Multivariate BYM

Proposal: sparse precision parametrisation for the multivariate BYM model.

In this note, we attempt at providing a parametrisation for the multivariate BYM model resulting in a sparse precision matrix.

Parametrisation for the univariate BYM Before doing so, we start by illustrating the well-established sparse parametrisation of the univariate BYM:

This model, proposed by (Riebler et al. 2016) takes the form:

$$y = \sigma\left(\sqrt{\phi}U + \sqrt{1-\phi}V\right)$$

Where $U \sim N(0, L^+)$, $V \sim N(0, I_n)$, L denotes the graph Laplacian matrix, already scaled in order that $\text{diag}(L)$ has a geometric mean equal to 1; $n = \text{card}(y)$. σ^2 is the scale parameter.

Now, despite $\text{Prec}[y \mid \phi, \sigma] = \sigma^{-2}\left(\phi L + (1-\phi)I_n\right)^{-1}$ which has no reason at all to be a sparse matrix, the joint random vector $\begin{pmatrix} y \\ U \end{pmatrix}$ has indeed a sparse precision. This can be seen considering that $\ln \pi(y, U) = \ln \pi(y|U) + \ln \pi(U)$ and $y|U \sim N(\sigma\sqrt{\phi}U, \sigma^2(1-\phi)I_n)$ thus, with some passages (Riebler et al. 2016),

$$\text{Prec}(y, U|\sigma, \phi) = \begin{pmatrix} \frac{1}{\sigma^2(1-\phi)}I_n & -\frac{\sqrt{\phi}}{\sigma(1-\phi)}I_n \\ -\frac{\sqrt{\phi}}{\sigma(1-\phi)}I_n & \frac{\phi}{1-\phi}I_n + L \end{pmatrix} \tag{1}$$

Which is made of four sparse blocks as long as L is sparse as well.

Hence the univariate BYM model, other than being scalable and allowing for PC priors setting on hyperparameters, can also be fitted in an efficient way leveraging on precision sparsity. And this is indeed the model implemented in `R-INLA`, using the specification `INLA::f(..., model = "bym2", ...)`.

While this parametrisation is essential for computational reasons, only the first half of the random vector, i.e. y, does enter the linear predictor.

Parametrisation for the multivariate BYM A direct extension of the BYM to the case of p variables (p diseases) is the following.

First let us consider the ICAR component. With no loss of generality, define $\mathbf{U} = (U_1, U_2, \dots U_p)$ and $\text{vec}(\mathbf{U}) = (U_1^\top U_2^\top \dots U_p^\top)^\top$. We suppose all its component to have the same prior distribution, i.e.

$$U_j \sim N(0, L^+) \quad \forall j \in [1, p]$$

We further assume independence among them, such that $\text{vec}(\mathbf{U}) \sim N(0, I_p \otimes L^+)$. The same assumption is made on the IID component, i.e. $\text{vec}(\mathbf{V}) \sim N(0, I_p \otimes I_n)$.

By doing so, we can use a unique scale parameter, say Σ, as in the univariate case. We define M as a generic full-rank matrix such that $M^\top M = \Sigma$. Additionally, we define the precision parameter $\Lambda =: \Sigma^{-1}$.

Please notice that M does not have to be the Cholesky factor; in fact, a rather convenient yet not unique definition is $M = D^{\frac{1}{2}}E^\top$, where D is the diagonal matrix of the eigenvalues of Σ and E are the eigenvectors of Σ.

In the more general case of the M-model (Botella-Rocamora, Martinez-Beneito, and Banerjee 2015), consider the matrix-valued mixing parameters $\tilde{\Phi} := \text{diag}(\sqrt{\phi_1}, \sqrt{\phi_2}, \dots \sqrt{\phi_p})$ and $\tilde{\bar{\Phi}} := \text{diag}(\sqrt{1-\phi_1}, \sqrt{1-\phi_2}, \dots \sqrt{1-\phi_p}) = (I_p - \tilde{\Phi})^{-1/2}$.

The convolution model is generalised to:

$$\mathbf{Y} = \mathbf{U}M\tilde{\Phi} + \mathbf{V}M\tilde{\bar{\Phi}} \tag{2}$$

We then have

$$\mathbb{E}[\text{vec}(\mathbf{Y}) \mid U, \tilde{\Phi}, \Sigma] = \text{vec}(\mathbf{U}M\tilde{\Phi}) = [(\tilde{\Phi}M^\top) \otimes I_n]\text{vec}(\mathbf{U})$$

and similarly

$$\text{VAR}[\text{vec}(\mathbf{Y}) \mid \mathbf{U}, \tilde{\Phi}, \Sigma] = \left[(\tilde{\bar{\Phi}}M^\top) \otimes I_n\right] \mathbb{E}\left[\text{vec}(\mathbf{V})\text{vec}(\mathbf{V})^\top\right] \left[(\tilde{\Phi}M^\top) \otimes I_n\right] = \left(\tilde{\bar{\Phi}}\Sigma\tilde{\bar{\Phi}}\right) \otimes I_n$$

The distribution of $\mathbf{Y} \mid \mathbf{U}, \Sigma, \tilde{\Phi}$ then reads:

$$\begin{aligned}
&-2\ln\pi\left(\text{vec}(\mathbf{Y}) \mid \mathbf{U}, \Sigma, \phi\right) = \\
&= \left\{\text{vec}(\mathbf{Y}) - [(\tilde{\Phi}M^\top) \otimes I_n]\text{vec}(\mathbf{U})\right\}^\top \left[\left(\tilde{\bar{\Phi}}^{-1}\Lambda\tilde{\bar{\Phi}}^{-1}\right) \otimes I_n\right] \left\{\text{vec}(\mathbf{Y}) - [(\tilde{\Phi}M^\top) \otimes I_n]\text{vec}(\mathbf{U})\right\} = \\
&= \text{vec}(\mathbf{Y})^\top \left[\left(\tilde{\bar{\Phi}}^{-1}\Lambda\tilde{\bar{\Phi}}^{-1}\right) \otimes I_n\right] \text{vec}(\mathbf{Y}) + \\
&-2\text{vec}(\mathbf{Y})^\top \left[\left(\tilde{\bar{\Phi}}^{-1}\Lambda\tilde{\bar{\Phi}}^{-1}\right) \otimes I_n\right] \left[(\tilde{\Phi}M^\top) \otimes I_n\right] \text{vec}(\mathbf{U}) + \\
&+\text{vec}(\mathbf{U})^\top \left[(M\tilde{\Phi}) \otimes I_n\right] \left[\left(\tilde{\bar{\Phi}}^{-1}\Lambda\tilde{\bar{\Phi}}^{-1}\right) \otimes I_n\right] \left[(\tilde{\Phi}M^\top) \otimes I_n\right] \text{vec}(\mathbf{U}) = \\
&\text{vec}(\mathbf{Y})^\top \left[\left(\tilde{\bar{\Phi}}^{-1}\Lambda\tilde{\bar{\Phi}}^{-1}\right) \otimes I_n\right] \text{vec}(\mathbf{Y}) + \\
&-2\text{vec}(\mathbf{Y})^\top \left[\left(\tilde{\bar{\Phi}}^{-1}\Lambda\tilde{\bar{\Phi}}^{-1}\tilde{\Phi}M^\top\right) \otimes I_n\right] \text{vec}(\mathbf{U}) + \\
&+\text{vec}(\mathbf{U})^\top \left[\left(M\tilde{\Phi}\tilde{\bar{\Phi}}^{-1}\Lambda\tilde{\bar{\Phi}}^{-1}\tilde{\Phi}M^\top\right) \otimes I_n\right] \text{vec}(\mathbf{U})
\end{aligned}$$

Now, for brevity let us define the following $p \times p$ matrices:

$$q_{11} := \tilde{\bar{\Phi}}^{-1}\Lambda\tilde{\bar{\Phi}}^{-1}; \quad q_{12} := q_{11}\tilde{\Phi}M^\top; \quad q_{22} := M\tilde{\Phi}q_{12}$$

Hence

$$\begin{aligned}
&-2\ln\pi\left(\text{vec}(\mathbf{Y}) \mid \mathbf{U}, \Sigma, \phi\right) = \\
&= \text{vec}(\mathbf{Y})^\top \left(q_{11} \otimes I_n\right) \text{vec}(\mathbf{Y}) - 2\text{vec}(\mathbf{Y})^\top \left(q_{12} \otimes I_n\right) \text{vec}(\mathbf{U}) + \text{vec}(\mathbf{U})^\top \left(q_{12} \otimes I_n\right) \text{vec}(\mathbf{U})
\end{aligned}$$

Then, we have

$$\begin{aligned}
&-2\ln\pi\left(\text{vec}(\mathbf{Y}), \text{vec}(\mathbf{U}) \mid \Sigma, \phi\right) = \\
&= \text{vec}(\mathbf{Y})^\top \left(q_{11} \otimes I_n\right) \text{vec}(\mathbf{Y}) - 2\text{vec}(\mathbf{Y})^\top \left(q_{12} \otimes I_n\right) \text{vec}(\mathbf{U}) + \text{vec}(\mathbf{U})^\top \left(q_{12} \otimes I_n + I_p \otimes L\right) \text{vec}(\mathbf{U})
\end{aligned}$$

Hence, with some straightforward algebra, it can be concluded that:

$$\begin{pmatrix}\text{vec}(\mathbf{Y}) \\ \text{vec}(\mathbf{U})\end{pmatrix} \sim N\left(0, \begin{pmatrix} q_{11} \otimes I_n & -q_{12} \otimes I_n \\ -q_{12}^\top \otimes I_n & q_{22} \otimes I_n + I_p \otimes L \end{pmatrix}^{-1}\right) \tag{3}$$

Which generalises to the multivariate case equation 1. The sparse parametrisation is thus also possible for the multivariate BYM.

Application to SIDS data

Here we attempt to an application to the well-known SIDS dataset. The model has the following structure:

$$y_{i,t} \sim \text{Poisson}(e^{E_{i,t} + \eta_{i,t}})$$

Where $y_{i,t}$ are the sudden infant death cases for $i = 1 \dots 100$ and $t = 1974, 1979$; $E_{i,t}$ are the expected SIDS cases, i.e. the global fatality rate times the number of births, and $\eta_{i,t} := \beta_0 + \beta X_{i,t} + z_{i,t}$ is the linear predictor. Specifically, β_0 is the intercept, $X_{i,t}$ is the non-white birth proportion (NWBIR), β is the effect of NWBIR, and $z_{i,t}$ is a spatially structure latent effect.

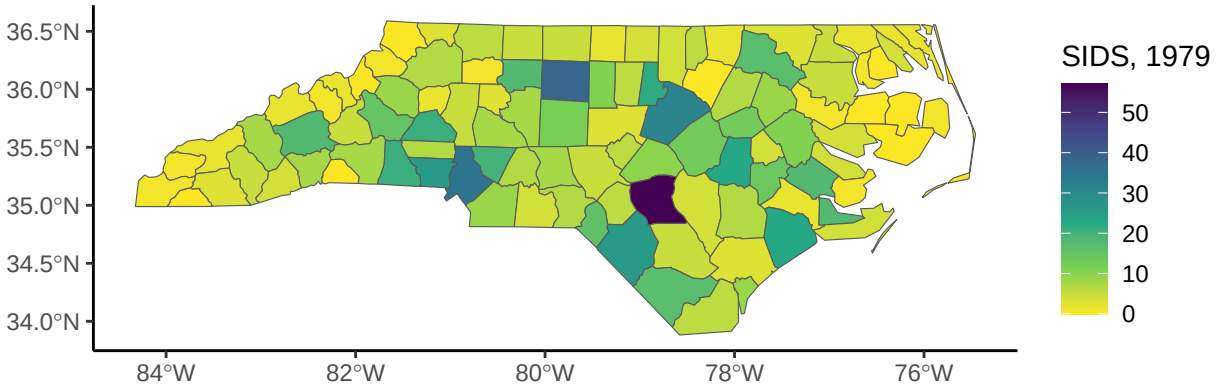
```
library(spdep)
nc <- st_read(system.file("shapes/sids.gpkg", package="spData")[1], quiet=TRUE)

# neighbouring/adjacency matrix
W<- spdep::nb2mat(spdep::poly2nb(nc), style = "B")
```

Here, a long version of the dataframe is employed. Expected cases are computed as in (Palmí-Perales, Gómez-Rubio, and Martinez-Beneito 2021)

```
r74 <- sum(nc.sids$SID74) / sum(nc.sids$BIR74)
r79 <- sum(nc.sids$SID79) / sum(nc.sids$BIR79)

nc.long <- data.frame(NAME = c(nc$NAME, nc$NAME),
                      SID = c(nc$SID74, nc$SID79),
                      BIR = c(nc$BIR74, nc$BIR79),
                      NWBIR = c(nc$NWBIR74, nc$NWBIR79),
                      EXP = c(r74 * nc.sids$BIR74, r79 * nc.sids$BIR79),
                      ID = c(1:2*nrow(nc))) %>%
  dplyr::mutate(NWPROP = as.vector(scale(.data$NWBIR/.data$BIR)))
```



A flexible class of models for the latent effect Z is that of M-models, which allow to employ disease-specific hyperparameters. As a baseline model one could think of the PCAR; which takes this form for $t = 1974, 1979$ and $n = 100$:

$$\text{vec}(Z) \sim N\left(0, (M^\top \otimes I_n)\,\text{Bdiag}(D - \alpha_t W)\,(M \otimes I_n)\right)$$

Where D is the graph degree matrix, W is the neighbourhood matrix, BDiag denotes a block-diagonal matrix, and α_t is the autoregressive parameter for year t. The matrix M is as defined in the previos section.

We use the `bigDM` function from the `bigDM` R package (Vicente et al. 2023) to fit the M-Model extension of the PCAR. This package has the advantage of automatically implementing models in which the Bartlett decomposition (see further) is used on the marginal scale parameter Σ, which allows to specify a smaller number of parameters than direct parametrisation of M; in brief, the marginal scale parameter can be decomposed as $\Sigma = AA^\top$, where A is a lower-triangular matrix. A χ^2 prior is assigned to the diagonal entries of A and a $N(0, 1)$ prior is assigned to its off-diagonal entries; this implies that Σ follows a Wishart distribution (Kabe 1964); lastly a Uniform prior on $[0, 1]$ is assigned to each α_t.

```
inla.PMMCAR.model <- function(...){
  INLA::inla.rgeneric.define(bigDM::Mmodel_pcar, ...)
}

pcar.inla.mmod <- inla(
  SID ~ 1 + NWPROP +
    f(ID, model = inla.PMMCAR.model(J=2, W = W, alpha.min = 0, alpha.max = 1,
                                    initial.values = c(0,0,0))),
  data = nc.long, E = EXP,
  family = "poisson", num.threads = 1,
```

```
  control.compute =list(waic = T, internal.opt =F),
  verbose = T)
```

BYM model implementation in INLA

Now, the PCAR is flexible and computationally efficient due to its sparse precision. However, it is not scalable. A flexible *and* scalable model, instead, is the Besag - York - Molliee convolution model, hereinafter referred to as BYM (Riebler et al. 2016). The drawback of the BYM model is that it does not have a sparse precision, which implies computational inefficiency. Here we provide an implementation of the BYM, loosely based on `bigDM` and `INLAMSM` codes:

```
inla.rgeneric.MMBYM.dense <-
  function (cmd = c("graph", "Q", "mu", "initial", "log.norm.const",
                    "log.prior", "quit"), theta = NULL) {
    envir <- parent.env(environment())
    #' Scaling the Laplacian matrix may be time-consuming,
    #' so it is better to do it just once.
    if(!exists("cache.done", envir=envir)){
    #' Unscaled Laplacian matrix (marginal precision of u_1, u_2 ... u_k)
      L_unscaled <- Matrix::Diagonal(nrow(W), rowSums(W)) -  W
      L_unscaled_block <- kronecker(diag(1,k), L_unscaled)
      A_constr <- t(pracma::nullspace(as.matrix(L_unscaled_block)))
      scaleQ <- INLA:::inla.scale.model.internal(
        L_unscaled_block, constr = list(A = A_constr, e = rep(0, nrow(A_constr))))
        #' Block Laplacian, i.e. precision of U = I_k \otimes L
      n <- nrow(W)
      L <- scaleQ$Q[c(1:n), c(1:n)]
      Sigma.u <- MASS::ginv(as.matrix(L))
      endtime.scale <- Sys.time()
      assign("Sigma.u", Sigma.u, envir = envir)
      assign("cache.done", TRUE, envir = envir)
    }
    interpret.theta <- function() {
      alpha <- 1/(1 + exp(-theta[as.integer(1:k)]))
      #' Bartlett decomposition ==> First define Sigma,
      #' then use its eigendecomposition to define M ==>
      #' ==> the function employs k(k+1)/2 parameters,
      #' i.e. lower-triangular factor in the Bartlett decomposition indeed.
      diag.N <- sapply(theta[as.integer(k + 1:k)], function(x) {
        exp(x)
      })
      no.diag.N <- theta[as.integer(2 * k + 1:(k * (k - 1)/2))]
      N <- diag(diag.N, k)
      N[lower.tri(N, diag = FALSE)] <- no.diag.N
      Sigma <- N %*% t(N)
      e <- eigen(Sigma)
      M <- t(e$vectors %*% diag(sqrt(e$values)))
      return(list(alpha = alpha, M = M))
    }
    graph <- function() {
      MI <- kronecker(Matrix::Matrix(1, ncol = k, nrow = k),
                      Matrix::Diagonal(nrow(W), 1))
      IW <- Matrix::Diagonal(nrow(W), 1) + W
      BlockIW <- Matrix::bdiag(replicate(k, IW, simplify = FALSE))
```

```
  G <- (MI %*% BlockIW) %*% MI
  return(G)
}
Q <- function() {
  param <- interpret.theta()
  M.inv <- solve(param$M)
  MI <- kronecker(M.inv, Matrix::Diagonal(nrow(W), 1))
  D <- as.vector(apply(W, 1, sum))
  BlockIW <- Matrix::bdiag(lapply(1:k, function(i) {
    solve(param$alpha[i]*Sigma.u +
            (1-param$alpha[i])*Matrix::Diagonal(nrow(W), 1))
  }))
  Q <- (MI %*% BlockIW) %*% kronecker(t(M.inv), Matrix::Diagonal(nrow(W),  1))
  return(Q)
}
mu <- function() {
  return(numeric(0))
}
log.norm.const <- function() {
  val <- numeric(0)
  return(val)
}
log.prior <- function() {
  param <- interpret.theta()
  val <- sum(-theta[as.integer(1:k)] - 2 * log(1 + exp(-theta[as.integer(1:k)])))
  #' Diagonal entries of the lower-triangular
  #' factor of Sigma: Chi-squared prior
  val <- val + k * log(2) + 2 * sum(theta[k + 1:k]) +
    sum(dchisq(exp(2 * theta[k + 1:k]),
               df = (k + 2) - 1:k + 1, log = TRUE))
    #' Off-diagonal entries of the factor:
    #' Normal prior
    val <- val + sum(dnorm(theta[as.integer((2 * k) + 1:(k *  (k - 1)/2))],
                           mean = 0, sd = 1, log = TRUE))
  return(val)
}
initial <- function() {
  return(c(rep(0, k * (k+3)/2)) )
}
quit <- function() {
  return(invisible())
}
if (as.integer(R.version$major) > 3) {
  if (!length(theta))
    theta = initial()
}
else {
  if (is.null(theta)) {
    theta <- initial()
  }
}
val <- do.call(match.arg(cmd), args = list())
return(val)
```

```
  }

inla.MMBYM.dense <- function (...)  INLA::inla.rgeneric.define(inla.rgeneric.MMBYM.dense, ...)
```

Specifically, we use a Uniform prior on the mixing parameters and we model the M matrix through the Bartlett decomposition, namely we define $\Sigma = AA^\top$, where A is a lower-triangular matrix whose squared diagonal elements are assigned a Chi-squared distribution and whose off-diagonal entries are assigned a Normal distribution. For more details on the Bartlett decomposition, see (Vicente et al. 2023).

Since the prior distribution of Z is proper, we do not set sum-to-zero constraints.

```
bym.dense.inla.mmod <- inla(
    SID ~ 1 + NWPROP +
    f(ID, model = inla.MMBYM.dense(k=2, W=W)#,
      #extraconstr = list(A = A_constr, e = c(0,0))
      ),
  data = nc.long, E = EXP,
  family = "poisson", num.threads = 1,
  control.compute =list(waic = T, internal.opt =F),
  verbose = T)
```

```
summary(bym.dense.inla.mmod)
```

```
## Time used:
##     Pre = 0.79, Running = 8.1, Post = 0.119, Total = 9.01
## Fixed effects:
##               mean    sd 0.025quant 0.5quant 0.975quant   mode kld
## (Intercept) -0.028 1.239     -2.572   -0.029      2.529 -0.028   0
## NWPROP       0.229 0.032      0.167    0.229      0.291  0.229   0
##
## Random effects:
##   Name     Model
##     ID RGeneric2
##
## Model hyperparameters:
##                mean    sd 0.025quant 0.5quant 0.975quant  mode
## Theta1 for ID 0.019 1.421     -2.773    0.017       2.82 0.008
## Theta2 for ID 0.089 1.449     -2.734    0.078       2.97 0.034
## Theta3 for ID 0.531 0.374     -0.245    0.544       1.22 0.607
## Theta4 for ID 0.350 0.440     -0.564    0.367       1.16 0.442
## Theta5 for ID 0.270 1.010     -1.730    0.274       2.25 0.291
##
## Watanabe-Akaike information criterion (WAIC) ...: 959.07
## Effective number of parameters .................: 6.10
##
## Marginal log-Likelihood:  -488.56
##  is computed
## Posterior summaries for the linear predictor and the fitted values are computed
## (Posterior marginals needs also 'control.compute=list(return.marginals.predictor=TRUE)')
```

We compare the posteriors of α for the PCAR and BYM models. Starting from the PCAR

```
# \alpha_{1974}
inla.zmarginal(inla.tmarginal(fun = function(X) exp(X)/(1 + exp(X)),
               marginal = pcar.inla.mmod$marginals.hyperpar[[1]]))
```

```
## Mean            0.485252
## Stdev           0.257423
## Quantile  0.025 0.0577171
## Quantile  0.25  0.266514
## Quantile  0.5   0.480312
## Quantile  0.75  0.700483
## Quantile  0.975 0.931046
```

```
# \alpha_{1979}
inla.zmarginal(inla.tmarginal(fun = function(X) exp(X)/(1 + exp(X)),
               marginal = pcar.inla.mmod$marginals.hyperpar[[2]]))
```

```
## Mean            0.489134
## Stdev           0.258192
## Quantile  0.025 0.058376
## Quantile  0.25  0.269832
## Quantile  0.5   0.485394
## Quantile  0.75  0.705724
## Quantile  0.975 0.933306
```

Then for the BYM:

```
# \alpha_{1974}
inla.zmarginal(inla.tmarginal(fun = function(X) exp(X)/(1 + exp(X)),
               marginal = bym.dense.inla.mmod$marginals.hyperpar[[1]]))
```

```
## Mean            0.503322
## Stdev           0.261985
## Quantile  0.025 0.0598766
## Quantile  0.25  0.280805
## Quantile  0.5   0.503945
## Quantile  0.75  0.726061
## Quantile  0.975 0.942444
```

```
# \alpha_{1979}
inla.zmarginal(inla.tmarginal(fun = function(X) exp(X)/(1 + exp(X)),
               marginal = bym.dense.inla.mmod$marginals.hyperpar[[2]]))
```

```
## Mean            0.514999
## Stdev           0.264773
## Quantile  0.025 0.062057
## Quantile  0.25  0.290239
## Quantile  0.5   0.518691
## Quantile  0.75  0.74244
## Quantile  0.975 0.949877
```

Results are similar.

Proposal - sparse precision multivariate BYM Here is the proposed code for the sparse BYM. Recall equation 3. Whereas $\pi(Y \mid \Sigma, \tilde{\Phi})$ is proper, the precision matrix of the joint model has rank deficiency p times the rank deficiency of L, hence the sum-to-zero constraint is necessary. This can be seen by computing its determinant, starting from the lemma

$$\begin{vmatrix} A & B \\ C & D \end{vmatrix} = \mid A \mid \cdot \mid D - CA^{-1}B \mid \propto \mid D - CA^{-1}B \mid$$

For the determinant of the augmented BYM precision we would therefore have: $A = q_{11} \otimes I_n$; $B = q_{11}\tilde{\Phi}M^{\top} \otimes I_n$,

$C = M\tilde{\Phi}q_1 1 \otimes I_n$ and $D = M\tilde{\Phi}q_{11}\tilde{\Phi}M^\top + I_p \otimes L$, hence

$$| D - CA^{-1}B | = | M\tilde{\Phi}q_{11}\tilde{\Phi}M^\top + I_p \otimes L - M\tilde{\Phi}q_{11}\tilde{\Phi}M^\top | = | I_p \otimes L | = 0$$

```
inla.rgeneric.MMBYM.sparse <-
  function (cmd = c("graph", "Q", "mu", "initial", "log.norm.const",
                    "log.prior", "quit"), theta = NULL) {
    envir <- parent.env(environment())
    #' Scaling the Laplacian matrix may be time-consuming,
    #' so it is better to do it just once.
    if(!exists("cache.done", envir=envir)){
      #' Unscaled Laplacian matrix (marginal precision of u_1, u_2 ... u_k)
      L_unscaled <- Matrix::Diagonal(nrow(W), rowSums(W)) -  W
      L_unscaled_block <- kronecker(diag(1,k), L_unscaled)
      A_constr <- t(pracma::nullspace(as.matrix(L_unscaled_block)))
      scaleQ <- INLA:::inla.scale.model.internal(
        L_unscaled_block, constr = list(A = A_constr, e = rep(0, nrow(A_constr))))
      #' Block Laplacian, i.e. precision of U = I_k \otimes L
      n <- nrow(W)
      L <- scaleQ$Q[c(1:n), c(1:n)]
      assign("L", L, envir = envir)
      assign("cache.done", TRUE, envir = envir)
    }
    interpret.theta <- function() {
      phi.vector <- 1/(1 + exp(-theta[as.integer(1:k)]))
      #' Bartlett decomposition ==> First define Sigma,
      #' then use its eigendecomposition to define M ==>
      #' ==> the function employs k(k+1)/2 parameters,
      #' i.e. lower-triangular factor in the Bartlett decomposition indeed.
      diag.N <- sapply(theta[as.integer(k + 1:k)], function(x) {
        exp(x)
      })
      no.diag.N <- theta[as.integer(2 * k + 1:(k * (k - 1)/2))]
      N <- diag(diag.N, k)
      N[lower.tri(N, diag = FALSE)] <- no.diag.N
      #' Marginal variance/scale:
      Sigma <- N %*% t(N)
      #' Eigendecomposition of Sigma ==> M
      e <- eigen(Sigma)
      M <- t(e$vectors %*% diag(sqrt(e$values)))
      return(list(phi.vector = phi.vector, M = M))
    }
    graph <- function() {
      #' Adapted from INLAMSM;
      #'  here dimensions of the G matrix are doubled.
      BPrec <- matrix(1, ncol = 2*k, nrow = 2*k)
      G <- kronecker(BPrec, Matrix::Diagonal(nrow(W), 1) +
                       W)
      return(G)
    }
    Q <- function() {
      param <- interpret.theta()
      M.inv <- solve(param$M)
      #' Matrix-valued mixing parameter, diagonal = sqrt(phi_1) ... sqrt(phi_k)
```

```
  Phi <- Matrix::Diagonal(sqrt(param$phi.vector), n=k)
  #' Diagonal of: 1/sqrt(1-phi_1), ... 1/sqrt(1-phi_k)
  invPhihat <- Matrix::Diagonal(1/sqrt(1-param$phi.vector), n=k)
  #' Precision blocks, defined as in equation 3
  q11 <- invPhihat %*% M.inv %*% t(M.inv) %*% invPhihat
  q12 <- q11 %*% Phi %*% t(param$M)
  q22 <- param$M %*% Phi %*% q12
  Q.11 <- kronecker(q11, Matrix::Diagonal(n=nrow(W), x = 1))
  Q.12 <- kronecker(-q12, Matrix::Diagonal(n=nrow(W), x = 1))
  Q.22 <- kronecker(q22, Matrix::Diagonal(n=nrow(W), x = 1)) +
    kronecker(Matrix::Diagonal(n=k, x=1), L)
  Q <- cbind(rbind(Q.11, Matrix::t(Q.12)),
             rbind(Q.12, Q.22))
  return(Q)
}
mu <- function() {
  return(numeric(0))
}
log.norm.const <- function() {
  val <- numeric(0)
  return(val)
}
#' Equivalent to bigDM::Mmodel_pcar or Mmodel_lcar
log.prior <- function() {
  param <- interpret.theta()
  #' Uniform prior on the mixing parameter
  val <- sum(-theta[as.integer(1:k)] - 2 * log(1 + exp(-theta[as.integer(1:k)])))
  #' Diagonal entries of the lower-triangular
  #' Bartlett factor of Sigma: Chi-squared prior
  val <- val + k * log(2) + 2 * sum(theta[k + 1:k]) +
    sum(dchisq(exp(2 * theta[k + 1:k]),
               df = (k + 2) - 1:k + 1, log = TRUE))
  #' Off-diagonal entries of the Bartlett factor:
  #' Normal prior
  val <- val + sum(dnorm(theta[as.integer((2 * k) + 1:(k *  (k - 1)/2))],
                         mean = 0, sd = 1, log = TRUE))
  return(val)
}
initial <- function() {
  return(c(rep(0, k * (k+3)/2)) )
}
quit <- function() {
  return(invisible())
}
if (as.integer(R.version$major) > 3) {
  if (!length(theta))
    theta = initial()
}
else {
  if (is.null(theta)) {
    theta <- initial()
  }
}
```

```
    val <- do.call(match.arg(cmd), args = list())
    return(val)
  }

inla.MMBYM.sparse<- function(...){
  INLA::inla.rgeneric.define(inla.rgeneric.MMBYM.sparse, ...)}

bym.sparse.inla.mmod <- inla(
    SID ~ 1 + NWPROP +
    f(ID, model = inla.MMBYM.sparse(k=2, W=W),
      extraconstr = list(A = cbind(matrix(0, nrow(A_constr), ncol = ncol(A_constr)), A_constr),
                         e = c(0, 0)),
      values = c(1:(2*nrow(nc.long)))),
  data = nc.long, E = EXP,
  family = "poisson", num.threads = 1,
  control.compute =list(waic = T, internal.opt =F),
  verbose = T)
```

The posterior distribution of the mixing parameter, here, is still flat.

```
# \alpha_{1974}
inla.zmarginal(inla.tmarginal(fun = function(X) exp(X)/(1 + exp(X)),
               marginal = bym.sparse.inla.mmod$marginals.hyperpar[[1]]))
```

```
## Mean            0.492778
## Stdev           0.260277
## Quantile  0.025 0.0575519
## Quantile  0.25  0.271283
## Quantile  0.5   0.490246
## Quantile  0.75  0.712309
## Quantile  0.975 0.936713
```

```
# \alpha_{1979}
inla.zmarginal(inla.tmarginal(fun = function(X) exp(X)/(1 + exp(X)),
               marginal = bym.sparse.inla.mmod$marginals.hyperpar[[2]]))
```

```
## Mean            0.494664
## Stdev           0.260226
## Quantile  0.025 0.0582823
## Quantile  0.25  0.273422
## Quantile  0.5   0.492736
## Quantile  0.75  0.714333
## Quantile  0.975 0.937347
```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