

Bivariate conditional spatial models: Case study in Section 5

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Setting up

An important component of this example is the slice sampler. Here we use the code by Jonathan Rougier, University of Bristol, which is not available from CRAN. As of writing, this was available from [his personal webpage](#). Once downloaded this package may be installed using

```
install.packages("./slice_0.9.tar.gz", type="source", repos=NULL)
```

We will also be needing part of the INLA package and installation instructions for this can be found on the [R-INLA homepage](#). Once these are installed we can load the required packages. As with the previous vignette (simulation example in Section 3.2), we will also need `dplyr`, `tidyr`, and `Matrix` for core operations and `ggplot2`, `gridExtra`, `grid`, `extrafont` and `maptools` for plotting purposes.

```
library(dplyr)
library(tidyr)
library(Matrix)
library(INLA)
library(slice)
library(ggplot2)
library(gridExtra)
library(grid)
library(extrafont)
library(maptools)
```

Finally, we will also need the package `bicon` to facilitate matrix construction.

```
library(bicon)
```

As detailed in Cressie & Zammit-Mangion (2015), we consider three models in this case study. These vary only through the interaction function $b_o(h)$ that, for each model, is given as

$$\begin{array}{ll} \text{Model 1 (independence):} & b_o(h) \equiv 0, \\ \text{Model 2 (pointwise dependence):} & b_o(h) \equiv A\delta(h), \\ \text{Model 3 (diffused dependence):} & b_o(h) \equiv \begin{cases} A\{1 - (\|h - \Delta\|/r)^2\}^2, & \|h - \Delta\| \leq r \\ 0, & \text{otherwise,} \end{cases} \end{array}$$

where $\Delta = (\Delta_1, \Delta_2)^T$ is a shift parameter vector that captures asymmetry, r is the aperture parameter, and A is the amplitude. In Model 3, $b_o(h)$ is a shifted bisquare function in \mathbb{R}^2 . The covariance functions $C_{11}(\cdot)$ and $C_{21}(\cdot)$ are Matérn covariance functions with $\nu_{11} = \nu_{21} = 1.5$.

The first thing we need to do is specify which model we are going to analyse. Since Model 3 is the most complicated, we will use this throughout this vignette. The second thing, is to indicate whether we want to run the full MCMC scheme (takes a long time!) or just generate a few samples to make sure the code is working. For the purpose of this vignette we will use a flag `long_analysis` to indicate whether we want to run the full MCMC chain or not.

```

### Model choice
### 1. Independent
### 2. Pointwise interaction
### 3. Smoothing
model = 3
model_name <- switch(model,"independent","pointwise","moving_average")
set.seed(1) ## Fix seed
img_path <- "../paper/art" ## Where to save the figures
show_figs <- 1 ## Show the figures in document
print_figs <- 0 ## Print figures to file (leave =0)
long_analysis <- 0 ## Run a long MCMC chain (1) or not (0)

```

The data

The data was made available through the work of Genton & Kleiber (2015) and is included in the package `extdata` folder. These have also been included as part of the package for convenience, by first preprocessing it using

```

temps_path <- system.file("extdata","COTemp20040919.txt", package = "bicon")
temps <- read.table(temps_path,header=T)
names(temps) <- c("minT","maxT","lon","lat")

```

Thus, these data can simply be loaded using the `data` command

```

### Import data
###-----
data(temps)

```

The above command loads the data `temps` in the the global environment as a data frame. The data frame stores the minimum temperature (`minT`), the maximum temperature (`maxT`) and the lon-lat coordinates of the measurement stations (`lon` and `lat`).

```
print(head(temps))
```

```

##      minT      maxT      lon      lat
## 1  4.752128  7.796809 -103.1417  40.1550
## 2 -7.547872 -5.003191 -105.8919  38.9933
## 3 -6.447872 -1.603191 -105.4767  39.4047
## 4 -3.647872  4.496809 -108.8903  38.3189
## 5 -3.647872 -5.503191 -107.6872  38.5547
## 6  3.052128  7.796809 -102.1192  39.6567

```

From this data frame we extract Z_1 and Z_2 and concatenate them into one long vector Z . We also define m_1 as the number of observations of Y_1 , m_2 as the number of observations of Y_2 and m as the total number of observations. Information pertaining to Z_1 and Z_2 are stored in the data frames `obs1` and `obs2`, respectively.

```

Z1 <- matrix(temps$minT)
Z2 <- matrix(temps$maxT)
Z <- rbind(Z1,Z2)
m1 <- length(Z1)

```

```

m2 <- length(Z2)
m <- m1 + m2

obs1 <- temps %>%
  mutate(x = lon, y = lat, z = minT) %>%
  select(x,y,z)

obs2 <- temps %>%
  mutate(x = lon, y = lat, z = maxT) %>%
  select(x,y,z)

```

Process discretisation

We approximate the processes as a sum of basis functions (tent functions) constructed on a triangulation. The triangulation is formed using the `mesher` in the `INLA` package, while we provide a tailored function `initFEbasis` which takes information from the `INLA` mesher and casts it into a `Mesh` object. We provide several methods associated with the `Mesh` class which will be useful for plotting later on. Importantly, the `Mesh` object also contains information on the areas of the elements in the Voronoi tessellation, which will be used to approximate the integrations.

```

### Construct mesh
###-----
mesh <- inla.mesh.2d(loc= temps[c("lon","lat")],cutoff=0.04,max.edge=0.3)
D <- as.matrix(dist(mesh$loc[,1:2]))
Dvec <- as.double(c(D))
distmat11 <- distmat12 <- distmat21 <- distmat22 <-
  as.matrix(dist( as.matrix(temps[c("lon","lat")]))))

Mesh <- initFEbasis(p = mesh$loc[,1:2],
                   t = mesh$graph$tv,
                   K = mesh$graph$vv)

```

```

##
##      PLEASE NOTE: The components "delsgs" and "summary" of the
##      object returned by deldir() are now DATA FRAMES rather than
##      matrices (as they were prior to release 0.0-18).
##      See help("deldir").
##
##      PLEASE NOTE: The process that deldir() uses for determining
##      duplicated points has changed from that used in version
##      0.0-9 of this package (and previously). See help("deldir").

```

We next establish the dimension of our grids. Since we will be evaluating Y_1 and Y_2 on the same grid, $n_1 = n_2$.

```

### Process models
###-----
n1 <- mesh$n
n2 <- mesh$n
n <- n1 + n2

```

As in the first vignette (simulation example of Section 3.2), we will approximate the integration using the rectangular rule. When using finite elements, this reduces to using the area of the Voronoi tessellation as the weight for the function values.

We first compute the vector of displacements h which will be of length $(n2 \times n1)$ and with each element associate an integration weight equal to the area of the Voronoi tessellation associated with the element:

```
### Mesh integration points
###-----
mesh_locs <- mesh$loc[,1:2]
h <- matrix(0,n1*n2,2)
areas <- rep(0,n1*n2)
for(i in 1:n2) {
  h[((i-1)*n1+1):(i*n1),] <- t(t(mesh_locs) - mesh_locs[i,])
  areas[((i-1)*n1+1):(i*n1)] <- Mesh["area_tess"]
}
h1_double <- as.double(h[,1])
h2_double <- as.double(h[,2])
```

The displacements (h1,h2) and the areas `areas` can then be used to construct the matrix B using the function `bisquare_B`.

```
#####
### Model specifics
#####
if (model == 1) B <- matrix(0,n2,n1)
if (model == 2) B <- diag(n1)
if (model == 3) B <- bisquare_B(h1 = h1_double,
                                h2 = h2_double,
                                delta=c(0,0),r=0.3,
                                n1 = n1,n2=n2,areas = areas)
```

Organising the observations

In order to map the process to the observations we construct an incidence matrix, which contains a 1 wherever the observation coincides with a vertex on the triangulation and a 0 otherwise. The dimension of this incidence matrix is $(m1 + m2) \times (n1 + n2)$, where $m1$, $m2$, are the number of observations in Z_1 , Z_2 , respectively. Since in this problem we have collocated observations, we find the incidence matrix for one of the observations, Z_1 , and then form the whole incidence matrix by simply carrying out `bdiag` (block diagonal) of the first matrix with itself. We find the points with which the observation locations coincide by using the function `left_join`, which returns an NA if no observation coincides with the vertex.

```
obs_locs <- as.matrix(temps[c("lon","lat")])      ## observation locations
mesh_locs <- data.frame(x=mesh$loc[,1],y=mesh$loc[,2]) ## mesh locations
idx <- which(!(is.na(left_join(mesh_locs,obs1)$z))) ## index of coincidence
C1 <- sparseMatrix(i=1:nrow(obs1),j=idx,x=1,dims=c(m1,n1)) ## incidence matrix of Z1
C <- bdiag(C1,C1)      ## incidence matrix
```

MCMC initialisation and prior specification

This is the computational and memory intensive part of the program. Since this is only a vignette we will only generate 10 samples. For the simulation study in Section 5, we used 50000 samples and thinned by only keeping every 100. To carry out the full analysis, please set `long_analysis = 1` above.

```

### MCMC initialisations
###-----
if(long_analysis){
  N = 50000
  thin = 100
  burn_in = 1000
} else {
  N = 10
  thin = 1
  burn_in = 2
}

```

The marginal precisions were initialised to $\sigma_{11}^{-2} = 0.25$ and $\sigma_{2|1}^{-2} = 5$. The scales were initialised to $\kappa_1 = \kappa_{2|1} = 2$, $\rho = 0.1$, $A = 0$, $r = 0.3$ and $\Delta = (0,0)'$. Recall that we use transformations for some of these parameters. Therefore, for example, we initialise a variable `log_kappa1_samp` as `log(2)`. Then, throughout, $\kappa_1 = \exp(\text{log_kappa1_samp})$.

```

Y_samp <- matrix(0,n,N/thin)
prec0_samp <- rep(1,N)
prec1_samp <- rep(0.25,N)
prec2_samp <- rep(5,N)

### kappa_1: init sample at log(2), kappa = exp(gamma)
log_kappa1_samp <- matrix(log(2),1,N)

### kappa_{2|1}: init sample at log(2), kappa = exp(gamma)
log_kappa2_samp <- matrix(log(2),1,N)

### rho_\epsilon: init sample at rho = 0.1, rho = 2*pnorm(gamma) - 1
rho_trans_samp <- rep(qnorm((0.1+1)/2),N)

### A: init sample at A = 0
A_samp <- rep(0,N)

### r: init sample at r = 0.3, r = exp(gamma)
log_r_samp <- rep(log(0.3),N)

### Delta_1 and Delta_2: init sample at Delta = (0,0)
d1_samp <- rep(0,N)
d2_samp <- rep(0,N)

### Sampling the Deviance
Deviance_samp <- rep(0,N)

```

We next specify the prior distributions over all unknown parameters. These are detailed in Table 2, Appendix 3 of Cressie & Zammit-Mangion (2015). In order to tune the prior distribution over the precision parameters we use a function `Findalphabeta_gamma` which, given the 5th and 95th percentiles for the desired standard deviations, finds appropriate values for α, β (shape and rate parameters) needed to define the Gamma distribution. Type `help(Findalphabeta_gamma)` for more details.

A new function appearing below is `makeQY`. This has an interface identical to `makeSY` but instead returns the precision matrix Σ^{-1} . This is useful since working with the precision matrices is slightly more computationally efficient than working with covariance matrices (even if the precision matrix is dense).

```
#####
### Parameter prior specification
#####

### Y1,Y2 mean and precision
muY = rep(0,n)
QY <- makeQY(r = Dvec,
             var1 = 4,
             var2 = 0.2,
             kappa1 = 2,
             kappa2 = 2,
             B = 0*B)
QY_chol <- chol(QY)

### observation error precision
hyp_prec0 <- optim(par=c(1,1),Findalphabeta_gamma, p5=0.5, p95=2)
alpha0 <- hyp_prec0$par[1]
beta0 <- hyp_prec0$par[2]
Qo_base <-diag(m)
chol_Qo_base <-chol(Qo_base)

### log(kappa_1)
mu_log_kappa1 = log(2)
prec_log_kappa1 = 1

### log(kappa_{2|1})
mu_log_kappa2 = log(2)
prec_log_kappa2 = 1

### gamma, where rho = 2*pnorm(theta) - 1
mu_rho_trans = qnorm((1)/2)
prec_rho_trans = 1

### precision(Y1) and precision(Y2)
hyp_prec1 <- optim(par=c(1,1),Findalphabeta_gamma, p5=1, p95=10)
alpha1 <- alpha2 <- hyp_prec1$par[1]
beta1 <- beta2 <- hyp_prec1$par[2]

### A (amplitude of bisquare function)
mu_A = 0
prec_A = 1/(0.2^2)

### Delta (shift parameter of bisquare function)
mu_delta1 = 0
prec_delta1 = 1/(0.5^2)
mu_delta2 = 0
prec_delta2 = 1/(0.5^2)

### r (aperture parameter of bisquare function)
mu_log_r = 1
prec_log_r = 1/(0.5^2)
```

The sampler

Before we start the MCMC routine, we need to initialise the slice sampler for those variables which have a conditional distribution that is not available in closed form. For the scales and observation correlation parameter we use univariate slice samplers, while for the bisquare function we use a tri-variate slice sampler.

```
#####
### Gibbs-slice sampler
#####

slice_log_kappa1 <- slice::slice(1)
slice_log_kappa2 <- slice::slice(1)
slice_rho_trans <- slice::slice(1)
slice_bisquare <- slice::slice(3)
```

We can now start the Gibbs sampler, for which we will be requiring the conditional distributions. Denote θ as the collection of unknown parameters and denote $\rho_\varepsilon = 2\Phi(\tilde{\rho}_\varepsilon) - 1$, $r = \exp(\tilde{r})$ and $\kappa_i = \exp(\tilde{\kappa}_i)$, where the sign \sim is used to note the (transformed) variable we actually sample from. Then

$$p(Y|Z, \theta) \propto p(Z|Y, \theta)p(Y|\theta) \quad (1)$$

$$p(\sigma_\varepsilon^{-2}|Y, Z, \theta/\sigma_\varepsilon^{-2}) \propto p(Z|Y, \theta)p(\sigma_\varepsilon^{-2}) \quad (2)$$

$$p(\tilde{\rho}_\varepsilon|Y, Z, \theta/\tilde{\rho}_\varepsilon) \propto p(Z|Y, \theta)p(\tilde{\rho}_\varepsilon) \quad (3)$$

$$p(\sigma_{11}^{-2}|Y, Z, \theta/\sigma_{11}^{-2}) \propto p(Y_1|\theta)p(\sigma_{11}^{-2}) \quad (4)$$

$$p(\sigma_{2|1}^{-2}|Y, Z, \theta/\sigma_{2|1}^{-2}) \propto p(Y_2|Y_1, \theta)p(\sigma_{2|1}^{-2}) \quad (5)$$

$$p(\tilde{\kappa}_{11}|Y, Z, \theta/\tilde{\kappa}_{11}) \propto p(Y_1|\theta)p(\tilde{\kappa}_{11}) \quad (6)$$

$$p(\tilde{\kappa}_{2|1}|Y, Z, \theta/\tilde{\kappa}_{2|1}) \propto p(Y_2|Y_1, \theta)p(\tilde{\kappa}_{2|1}) \quad (7)$$

$$p(A|Y, Z, \theta/A) \propto p(Y_2|Y_1, \theta)p(A) \quad (8)$$

$$p(\Delta, \tilde{r}|Y, Z, \theta/(\Delta, \tilde{r})) \propto p(Y_2|Y_1, \theta)p(\Delta)p(\tilde{r}) \quad (9)$$

We do not discuss the algorithm below in detail, as it simply carries out the updates according to the conditional distributions listed above. However, a couple points are worth mentioning:

- Where appropriate, we sample directly using functions such as `rgamma`. When the conditional distribution is not available in closed form we use the slice sampler. When slice sampling, all we need to do is supply the sampler with the logarithm of the conditional distribution and a `learn` parameter, which indicates for how many samples we are adapting the interval width in the slice sampler. This is set equal to the burn-in in each case.
- To sample the precision and scale parameters, we need to construct the covariance and precision matrices corresponding to $C_{11}(\cdot)$ and $C_{2|1}(\cdot)$. For this we use the functions `makeS` and `makeQ` respectively.

```
Ycount=1
I_m1 <- Imat(m1)
set.seed(1)
for(i in 2:N) {
  ## Sample Y
  Qo_new <- prec0_samp[i-1]*Qo_base
  QY_new <- QY + prec0_samp[i-1] * as(crossprod(chol_Qo_base %*% C), "matrix")
  R <- chol(QY_new)
```

```

muY_new <- matrix(backsolve(R,backsolve(R,t(C) %*% Qo_new %*% Z,transpose=T)),ncol=1)
Yi <- (muY_new + backsolve(R,rnorm(n = n)))[,1]

Y1i <- Yi[1:n1]
Y2i <- Yi[-(1:n1)]
if (i %% thin == 0) {
  Y_samp[,Ycount] <- Yi
  Ycount <- Ycount + 1
}

### Observation model parameters

## Sample prec(epsilon)
alpha0_new <- alpha0 - 1 + m/2
beta0_new <- beta0 + 0.5*crossprod(chol_Qo_base %*% (Z - C %*%Yi))
prec0_samp[i] <- rgamma(n = 1,shape = alpha0_new,rate = as.numeric(beta0_new))

## Sample rho
ZCY <- (Z - C %*%Yi)
logf_a <- function(x) {
  a <- 2*(pnorm(x)) - 1
  Qo <- prec0_samp[i] * kronecker(solve(matrix(c(1,a,a,1),2,2)),I_m1)
  chol_Qo <- chol(Qo)
  as.numeric(0.5*(2 * sum(log(diag(chol_Qo)))) -
    0.5*crossprod(chol_Qo %*% ZCY) -
    0.5*(x - mu_rho_trans)^2*prec_rho_trans)
}

rho_trans_samp[i] <- slice_rho_trans(rho_trans_samp[i-1] , logf_a, learn = i <= burn_in)
Qo_base <- kronecker(solve(matrix(c(1,2*pnorm(rho_trans_samp[i]) - 1,
  2*pnorm(rho_trans_samp[i]) - 1,1),2,2)),I_m1)

chol_Qo_base <- chol(Qo_base)

### Precision parameters

## Sample precision(Y1)
Q11base <- makeQ(r = Dvec,var = 1, kappa = exp(log_kappa1_samp[1,i-1]))
alpha1_new <- alpha1 - 1 + n1/2
beta1_new <- beta1 + 0.5*(t(Y1i) %*% Q11base %*% Y1i)[,1]
prec1_samp[i] <- rgamma(n = 1,shape = alpha1_new,rate = beta1_new)

## Sample precision(Y2)
Q2_1base <- makeQ(r = Dvec, var=1,kappa= exp(log_kappa2_samp[1,i-1]))
alpha2_new <- alpha2 - 1 + n2/2
YB <- Y2i - A_samp[i-1]*B %*% Y1i
beta2_new <- beta2 + 0.5*(t(YB) %*% Q2_1base %*% YB)[,1]
prec2_samp[i] <- rgamma(n = 1,shape = alpha2_new,rate = beta2_new)

### Interaction parameters

## Sample A
if(model %in% 2:3) {
  Q2_1 <- prec2_samp[i]*Q2_1base

```



```

Y1_sub <- B %*% Y1i
precA_new <- t(Y1_sub) %*% Q2_1 %*% Y1_sub + prec_A
muA_new <- solve(precA_new, t(Y1_sub) %*% Q2_1 %*% Y2i + prec_A*mu_A)
A_samp[i] <- as.numeric(muA_new + solve(chol(precA_new), rnorm(n = 1)))
}

## Sample delta, r
if(model == 3) {
  Q2_1 <- prec2_samp[i]*Q2_1base
  logf_B <- function(x) {
    BB <- bisquare_B(h1_double, h2_double,
                     delta=x[1:2], r=exp(x[3]),
                     n1 = n1, n2=n2, areas = areas)
    (-0.5*t(Y2i - A_samp[i]*BB %*% Y1i) %*% Q2_1 %*% (Y2i - A_samp[i]*BB %*% Y1i) -
     0.5*(x[1] - mu_delta1)^2*prec_delta1 -
     0.5*(x[2] - mu_delta2)^2*prec_delta2 -
     0.5*(x[3] - mu_log_r)^2*prec_log_r)[,1]
  }
  all_samp <- slice_bisquare(c(d1_samp[i-1], d2_samp[i-1], log_r_samp[i-1]),
                           logf_B, learn = i <= burn_in)

  d1_samp[i] <- all_samp[1]
  d2_samp[i] <- all_samp[2]
  log_r_samp[i] <- all_samp[3]
  B <- bisquare_B(h1_double, h2_double,
                  delta=all_samp[1:2], r=exp(all_samp[3]),
                  n1 = n1, n2=n2, areas = areas)
}

### Scale parameters

## Sample scale1
logf_k1 <- function(x) {
  SY <- makeS(r = Dvec, var = 1/prec1_samp[i], kappa = exp(x))
  R <- chol(SY)
  (-0.5*logdet(R) -
   0.5*crossprod(forwardsolve(t(R), Y1i)) -
   0.5*(x[1] - mu_log_kappa1)^2*prec_log_kappa1)[,1]
}
log_kappa1_samp[1,i] <- slice_log_kappa1(log_kappa1_samp[1,(i-1)],
                                       logf_k1, learn = i <= burn_in)

## Sample scale2
YB <- Y2i - A_samp[i]*B %*% Y1i
logf_k2 <- function(x) {
  SY <- makeS(r = Dvec, var = 1/prec2_samp[i], kappa = exp(x))
  R <- chol(SY)
  (-0.5*logdet(R) -
   0.5*crossprod(forwardsolve(t(R), YB)) -
   0.5*(x - mu_log_kappa2)^2*prec_log_kappa2)[,1]
}
log_kappa2_samp[1,i] <- slice_log_kappa1(log_kappa2_samp[1,(i-1)],

```

```

logf_k2, learn = i <= burn_in)

### Form prevision matrix from updated parameters
QY <- makeQY(r = Dvec,
             1/prec1_samp[i],
             1/prec2_samp[i],
             exp(log_kappa1_samp[1,i]),
             exp(log_kappa2_samp[1,i]),
             A_samp[i]*B)

### Compute deviance
Deviance_samp[i] <-
  as.numeric(-2*( -0.5*m*log(2*pi) +
    0.5*logdet(L = sqrt(prec0_samp[i])*chol_Qo_base) -
    0.5*prec0_samp[i] * t(ZCY) %*% Qo_base %*% ZCY))

if(!(i%1)) cat(paste0("Iteration ",i),sep="\n")
}

```

```

## Iteration 2
## Iteration 3
## Iteration 4
## Iteration 5
## Iteration 6
## Iteration 7
## Iteration 8
## Iteration 9
## Iteration 10

```

Computing the DIC

The discrepancy between data and model can be assessed using the *deviance*

$$D(Z, Y, \theta) \equiv -2 \log p(Z \mid Y, \theta). \quad (10)$$

Since the deviance is a function of the unknowns Y and θ we use the average deviance from the posterior realisations of (Y, θ)

$$\hat{D}(Z) \equiv \frac{1}{N} \sum_{i=1}^N D(Z, Y^{(i)}, \theta^{(i)}). \quad (11)$$

where N is the number of samples.

The average deviance alone is not sufficient when comparing across models with differing complexities. In deviance-based strategies, a penalty for model complexity p_D is obtained by computing the difference between $\hat{D}(Z)$ and the deviance at the posterior means of Y, θ , $D(Z; \hat{Y}, \hat{\theta})$. Then the *Deviance Information Criterion* (DIC) is simply the addition of these two quantities (Spiegelhalter, Best, Carlin, & Van Der Linde, 2002):

$$DIC \equiv 2\hat{D}(Z) - D(Z; \hat{Y}, \hat{\theta}). \quad (12)$$

We find the mean deviance and the DIC from the samples as follows.

```
MCMC_sub <- seq(burn_in,N,by=thin)
Qo_base <- kronecker(solve(matrix(c(1,2*pnorm(mean(rho_trans_samp[MCMC_sub]))-1,
2*pnorm(mean(rho_trans_samp[MCMC_sub]))-1,1),2,2)),I_m1)
Deviance_mean <- as.numeric(-2*( -0.5*m*log(2*pi) +
0.5*logdet(L = chol(mean(prec0_samp[MCMC_sub])*Qo_base)) -
0.5*crossprod(chol(mean(prec0_samp[MCMC_sub])*Qo_base) %%%
(Z - C %%%apply(Y_samp,1,mean))))))
DIC <- 2*mean(Deviance_samp[MCMC_sub]) - Deviance_mean
```

Obviously, with such few samples the results are not of much use. Instead, we saved the results using $N=50000$, $\text{burn_in} = 1000$ and $\text{thin} = 100$ using the following piece of code

```
### Should only be run with path set as vignette source directory
if (long_analysis)
save(model_name,
MCMC_sub,
Y_samp,
prec0_samp,
rho_trans_samp,
prec1_samp,
prec2_samp,
log_kappa1_samp,
log_kappa2_samp,
A_samp,
log_r_samp,
d1_samp,
d2_samp,
Deviance_samp,
Deviance_mean,
DIC,
file=paste0("../data/",model_name,".rda"))
```

and now re-load these results using

```
data(moving_average)
```

If we wish to write out the results to a text file we can use the following code (not evaluated)

```
fileConn<-file(paste0("../paper/",model_name,".txt"))
print_row <- function(x) {
fline <- paste0(round(median(x[MCMC_sub]),digits=2)," [",
round(quantile(x[MCMC_sub],c(0.25)),digits=2)," , ",
round(quantile(x[MCMC_sub],c(0.75)),digits=2)," ]")
}
writeLines(c(print_row(1/prec0_samp),
print_row(2*pnorm(rho_trans_samp)-1),
```

```

    print_row(1/prec1_samp),
    print_row(1/prec2_samp),
    print_row(exp(log_kappa1_samp[1,])),
    print_row(exp(log_kappa2_samp[1,])),
    print_row(A_samp),
    print_row(exp(log_r_samp)),
    print_row(d1_samp),
    print_row(d2_samp),
    print_row(Deviance_samp),
    paste0(round(mean(Deviance_samp[MCMC_sub]),digits=2)),
    paste0(round(mean(Deviance_samp[MCMC_sub]) - Deviance_mean,digits=2)),
    paste0(round(DIC,digits=2))),
  fileConn)
close(fileConn)

```

Plotting

As in the previous vignette, we only briefly describe the code used to plot the results. The first plot shows the domain of interest around the state of Colorado. The shapefile required is available in the `extdata` folder of the package and is accessible through

```

shapefile_path <- system.file("extdata", "cb_2013_us_state_5m.shp", package = "bicon")
States <- maptools::readShapeSpatial(shapefile_path)

```

We now extract these data into a data frame, and add coordinates for the labels in a data frame `State_summaries`. We then find the convex hull of our triangulation (domain boundary) using `chull`.

```

### DOMAIN PLOT
States_fort <- fortify(States) %>% mutate( id= as.numeric(id))
State_names <- data.frame(Name = States$NAME, id = 0:(length(States$NAME)-1))

States_fort <- left_join(States_fort,State_names)
State_summaries <- group_by(States_fort,Name) %>%
  summarise(long = mean(long), lat = mean(lat))
State_summaries[4,c("long","lat")] <- c(-112,35.22)
State_summaries[46,c("long","lat")] <- c(-101.09198, 43.80577)
State_summaries[32,c("long","lat")] <- c(-118.75965, 37.96324)
State_summaries[31,c("long","lat")] <- c(-99.79460, 41.49899)
State_summaries[20,c("long","lat")] <- c(-99.10218, 38.75878)
State_summaries[35,c("long","lat")] <- c(-105.71772, 34.71201)
State_summaries[40,c("long","lat")] <- c(-97.32183, 35.72782)

conv_hull <- Mesh[c("x","y")][chull(Mesh[c("x","y")]),]
conv_hull <- rbind(conv_hull,conv_hull[1,])

```

We can now plot the domain of interest overlaying the state boundaries.

```

Stateplot <- LinePlotTheme() +
  geom_path(data=States_fort,aes(long,lat,group=group,label=Name),linetype="dashed") +
  geom_text(data=State_summaries,aes(long,lat,label=Name)) +
  coord_fixed(,xlim=c(-115,-95),ylim=c(33,45)) +
  geom_path(data=conv_hull,aes(x,y),size=1,,colour="black") +

```

```

theme(plot.margin = grid::unit(c(2, 2, 2, 2),units="mm")) + xlab("lon")
if(print_figs)
  ggsave(Stateplot,
    filename = file.path(img_path,"Stateplot.eps"),
    width=7,height=4,family="Arial")
if(show_figs)
  print(Stateplot,family="Arial")

```

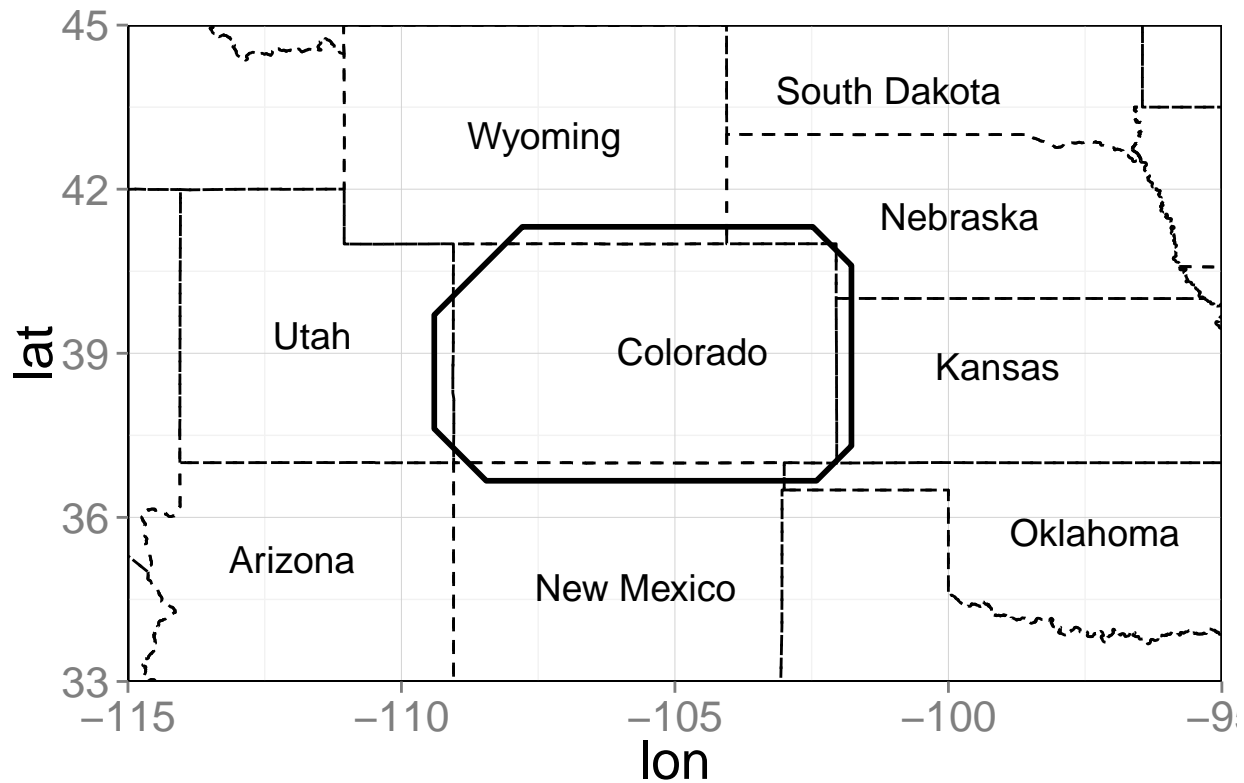


Figure 1: State boundaries in a region of the USA (dashed lines), with the domain of interest enclosed by a bounding polygon (solid line).

The following code plots the triangulation together with the observation locations.

```

### MESH PLOT
meshplot <- function(g,include_obs=1L) {
  p <- plot(Mesh,g=g,plot_dots=F)
  p <- p +
    xlab('lon') + ylab('lat') +
    coord_fixed(xlim=c(-110,-101.5),ylim=c(36.5,41.5)) +
    geom_path(data=States_fort,aes(long,lat,group=group,label=Name),linetype="dashed") +
    geom_path(data=conv_hull,aes(x,y),size=1,,colour="black")
  if(include_obs) p <- p + geom_point(data = temps,aes(lon,lat),size=3)
  p
}
Colorado_Mesh <- meshplot(LinePlotTheme())
if(print_figs)
  ggsave(Colorado_Mesh,

```

```

filename = file.path(img_path,"meshplot.eps"),
width=7,height=4,family="Arial")
if(show_figs)
  print(Colorado_Mesh,family="Arial")

```

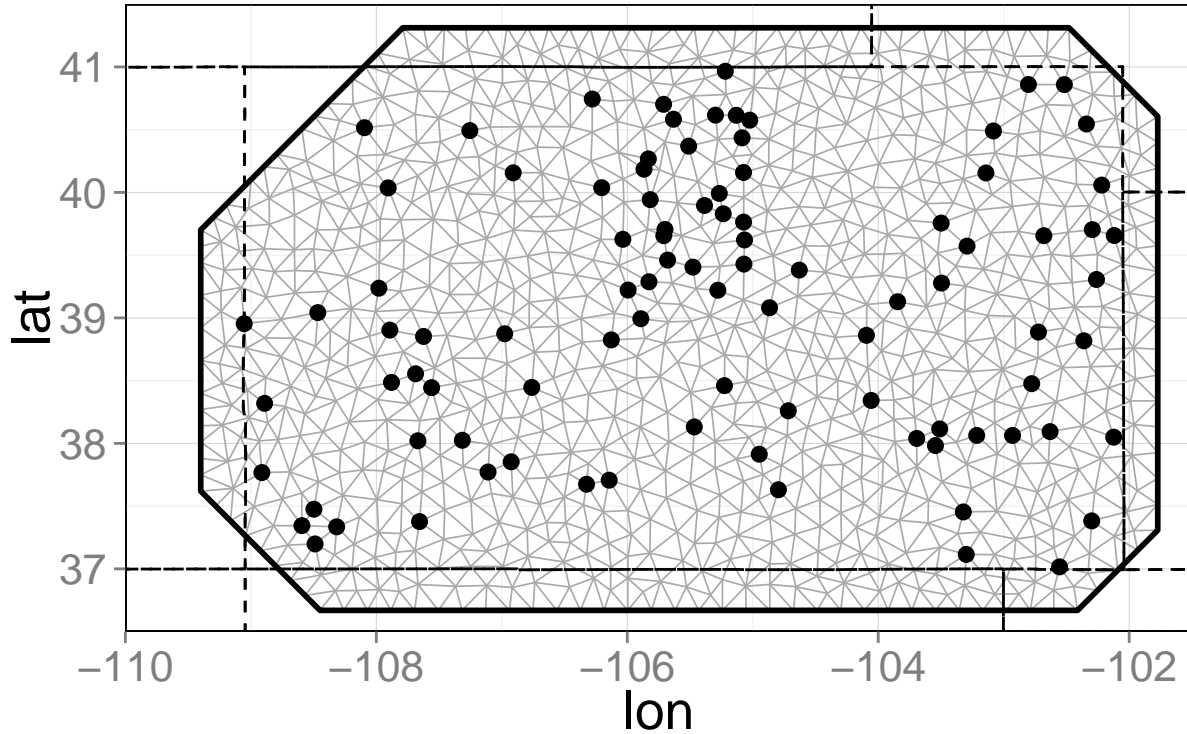


Figure 2: The irregular triangular grid used for discretising D . The observation locations given by D^O consist of the large dots and the discretized spatial domain D^L consists of the mesh nodes.

To combine the figures into a single panel we use

```

library(gridExtra)
g <- arrangeGrob(Stateplot,Colorado_Mesh,ncol=2)
if(print_figs) ggsave(g,
  filename = file.path(img_path,"Fig2.eps"),
  width=14,height=4,family="Arial")

```

Next, we plot the estimated fields together with some major cities in the state of Colorado. For the cities, we need the shapefile `ci08au12.shp`, also available in `extdata`. This can be loaded and subsetted using:

```

shapefile_path <- system.file("extdata", "ci08au12.shp", package = "bicon")
Cities <- maptools::readShapeSpatial(shapefile_path) %>%
  as.data.frame() %>%
  subset(STATE == "COLORADO" &
    NAME %in% c("DENVER","COLORADO SPRINGS","PUEBLO","FORT COLLINS"))

```

Now we do some pre-processing and print the required plots

```

Cities$NAME <- as.character(Cities$NAME)
Cities$n <- sapply(Cities$NAME,nchar)
Cities[which(Cities$NAME == "COLORADO SPRINGS"),]$NAME <- "COL. SPRINGS"
Denver <- subset(Cities,NAME == "DENVER")

mesh_cities <- function(g,pt_size=3,txt_size=6) {
  g + geom_point(data=Cities,aes(LON,LAT),size=pt_size,shape=17,colour="black") +
    geom_text(data=Cities,aes(LON,LAT,label=NAME),hjust=-0.07,vjust=0,size=txt_size)
}

Mesh["Y1"] <- apply(Y_samp,1,mean)[1:n1]
Mesh["Y2"] <- apply(Y_samp,1,mean)[-1:n1]
Mesh["diffY"] <- Mesh["Y2"] - Mesh["Y1"]

Y1plot <- plot_interp(Mesh,"Y1",ds=200,min=-7.9,max=7.9,leg_title="Y1 (degC)",reverse=T) %>%
  meshplot(include_obs=0L)

Y1plot2 <- LinePlotTheme() %>% ## BW version
  meshplot(include_obs=0L) %>%
  mesh_cities(pt_size=6,txt_size=10) +
  geom_point(data=Mesh@pars$vars,aes(x=x,y=y,size=abs(Y1),shape=Y1>0))+
  scale_size_continuous((name="Y2 (deg C)")) +
  scale_shape_manual(values = c(19,1),guide=F) + xlab("") +
  theme(text = element_text(size = 35))

Y2plot <- plot_interp(Mesh,"Y2",ds=200,min=-7.9,max=7.9,leg_title="Y2 (degC)",reverse=T) %>%
  meshplot(include_obs=0L)

Y2plot2 <- LinePlotTheme() %>% ## BW version
  meshplot(include_obs=0L) %>%
  mesh_cities(pt_size=6,txt_size=10) +
  geom_point(data=Mesh@pars$vars,aes(x=x,y=y,size=abs(Y2),shape=Y2>0))+
  scale_size_continuous(name="Y2 (deg C)") +
  scale_shape_manual(values = c(19,1),guide=F) + xlab("") +
  theme(text = element_text(size = 35))

if(print_figs) {
  ggsave(Y1plot %>%
    mesh_cities(pt_size=6,txt_size=10) + xlab(""),
    filename = file.path(img_path,"Y1est.png"),width=13,height=7)
  ggsave(Y2plot %>%
    mesh_cities(pt_size=6,txt_size=10) ,
    filename = file.path(img_path,"Y2est.png"),width=13,height=7)
}

knitr::opts_chunk$set(dev = 'pdf')
if(show_figs) print(Y1plot %>%
  mesh_cities(pt_size=6,txt_size=6)+
  theme(text = element_text(size = 15)) +
  theme(legend.key.height=unit(2,"line")),
  width=13,height=7)

```

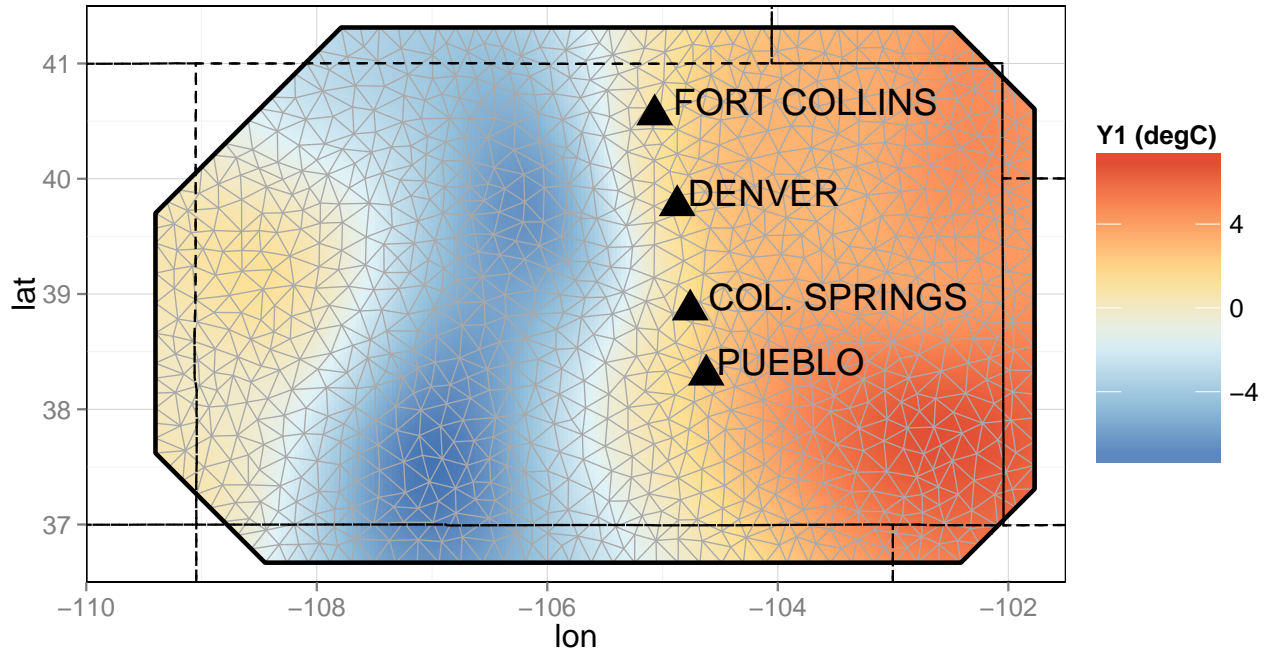



Figure 3: Interpolated map in degrees Celsius (degC) of $E(Y_1 | Z_1, Z_2)$

```
if(show_figs) print(Y2plot %>%
  mesh_cities(pt_size=6,txt_size=6) +
  theme(text = element_text(size = 15)) +
  theme(legend.key.height=unit(2,"line")),
  width=13,height=7)

### KERNEL VECTOR PLOT
if(model==2) {

  ## Kernel plots
  dh = 0.04
  d1_samp_prior <- rnorm(mu_delta1,sd=1/sqrt(prec_delta1),n=length(MCMC_sub))
  d2_samp_prior <- rnorm(mu_delta1,sd=1/sqrt(prec_delta2),n=length(MCMC_sub))
  log_r_samp_prior <- rnorm(mu_log_r,sd=1/sqrt(prec_log_r),n=length(MCMC_sub))
  A_samp_prior <- rnorm(mu_A,sd=1/sqrt(prec_A),n = length(MCMC_sub))

  dir_vector <- subset(Cities,NAME %in% c("DENVER","FORT COLLINS")) %>%
    select(LON,LAT) %>%
    summarise(x = diff(LON),y=diff(LAT))
  abs_dv <- sqrt(sum(dir_vector^2))
  hplot_post <- hplot_prior <- outer(seq(0,3,by=dh),t(dir_vector)[,1] %>%
    data.frame() %>%
    mutate(he = sqrt(x^2 + y^2))

  for(i in MCMC_sub[-1])
    hplot_post[,paste0("MCMC.",i)] <- bisquare_2d(hplot_post$x,
      hplot_post$y,
      delta = c(d1_samp[i],
```

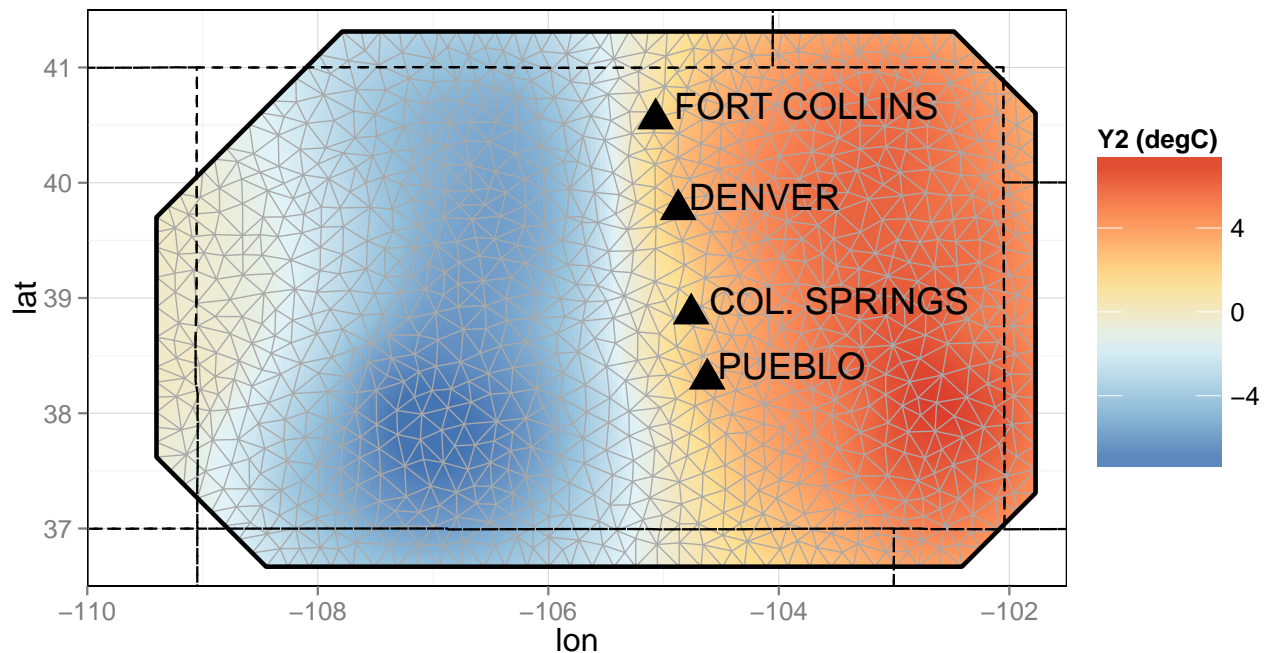



Figure 4: Interpolated map in degrees Celsius (degC) of $E(Y_2 \mid Z_1, Z_2)$

```

                                d2_samp[i]),
                                r = exp(log_r_samp[i]),
                                A = A_samp[i])

for(i in 1:length(MCMC_sub))
  hplot_prior[,paste0("MCMC.",i)] <- bisquare_2d(hplot_prior$x,
                                                  hplot_prior$y,
                                                  delta = c(d1_samp_prior[i],
                                                            d2_samp_prior[i]),
                                                  r = exp(log_r_samp_prior[i]),
                                                  A = A_samp_prior[i])

process_h <- function(h) {
  select(h,-x,-y) %>%
    gather(MCMC,z,-he) %>%
    group_by(he) %>%
    summarise(lq = quantile(z,0.25),
              mq = quantile(z,0.5),
              uq = quantile(z,0.75))
}

hpost <- process_h(hplot_post)
hprior <- process_h(hplot_prior)

plot_h <- function(g,h,col="red",al=0.9) {
  g + geom_ribbon(data=h,aes(x = he, ymin = lq, ymax = uq),
                 fill=col,alpha=al) +
    geom_line(data=h,aes(x=he,y=lq),linetype=2,size=0.4) +
    geom_line(data=h,aes(x=he,y=mq),linetype=1,size=0.4) +

```

```

    geom_line(data=h,aes(x=he,y=uq),linetype=2,size=0.4)
  }
g <- plot_h(LinePlotTheme(),hprior,col="light grey",al=1) %>%
plot_h(hpost,col="dark grey",al=1) +
  ylim(-0.15,0.4) +
  ylab(expression(paste(b[o],"(h",bold(e),"",sep = ""))) +
  xlab("h") +
  coord_fixed(xlim=c(0,2.43),ratio = 5,ylim = c(-0.15,0.4)) +
  geom_line(data= data.frame(x = c(0,0,abs_dv,abs_dv),
                                y=c(-0.15,-0.14,-0.15,-0.14),
                                group=c(1,1,2,2)),
            aes(x,y,group=group),size=4) +
  theme(plot.margin=grid::unit(c(2.5,2.5,0,0),"mm"))
gshow <- g + geom_text(data=data.frame(x=c(0.13,abs_dv+0.13),
                                y=c(-0.125,-0.125),
                                txt=c("DE","FC")),
                      aes(x,y,label=txt),size=6)
g <- g + geom_text(data=data.frame(x=c(0.13,abs_dv+0.13),
                                y=c(-0.125,-0.125),
                                txt=c("DE","FC")),
                      aes(x,y,label=txt),size=20)

if (print_figs) ggsave(g,filename=file.path(img_path,"Denver_FortCollins_vector.png"))
if (show_figs) print(gshow)

g_all <- arrangeGrob(arrangeGrob(Y1plot,Y2plot,ncol=1),g +
                      theme(text = element_text(size = 50)),ncol=2)
if (print_figs) ggsave(g_all,
                      filename = file.path(img_path,"Fig3.eps"),
                      width=28,height=16,family="Arial")
g_all <- arrangeGrob(arrangeGrob(Y1plot2,Y2plot2,ncol=1),g +
                      theme(text = element_text(size = 50)),ncol=2)
if (print_figs) ggsave(g_all,
                      filename = file.path(img_path,"Fig3BW.eps"),
                      width=28,height=16,family="Arial")
}

```

References

- Cressie, N., & Zammit-Mangion, A. (2015). Multivariate spatial covariance models: A conditional approach. *Submitted*.
- Genton, M. G., & Kleiber, W. (2015). Cross-covariance functions for multivariate geostatistics. *Statistical Science*, 30, to appear.
- Spiegelhalter, D. J., Best, N. G., Carlin, B. P., & Van Der Linde, A. (2002). Bayesian measures of model complexity and fit. *Journal of the Royal Statistical Society, Series B*, 64, 583–639.