

PRACTICAL 5



Aim of this practical:

In this first practical we are going to fit spatial modes for Areal, Geostatistical and Point-Process Data.

1 Models for areal data

In this practical we are going to fit an areal model. We will:

- Learn how to fit an areal model in `inlabru`
 - Learn how to add spatial covariates to the model
 - Learn how to do predictions
 - Learn how to simulate from the fitted model
-

Libraries to load:

```
library(dplyr)
library(INLA)
library(ggplot2)
library(patchwork)
library(inlabru)
library(mapview)

# load some libraries to generate nice map plots
library(scico)
```

1 The data

We consider data on respiratory hospitalizations for Greater Glasgow and Clyde in 2007. The data are available from the CARBayesdata R Package:

```
library(CARBayesdata)

data(pollutionhealthdata)
data(GGHB.IZ)
```

The `pollutionhealthdata` contains the spatiotemporal data on respiratory hospitalizations, air pollution concentrations and socio-economic deprivation covariates for the 271 Intermediate Zones (IZ) that make up the Greater Glasgow and Clyde health board in Scotland. Data are provided by the [Scottish Government](#) and the available variables are:

- `IZ`: unique identifier for each IZ.
- `year`: the year when the measurements were taken

- observed: observed numbers of hospitalizations due to respiratory disease.
- expected: expected numbers of hospitalizations due to respiratory disease computed using indirect standardisation from Scotland-wide respiratory hospitalization rates.
- pm10: Average particulate matter (less than 10 microns) concentrations.
- jsa: The percentage of working age people who are in receipt of Job Seekers Allowance
- price: Average property price (divided by 100,000).

The GGHB.IZ data is a Simple Features (sf) object containing the spatial polygon information for the set of 271 Intermediate Zones (IZ), that make up of the Greater Glasgow and Clyde health board in Scotland (Figure 1).

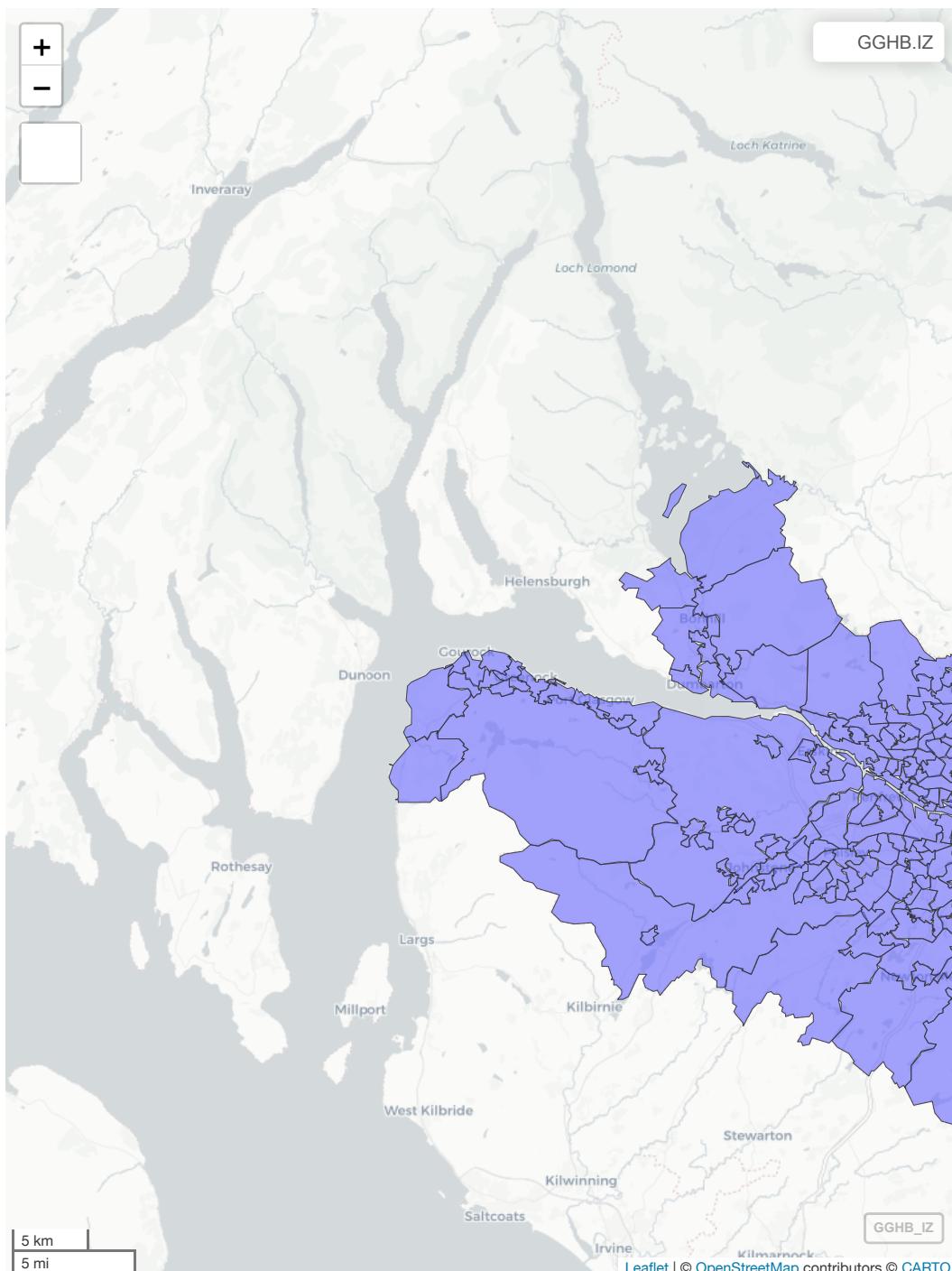
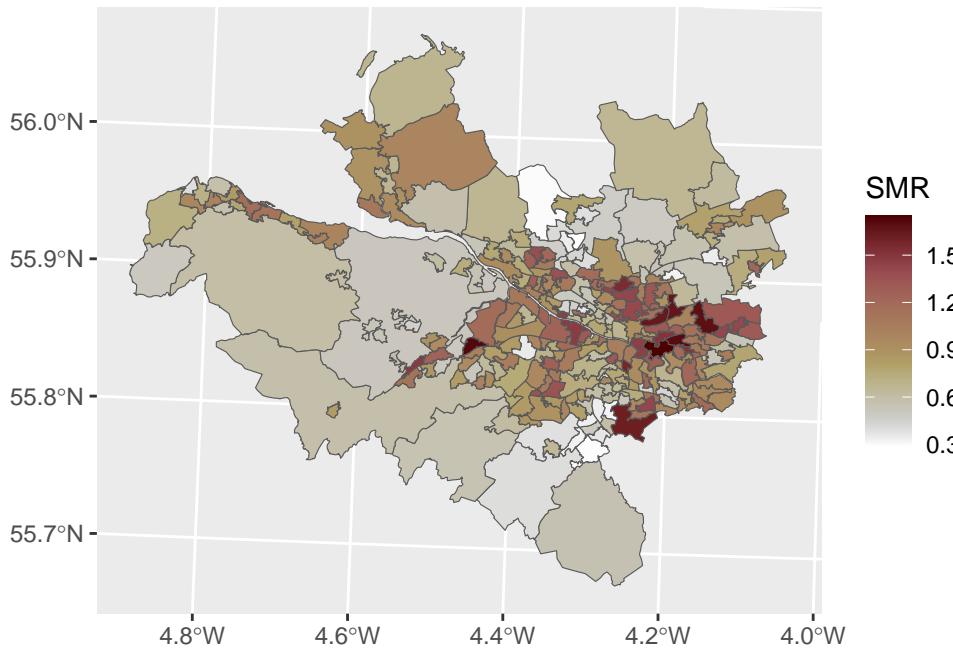


Figure 1: Greater Glasgow and Clyde health board represented by 271 Intermediate Zones

We first merge the two dataset and select only one year of data, compute the SME and plot the observed

```
resp_cases <- merge(GGHB.IZ %>%
  mutate(space = 1:dim(GGHB.IZ)[1]),
  pollutionhealthdata, by = "IZ") %>%
filter(year == 2007) %>%
mutate(SMR = observed/expected)

ggplot() + geom_sf(data = resp_cases, aes(fill = SMR)) + scale_fill_scico(direction = -1)
```



Then we compute the adjacency matrix using the functions `poly2nb()` and `nb2mat()` in the `spdep` library. We then convert the adjacency matrix into the precision matrix \mathbf{Q} of the CAR model. Remember this matrix has, on the diagonal the number of e

```
library(spdep)

W.nb <- poly2nb(GGHB.IZ,queen = TRUE)
R <- nb2mat(W.nb, style = "B", zero.policy = TRUE)

diag = apply(R,1,sum)
Q = -R
diag(Q) = diag
```

1 The model

We fit a first model to the data where we consider a Poisson model for the observed cases.

Stage 1 Model for the response

$$y_i | \eta_i \sim \text{Poisson}(E_i \lambda_i)$$

where E_i are the expected cases for area i .

Stage 2 Latent field model

$$\eta_i = \log(\lambda_i) = \beta_0 + \omega_i + z_i$$

where

- β_0 is a common intercept
- $= (\omega_1, \dots, \omega_k)$ is a conditional Autoregressive model (CAR) with precision matrix $\tau_1 Q$
- $\mathbf{z} = (z_1, \dots, z_k)$ is an unstructured random effect with precision τ_2

Stage 3 Hyperparameters

The hyperparameters of the model are τ_1 and τ_2

NOTE In this case the linear predictor η consists of three components!!

Task

Fit the above model in using `inlabru` by completing the following code:

```
cmp = ~ Intercept(1) + space(...) + iid(...)

formula = ...

lik = bru_obs(formula = formula,
              family = ...,
              E = ...,
              data = ...)

fit = bru(cmp, lik)
```

Answer

```
cmp = ~ Intercept(1) + space(space, model = "besag", graph = Q) + iid(space, model = "iid")

formula = observed ~ Intercept + space + iid

lik = bru_obs(formula = formula,
              family = "poisson",
              E = expected,
              data = resp_cases)

fit = bru(cmp, lik)
```

After fitting the model we want to extract results.

Question

1. What is the estimated value for β_0 ? _____
2. Look at the estimated values of the hyperparameters using `fit$summary.hyperpar`, which of the two spatial components (structured or unstructured) explains more of the variability in the counts?
 - (A) structured

- (B) unstructured

We now look at the predictions over space.

Task

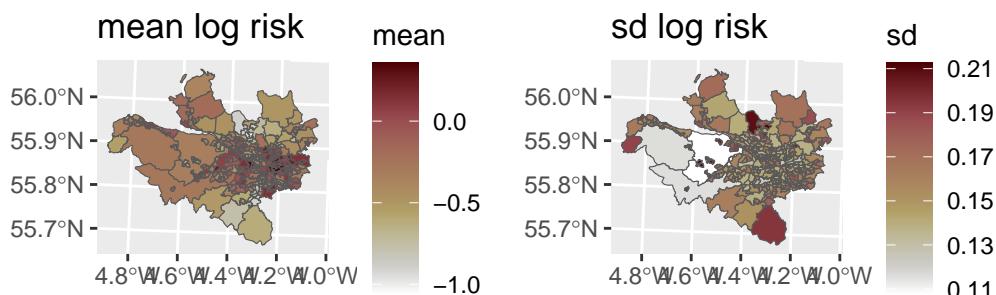
Complete the code below to produce prediction of the linear predictor η_i and of the risk λ_i and of the expected cases $E_i \exp(\lambda_i)$ over the whole space of interest. Then plot the mean and sd of the resulting surfaces.

```
pred = predict(fit, resp_cases, ~data.frame(log_risk = ...,
                                             risk = exp(...),
                                             cases = ...),
               n.samples = 1000)
```

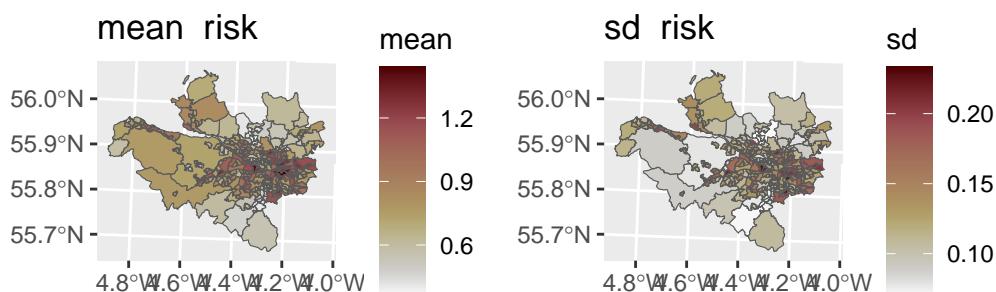
Show Answer

```
# produce predictions
pred = predict(fit, resp_cases, ~data.frame(log_risk = Intercept + space,
                                             risk = exp(Intercept + space),
                                             cases = expected * exp(Intercept + space),
                                             ),
               n.samples = 1000)
# plot the predictions

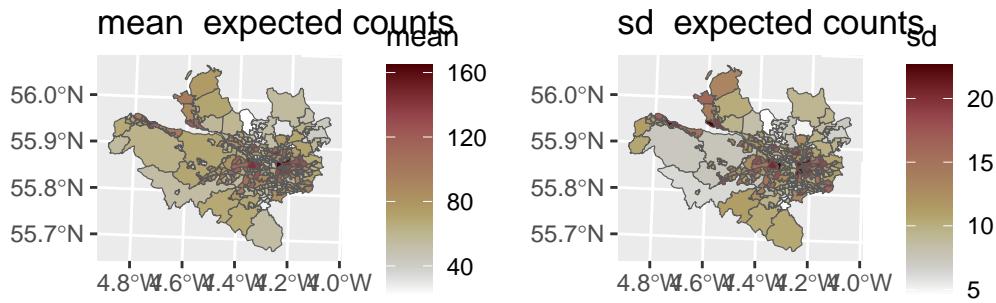
p1 = ggplot() + geom_sf(data = pred$log_risk, aes(fill = mean)) + scale_fill_scico(direction = -1)
p2 = ggplot() + geom_sf(data = pred$log_risk, aes(fill = sd)) + scale_fill_scico(direction = -1)
p1 + p2
```



```
p1 = ggplot() + geom_sf(data = pred$risk, aes(fill = mean)) + scale_fill_scico(direction = -1)
p2 = ggplot() + geom_sf(data = pred$risk, aes(fill = sd)) + scale_fill_scico(direction = -1)
p1 + p2
```

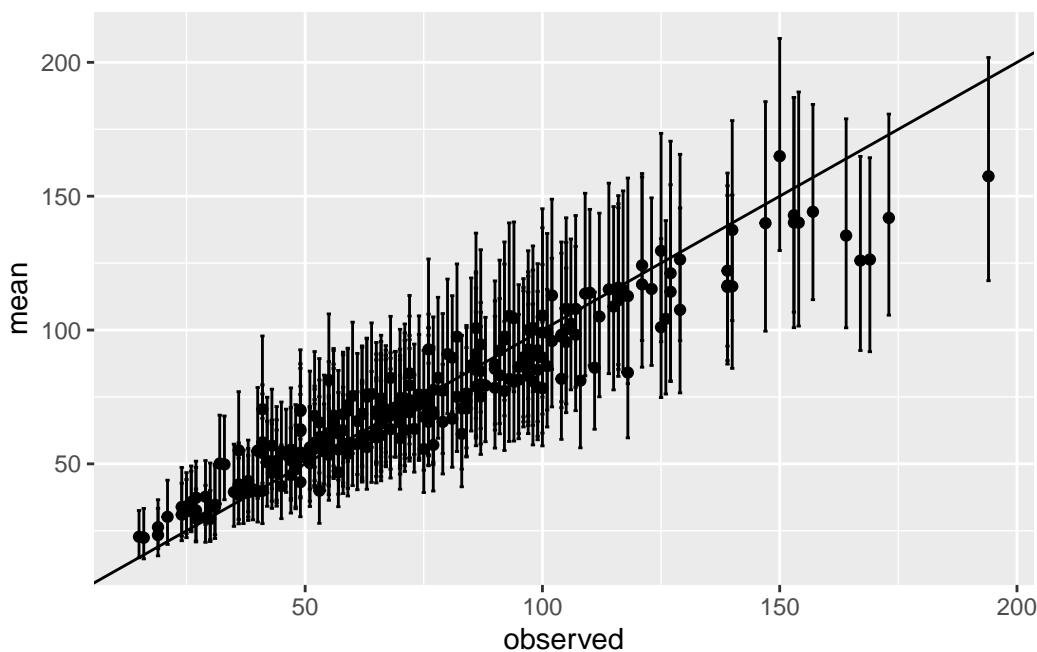


```
p1 = ggplot() + geom_sf(data = pred$cases, aes(fill = mean)) + scale_fill_scico(direction = 1)
p2 = ggplot() + geom_sf(data = pred$cases, aes(fill = sd)) + scale_fill_scico(direction = -1)
p1 + p2
```



Finally we want to compare our observations y_i with the predicted means of the Poisson distribution $E_i \exp(\lambda_i)$

```
pred$cases %>% ggplot() + geom_point(aes(observed, mean)) +
  geom_errorbar(aes(observed, ymin = q0.025, ymax = q0.975)) +
  geom_abline(intercept = 0, slope = 1)
```



Note: Here we are predicting the *mean* of counts, not the counts!!! Predicting counts is the theme of the next task!

1 Getting prediction densities

Posterior predictive distributions, that is $\pi(y_i^{\text{new}} | \mathbf{y})$ are of interest in many applied problems. The `bru()` function does not return predictive densities. In the previous step we have computed predictions for the expected counts $\pi(E_i \lambda_i | \mathbf{y})$. The predictive distribution is then:

$$\pi(y_i^{\text{new}} | \mathbf{y}) = \int \pi(y_i | E_i \lambda_i) \pi(E_i \lambda_i | \mathbf{y}) dE_i \lambda_i$$

where, in our case, $\pi(y_i|E_i\lambda_i)$ is Poisson with mean $E_i\lambda_i$. We can achieve this using the following algorithm:

1. Simulate n replicates of $g^k = E_i\lambda_i$ for $k = 1, \dots, n$ using the function `generate()` which takes the same input as `predict()`
2. For each of the k replicates simulate a new value y_i^{new} using the function `rpois()`
3. Summarise the n samples of y_i^{new} using, for example the mean and the 0.025 and 0.975 quantiles.

Here is the code:

```
# simulate 1000 realizations of E_i\lambda_i
expected_counts = generate(fit, resp_cases,
                            ~ expected * exp(Intercept + space),
                            n.samples = 1000)

# simulate poisson data
aa = rpois(271*1000, lambda = as.vector(expected_counts))
sim_counts = matrix(aa, 271, 1000)

# summarise the samples with posterior means and quantiles
pred_counts = data.frame(observed = resp_cases$observed,
                          m = apply(sim_counts, 1, mean),
                          q1 = apply(sim_counts, 1, quantile, 0.025),
                          q2 = apply(sim_counts, 1, quantile, 0.975),
                          vv = apply(sim_counts, 1, var)
                          )
```

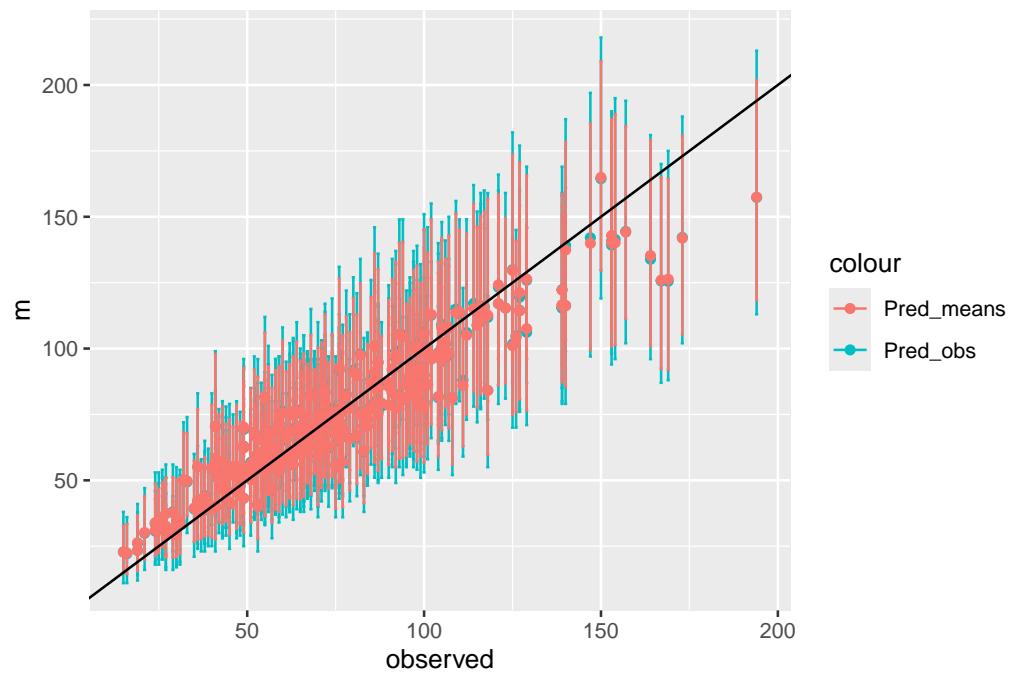
Task

Plot the observations against the predicted new counts and the predicted expected counts. Include the uncertainty and compare the two.

[Click here to see the solution](#)

```
ggplot() +
  geom_point(data = pred_counts, aes(observed, m, color = "Pred_obs")) +
  geom_errorbar(data = pred_counts, aes(observed, ymin = q1, ymax = q2, color = "Pred_obs"))
  geom_point(data = pred$cases, aes(observed, mean, color = "Pred_means")) +
  geom_errorbar(data = pred$cases, aes(observed, ymin = q0.025, ymax = q0.975, color = "Pred_means"))

  geom_abline(intercept = 0, slope = 1)
```



1 Adding a spatial covariate

Finally, we want to add a covariate to the model. We are going to check if the PM10 levels influence the numbers of hospitalizations.

Task

Add the effect of PM10 in the previous model. First as a linear effect and then as a smooth effect (RW2). Check the results.

Take hint

To use the RW2 model you first need to group the values of the PM10 using the `inla.group()` function.

[Click here to see the solution](#)

```

## Linear Effect
cmp = ~ Intercept(1) + space(space, model = "besag", graph = Q) + iid(space, model = "iid")
  cov(pm10, model = "linear")

formula = observed ~ Intercept + space + iid + cov

lik = bru_obs(formula = formula,
              family = "poisson",
              E = expected,
              data = resp_cases)

fit_lin = bru(cmp, lik)
# effect of the covaraite
# fit_lin$summary.fixed

## Linear Effect
resp_cases$pm10_group= inla.group(resp_cases$pm10)
cmp = ~ Intercept(1) + space(space, model = "besag", graph = Q) + iid(space, model = "iid")
  cov(pm10_group, model = "rw2")

formula = observed ~ Intercept + space + iid + cov

lik = bru_obs(formula = formula,
              family = "poisson",
              E = expected,
              data = resp_cases)

fit_smooth = bru(cmp, lik)

#check the smooth effect of the covariate
#fit_smooth$summary.random$cov %>% ggplot() + geom_line(aes(ID,mean)) +
#  geom_ribbon(aes(ID, ymin = `0.025quant`, ymax = `0.975quant`), alpha = 0.5)

```

2 Geostatistics

In this practical we are going to fit a geostatistical model. We will:

- Learn how to fit a geostatistical model in `inlabru`
- Learn how to build a mesh for the SPDE representation
- Learn how to add spatial covariates to the model
- Learn how to do predictions
- Learn how to simulate from the fitted model

Libraries to load:

```

library(dplyr)
library(INLA)
library(inlabru)
library(sf)
library(terra)

# load some libraries to generate nice map plots
library(scico)
library(ggplot2)
library(patchwork)
library(mapview)
library(tidyterra)

```

2 The data

In this practical, we will explore data on the Pacific Cod (*Gadus macrocephalus*) from a trawl survey in Queen Charlotte Sound. The pcod dataset is available from the sdmTMB package and contains the presence/absence records of the Pacific Cod during each surveys along with the biomass density of Pacific cod in the area swept (kg/Km²). The qcs_grid data contain the depth values stored as 2 × 2 km grid for Queen Charlotte Sound.

The dataset contains presence/absence data from 2003 to 2017. In this practical we only consider year 2003.

We first load the dataset and select the year of interest

```

library(sdmTMB)

pcod_df = sdmTMB::pcod %>% filter(year==2003)
qcs_grid = sdmTMB::qcs_grid

```

Then, we create an sf object and assign the rough coordinate reference to it:

```

pcod_sf = st_as_sf(pcod_df, coords = c("lon","lat"), crs = 4326)
pcod_sf = st_transform(pcod_sf,
  crs = "+proj=utm +zone=9 +datum=WGS84 +no_defs +type=crs +units=km" )

```

We convert the covariate into a raster and assign the same coordinate reference:

```

depth_r <- rast(qcs_grid, type = "xyz")
crs(depth_r) <- crs(pcod_sf)

```

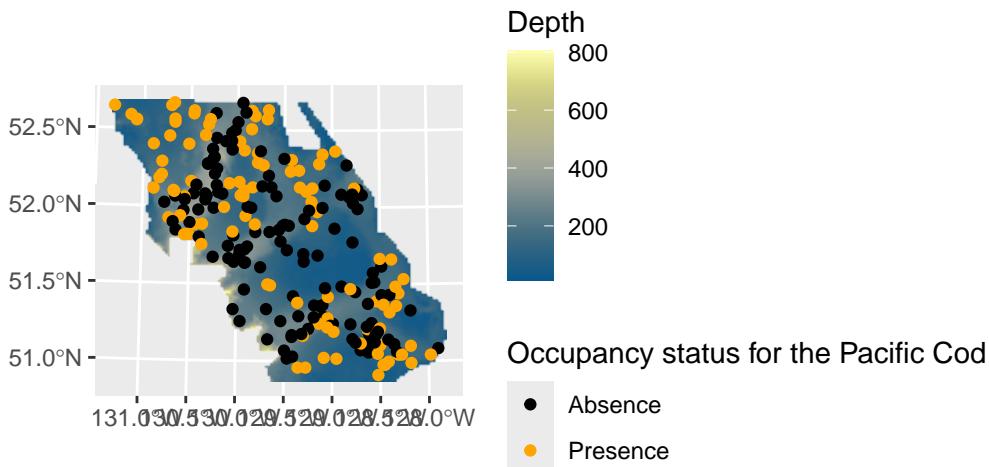
Finally we can plot our dataset. Note that to plot the raster we need to upload also the tidyterra library.

```

ggplot()+
  geom_spatraster(data=depth_r$depth)+
  geom_sf(data=pcod_sf,aes(color=factor(present)))+
  scale_color_manual(name="Occupancy status for the Pacific Cod",
                     values = c("black","orange"),
                     labels= c("Absence","Presence"))+

```

```
scale_fill_scico(name = "Depth",
                  palette = "nuuk",
                  na.value = "transparent" ) + xlab("") + ylab("")
```



2 The model

We first fit a simple model where we consider the observation as Bernoulli and where the linear predictor contains only one intercept and the GR field defined through the SPDE approach. The model is defined as:

Stage 1 Model for the response

$$y(s)|\eta(s) \sim \text{Binom}(1, p(s))$$

Stage 2 Latent field model

$$\eta(s) = \text{logit}(p(s)) = \beta_0 + \omega(s)$$

with

$$\omega(s) \sim \text{GF with range } \rho \text{ and marginal variance } \sigma^2$$

Stage 3 Hyperparameters

The hyperparameters of the model are ρ and σ

NOTE In this case the linear predictor η consists of two components!!

2.2.1 The workflow

When fitting a geostatistical model we need to fulfill the following tasks:

1. Build the mesh
2. Define the SPDE representation of the spatial GF. This includes defining the priors for the range and sd of the spatial GF
3. Define the *components* of the linear predictor. This includes the spatial GF and all eventual covariates

4. Define the observation model using the `bru_obs()` function

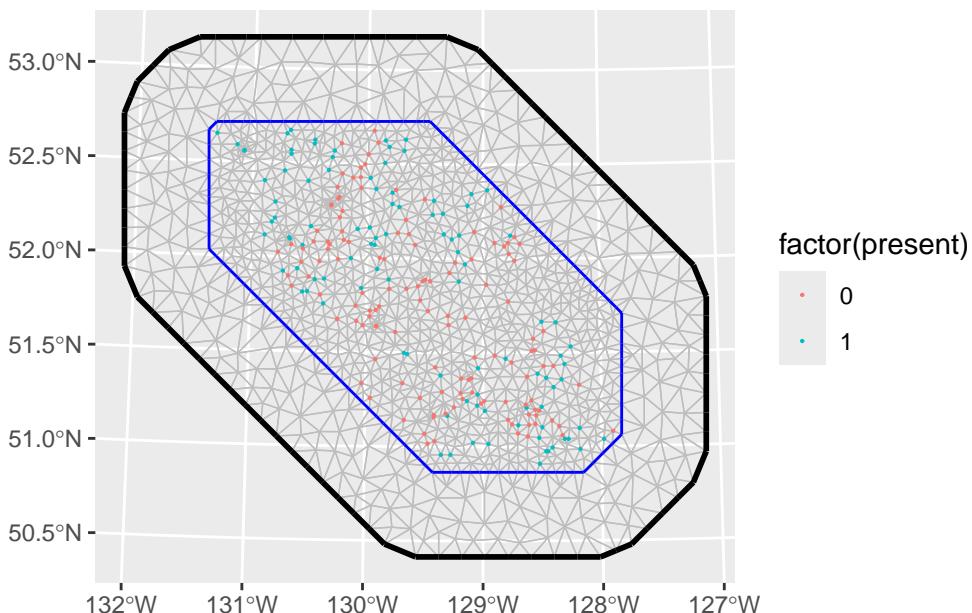
5. Run the model using the `bru()` function

2.2.2 1. Building the mesh

The first task, when dealing with geostatistical models in `inlabru` is to build the mesh that covers the area of interest. For this purpose we use the function `fm_mesh_2d`.

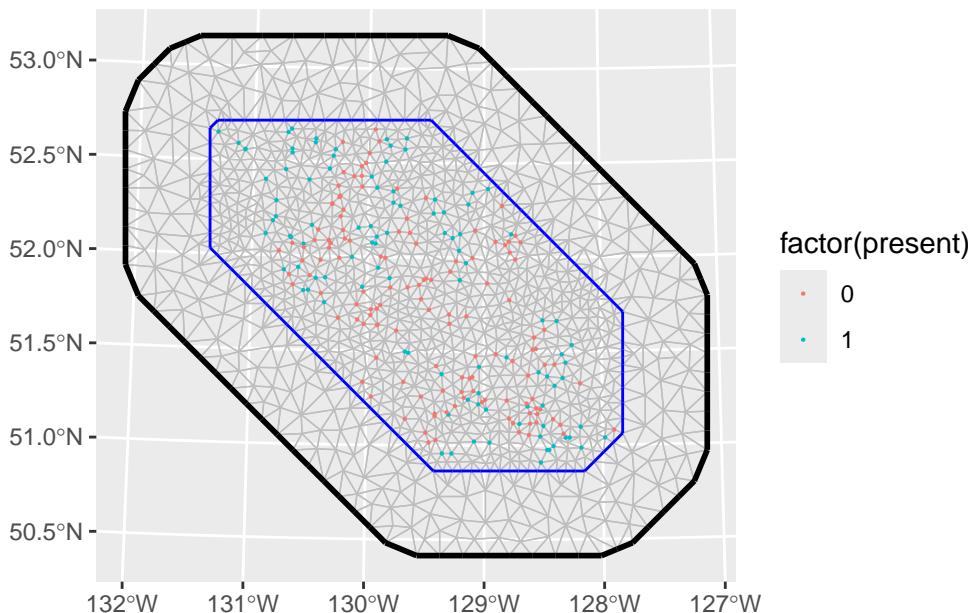
One way to build the mesh is to start from the locations where we have observations, these are contained in the dataset `pcod_sf`.

```
mesh = fm_mesh_2d(loc = pcod_sf,           # Build the mesh
                  max.edge = c(10,20),    # The largest allowed triangle edge length.
                  offset = c(5,50))      # The automatic extension distance
ggplot() + gg(mesh) + geom_sf(data= pcod_sf, aes(color = factor(present)), size = 0.1) + xla
```



As you can see from the plot above, some of the locations are very close to each other, this causes some very small triangles. This can be avoided using the option `cutoff` = which collapses the locations that are closer than a cutoff (those points are collapsed in the mesh construction but, of course, not when it come to estimation.)

```
mesh = fm_mesh_2d(loc = pcod_sf,           # Build the mesh
                  cutoff = 2,
                  max.edge = c(10,20),    # The largest allowed triangle edge length.
                  offset = c(5,50))      # The automatic extension distance
ggplot() + gg(mesh) + geom_sf(data= pcod_sf, aes(color = factor(present)), size = 0.1) + xla
```



Key parameters in mesh construction include: `max.edge` for maximum triangle edge lengths, `offset` for inner and outer extensions (to prevent edge effects), and `cutoff` to avoid overly small triangles in clustered areas.

Note

General guidelines for creating the mesh

1. Create triangulation meshes with `fm_mesh_2d()`
2. Move undesired boundary effects away from the domain of interest by extending to a smooth external boundary
3. Use a coarser resolution in the extension to reduce computational cost (`max.edge=c(inner, outer)`)
4. Use a fine resolution (subject to available computational resources) for the domain of interest (inner correlation range) and filter out small input point clusters ($0 < \text{cutoff} < \text{inner}$)
5. Coastlines and similar can be added to the domain specification in `fm_mesh_2d()` through the `boundary` argument.

Task

Look at the documentation for the `fm_mesh_2d` function typing

```
?fm_mesh_2d
```

play around with the different options and create different meshes.

The *rule of thumb* is that your mesh should be:

- fine enough to well represent the spatial variability of your process, but not too fine in order to avoid computation burden
- the triangles should be regular, avoid long and thin triangles.
- The mesh should contain a buffer around your area of interest (this is what is defined in the `offset` option) in order to avoid boundary artefact in the estimated variance.

2.2.3 2. Define the SPDE representation of the spatial GF

To define the SPDE representation of the spatial GF we use the function `inla.spde2.pcmatern`. This takes as input the mesh we have defined and the PC-priors definition for ρ and σ (the range and the marginal standard deviation of the field).

PC priors Gaussian Random field are defined in (Fuglstad et al. 2018). From a practical perspective for the range ρ you need to define two paramters ρ_0 and p_ρ such that you believe it is reasonable that

$$P(\rho < \rho_0) = p_\rho$$

while for the margianal variance σ you need to define two parameters σ_0 and p_σ such that you believe it is reasonable that

$$P(\sigma < \sigma_0) = p_\sigma$$

You can use the following function to compute and plot the prior distributions for the range and sd of the Matern field.

```

dens_prior_range = function(rho_0, p_alpha)
{
  # compute the density of the PC prior for the
  # range rho of the Matern field
  # rho_0 and p_alpha are defined such that
  # P(rho<rho_0) = p_alpha
  rho = seq(0, rho_0*10, length.out =100)
  alpha1_tilde = -log(p_alpha) * rho_0
  dens_rho = alpha1_tilde / rho^2 * exp(-alpha1_tilde / rho)
  return(data.frame(x = rho, y = dens_rho))
}

dens_prior_sd = function(sigma_0, p_sigma)
{
  # compute the density of the PC prior for the
  # sd sigma of the Matern field
  # sigma_0 and p_sigma are defined such that
  # P(sigma>sigma_0) = p_sigma
  sigma = seq(0, sigma_0*10, length.out =100)
  alpha2_tilde = -log(p_sigma)/sigma_0
  dens_sigma = alpha2_tilde* exp(-alpha2_tilde * sigma)
  return(data.frame(x = sigma, y = dens_sigma))
}

```

Here are some alternatives for defining priors for our model

```

spde_model1 = inla.spde2.pcmatern(mesh,
                                     prior.sigma = c(.1, 0.5),
                                     prior.range = c(30, 0.5))
spde_model2 = inla.spde2.pcmatern(mesh,
                                     prior.sigma = c(10, 0.5),
                                     prior.range = c(1000, 0.5))
spde_model3 = inla.spde2.pcmatern(mesh,

```

```
prior.sigma = c(1, 0.5),
prior.range = c(100, 0.5))
```

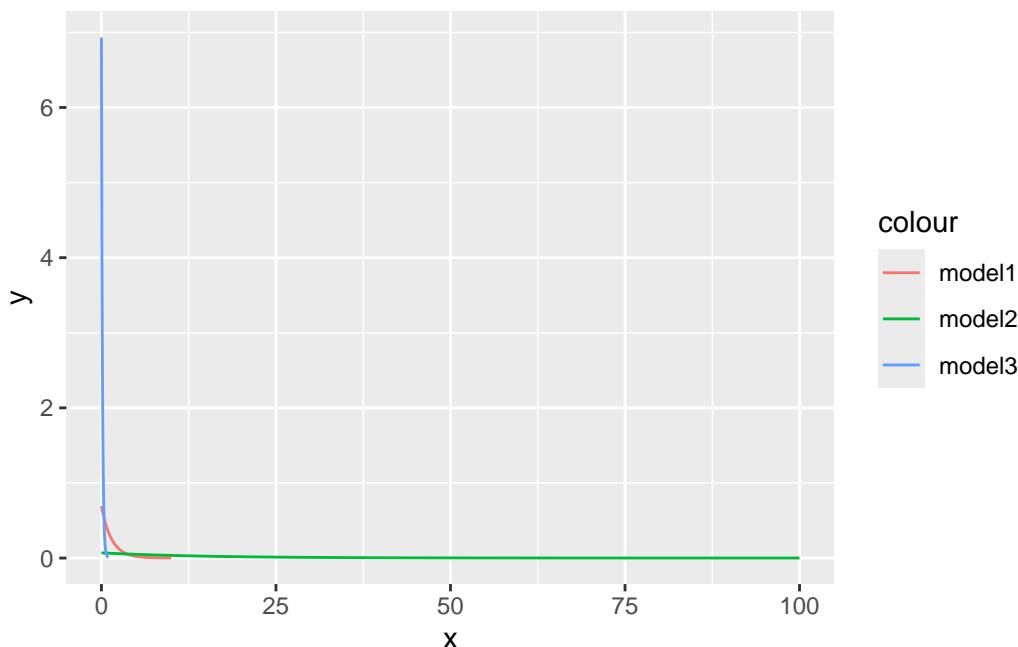
And here we plot the different priors for the range:

```
ggplot() +
  geom_line(data = dens_prior_range(30,.5), aes(x,y, color = "model1")) +
  geom_line(data = dens_prior_range(1000,.5), aes(x,y, color = "model2")) +
  geom_line(data = dens_prior_range(100,.5), aes(x,y, color = "model3"))
```



and for the sd:

```
ggplot() +
  geom_line(data = dens_prior_sd(1,.5), aes(x,y, color = "model1")) +
  geom_line(data = dens_prior_sd(10,.5), aes(x,y, color = "model2")) +
  geom_line(data = dens_prior_sd(.1,.5), aes(x,y, color = "model3"))
```



Question

Consider the `pcod_sf`, the spatial extension and type of the data...is some of the previous choices more reasonable than other?

- (A) `spde_model1`
- (B) `spde_model2`
- (C) `spde_model3`

NOTE Remember that a prior should be reasonable..but the model should not totally depend on it.

2.2.4 3. Define the components of the linear predictor

We have now defined a mesh and a SPDE representation of the spatial GF. We now need to define the model components:

```
cmp = ~ Intercept(1) + space(geometry, model = spde_model3)
```

NOTE since the dataframe we use (`pcod_sf`) is an `sf` object the input in the `space()` component is the geometry of the dataset.

2.2.5 4. Define the observation model

Our data are Bernoulli distributed so we can define the observation model as:

```
formula = present ~ Intercept + space

lik = bru_obs(formula = formula,
              data = pcod_sf,
              family = "binomial")
```

2.2.6 5. Run the model

Finally we are ready to run the model

```
fit1 = bru(cmp,lik)
```

2 Extract results

2.3.1 Hyperparameters

Task

Plot the posterior densities for the range ρ and the standard deviation σ along with the prior for both parameters.

Take hint

Posterior marginals for the hyperparameters can be extracted from the fitted model as:

[Click here to see the solution](#)

```
fit1$marginals.hyperpar$name of the parameter'
```

[Click here to see the solution](#)

```
# Extract marginal for the range

ggplot() +
  geom_line(data = fit1$marginals.hyperpar`Range for space`,
            aes(x,y, color = "Posterior")) +
  geom_line(data = dens_prior_range(100,.5),
            aes(x,y, color = "Prior"))

ggplot() +
  geom_line(data = fit1$marginals.hyperpar`Stdev for space`,
            aes(x,y, color = "Posterior")) +
  geom_line(data = dens_prior_sd(1,.5), aes(x,y, color = "Prior"))
```

2 Spatial prediction

We now want to extract the estimated posterior mean and sd of spatial GF. To do this we first need to define a grid of points where we want to predict. We do this using the function `fm_pixels()` which creates a regular grid of points covering the mesh

```
pxl = fm_pixels(mesh)
```

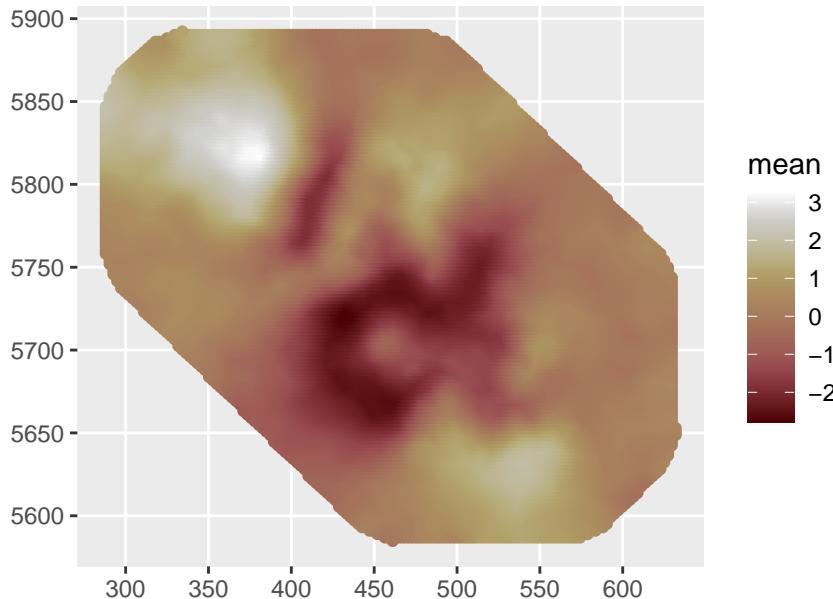
then compute the prediction for both the spatial GF and the linear predictor (spatial GF + intercept)

```
preds = predict(fit1, ppx, ~data.frame(spatial = space,
                                         total = Intercept + space))
```

Finally, we can plot the maps

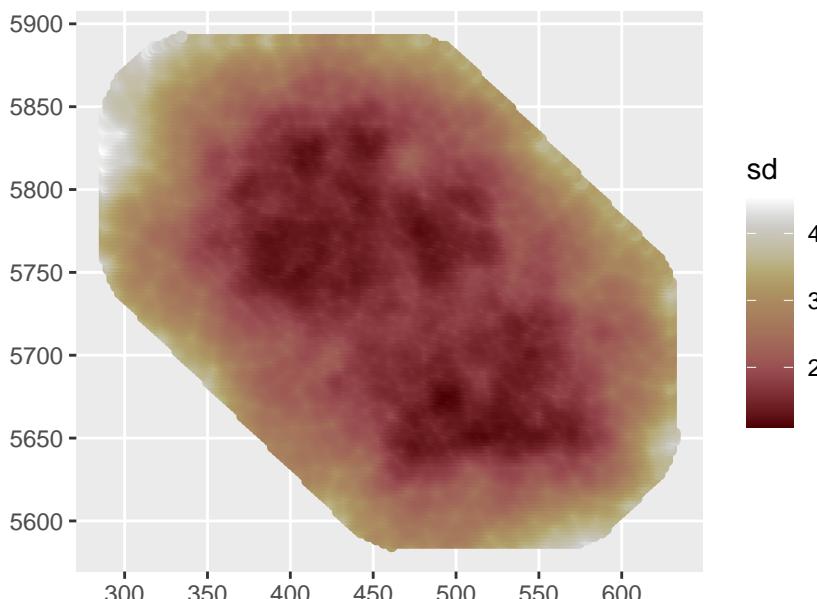
```
ggplot() + geom_sf(data = preds$spatial,aes(color = mean)) + scale_color_scico() + ggtitle("Posterior mean")
```

Posterior mean



```
ggplot() + geom_sf(data = preds$spatial,aes(color = sd)) + scale_color_scico() + ggtitle("Posterior sd")
```

Posterior sd



Note The posterior sd is lowest at the observation points. Note how the posterior sd is inflated around the border, this is the “border effect” due to the SPDE representation.

Instead of predicting over a grid covering the whole mesh, we can limit our predictions to the points where the covariate is defined. We can do this by defining a sf object using coordinates in the object `depth_r`.

```
pxl1 = data.frame(crds(depth_r),
                  as.data.frame(depth_r$depth)) %>%
  filter(!is.na(depth)) %>%
  st_as_sf(coords = c("x","y"))
```

Task

Produce prediction over pxl1 unsing the same techniques as before. Plot your results.

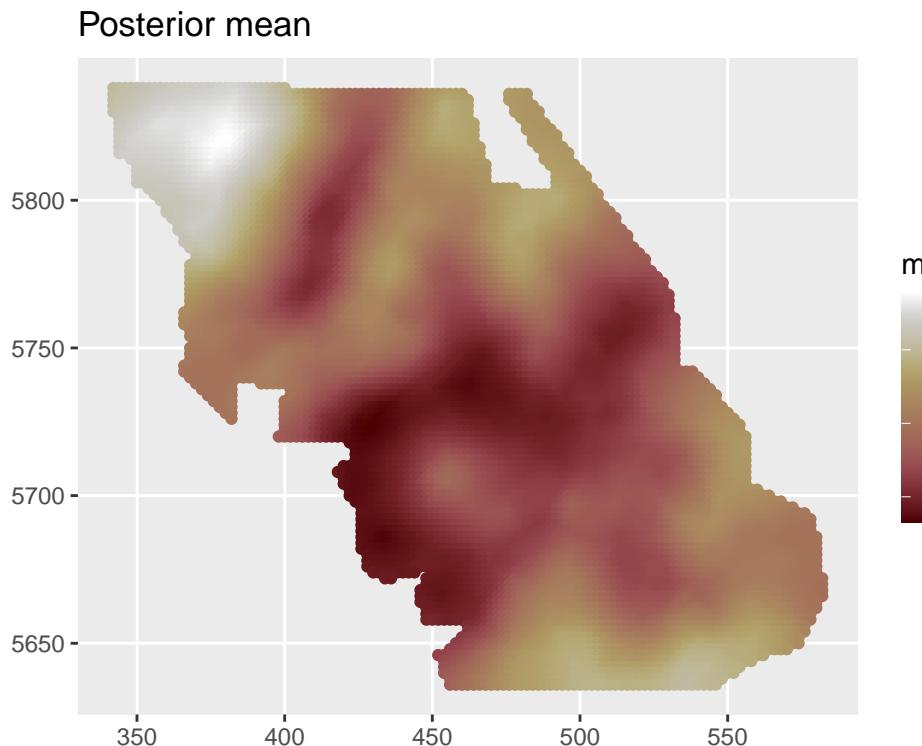
[Take hint](#)

Add hint details here...

[Click here to see the solution](#)

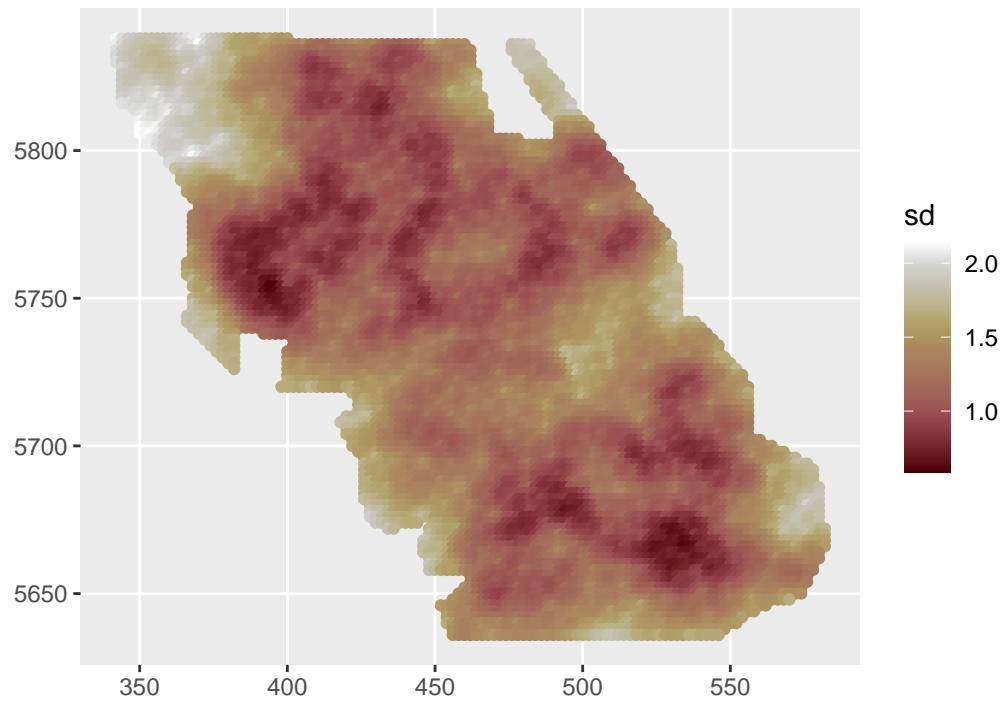
```
pred_pxl1 = predict(fit1, pxl1, ~data.frame(spatial = space,
                                              total = Intercept + space))
```

```
ggplot() + geom_sf(data = pred_pxl1$total,aes(color = mean)) + scale_color_scico() + ggtitle("Posterior mean")
```



```
ggplot() + geom_sf(data = pred_pxl1$total,aes(color = sd)) + scale_color_scico() + ggtitle("Posterior standard deviation")
```

Posterior sd



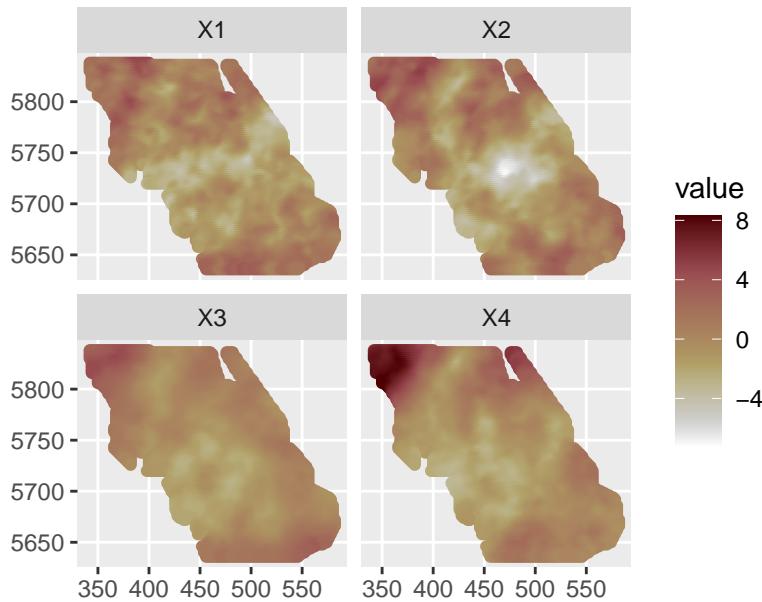
Instead of computing the posterior mean and standard deviations of the estimated surface, one can also *simulate* possible realizations of such surface. This will give the user a better idea of the type of realized surfaces one can expect. We can do this using the function `generate()`.

```
# we simulate 4 samples from the
gens = generate(fit1, pxl1, ~ (Intercept + space),
                n.samples = 4)

pp = cbind(pxl1, gens)

pp %>% select(-depth) %>%
  pivot_longer(-geometry) %>%
  ggplot() +
  geom_sf(aes(color = value)) +
  facet_wrap(.~name) +
  scale_color_scico(direction = -1) +
  ggtitle("Sample from the fitted model")
```

Sample from the fitted model



2 An alternative model

We now want to check if the depth covariate has an influence on the probability of presence. We do this in two different models

1. **Model 1** The depth enters the model in a linear way. The linear predictor is then defined as:

$$\eta(s) = \text{logit}(p(s)) = \beta_0 + \omega(s) + \beta_1 \text{depth}(s)$$

2. **Model 1** The depth enters the model in a non linear way. The linear predictor is then defined as:

$$\eta(s) = \text{logit}(p(s)) = \beta_0 + \omega(s) + f(\text{depth}(s))$$

where $f(\cdot)$ is a smooth function. We will use a RW2 model for this.

Task

Fit model 1. Define components, observation model and use the `bru()` function to estimate the parameters.

Note Use the scaled version of the covariate stored in `depth_r$depth_scaled`. What is the liner effect of depth on the logit probability?

Take hint

Add hint details here...

[Click here to see the solution](#)

```

cmp = ~ Intercept(1) + space(geometry, model = spde_model3) +
      covariate(depth_r$depth_scaled, model = "linear")

formula = present ~ Intercept + space + covariate

lik = bru_obs(formula = formula,
              data = pcod_sf,
              family = "binomial")

fit2 = bru(cmp, lik)

```

We now want to fit **Model 2** where we allow the effect of depth to be non-linear. To use the RW2 model we need to *group* the values of depth into distinct classes. To do this we use the function `inla.group()` which, by default, creates 20 groups. Then we can fit the model as usual

```

# create the grouped variable
depth_r$depth_group = inla.group(values(depth_r$depth_scaled))

# run the model
cmp = ~ Intercept(1) + space(geometry, model = spde_model3) +
      covariate(depth_r$depth_group, model = "rw2")

formula = present ~ Intercept + space + covariate

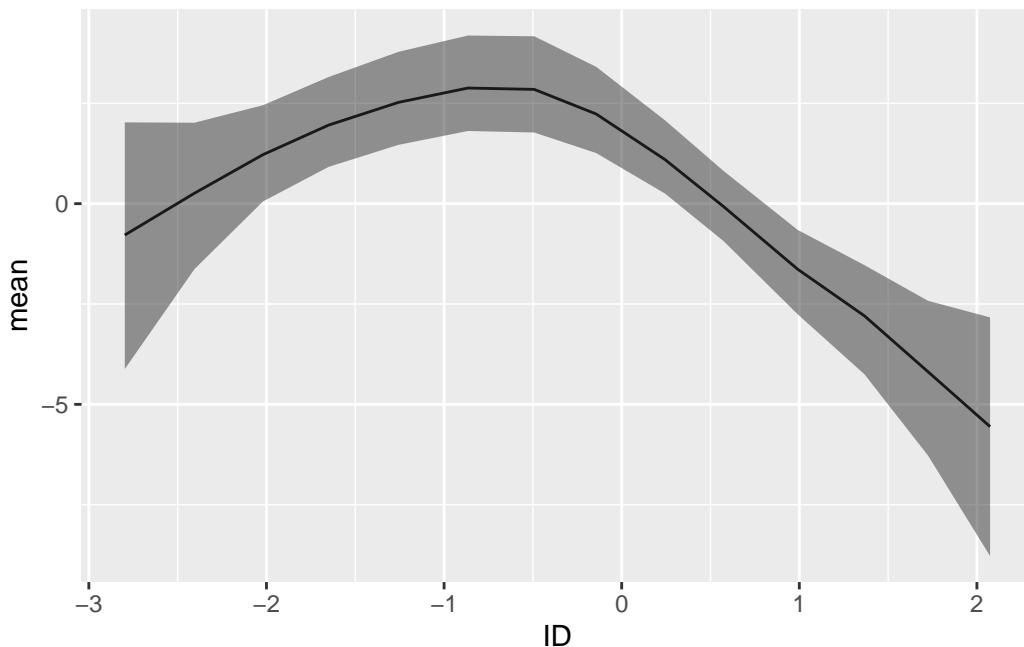
lik = bru_obs(formula = formula,
              data = pcod_sf,
              family = "binomial")

fit3 = bru(cmp, lik)

# plot the estimated effect of depth

fit3$summary.random$covariate %>%
  ggplot() + geom_line(aes(ID, mean)) +
  geom_ribbon(aes(ID, ymin = `0.025quant`,
                  ymax = `0.975quant`), alpha = 0.5)

```



Task

Create a map of predicted *probability* from Model 3. You can use a inverse logit function defined as

```
inv_logit = function(x) (1+exp(-x))^-1
```

Take hint

The `predict()` function can take as input also functions of elements of the components you want to consider

[Click here to see the solution](#)

```
inv_logit = function(x) (1+exp(-x))^-1

pred3  = predict(fit3, pxl1, ~inv_logit(Intercept + space + covariate) )

pred3 %>% ggplot() +
  geom_sf(aes(color = mean)) +
  scale_color_scico(direction = -1) +
  ggtitle("Sample from the fitted model")
```

Sample from the fitted model

