites
y <- d[, "CMEDV"]
x <- d[,c("ZN","INDUS","NOX","RM","AGE","DIS")]
coords <- d[,c("LON","LAT")]

d0 <- boston.c[-samp,][1,]  ## Data at unobserved sites
y0 <- d0[, "CMEDV"]
x0 <- d0[,c("ZN","INDUS","NOX","RM","AGE","DIS")]
coords0 <- d0[,c("LON","LAT")]

############ Model estimation
meig <- meigen(coords = coords )
mod <- resf(y=y, x=x, meig=meig)  ## or
# mod <- esf(y=y,x=x,meig=meig)

############ Spatial prediction
meig0 <- meigen0( meig = meig, coords0 = coords0 )
pred0 <- predict0( mod = mod, x0 = x0, meig0 = meig0 )
pred0$pred[1:10,]

# If NVCs are assumed
#mod2 <- resf(y=y, x=x, meig=meig, nvc=TRUE)
#pred02 <- predict0( mod = mod2, x0 = x0, meig0 = meig0 )
#pred02$pred[1:10,] # Predicted explained variables
#pred02$c_vc[1:10,] # Predicted NVCs
```

**predict0_vc**  
*Prediction of explained variables and spatially varying coefficients*

Description

This function predicts explained variables and spatially and non-spatially varying coefficients. The Nystrom extension is used to perform a prediction minimizing the expected prediction error.

Usage

```r
predict0_vc( mod, meig0, x0 = NULL, xgroup0 = NULL, xconst0 = NULL )
```

Arguments

- `mod`: Output from `resf_vc` or `besf_vc`
- `meig0`: Moran eigenvectors at predicted sites. Output from `meigen0`
predict0_vc

x0  Matrix of explanatory variables at predicted sites whose coefficients are allowed to vary across geographical space (N_0 x K). Default is NULL.

xgroup0  Matrix of group indices that may be group IDs (integers) or group names (N_0 x K_group). Default is NULL.

xconst0  Matrix of explanatory variables at predicted sites whose coefficients are assumed constant (or NVC) across space (N_0 x K_const). Default is NULL.

Value

pred  Matrix with the first column for the predicted values (pred). The second and the third columns are the predicted trend component (i.e., component explained by x0 and xconst0) (xb) and the residual spatial process (sf_residual). If xgroup0 is specified, the fourth column is the predicted group effects (group).

b_vc  Matrix of estimated spatially (and non-spatially) varying coefficients (S(N)VCs) on x0 (N_0 x K).

bse_vc  Matrix of estimated standard errors for the S(N)VCs (N_0 x K).

t_vc  Matrix of estimated t-values for the S(N)VCs (N_0 x K).

p_vc  Matrix of estimated p-values for the S(N)VCs (N_0 x K).

c_vc  Matrix of estimated non-spatially varying coefficients (NVCs) on xconst0 (N_0 x K).

cse_vc  Matrix of estimated standard errors for the NVCs (N_0 x K).

tc_vc  Matrix of estimated t-values for the NVCs (N_0 x K).

References


See Also

meigen0, predict0

Examples

```r
require(spdep)
data(boston)
samp <- sample( dim( boston.c )[1], 300)
d <- boston.c[ samp, ]  ## Data at observed sites
y <- d[, "CMEDV"]
x <- d[, c("ZN", "LSTAT")]
xconst <- d[, c("CRIM", "NOX", "AGE", "DIS", "RAD", "TAX", "PTRATIO", "B", "RM")]
coords <- d[, c("LON", "LAT")]
```
d0 <- boston.c[-samp,]  ## Data at unobserved sites
x0 <- d0[,c("ZN", "LSTAT")]
xconst0 <- d0[,c("CRIM", "NOX", "AGE", "DIS", "RAD", "TAX", "PTRATIO", "B", "RM")]
coords0 <- d0[,c("LON", "LAT")]

############ Model estimation
meig <- meigen( coords = coords )
mod <- resf_vc(y=y, x=x, xconst=xconst, meig=meig )

############ Spatial prediction of y and spatially varying coefficients
meig0 <- meigen0( meig = meig, coords0 = coords0 )
pred0 <- predict0_vc( mod = mod, x0 = x0, xconst0=xconst0, meig0 = meig0 )
pred0$pred[1:10,] # Predicted explained variables
pred0$b_vc[1:10,] # Predicted SVCs
pred0$bse_vc[1:10,]# Predicted standard errors of the SVCs
pred0$t_vc[1:10,] # Predicted t-values of the SNVCs
pred0$p_vc[1:10,] # Predicted p-values of the SNVCs

############ or spatial prediction of spatially varying coefficients only
# pred00 <- predict0_vc( mod = mod, meig0 = meig0 )
# pred00$b_vc[1:10,]
# pred00$bse_vc[1:10,]
# pred00$t_vc[1:10,]
# pred00$p_vc[1:10,]

########################################################################
# If SNVCs are assumed on x
# mod2 <- resf_vc(y=y, x=x, xconst=xconst, meig=meig, x_nvc=TRUE,xconst_nvc=TRUE )
# pred02 <- predict0_vc( mod = mod2, x0 = x0, xconst0=xconst0 ,meig0 = meig0 )
# pred02$pred[1:10,] # Predicted explained variables
# pred02$b_vc[1:10,] # Predicted SNVCs
# pred02$bse_vc[1:10,]# Predicted standard errors of the SNVCs
# pred02$t_vc[1:10,] # Predicted t-values of the SNVCs
# pred02$p_vc[1:10,] # Predicted p-values of the SNVCs

resf  Spatial regression with random effects eigenvector spatial filtering
       (RE-ESF)

Description

RE-ESF-based spatial regression modeling. This model estimates residual spatial dependence, constant coefficients, non-spatially varying coefficients (NVC; coefficients varying with respect to explanatory variable value), and group effects.

Usage

resf( y, x = NULL, xgroup = NULL, nvc = FALSE, nvc_sel = TRUE, 
      nvc_num = 5, meig, method = "reml", penalty = "bic" )
Arguments

- **y**: Vector of explained variables (N x 1)
- **x**: Matrix of explanatory variables (N x K). Default is NULL
- **xgroup**: Matrix of group IDs. The IDs may be group numbers or group names (N x K_group). Default is NULL
- **nvc**: If TRUE, non-spatially varying coefficients (NVCs; coefficients varying with respect to explanatory variable value) are assumed. If FALSE, constant coefficients are assumed. Default is FALSE
- **nvc_sel**: If TRUE, type of each coefficient (NVC or constant) is selected through a BIC (default) or AIC minimization. If FALSE, NVCs are assumed across x. Alternatively, nvc_sel can be given by column number(s) of x. For example, if nvc_sel = 2, the coefficient on the second explanatory variable is NVC and the other coefficients are constants. Default is TRUE
- **nvc_num**: Number of basis functions used to model NVC. An intercept and nvc_num natural spline basis functions are used to model each NVC. Default is 5
- **meig**: Moran eigenvectors and eigenvalues. Output from `meigen` or `meigen_f`
- **method**: Estimation method. Restricted maximum likelihood method ("reml") and maximum likelihood method ("ml") are available. Default is "reml"
- **penalty**: Penalty to select type of coefficients (NVC or constant) to stabilize the estimates. The current options are "bic" for the Bayesian information criterion-type penalty (N x log(K)) and "aic" for the Akaike information criterion (2K). Default is "bic"

Value

- **b**: Matrix with columns for the estimated coefficients on x, their standard errors, t-values, and p-values (K x 4)
- **b_g**: List of K_group matrices with columns for the estimated group effects, their standard errors, and t-values
- **c_vc**: Matrix of estimated NVCs on x (N x K). Effective if nvc = TRUE
- **cse_vc**: Matrix of standard errors for the NVCs on x (N x K). Effective if nvc = TRUE
- **ct_vc**: Matrix of t-values for the NVCs on x (N x K). Effective if nvc = TRUE
- **cp_vc**: Matrix of p-values for the NVCs on x (N x K). Effective if nvc = TRUE
- **s**: Vector of estimated variance parameters (2 x 1). The first and the second elements are the standard error and the Moran’s I value of the estimated spatially dependent process, respectively. The Moran’s I value is scaled to take a value between 0 (no spatial dependence) and 1 (the maximum possible spatial dependence). Based on Griffith (2003), the scaled Moran'I value is interpretable as follows: 0.25-0.50:weak; 0.50-0.70:moderate; 0.70-0.90:strong; 0.90-1.00:marked
- **s_c**: Vector of standard errors of the NVCs on xconst
- **s_g**: Vector of estimated standard errors of the group effects
resf

Vector whose elements are residual standard error (resid_SE), adjusted conditional R2 (adjR2(cond)), restricted log-likelihood (rlogLik), Akaike information criterion (AIC), and Bayesian information criterion (BIC). When method = "ml", restricted log-likelihood (rlogLik) is replaced with log-likelihood (logLik)

vc
List indicating whether NVC are removed or not during the BIC/AIC minimization. 1 indicates not removed whereas 0 indicates removed

r
Vector of estimated random coefficients on Moran’s eigenvectors (L x 1)

sf
Vector of estimated spatial dependent component (N x 1)

pred
Vector of predicted values (N x 1)

resid
Vector of residuals (N x 1)

other
List of other outcomes, which are internally used

Author(s)

Daisuke Murakami

References


See Also

meigen, meigen_f, besf

Examples

require(spdep);require(Matrix)
data(boston)
y <- boston.c[, "CMEDV"]
x <- boston.c[,c("CRIM","ZN","INDUS","CHAS","NOX","RM","AGE","DIS","RAD","TAX","PTRATIO","B","LSTAT")]
xgroup<- boston.c[,"TOWN"]
coords<- boston.c[,c("LON","LAT")]
meig <- meigen(coords=coords)
# meig<- meigen_f(coords=coords) ## for large samples

######### Regression considering residual spatially dependence
res <- resf(y = y, x = x, meig = meig)
res
plot_s(res) ## spatially dependent component (intercept)

######### Regression considering residual spatially dependence and NVC
######### (coefficients or NVC is selected)
#res2 <- resf(y = y, x = x, meig = meig, nvc = TRUE)
#res2 ## Note: Coefficients on 5,6,and 13-th covariates
## are estimated non-spatially varying (NVC)
resf_qr

Spatial filter unconditional quantile regression

Description
This function estimates the spatial filter unconditional quantile regression (SF-UQR) model.

Usage
resf_qr( y, x = NULL, meig, tau = NULL, boot = TRUE, iter = 200, cl=NULL )

Arguments
y  Vector of explained variables (N x 1)
x  Matrix of explanatory variables (N x K). Default is NULL
meig Moran eigenvectors and eigenvalues. Output from meigen or meigen_f
tau The quantile(s) to be modeled. It must be a number (or a vector of numbers) strictly between 0 and 1. By default, tau = c(0.1, 0.2, ..., 0.9)
boot If it is TRUE, confidence intervals of regression coefficients are estimated by a semiparametric bootstrapping. Default is TRUE
iter The number of bootstrap replications. Default is 200
cl  Number of cores used for the parallel computation. If cl=NULL, which is the default, the number of available cores is detected and used
Value

- **b**: Matrix of estimated regression coefficients (K x Q), where Q is the number of quantiles (i.e., the length of tau)
- **r**: Matrix of estimated random coefficients on Moran eigenvectors (L x Q)
- **s**: Vector of estimated variance parameters (2 x 1). The first and the second elements denote the standard error and the Moran’s I value of the estimated spatially dependent component, respectively. The Moran’s I value is scaled to take a value between 0 (no spatial dependence) and 1 (the maximum possible spatial dependence). Based on Griffith (2003), the scaled Moran’s I value is interpretable as follows: 0.25-0.50: weak; 0.50-0.70: moderate; 0.70-0.90: strong; 0.90-1.00: marked
- **e**: Vector whose elements are residual standard error (resid_SE) and adjusted quasi conditional R2 (quasi_adjR2(cond))
- **B**: Q matrices (K x 4) summarizing bootstrapped estimates for the regression coefficients. Columns of these matrices consist of the estimated coefficients, the lower and upper bounds for the 95 percent confidence intervals, and p-values. It is returned if boot = TRUE
- **S**: Q matrices (2 x 3) summarizing bootstrapped estimates for the variance parameters. Columns of these matrices consist of the estimated parameters, the lower and upper bounds for the 95 percent confidence intervals. It is returned if boot = TRUE
- **B_0**: List of Q matrices (K x iter) summarizing bootstrapped coefficients. The q-th matrix consists of the coefficients on the q-th quantile. Effective if boot = TRUE
- **S_0**: List of Q matrices (2 x iter) summarizing bootstrapped variance parameters. The q-th matrix consists of the parameters on the q-th quantile. Effective if boot = TRUE

Author(s)

Daisuke Murakami

References


See Also

plot_qr

Examples

```r
require(spdep)
data(boston)
y <- boston.c[, "CMEDV"]
x <- boston.c[,c("CRIM","ZN","INDUS","CHAS","NOX","RM","AGE",
              "DIS","RAD","TAX","PFRATIO","B","LSTAT")]
coords <- boston.c[,c("LON", "LAT")]
```
resf_vc <- meigen(coords=coords)
res <- resf_qr(y=y,x=x,meig=meig, boot=FALSE)
res
plot_qr(res,1)  # Intercept
plot_qr(res,2)  # Coefficient on CRIM
plot_qr(res,1,"s")  # spcomp_SE
plot_qr(res,2,"s")  # spcomp_Moran.I/max(Moran.I)

###Not run
#res <- resf_qr(y=y,x=x,meig=meig, boot=TRUE)
#res
#plot_qr(res,1)  # Intercept + 95 percent confidence interval (CI)
#plot_qr(res,2)  # Coefficient on CRIM + 95 percent CI
#plot_qr(res,1,"s")  # spcomp_SE + 95 percent CI
#plot_qr(res,2,"s")  # spcomp_Moran.I/max(Moran.I) + 95 percent CI

resf_vc  

Spatially and non-spatially varying coefficient (SNVC) modeling

Description

The model estimates residual spatial dependence, constant coefficients, spatially varying coefficients (SVCs), non-spatially varying coefficients (NVC; coefficients varying with respect to explanatory variable value), SNVC (= SVC + NVC), and group effects. Type of coefficients can be selected through BIC/AIC minimization. By default, it estimates a SVC model.

Note: SNVCs can be mapped just like SVCs. SNVC model is more robust against spurious correlation (multicollinearity) and stable than SVC models (see Murakami and Griffith, 2020).

Usage

```
resf_vc(y, x, xconst = NULL, xgroup = NULL, x_nvc = FALSE, xconst_nvc = FALSE,
        x_sel = TRUE, x_nvc_sel = TRUE, xconst_nvc_sel = TRUE, nvc_num = 5,
        meig, method = "reml", penalty = "bic", maxiter = 30 )
```

Arguments

- **y**: Vector of explained variables (N x 1)
- **x**: Matrix of explanatory variables with spatially varying coefficients (SVC) (N x K)
- **xconst**: Matrix of explanatory variables with constant coefficients (N x K_c). Default is NULL
- **xgroup**: Matrix of group IDs. The IDs may be group numbers or group names (N x K_g). Default is NULL
- **x_nvc**: If TRUE, SNVCs are assumed on x. Otherwise, SVCs are assumed. Default is FALSE
- **xconst_nvc**: If TRUE, NVCs are assumed on xconst. Otherwise, constant coefficients are assumed. Default is FALSE
x_sel

If TRUE, type of coefficient (SVC or constant) on x is selected through a BIC (default) or AIC minimization. If FALSE, SVCs are assumed across x. Alternatively, x_sel can be given by column number(s) of x. For example, if x_sel = 2, the coefficient on the second explanatory variable in x is SVC and the other coefficients are constants. The Default is TRUE

x_nvc_sel

If TRUE, type of coefficient (NVC or constant) on x is selected through the BIC (default) or AIC minimization. If FALSE, NVCs are assumed across x. Alternatively, x_nvc_sel can be given by column number(s) of x. For example, if x_nvc_sel = 2, the coefficient on the second explanatory variable in x is NVC and the other coefficients are constants. The Default is TRUE

xconst_nvc_sel

If TRUE, type of coefficient (NVC or constant) on xconst is selected through the BIC (default) or AIC minimization. If FALSE, NVCs are assumed across xconst. Alternatively, xconst_nvc_sel can be given by column number(s) of xconst. For example, if xconst_nvc_sel = 2, the coefficient on the second explanatory variable in xconst is NVC and the other coefficients are constants. The Default is TRUE

nvc_num

Number of basis functions used to model NVC. An intercept and nvc_num natural spline basis functions are used to model each NVC. Default is 5

meig

Moran eigenvectors and eigenvalues. Output from meigen or meigen_f

method

Estimation method. Restricted maximum likelihood method ("reml") and maximum likelihood method ("ml") are available. Default is "reml"

penalty

Penalty to select varying coefficients and stabilize the estimates. The current options are "bic" for the Baysian information criterion-type penalty (N x log(K)) and "aic" for the Akaike information criterion (2K) (see Muller et al., 2013). Default is "bic"

maxiter

Maximum number of iterations. Default is 30

Value

b_vc

Matrix of estimated spatially and non-spatially varying coefficients (SNVC = SVC + NVC) on x (N x K)

bse_vc

Matrix of standard errors for the SNVCs on x (N x k)

t_vc

Matrix of t-values for the SNVCs on x (N x K)

p_vc

Matrix of p-values for the SNVCs on x (N x K)

B_vc_s

List summarizing estimated SVCs (in SNVC) on x. The four elements are the SVCs (N x K), the standard errors (N x K), t-values (N x K), and p-values (N x K), respectively

B_vc_n

List summarizing estimated NVCs (in SNVC) on x. The four elements are the NVCs (N x K), the standard errors (N x K), t-values (N x K), and p-values (N x K), respectively

c

Matrix with columns for the estimated coefficients on xconst, their standard errors, t-values, and p-values (K_c x 4). Effective if xconst_nvc = FALSE

c_vc

Matrix of estimated NVCs on xconst (N x K_c). Effective if xconst_nvc = TRUE

cse_vc

Matrix of standard errors for the NVCs on xconst (N x k_c). Effective if xconst_nvc = TRUE
Matrix of t-values for the NVCs on xconst (N x K_c). Effective if xconst_nvc = TRUE

Matrix of p-values for the NVCs on xconst (N x K_c). Effective if xconst_nvc = TRUE

List of K_g matrices with columns for the estimated group effects, their standard errors, and t-values

List of variance parameters in the SNVC (SVC + NVC) on x. The first element is a 2 x K matrix summarizing variance parameters for SVC. The (1, k)-th element is the standard error of the k-th SVC, while the (2, k)-th element is the Moran’s I value is scaled to take a value between 0 (no spatial dependence) and 1 (strongest spatial dependence). Based on Griffith (2003), the scaled Moran’s I value is interpretable as follows: 0.25-0.50:weak; 0.50-0.70:moderate; 0.70-0.90:strong; 0.90-1.00:marked. The second element of s is the vector of standard errors of the NVCs

Vector of standard errors of the NVCs on xconst

Vector of standard errors of the group effects

List indicating whether SVC/NVC are removed or not during the BIC/AIC minimization. 1 indicates not removed (replaced with constant) whereas 0 indicates removed

Vector whose elements are residual standard error (resid_SE), adjusted conditional R2 (adjR2(cond)), restricted log-likelihood (rlogLik), Akaike information criterion (AIC), and Bayesian information criterion (BIC). When method = "ml", restricted log-likelihood (rlogLik) is replaced with log-likelihood (logLik)

Vector of predicted values (N x 1)

Vector of residuals (N x 1)

List of other outcomes, which are internally used

Author(s)
Daisuke Murakami

References


resf_vc

See Also
meigen, meigen_f, besf_vc

Examples

```
require(spdep)
data(boston)
y <- boston.c[, "CMEDV"]
x <- boston.c[,c("CRIM", "AGE")]
xconst <- boston.c[,c("ZN","DIS","RAD","NOX", "TAX","RM", "PTRATIO", "B")]
xgroup <- boston.c[,"TOWN"]
coords <- boston.c[,c("LON", "LAT")]
meig <- meigen(coords=coords)
# meig <- meigen_f(coords=coords) ## for large samples

############## SVC modeling1 ####################
(SVC or constant coefficients on x; Constant coefficients on xconst)
res <- resf_vc(y=y, x=x, xconst=xconst, meig=meig)
res
plot_s(res,0) # Spatially varying intercept
plot_s(res,1) # 1st SVC (Not shown because the SVC is estimated constant)
plot_s(res,2) # 2nd SVC

############## SVC modeling2 ####################
(SVC on x; Constant coefficients on xconst)
#res2 <- resf_vc(y=y, x=x, xconst=xconst, meig=meig, x_sel = FALSE)

############## SVC modeling3 ####################
- Group-level SVC or constant coefficients on x
- Constant coefficients on xconst
- Group effects

#meig_g <- meigen(coords, s_id=xgroup)
#res3 <- resf_vc(y=y, x=x, xconst=xconst, meig=meig_g, xgroup=xgroup)

############## SNVC modeling1 ####################
(SNVC, SVC, NVC, or constant coefficients on x)
- Constant coefficients on xconst

#res4 <- resf_vc(y=y, x=x, xconst=xconst, meig=meig, x_nvc =TRUE)

############## SNVC modeling2 ####################
- SNVC, SVC, NVC, or constant coefficients on x
- NVC or Constant coefficients on xconst

#res5 <- resf_vc(y=y, x=x, xconst=xconst, meig=meig, x_nvc =TRUE, xconst_nvc=TRUE)
#plot_s(res5,0) # Spatially varying intercept
#plot_s(res5,1) # Spatial plot of 1st SNVC (SVC + NVC)
#plot_s(res5,1,btype="svc") # Spatial plot of SVC in the SNVC on x[,1]
#plot_s(res5,1,btype="nvc") # Spatial plot of NVC in the SNVC on x[,1]
#plot_n(res5,1) # 1D plot of NVC in the SNVC on x[,1]
```
Description

This function extracts eigenvectors and eigenvalues from a spatial weight matrix.

Usage

weigen( x = NULL, type = "knn", k = 4, threshold = 0.25, enum = NULL )

Arguments

x Matrix of spatial point coordinates (N x 2), ShapePolygons object (N spatial units), or an user-specified spatial weight matrix (N x N) (see Details)
type Type of spatial weights. The currently available options are "knn" for the k-nearest neighbor-based weights, and "tri" for the Delaunay triangulation-based weights. If ShapePolygons are provided for x, type is ignored, and the rook-type neighborhood matrix is created
k Number of nearest neighbors. It is used if type = "knn"
threshold Threshold for the eigenvalues (scalar). Suppose that lambda_1 is the maximum eigenvalue. Then, this function extracts eigenvectors whose corresponding eigenvalues are equal or greater than [threshold x lambda_1]. It must be a value between 0 and 1. Default is 0.25 (see Details)
enum Optional. The maximum acceptable number of eigenvectors to be used for spatial modeling (scalar)

Details

If user-specified spatial weight matrix is provided for x, this function returns the eigen-pairs of the matrix. Otherwise, if a SpatialPolygons object is provided to x, the rook-type neighborhood matrix is created using this polygon, and eigen-decomposed. Otherwise, if point coordinates are provided to x, a spatial weight matrix is created according to type, and eigen-decomposed.

By default, the ARPACK routine is implemented for fast eigen-decomposition.

threshold = 0.25 (default) is a standard setting for topology-based ESF (see Tiefelsdorf and Griffith, 2007) while threshold = 0.00 is a usual setting for distance-based ESF.

Value

sf Matrix of the first L eigenvectors (N x L)
ev Vector of the first L eigenvalues (L x 1)
other List of other outcomes, which are internally used
weigen

Author(s)
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References

See Also
meigen, meigen_f

Examples

```r
require(spdep);library(rgdal)
data(boston)

########## Rook adjacency-based W
poly <- readOGR(system.file("shapes/boston_tracts.shp",package="spData") [1])
weig1 <- weigen( poly )

########## knn-based W
coords <- boston.c[,c("LON", "LAT")]
weig2 <- weigen( coords, type = "knn" )

########## Delaunay triangulation-based W
coords <- boston.c[,c("LON", "LAT")]
weig3 <- weigen( coords, type = "tri" )

########## User-specified W
dmat <- as.matrix(dist(coords))
cmat <- exp(-dmat)
diag(cmat)<- 0
weig4 <- weigen( cmat, threshold = 0 )
```
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