Transformation-based generalized spatial regression using the spmoran package: Case study examples

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1. Introduction

1.1. Outline

Application examples of generalized spatial regression modeling for count data and continuous non-Gaussian data using the spmoran package (version 0.2.2 onward) are presented. In Section 2, the model is introduced. In the subsequent sections, applications of the model for disease mapping, spatial prediction and uncertainty modeling, and hedonic analysis are presented.

The R codes used are available at https://github.com/dmuraka/spmoran. Another coding examples focusing on Gaussian spatial regression modeling is also available on the same GitHub page.

1.2. Model

The following generalized spatial regression model (Murakami et al., 2021) is considered:

$$\varphi_{\boldsymbol{\theta}}(y_i) = z_i, \quad z_i = \sum_{k=1}^{K} x_{i,k}\beta_{i,k} + w_i + \varepsilon_i, \quad w_i \sim N(0, c(d_{ij})), \quad \varepsilon_i \sim N(0, \sigma^2), \tag{1}$$

where $\varphi_{\boldsymbol{\theta}}(\cdot)$ is a transformation function normalizing the i-th explained variable y_i, $x_{i,k}$ is the k-th explanatory variable, $\beta_{i,k}$ is a fixed or random coefficient, which may vary spatially and/or non-spatially (the distribution for $\beta_{i,k}$ is omitted from Eq. (1) for simplicity), and w_i is a term that captures residual spatial dependence. Moran eigenvectors, which are spatial basis functions, are used to model the spatially dependent processes in $\beta_{i,k}$ and w_i. This model can be rewritten as follows:

$$y_i = \varphi_{\boldsymbol{\theta}}^{-1}(z_i), \quad z_i = \sum_{k=1}^{K} x_{i,k}\beta_{i,k} + w_i + \varepsilon_i, \quad w_i \sim N(0, c(d_{ij})), \quad \varepsilon_i \sim N(0, \sigma^2). \tag{2}$$

Eq. (2) suggests that y_i is assumed to have a distribution obtained by transforming a Gaussian distributed z_i using the $\varphi_{\boldsymbol{\theta}}^{-1}(\cdot)$ function. This model describes a wide variety of non-Gaussian data, including count data, by flexibly specifying the transformation function.

The transformation function is defined by concatenating D sub-transformation functions:

$$\varphi_{\boldsymbol{\theta}}(y_i) = \varphi_{\boldsymbol{\theta}_D}\left(\varphi_{\boldsymbol{\theta}_{D-1}}\left(\cdots \varphi_{\boldsymbol{\theta}_2}\left(\varphi_{\boldsymbol{\theta}_1}(y_i)\right) \cdots\right)\right), \tag{3}$$

where $\varphi_{\boldsymbol{\theta}_d}(\cdot)$ is the d-th sub-transformation function, which depends on the set of parameters $\boldsymbol{\theta}_d$. For continuous explained variables, the spmoran package provides the following specifications for $\varphi_{\boldsymbol{\theta}}(\cdot)$ (see Figure 1).

(a) For non-negative y_i, the Box–Cox transformation is available (left of Figure 1).

(b) For non-Gaussian y_i (e.g., skew and fat-tail distribution), the SAL transformation in Eq. (4) (Rios and Tobar, 2019), which is a nonlinear transformation, is iterated D times to normalize y_i accurately (middle of Figure 1):

$$\varphi_{\boldsymbol{\theta}_d}(y_i) = \theta_{d,1} + \theta_{d,2}\sinh\left(\theta_{d,3}\,\mathrm{arcsinh}(y_i) - \theta_{d,4}\right), \tag{4}$$

where $\boldsymbol{\theta}_d \in \{\theta_{d,1}, \theta_{d,2}, \theta_{d,3}, \theta_{d,4}\}$.

(c) For non-negative and non-Gaussian y_i, the Box–Cox transformation is applied first, and the SAL transformation is iterated D times thereafter to normalize y_i accurately (right of Figure 1).

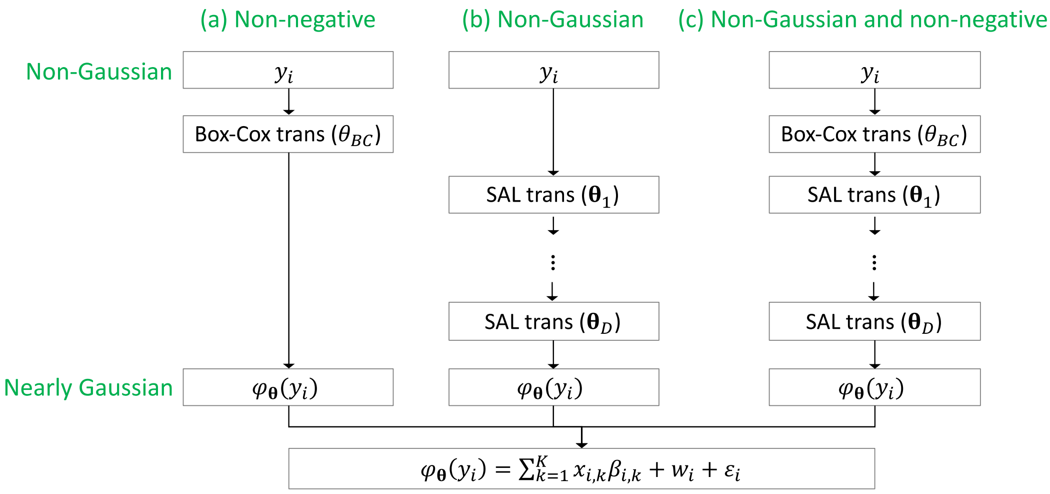


Figure 1: Transformation functions for continuous variables.

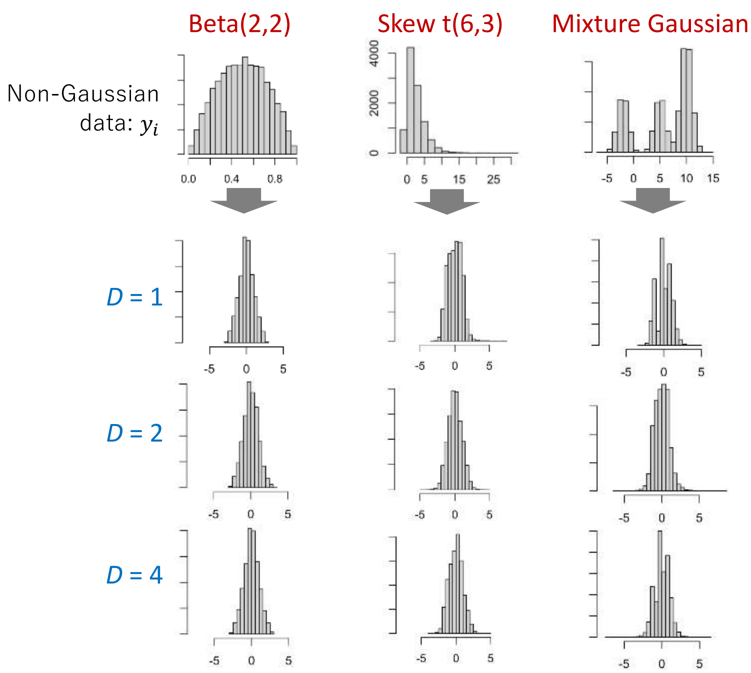


Figure 2: Results of applying the iterative SAL transformations to simulated data generated from beta, skew t, and Gaussian mixture distributions. The top three panels represent histograms of the simulated non-Gaussian data, and the bottom nine panels show the histograms after the transformations. D is the number of transformations.

As illustrated in Figure 2, the iteration of the SAL transformations converts a wide variety of non-Gaussian data y_i to Gaussian data $\varphi_{\boldsymbol{\theta}}(y_i)$ flexibly. Thus, the generalized regression model in Eq. (1) is available for a wide variety of non-Gaussian data.

This model in Eq. (1) is also available for count data by applying a (log-)Gaussian transformation approximating the count data distribution. The following transformations are implemented in the spmoran package:

(d) For (over-dispersed) Poisson counts, a log-Gaussian approximation proposed by Murakami and Matsui (2021) is available (left of Figure 3). Based on these results, the accuracy of the approximate model is almost the same as that of conventional over-dispersed Poisson regression.

(e) For counts that do not obey the Poisson distribution, the log-Gaussian approximation is applied first to normalize the data roughly, and the SAL transformation is iterated to identify the most likely distribution (i.e., probability mass function) (right of Figure 3).

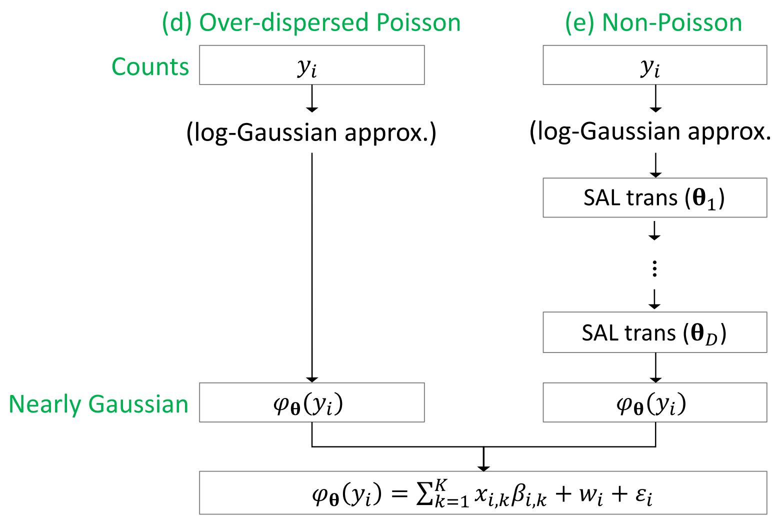


Figure 3: Transformation functions for count variables.

1.3. Coding for specifying the transformation

In the spmoran package, the transformation function $\varphi_{\boldsymbol{\theta}}(\cdot)$ in Eq. (1) is specified using the nongauss_y function. The following is a code (blue part) to specify (a) for non-negative y_i:

```
> ng_a     <- nongauss_y(y_nonneg=TRUE)
Box-cox transformation f() is applied to y to estimate
y ~ P( xb, par )   (or f(y,par)~N(xb, sig) )

 - P(): Distribution estimated through the transformation
 - xb : Regression term with fixed and random coefficients in b
        which is specified by resf or resf_vc function
 - par: Parameter estimating data distribution
```

Here, y_nonneg = TRUE constrains the explained variables to avoid negative values. The output from the nongauss_y function is used as an input of the resf or resf_vc function to estimate Eq. (1). The transformations (b) for non-Gaussian y_i and (c) for non-negative and non-Gaussian y_i are specified as follows (D = 2 is assumed):

```
> ng_b     <- nongauss_y(tr_num=2)
2 SAL transformations are applied to y to estimate
y ~ P( xb, par )   (or f(y,par)~N(xb, sig) )

 - P(): Distribution estimated through the transformation(s)
 - xb : Regression term with fixed and random coefficients in b
        which is specified by resf or resf_vc function
 - par: Parameters estimating data distribution
```

```
> ng_c     <- nongauss_y(y_nonneg=TRUE,tr_num=2)
Box-Cox and 2 SAL transformations f() are applied to y to estimate
y ~ P( xb, par )   (or f(y,par)~N(xb, sig) )

 - P(): Distribution estimated through the transformation(s)
 - xb : Regression term with fixed and random coefficients in b
        which is specified by resf or resf_vc function
 - par: Parameters estimating data distribution
```

where tr_num (=D) specifies the number of SAL transformations. Finally, the transformations (d) for over-dispersed Poisson counts and (e) for other counts are specified as follows:

```
> ng_d     <- nongauss_y(y_type="count")
Log-Gaussian approximation estimating
y ~ oPois( mu, sig ), mu = exp( xb )

 - oPois(): Overdispersed Poisson distribution
 - xb     : Regression term with fixed and random coefficients in b
            which is specified by resf or resf_vc function
 - sig    : Dispersion parameter (overdispersion if sig > 1)
```

```
> ng_e    <- nongauss_y(y_type="count",tr_num=2)
Log-Gaussian and 2 SAL transformations are applied to y to estimate
 y ~ P( mu, par ), mu = exp( xb )

 - P(): Distribution estimated through the transformations
 - xb : Regression term with fixed and random coefficients in b
        which is specified by resf or resf_vc function
 - par: Parameters estimating data distribution
```

where y_type specifies the data type ("count" for count variables and "continuous" for continuous variables (default)).

The subsequent sections present application examples of the model for count data (Section 2) and continuous data (Sections 3 and 4).

2. Example 1: Disease mapping and regression with count data

In this section, a count regression model for epidemic data that considers spatially varying coefficients (SVCs), residual spatial dependence, and heterogeneity across years is demonstrated. The estimated model is used mainly for disease mapping and uncertainty modeling.

2.1. Data

The study described in this section uses the sf, rgeos, CARBayesdata, spdep, and spmoran packages:

```
> library(sf);library(rgeos);library(CARBayesdata);library(spdep);library(spmoran)
```

Pollution-health data (pollutionhealthdata) available from the CARBayesdata package are employed. The data consist of respiratory hospitalization data, air pollution data, and covariate data for greater Glasgow (2007–2011) by 271 Intermediate Geographies (IG).

```
> data("pollutionhealthdata")
> head(pollutionhealthdata)
         IG year observed  expected     pm10  jsa price
1 S02000260 2007       97  98.24602 14.02699 2.25 1.150
2 S02000261 2007       15  45.26085 13.30402 0.60 1.640
3 S02000262 2007       49  92.36517 13.30402 0.95 1.750
4 S02000263 2007       44  72.55324 14.00985 0.35 2.385
5 S02000264 2007       68 125.41904 14.08074 0.80 1.645
6 S02000265 2007       24  55.04868 14.08884 1.25 1.760
```

The explained variable (y) is the number of hospitalizations resulting from respiratory disease (observed). Explanatory variables (x) are the average particulate matter concentration (pm10), the percentage of working-age people who are in receipt of Job Seekers Allowance, a benefit paid to unemployed people looking for work (jsa), and the average property price (divided by 100,000) (price). Random effects by year are considered to estimate the heterogeneity across years (xgroup). Furthermore, the expected number of hospitalizations based on Scotland-wide respiratory hospitalization rates (expected) is used as an offset variable. These variables are specified as follows:

```
> y      <- pollutionhealthdata[,"observed"]
> x      <- pollutionhealthdata[,c("jsa","price","pm10")]
> xgroup <- pollutionhealthdata[,"year"]
> offset <- pollutionhealthdata[,"expected"]
```

A binary contiguity matrix generated from the spatial polygons by IGs (GGHB.IG) is used to model spatial dependence:

```
> data("GGHB.IG")
> W.nb   <- poly2nb(GGHB.IG)
> W.list <- nb2listw(W.nb, style = "B")
> W      <- nb2mat(W.nb, style = "B")
```

As explained, Moran eigenvectors are used to model spatially dependent processes. The following is a code that generates eigenvectors from the W matrix:

```
> s_id   <- pollutionhealthdata[,"IG"]
> meig   <- meigen(cmat=W, s_id = s_id )
 109/271 eigen-pairs are extracted
```

where cmat specifies a spatial proximity matrix, and s_id specifies the zone ID (the *i*-th row of cmat and the element of s_id that appears in the *i*-th are associated).

2.2. Model

In this section, two specifications of y are considered. The former (ng1) assumes that y obeys an over-dispersed Poisson distribution. The latter assumes a more general distribution and estimates it through the SAL transformation (ng2):

```
> ng1    <- nongauss_y( y_type = "count")
Log-Gaussian approximation estimating
y ~ oPois( mu, sig ), mu = exp( xb )

 - oPois(): Overdispersed Poisson distribution
 - xb     : Regression term with fixed and random coefficients in b
            which is specified by resf or resf_vc function
 - sig    : Dispersion parameter (overdispersion if sig > 1)


> ng2    <- nongauss_y( y_type = "count", tr_num=1 )
Log-Gaussian and 1 SAL transformations are applied to y to estimate
 y ~ P( mu, par ), mu = exp( xb )

 - P(): Distribution estimated through the transformations
 - xb : Regression term with fixed and random coefficients in b
        which is specified by resf or resf_vc function
 - par: Parameters estimating data distribution
```

The outputs ng1 and ng2 are used as inputs for the resf function or resf_cv function. The resf function estimates spatial regression models without SVCs, whereas the resf_vc function estimates models with SVCs (see Murakami, 2017). Here, the following models are estimated.

```
> mod1   <- resf(y=y, x=x, meig=meig, xgroup=xgroup,nongauss=ng1)
> mod2   <- resf(y=y, x=x, meig=meig, xgroup=xgroup,nongauss=ng2)
> mod3   <- resf_vc(y=y, x=x, xgroup=xgroup, offset=offset,meig=meig,nongauss=ng1)
> mod4   <- resf_vc(y=y, x=x, xgroup=xgroup, offset=offset,meig=meig,nongauss=ng2)
```

where mod1 and mod2 assume constant coefficients, and mod3 and mod4 assume SVCs on x. For the distribution of y, mod1 and mod3 assume an over-dispersed Poisson distribution, and mod2 and mod3 adjust the distribution using the SAL transformation to identify the most likely distribution. The Bayesian information criterion (BIC) values are -260.1 (mod1), -256.2 (mod2), -274.2 (mod3), and -271.7 (mod4). Here, mod3, which is an over-dispersed Poisson SVC model, is selected as the best model. The BIC is based on a Gaussian likelihood approximating the Poisson model, which differs from the conventional Poisson likelihood.

The estimation result of mod3 is as follows. The intercept and coefficient on price are estimated to vary spatially, whereas the coefficients on jsa and pm10 are estimated to be constant. As shown at the bottom, the BIC of mod3 is considerably better than that of the NULL model (74.9), which is a log-Gaussian model approximating conventional Poisson regression:

```
> mod3
Call:
resf_vc(y = y, x = x, xgroup = xgroup, offset = offset, meig = meig,
    nongauss = ng1)

----Spatially varying coefficients on x (summary)----

Coefficient estimates:
  (Intercept)          jsa               price              pm10
 Min.   :-0.6504   Min.   :0.06149   Min.   :-0.33538   Min.   :0.02834
 1st Qu.:-0.5831   1st Qu.:0.06149   1st Qu.:-0.23431   1st Qu.:0.02834
 Median :-0.5526   Median :0.06149   Median :-0.19311   Median :0.02834
 Mean   :-0.5478   Mean   :0.06149   Mean   :-0.18184   Mean   :0.02834
 3rd Qu.:-0.5163   3rd Qu.:0.06149   3rd Qu.:-0.13469   3rd Qu.:0.02834
 Max.   :-0.3929   Max.   :0.06149   Max.   : 0.04439   Max.   :0.02834

Statistical significance:
                        Intercept  jsa price pm10
Not significant                 0    0   205    0
Significant (10% level)         0    0    70    0
Significant ( 5% level)         0    0   180    0
Significant ( 1% level)      1355 1355   900 1355

----Variance parameters----------------------------------

Spatial effects (coefficients on x):
                     (Intercept) jsa      price pm10
random_SE             0.07496275   0 0.09383671    0
Moran.I/max(Moran.I)  0.72069442  NA 0.37600487   NA

Group effects:
             xgroup
ramdom_SE 0.1219861

----Estimated probability distribution of y--------------
                Estimates
skewness         1.026517
excess kurtosis  1.752394

----Error statistics-------------------------------------
                                               stat
dispersion parameter                       3.132744
deviance explained (%)                    82.977533
Gaussian rlogLik approximating the model  173.152374
AIC                                      -326.304748
BIC                                      -274.189181

NULL model: glm( y ~ x, offset = log( offset ), family = poisson )
   Gaussian (r)loglik approximating the model: -19.4258
   ( AIC: 48.85159,  BIC: 74.90938 )
```

The estimated group effects are as follows:

```
> mod3$b_g
[[1]]
                 Estimate         SE   t_value
xgroup_2007  0.052882464 0.02678485  1.974343
xgroup_2008  0.107183516 0.02409724  4.447959
xgroup_2009  0.007175285 0.02767944  0.259228
xgroup_2010 -0.083975107 0.02474086 -3.394187
xgroup_2011 -0.083266159         NA        NA
```

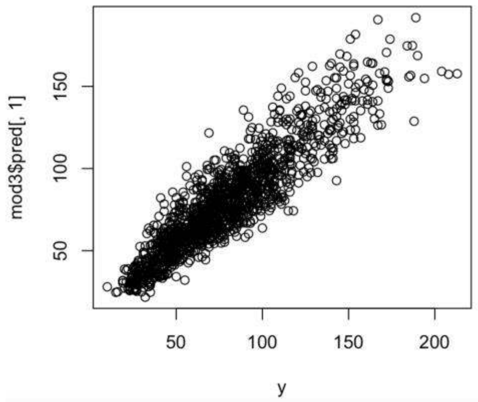
Although regression coefficients for the transformed y are often difficult to interpret, marginal effect $dy_i/dx_{i,k}$, which quantifies the magnitude of change in the i-th explained variable (y_i) for one unit change in the k-th explanatory variable ($x_{i,k}$), can be evaluated using the coef_marginal function if the resf function is used and the coef_marginal_vc function if the resf_vc function is used:

```
> coef_marginal_vc(mod3)
Call:
coef_marginal_vc(mod = mod3)

----Marginal effects from x (dy_i/dx_i) (summary)----
 (Intercept)         jsa              price               pm10
 Mode:logical   Min.   : 1.333   Min.   :-34.568   Min.   :0.6144
 NA's:1355      1st Qu.: 3.584   1st Qu.:-17.135   1st Qu.:1.6520
                Median : 4.652   Median :-12.722   Median :2.1441
                Mean   : 4.915   Mean   :-13.342   Mean   :2.2654
                3rd Qu.: 5.979   3rd Qu.: -9.379   3rd Qu.:2.7556
                Max.   :11.795   Max.   :  7.291   Max.   :5.4363

 Note: Medians are recommended summary statistics
```

For example, the median of pm10 suggests that the number of hospitalizations increases 2.1441 for every 1.0 increase in pm10.

The explained variables and predicted values are plotted below. This result confirms the accuracy of the model:

```
> plot(y,mod3$pred[,1])
```



In addition to the predicted values plotted above, the resf and resf_vc functions return quantiles of the predicted values, which are estimated based on the modeled probability density/mass function. These are as follows:

```
> mod3$pred_quantile[1:2,]
     q0.01   q0.025     q0.05      q0.1      q0.2      q0.3      q0.4      q0.5      q0.6
1 52.05107 56.02032 59.67535 64.18632 70.10760 74.71338 78.88783 83.00021 87.32698
2 16.12654 17.23963 18.25821 19.50748 21.13521 22.39256 23.52602 24.63725 25.80097
      q0.7     q0.8      q0.9     q0.95     q0.975      q0.99
1 92.20619 98.26375 107.32872 115.4419 122.97388 132.35148
2 27.10695 28.71957  31.11597  33.2450  35.20924  37.63946
```

The quantiles are useful for evaluating uncertainty in disease mapping (see below).

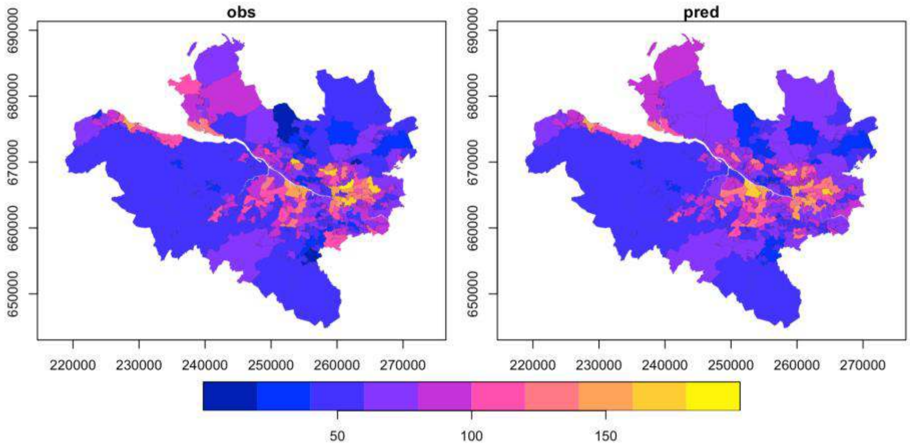
2.3. Regression and disease mapping

The predicted values are available for disease mapping. Here, mapping the patterns for 2007 is considered. A code to create a dataset including observed counts in 2007 (obs), predicted counts and their standard errors (pred), estimated varying coefficients (b_est), and quantiles of the predicted values (pred_qt) is presented as follows, and the dataset is converted to sf format, which is a spatial data format, for mapping:

```
> obs     <- y[pollutionhealthdata[,"year"] == 2007]
> pred    <- mod3$pred[pollutionhealthdata[,"year"] == 2007, ]
> b_est   <- mod3$b_vc[pollutionhealthdata[,"year"] == 2007,]
> pred_qt<- mod3$pred_quantile[pollutionhealthdata[,"year"] == 2007,]
>
> poly    <- st_as_sf(GGHB.IG)
> poly    <- cbind(poly, obs, pred, b_est, pred_qt)
```

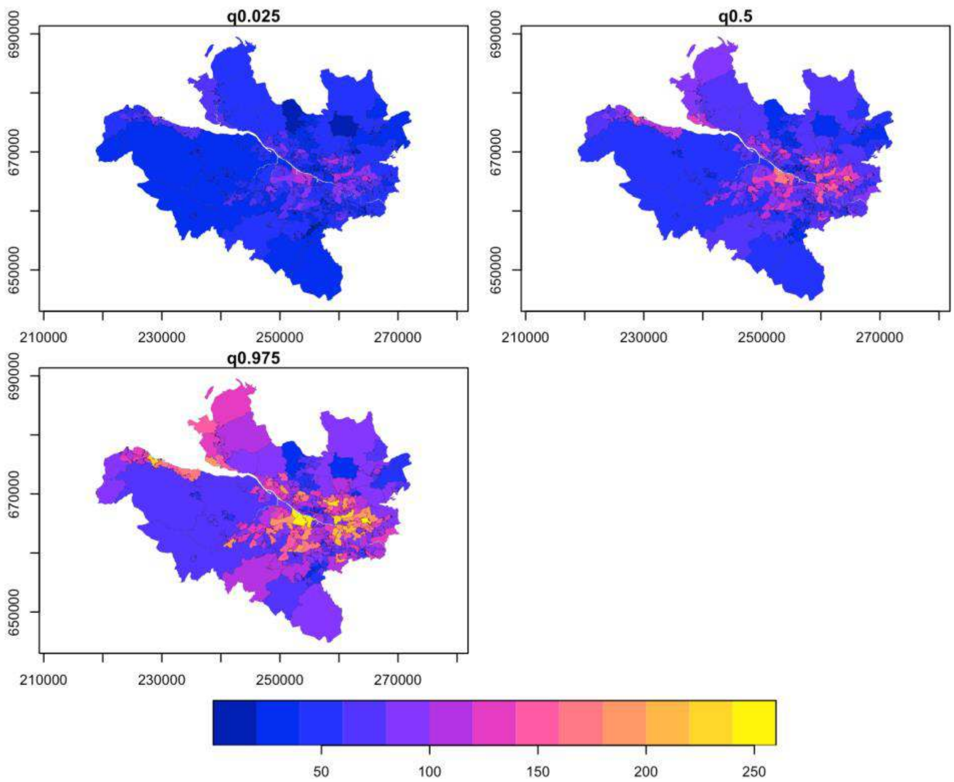
The predicted counts are as mapped together with the observed counts below. The result suggests that the estimated model accurately identifies the spatial pattern underlying respiratory disease.

```
> plot(poly[,c("obs","pred")],axes=TRUE, lwd=0.1, key.pos = 1)
```



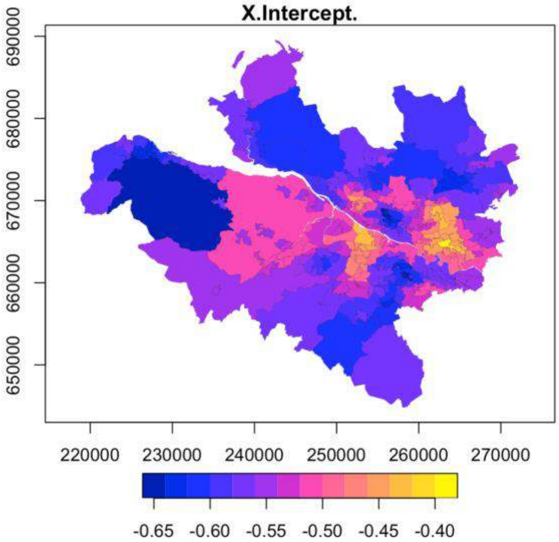
The following is a code to map the percentile (0.025%, 0.50%, 0.975%) of the predicted values. This map suggests higher uncertainty in the central urban area and lower uncertainty in the suburban areas.

```
> plot(poly[,c("q0.025","q0.5","q0.975")],axes=TRUE, lwd=0.1, key.pos = 1)
```

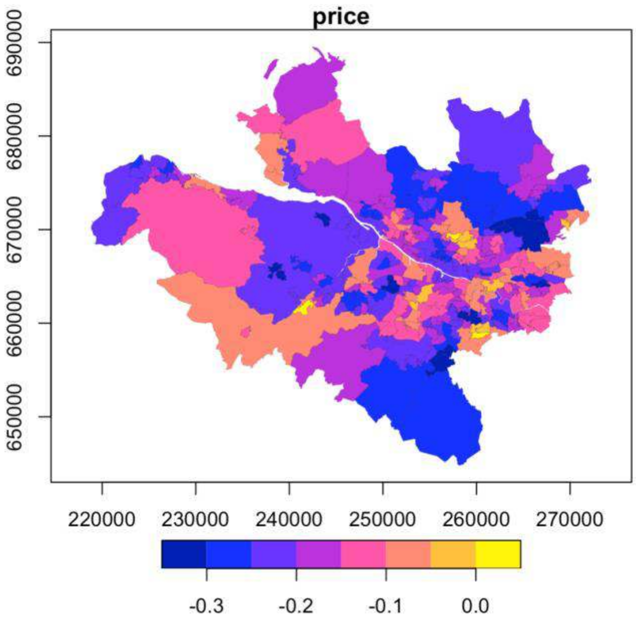


Finally, the estimated spatially varying intercept and coefficients on price are plotted below:

```
> plot(poly[,"X.Intercept."],axes=TRUE,lwd=0.1, key.pos = 1)
```




```
> plot(poly[,"price"],axes=TRUE,lwd=0.1, key.pos = 1)
```



3. Example 2: Spatial prediction and uncertainty analysis for non-Gaussian data

In this section, a non-Gaussian spatial regression modeling for spatial interpolation and uncertainty modeling is demonstrated.

3.1. Data

Here, the sf, automap, and spmoran packages are used:

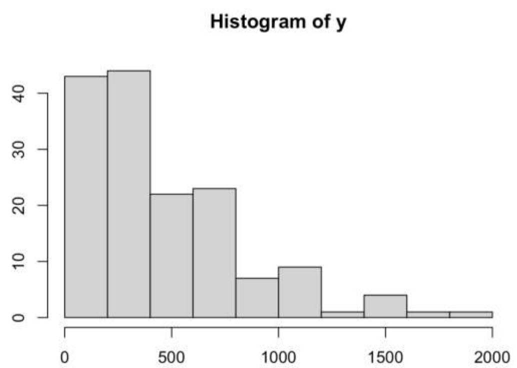
```
> library(sf);library(automap);library(spmoran)
```

The meuse data, which are used in this section, consist of heavy metal concentrations (cadmium, copper, lead, and zinc) measured in a flood plain along the river Meuse and explanatory variates:

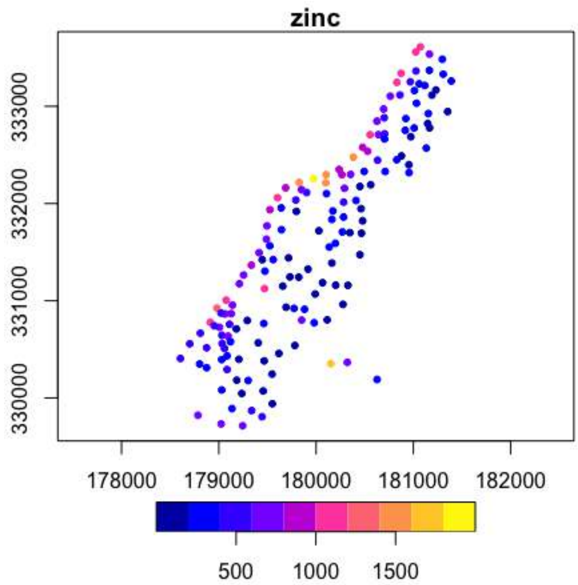
```
> data(meuse)
> meuse[1:5,]
       x      y cadmium copper lead zinc  elev       dist   om ffreq soil lime landuse dist.m
1 181072 333611    11.7     85  299 1022 7.909 0.00135803 13.6     1    1    1      Ah     50
2 181025 333558     8.6     81  277 1141 6.983 0.01222430 14.0     1    1    1      Ah     30
3 181165 333537     6.5     68  199  640 7.800 0.10302900 13.0     1    1    1      Ah    150
4 181298 333484     2.6     81  116  257 7.655 0.19009400  8.0     1    2    0      Ga    270
5 181307 333330     2.8     48  117  269 7.480 0.27709000  8.7     1    2    0      Ah    380
```

The zinc concentration in ppm (zinc) is analyzed. As shown in the histogram below, the zinc data do not exhibit a Gaussian distribution:

```
> y     <-meuse$zinc
> hist(y)
```



The following is the spatial plot of the zinc concentration:



Here, dist (distance to the river Meuse), ffreq2 (1 if flooding frequency class is 2, and 0 otherwise), and ffreq3 (1 if flooding frequency class is 3) are used for the explanatory variables:

```
> x     <-data.frame(dist= meuse[,"dist"],
+                    ffreq2=ifelse(meuse$ffreq==2,1,0),
+                    ffreq3=ifelse(meuse$ffreq==3,1,0))
```

3.2. Model

The Moran eigenvectors, which are the basis functions used for spatial process modeling, are constructed as follows:

```
> meig  <-meigen(coords)
 25/155 eigen-pairs are extracted
```

First, the classical Gaussian regression model is estimated using the resf function. The error statistics, including the restricted log-likelihood (rlogLik), Akaike information criterion (AIC), and BIC, are as follows:

```
> mod0  <-resf(y=y, x=x,meig=meig)
> mod0$e
                     stat
resid_SE      172.9239783
adjR2(cond)     0.7720376
rlogLik     -1032.7022760
AIC          2079.4045520
BIC          2100.7085278
```

Unfortunately, this model is not appropriate because of the non-Gaussianity of y. For non-negative explained variables, such as zinc concentration, the user can specify y_nonneg = TRUE in the nongauss_y function. If it is specified, the explanatory variable y is assumed to be non-negative, and the Box–Cox transformation is applied:

```
> ng1    <-nongauss_y(y_nonneg=TRUE)
Box-cox transformation f() is applied to y to estimate
y ~ P( xb, par )   (or f(y,par)~N(xb, sig) )

 - P(): Distribution estimated through the transformation
 - xb : Regression term with fixed and random coefficients in b
        which is specified by resf or resf_vc function
 - par: Parameter estimating data distribution
```

The output ng1 is used as an output of the resf function to estimate a regression model with residual spatial dependence and the Box–Cox transformation for y:

```
> mod1  <-resf(y=y,x=x, meig=meig, nongauss=ng1)
> mod1
Call:
resf(y = y, x = x, meig = meig, nongauss = ng1)

----Coefficients------------------------------
              Estimate         SE    t_value      p_value
(Intercept)  3.1550749 0.01777841 177.466681 0.000000e+00
dist        -0.5160247 0.07024097  -7.346492 1.956835e-11
ffreq2      -0.1248181 0.01390843  -8.974277 2.664535e-15
ffreq3      -0.1318089 0.02119947  -6.217554 6.298492e-09

----Variance parameter------------------------

Spatial effects (residuals):
                     (Intercept)
random_SE             0.09615471
Moran.I/max(Moran.I)  0.41327562


----Estimated probability distribution of y--------------
                 Estimates
skewness          2.488325
excess kurtosis   7.972227
(Box-Cox parameter: -0.263962)

----Error statistics--------------------------
                   stat
resid_SE      0.0581104
adjR2(cond)   0.8453350
rlogLik    -971.3835963
AIC        1958.7671926
BIC        1983.1145935

NULL model: lm( y ~ x )
   (r)loglik: -1083.605 ( AIC: 2177.211,  BIC: 2192.428 )
```

The resf_vc function is available when assuming SVCs. The estimated skewness, excess kurtosis, and Box–Cox parameter confirm the non-Gaussianity of the data. The BIC of the model (1983.114), which considers residual spatial dependence, is considerably better than that of the ordinary linear regression model (2192.428). The accuracy of the model is confirmed.

In addition to the Box–Cox transformation, the SAL transformation can be iterated to estimate the probability density function (PDF), most likely behind y. The number of iterations is specified by an argument tr_num. The models with tr_num=1 (ng2) and tr_num=2 (ng3) are compared:

```
> ng2    <-nongauss_y(y_nonneg=TRUE, tr_num=1)
Box-Cox and 1 SAL transformations f() are applied to y to estimate
y ~ P( xb, par )   (or f(y,par)~N(xb, sig) )

 - P(): Distribution estimated through the transformation(s)
 - xb : Regression term with fixed and random coefficients in b
        which is specified by resf or resf_vc function
 - par: Parameters estimating data distribution
> ng3    <-nongauss_y(y_nonneg=TRUE, tr_num=2)
Box-Cox and 2 SAL transformations f() are applied to y to estimate
y ~ P( xb, par )   (or f(y,par)~N(xb, sig) )

 - P(): Distribution estimated through the transformation(s)
 - xb : Regression term with fixed and random coefficients in b
        which is specified by resf or resf_vc function
 - par: Parameters estimating data distribution
```

The following non-Gaussian models considering residual spatial dependence are estimated:

```
> mod2  <-resf(y=y, x=x,meig=meig, nongauss=ng2)
> mod3  <-resf(y=y, x=x,meig=meig, nongauss=ng3)
```

The model accuracies can be compared using the BIC (or AIC) values. Based on the BIC, mod2, which applies the Box–Cox transformation first and then an SAL transformation, is the best model.

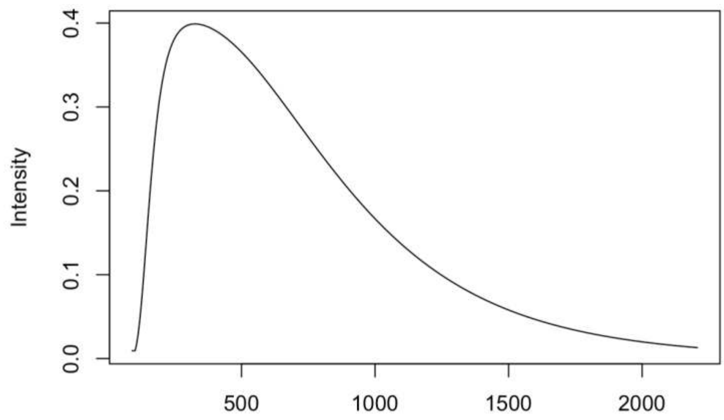
```
> mod2$e
                 stat
resid_SE      0.3976609
adjR2(cond)   0.8341787
rlogLik    -958.5890848
AIC        1937.1781696
BIC        1967.6124208
> mod3$e
                 stat
resid_SE      0.3996559
adjR2(cond)   0.8277254
rlogLik    -958.8305130
AIC        1945.6610260
BIC        1988.2689776
```

The estimated parameters are as follows:

```
> mod2  <-resf(y=y, x=x,meig=meig, nongauss=ng2)
> mod2
Call:
resf(y = y, x = x, meig = meig, nongauss = ng2)

----Coefficients------------------------------
              Estimate         SE   t_value      p_value
(Intercept)  1.2100004 0.11458914 10.559468 0.000000e+00
dist        -3.5209129 0.45132654 -7.801254 1.716405e-12
ffreq2      -0.7826159 0.09477395 -8.257712 1.421085e-13
ffreq3      -0.8259699 0.14323514 -5.766531 5.544422e-08

----Variance parameter------------------------

Spatial effects (residuals):
                     (Intercept)
random_SE              0.6035734
Moran.I/max(Moran.I)   0.3693597

----Estimated probability distribution of y--------------
                Estimates
skewness         1.717799
excess kurtosis  3.327901
(Box-Cox parameter: -0.2819055)

----Error statistics--------------------------
                 stat
resid_SE      0.3976609
adjR2(cond)   0.8341787
rlogLik    -958.5890848
AIC        1937.1781696
BIC        1967.6124208

NULL model: lm( y ~ x )
   (r)loglik: -1083.605 ( AIC: 2177.211,  BIC: 2192.428 )
```

The estimated PDF for y can be plotted as follows:

```
> plot(mod2$pdf,type="l")
```



The estimated PDF is reasonably similar to the histogram of y.

Although regression coefficients for transformed y are often difficult to interpret, the marginal effect of each explanatory variable ($dy_i/dx_{i,k}$), which quantifies the magnitude of change in the i-th explained variable (y_i) for one unit change in the k-th explanatory variable ($x_{i,k}$), is evaluated using the coef_marginal function:

```
> coef_marginal(mod2)
Call:
coef_marginal(mod = mod2)

----Marginal effects from x (dy_i/dx_i) (summary)-------
 (Intercept)          dist                ffreq2              ffreq3
 Mode:logical   Min.   :-3832.79   Min.   :-851.94   Min.   :-899.13
 NA's:155       1st Qu.:-1858.62   1st Qu.:-413.13   1st Qu.:-436.01
                Median :-1173.63   Median :-260.87   Median :-275.32
                Mean   :-1195.47   Mean   :-265.73   Mean   :-280.45
                3rd Qu.: -368.10   3rd Qu.: -81.82   3rd Qu.: -86.35
                Max.   :  -98.77   Max.   : -21.95   Max.   : -23.17

 Note: Medians are recommended summary statistics
```

For example, the median for ffreq2 suggests that areas with flooding frequency class 2 have a 260.87 ppm smaller median zinc concentration than other areas.

3.3. Spatial prediction and uncertainty analysis

The estimated model (mod2) is applied to spatially predict the zinc concentration on 3103 grid points with a 40 × 40-m spacing (meuse.grid). Spatial coordinates (coords0) and the explanatory variables in the grids are used for the prediction:

```
> data(meuse.grid)
> coords0<-meuse.grid[,c("x","y")]
> x0      <-data.frame(dist= meuse.grid$dist,
+                      ffreq2=ifelse(meuse.grid$ffreq==2,1,0),
+                      ffreq3=ifelse(meuse.grid$ffreq==3,1,0))
```

The Moran eigenvectors at the prediction sites are generated using the meigen0 function:

```
> meig0  <-meigen0(meig=meig, coords0=coords0)
> pres   <-predict0(mod=mod2,x0=x0,meig0=meig0, compute_quantile = TRUE)
```

The spatial prediction is performed using the predict0 function. If compute_quantile=TRUE, the quantiles for the predicted values are evaluated based on the PDF estimated in Section 1.2:


```
> meig0  <-meigen0(meig=meig, coords0=coords0)
> pres   <-predict0(mod=mod2,x0=x0,meig0=meig0, compute_quantile = TRUE)
```


The outputs are as follows:

```
> pres$pred[1:2,]
      pred pred_transG pred_transG_se   xb  sf_residual
1 916.2723    1.191011      0.4128080 1.21 -0.018989791
2 923.0430    1.201812      0.4132363 1.21 -0.008188592
```

The output includes the predicted values on the original scale (pred), the predicted value on the transformed scale (pred_transG), and the standard error (pred_transG_se). The estimated quantiles for the predicted values are as follows:

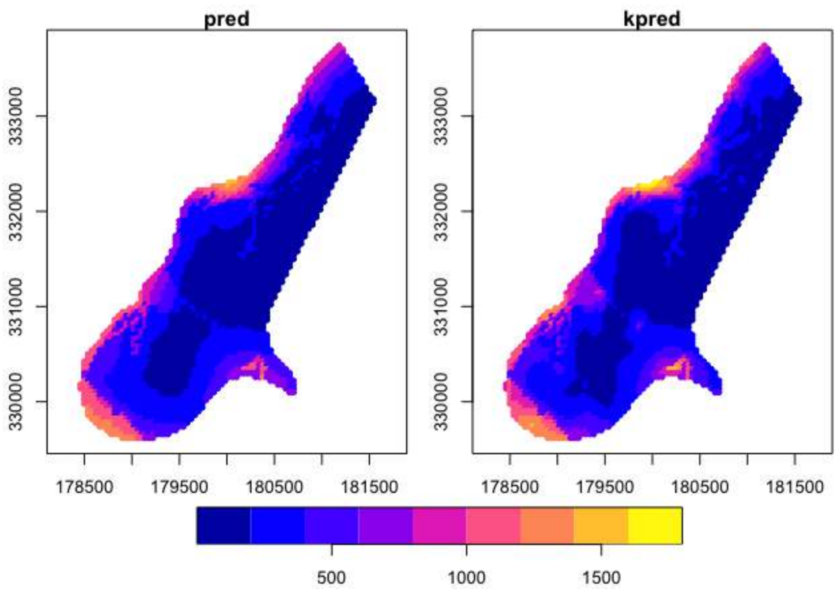
```
> pres$pred_quantile[1:2,]
     q0.01   q0.025     q0.05     q0.1     q0.2     q0.3     q0.4     q0.5
1 414.9931 482.7518 544.3806 618.7869 714.1259 786.9783 852.3321 916.2723
2 419.2256 487.3734 549.2768 624.0092 719.8005 793.0283 858.7385 923.0430
      q0.6     q0.7     q0.8     q0.9    q0.95   q0.975     q0.99
1 983.2187 1058.455 1151.664 1291.096 1416.133 1532.610 1678.346
2 990.3854 1066.082 1159.881 1300.232 1426.124 1543.421 1690.210
```

To map the outputs, pred, pred_transG, pred_transG_se, and quantiles for the predicted values (pred_quantile) are summarized into a data.frame object. As a measure of uncertainty, the length of the 95% confidence interval for the predicted value (len95) is added. In addition, the predicted values of a regression kriging, which is widely used for spatial prediction, are also added (kpred). In sequence, the data.frame object is converted to an sf object for mapping:

```
> pred   <- data.frame(coords0,pred=pres$pred[,"pred"],
+                      len95=pres$pred_quantile$q0.975 - pres$pred_quantile$q0.025,
+                      pred_transG=pres$pred[,"pred_transG"],
+                      pred_transG_se=pres$pred[,"pred_transG_se"],
+                      pres$pred_quantile,
+                      kpred=exp(kres$krige_output$var1.pred))
> coordinates(pred)<-c("x","y")
> pred_sf <-st_as_sf(pred)
```

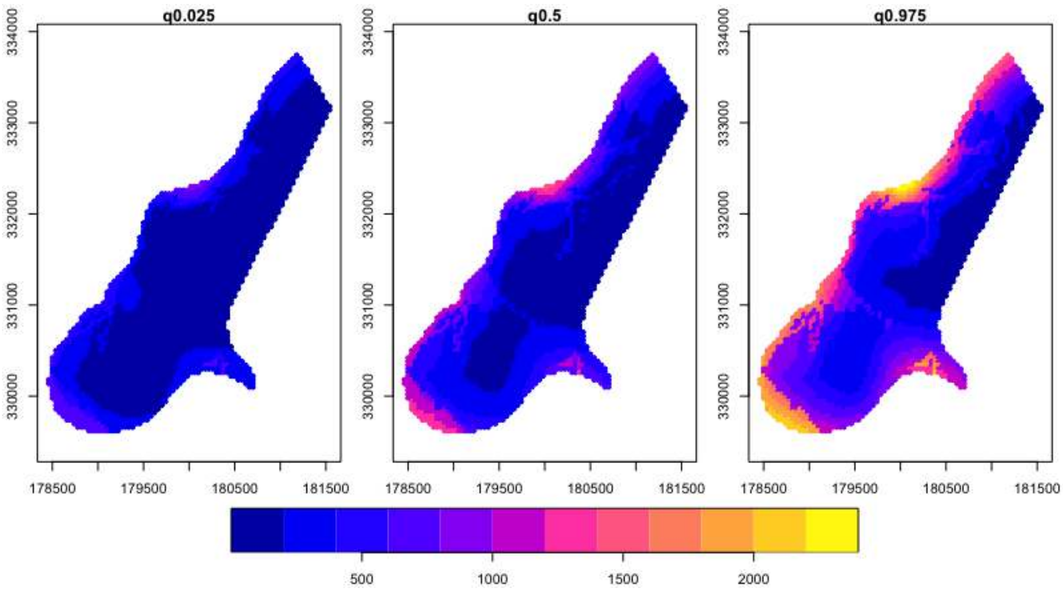
The prediction result (pred) and the kriging-based prediction result (kpred) are quite similar:

```
> plot(pred_sf[,c("pred","kpred")], pch=20, axes=TRUE, key.pos = 1)
```

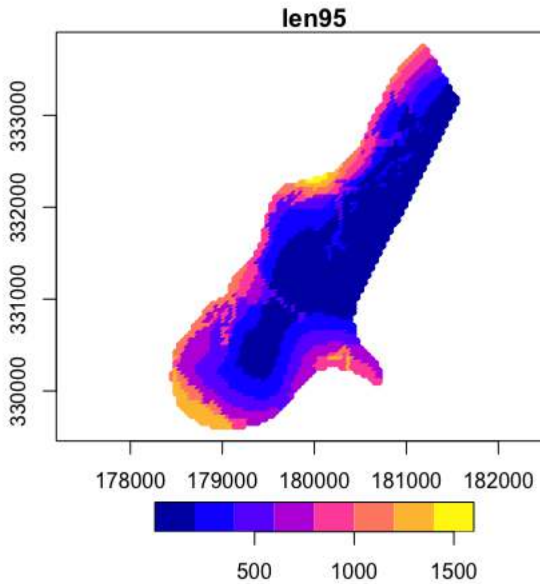


As shown in the maps below exhibiting the 2.5%, 50%, and 97.5% quantiles, the predicted values have larger uncertainty in the northern area that faces the river Meuse:

```
> plot(pred_sf[,c("q0.025","q0.5","q0.975")], pch=20, axes=TRUE, key.pos = 1)
```

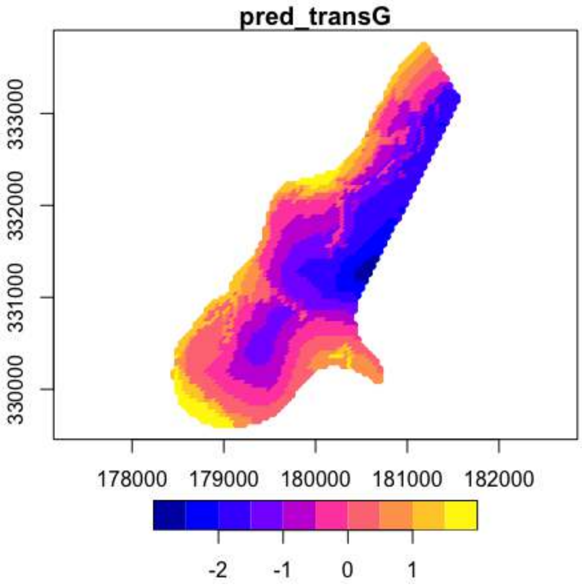


The map below shows the length of the 95% confidence interval (len95), which is another manner to visualize the uncertainty in the original scale:



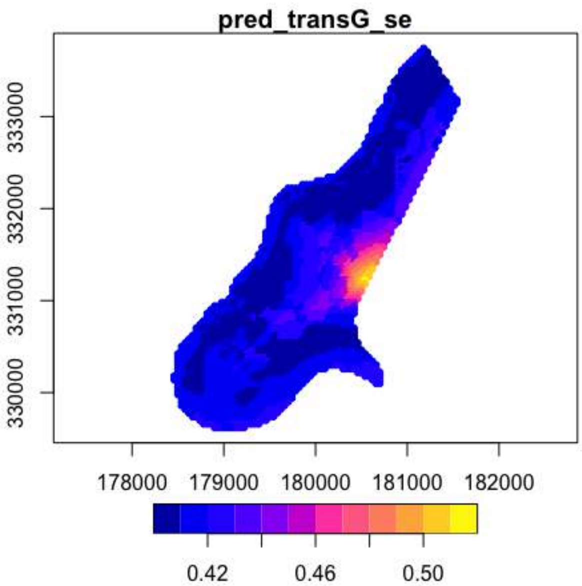
The predicted values can also be visualized in the transformed/normalized scale:

```
> plot(pred_sf[,"pred_transG"], pch=20, axes=TRUE, key.pos = 1)
```



As shown below, in the transformed scale, the predictive errors are large in the eastern central area, where the samples are relatively limited (however, as observed in the maps for len95 or the quantiles, this error has a slight impact on the original scale as a result of the rescaling/transformation to the real scale).

```
> plot(pred_sf[,"pred_transG_se"], pch=20, axes=TRUE, key.pos = 1)
```



3.4. Limitation

The Moran eigenvector approach provides a type of low rank approximation for spatial process modeling (similar to fixed rank kriging and predictive process modeling; see Sun et al., 2012). Although the modeling accuracy is sufficient in many cases, it can provide overly smoothed spatial prediction results for very large samples (e.g., N > 10,000; see, Stein, 2014). For spatial prediction using large samples, it should be used with caution (this approach is still useful even in such a case to understand underlying map patterns in a computationally efficient manner).

4. Example 3: Non-Gaussian spatial hedonic analysis

In this section, the importance of considering non-Gaussianity in hedonic housing price analysis is demonstrated. Gaussian and non-Gaussian SVC models are used.

4.1. Data

This section uses the spdep, sf, and spmoran packages:

```
> library(spdep);library(sf);library(spmoran)
```

In this section, the housing data for 506 census tracts in Boston in 1970 are analyzed. The explained variable (y) is the median housing value in USD 1000s (CMEDV). The explained variables, whose coefficients are allowed to vary over space (x), those whose coefficients are assumed to be constant (xconst), and spatial coordinates (coords) are used in this analysis:

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

Moran eigenvectors are extracted as follows:

```
> meig    <- meigen(coords=coords)
 55/506 eigen-pairs are extracted
```

4.2. Model

In this section, three transformation functions are considered:

```
> ng1     <- nongauss_y(y_nonneg=TRUE)
Box-cox transformation f() is applied to y to estimate
y ~ P( xb, par )   (or f(y,par)~N(xb, sig) )

 - P(): Distribution estimated through the transformation
 - xb : Regression term with fixed and random coefficients in b
        which is specified by resf or resf_vc function
 - par: Parameter estimating data distribution
```

```
> ng2     <- nongauss_y(y_nonneg=TRUE,tr_num=1)
Box-Cox and 1 SAL transformations f() are applied to y to estimate
y ~ P( xb, par )   (or f(y,par)~N(xb, sig) )

 - P(): Distribution estimated through the transformation(s)
 - xb : Regression term with fixed and random coefficients in b
        which is specified by resf or resf_vc function
 - par: Parameters estimating data distribution
```

```
> ng3     <- nongauss_y(y_nonneg=TRUE,tr_num=2)
Box-Cox and 2 SAL transformations f() are applied to y to estimate
y ~ P( xb, par )   (or f(y,par)~N(xb, sig) )

 - P(): Distribution estimated through the transformation(s)
 - xb : Regression term with fixed and random coefficients in b
        which is specified by resf or resf_vc function
 - par: Parameters estimating data distribution
```

Although ng3 is the most flexible, it can result in overfitting. To identify the best model, the Gaussian SVC (mod0) and non-Gaussian SVC models (mod1, mod2, and mod3) are fitted, and their BIC values are compared:

```
> mod0    <- resf_vc(y=y,x=x, x_nvc=TRUE,xconst=xconst,meig=meig )
> mod1    <- resf_vc(y=y,x=x, x_nvc=TRUE,xconst=xconst,meig=meig, nongaus=ng1 )
> mod2    <- resf_vc(y=y,x=x, x_nvc=TRUE,xconst=xconst,meig=meig, nongaus=ng2 )
> mod3    <- resf_vc(y=y,x=x, x_nvc=TRUE,xconst=xconst,meig=meig, nongaus=ng3 )
```

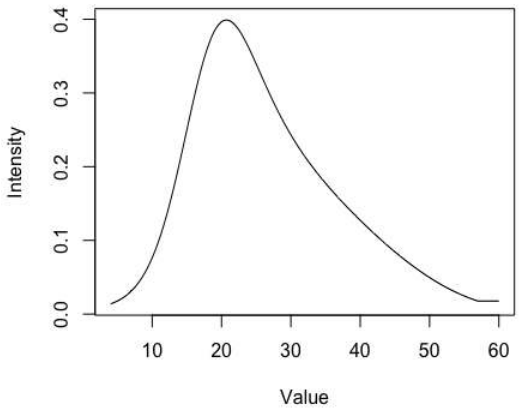
The resulting BICs are 3110.5 (mod0), 2950.5 (mod1), 2901.6 (mod2), 2931.4 (mod3), and 3178.4 for the ordinary linear regression model. mod2, which applies the Box-Cox transformation and an SAL transformation, was selected as the best model.

The parameters estimated from mod2 are as follows:

```
> mod2
Call:
resf_vc(y = y, x = x, xconst = xconst, x_nvc = TRUE, meig = meig,
    nongauss = ng2)

----Spatially and non-spatially varying coefficients on x (summary)----

Coefficient estimates:
  (Intercept)           CRIM                  AGE
 Min.   :-0.02244   Min.   :-0.2740242   Min.   :-0.018914
 1st Qu.:-0.02244   1st Qu.:-0.0599508   1st Qu.:-0.010591
 Median :-0.02244   Median :-0.0322745   Median :-0.007599
 Mean   :-0.02244   Mean   :-0.0329763   Mean   :-0.007425
 3rd Qu.:-0.02244   3rd Qu.: 0.0004135   3rd Qu.:-0.004354
 Max.   :-0.02244   Max.   : 0.1070968   Max.   : 0.005453

Statistical significance:
                        Intercept CRIM AGE
Not significant               506  410 117
Significant (10% level)         0   18  24
Significant ( 5% level)         0   19  52
Significant ( 1% level)         0   59 313
----Constant coefficients on xconst----------------------------
            Estimate           SE    t_value      p_value
ZN       0.002027180 0.0011645284  1.740773 8.243151e-02
DIS     -0.131266652 0.0237841152 -5.519089 5.869668e-08
RAD      0.052234354 0.0085592354  6.102689 2.312320e-09
NOX     -3.124557004 0.4565365150 -6.844046 2.632916e-11
TAX     -0.001635874 0.0003135737 -5.216872 2.823456e-07
RM       0.506995252 0.0296312602 17.110148 0.000000e+00
PTRATIO -0.056300954 0.0135694652 -4.149092 4.017337e-05
B        0.002452484 0.0002849729  8.606026 0.000000e+00

----Variance parameters----------------------------------

Spatial effects (coefficients on x):
                     (Intercept)       CRIM         AGE
random_SE           3.398454e-06 0.12892890 0.007028641
Moran.I/max(Moran.I) 4.631293e-01 0.05171784 0.273869153

Non-spatial effects (coefficients on x):
                  CRIM AGE
random_SE 0.003807227   0

----Estimated probability distribution of y--------------
                Estimates
skewness         1.200526
excess kurtosis  1.765607
(Box-Cox parameter: 1.691544)

----Error statistics-------------------------------------
                    stat
resid_SE       0.3303358
adjR2(cond)    0.8881671
rlogLik    -1382.3284183
AIC         2808.6568365
BIC         2901.6406432

NULL model: lm( y ~ x + xconst )
   (r)loglik: -1551.857 ( AIC: 3127.715,  BIC: 3178.433 )
```

The "Estimated probability distribution of y" section suggests that the data are positively skewed (skewness > 0) and exhibit a fat tail (excess kurtosis > 0). The estimated probability density distribution can be visualized as follows:

```
> plot(mod2$pdf,type="l")
```



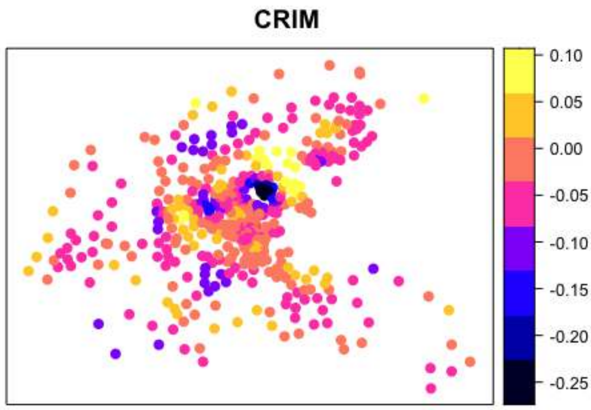
The marginal effect of each explanatory variable ($dy_i/dx_{i,k}$), which quantifies the magnitude of change in the i-th explained variable (y_i) for one unit change in the k-th explanatory variable ($x_{i,k}$), is evaluated using the coef_marginal function if the resf function is used and the coef_marginal_vc function if the resf_vc function is used, as in the present case:

```
> coef_marginal_vc(mod2)
Call:
coef_marginal_vc(mod = mod2)

----Marginal effects from x (dy_i/dx_i) (summary)----
 (Intercept)         CRIM                AGE           
 Mode:logical   Min.   :-3.186702   Min.   :-0.32519  
 NA's:506       1st Qu.:-0.485693   1st Qu.:-0.08374  
                Median :-0.240681   Median :-0.05859  
                Mean   :-0.285872   Mean   :-0.05956  
                3rd Qu.: 0.003341   3rd Qu.:-0.03813  
                Max.   : 1.443992   Max.   : 0.09132  

----Marginal effects from xconst (dy_i/dx_i)(summary)----
       ZN               DIS                RAD              NOX        
 Min.   :0.01145   Min.   :-2.7675   Min.   :0.2950   Min.   :-65.88  
 1st Qu.:0.01209   1st Qu.:-1.2022   1st Qu.:0.3114   1st Qu.:-28.62  
 Median :0.01402   Median :-0.9079   Median :0.3613   Median :-21.61  
 Mean   :0.01841   Mean   :-1.1922   Mean   :0.4744   Mean   :-28.38  
 3rd Qu.:0.01857   3rd Qu.:-0.7826   3rd Qu.:0.4784   3rd Qu.:-18.63  
 Max.   :0.04274   Max.   :-0.7412   Max.   :1.1013   Max.   :-17.64  
      TAX                 RM             PTRATIO              B          
 Min.   :-0.034490   Min.   : 2.863   Min.   :-1.1870   Min.   :0.01385  
 1st Qu.:-0.014982   1st Qu.: 3.023   1st Qu.:-0.5156   1st Qu.:0.01462  
 Median :-0.011315   Median : 3.507   Median :-0.3894   Median :0.01696  
 Mean   :-0.014857   Mean   : 4.605   Mean   :-0.5113   Mean   :0.02227  
 3rd Qu.:-0.009753   3rd Qu.: 4.643   3rd Qu.:-0.3357   3rd Qu.:0.02246  
 Max.   :-0.009238   Max.   :10.689   Max.   :-0.3179   Max.   :0.05171  

 Note: Medians are recommended summary statistics
```

For example, the median of per capita crime rate (CRIM) suggests that, on average, the housing price decreases 0.24 (1000 USD) for every 1.0 increase of CRIM.

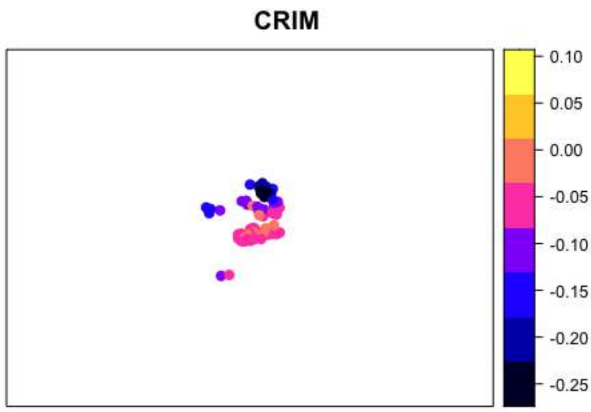
The estimated SVCs on x (CRIM, AGE, and Intercept) can be plotted using the plot_s function. For example, SVC on CRIM, which is the first column of x, is mapped as follows:

```
> plot_s(mod2,1)
```



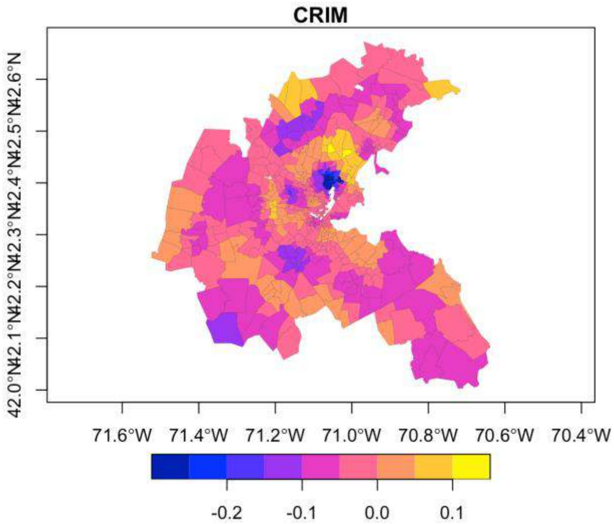
The output suggests a strong negative impact of CRIM in the central area. An argument pmax is useful for displaying statistically significant coefficients only. For example, the following is the code to display the coefficients that are statistically significant at the 5% level:

```
> plot_s(mod2,1,pmax=0.05)
```



This map demonstrates that the crime rate has a statistically significant negative impact on housing price only in the central area. Alternatively, the SVCs can be plotted using the sf package, as follows:

```
> boston.tr <- boston.tr0[order(boston.tr0$TOWNNO),1:8]
> b_est     <- mod2$b_vc
> boston.tr <- cbind(boston.tr, b_est)
> names(boston.tr)
 [1] "poltract"     "TOWN"         "TOWNNO"
 [4] "TRACT"        "LON"          "LAT"
 [7] "MEDV"         "CMEDV"        "X.Intercept."
[10] "CRIM"         "AGE"          "geometry"
> plot(boston.tr[,"CRIM"],axes=TRUE,lwd=0.1, key.pos = 1)
```



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