

PRACTICAL 2



Aim of this practical:

In this practical we are going to look at commonly used spatial models

1. CAR model for areal data
2. A geostatistical model for binary presence-absence species distribution data
3. A Point process model for georeferenced species occurrence data

0 Areal (lattice) data

In this practical we will:

- Explore tools for areal spatial data wrangling and visualization.
- Learn how to fit an areal model in `inlabru`

In areal data our measurements are summarised across a set of discrete, non-overlapping spatial units such as postcode areas, health board or pixels on a satellite image. In consequence, the spatial domain is a countable collection of (regular or irregular) areal units at which variables are observed. Many public health studies use data aggregated over groups rather than data on individuals - often this is for privacy reasons, but it may also be for convenience.

In the next example we are going to explore data on respiratory hospitalisations for Greater Glasgow and Clyde between 2007 and 2011. The data are available from the CARBayesdata R Package:

```
library(CARBayesdata)

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

The `pollutionhealthdata` contains the spatiotemporal data on respiratory hospitalisations, 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 were the measurements were taken
- observed: observed numbers of hospitalisations due to respiratory disease.
- expected: expected numbers of hospitalisations due to respiratory disease computed using indirect standardisation from Scotland-wide respiratory hospitalisation 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).

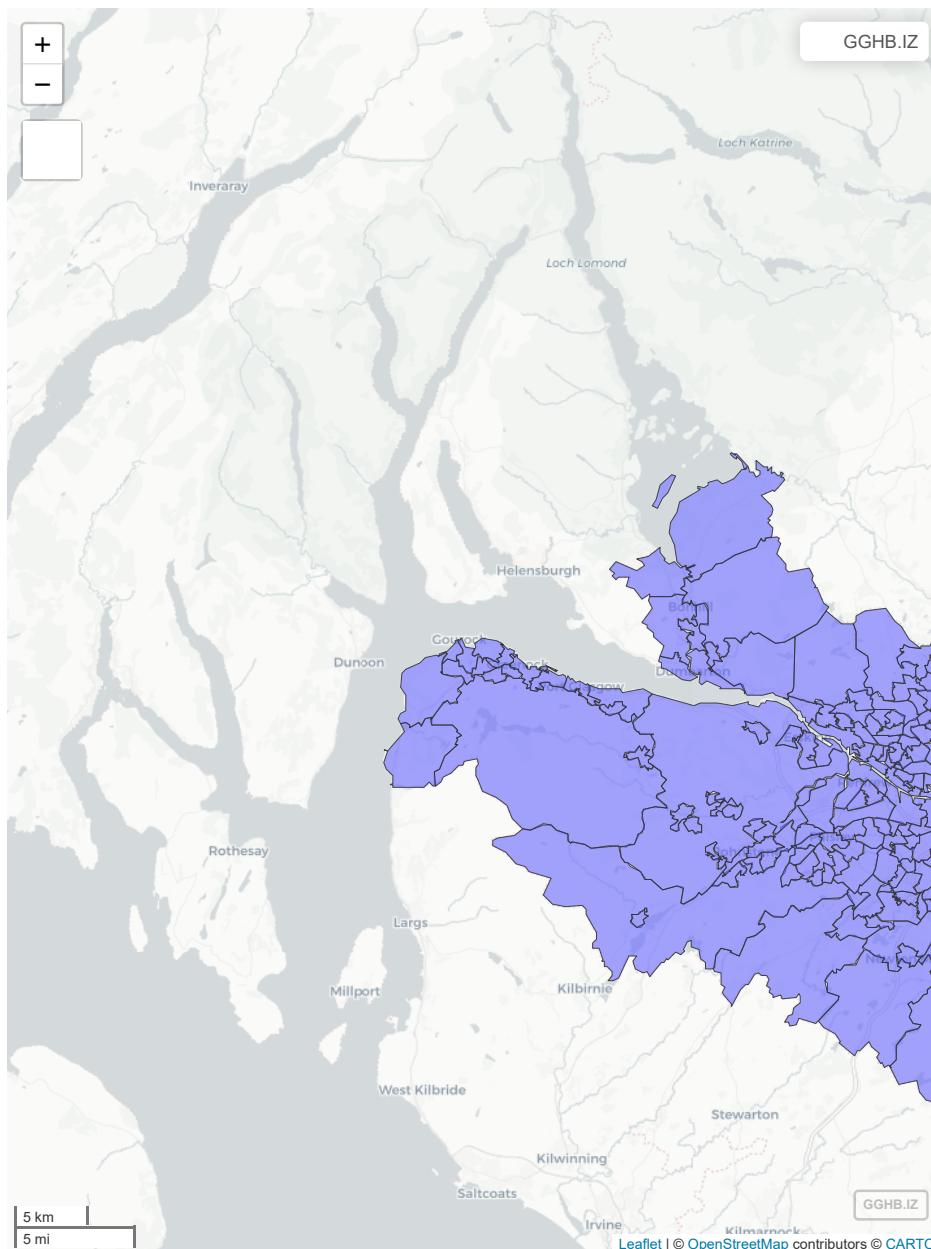


Figure 1: Greater Glasgow and Clyde health board represented by 271 Intermediate Zones

0.1.1 Manipulating and visualizing areal data

Let's start by loading useful libraries:

```
library(dplyr)
library(INLA)
library(ggplot2)
```

```
library(patchwork)
library(inlabru)
library(mapview)
library(sf)

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

The `sf` package allows us to work with vector data which is used to represent points, lines, and polygons. It can also be used to read vector data stored as a shapefiles.

First, lets combine both data sets based on the Intermediate Zones (IZ) variable using the `merge` function from base R, and select only one year of data

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

In epidemiology, disease risk is usually estimated using Standardized Mortality Ratios (SMR). The SMR for a given spatial areal unit i is defined as the ratio between the observed (Y_i) and expected (E_i) number of cases:

$$SMR_i = \frac{Y_i}{E_i}$$

A value $SMR > 1$ indicates that there are more observed cases than expected which corresponds to a high risk area. On the other hand, if $SMR < 1$ then there are fewer observed cases than expected, suggesting a low risk area.

We can manipulate `sf` objects the same way we manipulate standard data frame objects via the `dplyr` package. Lets use the pipeline command `%>%` and the `mutate` function to calculate the yearly SMR values for each IZ:

```
resp_cases <- resp_cases %>%
  mutate(SMR = observed/expected )
```

Now we use `ggplot` to visualize our data by adding a `geom_sf` layer and coloring it according to our variable of interest (i.e., SMR).

```
ggplot()+
  geom_sf(data=resp_cases,aes(fill=SMR))+
  scale_fill_scico(palette = "roma")
```



As with the other types of spatial modelling, our goal is to observe and explain spatial variation in our data. Generally, we are aiming to produce a smoothed map which summarises the spatial patterns we observe in our data.

0.1.2 Spatial neighbourhood structures

A key aspect of any spatial analysis is that observations closer together in space are likely to have more in common than those further apart. This can lead us towards approaches similar to those used in time series, where we consider the spatial *closeness* of our regions in terms of a *neighbourhood structure*.

The function `poly2nb()` of the `spdep` package can be used to construct a list of neighbors based on areas with contiguous boundaries (e.g., using Queen contiguity).

```
library(spdep)

W.nb <- poly2nb(GGHB.IZ,queen = TRUE)
W.nb
```

Neighbour list object:
Number of regions: 271
Number of nonzero links: 1424
Percentage nonzero weights: 1.938971
Average number of links: 5.254613
2 disjoint connected subgraphs

```
plot(st_geometry(GGHB.IZ), border = "lightgray")
plot.nb(W.nb, st_geometry(GGHB.IZ), add = TRUE)
```



i Note

You could use the `snap` argument within `poly2nb` to set a distance at which the different regions centroids are consider neighbours.

With this neighborhood matrix, we can then fit a conditional autoregressive (CAR) model. One of the most popular CAR approaches to model spatial correlation is the Besag model a.k.a. Intrinsic Conditional Autoregressive (ICAR) model.

The conditional distribution for u_i given $\mathbf{u}_{-i} = (u_i, \dots, u_{i-1}, u_{i+1}, \dots, u_n)^T$ is

$$u_i | \mathbf{u}_{-i} \sim N \left(\frac{1}{d_i} \sum_{j \sim i} u_j, \frac{1}{d_i \tau_u} \right)$$

where τ_u is the precision parameter, $j \sim i$ denotes that i and j are neighbors, and d_i is the number of neighbors. Thus, the mean of u_i is equivalent to the the mean of the effects over all neighbours, and the precision is proportional to the number of neighbors. The joint distribution is given by:

$$\mathbf{u} | \tau_u \sim N \left(0, \frac{1}{\tau_u} Q^{-1} \right),$$

Where Q denotes the structure matrix defined as

$$Q_{i,j} = \begin{cases} d_i, & i = j \\ -1, & i \sim j \\ 0, & \text{otherwise} \end{cases}$$

This structure matrix directly defines the neighbourhood structure and is sparse. We can compute the adjacency matrix using the function `nb2mat()` in the `spdep` library. Then convert the adjacency matrix into the precision matrix \mathbf{Q} of the CAR model as follows:

```
library(spdep)
R <- nb2mat(W.nb, style = "B", zero.policy = TRUE)
diag = apply(R, 1, sum)
Q = -R
diag(Q) = diag
```

The ICAR model accounts only for spatially structured variability and does not include a limiting case where no spatial structure is present. Therefore, it is typically combined with an additional unstructured random effect $z_i | \tau_z \sim N(0, \tau_z^{-1})$. The resulting model $v_i = u_i + z_i$ is known as the Besag-York-Molié model (BYM) which is an extension to the intrinsic CAR model that contains an i.i.d. model component.

0.1.3 Fitting an ICAR model in `inlabru`

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

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

where

- β_0 is a common intercept
- $\mathbf{u} = (u_1, \dots, u_k)$ is a conditional Autoregressive model (CAR) with precision matrix $\tau_u \mathbf{Q}$
- $\mathbf{z} = (z_1, \dots, z_k)$ is an unstructured random effect with precision τ_z

Stage 3 Hyperparameters

The hyperparameters of the model are τ_u and τ_z

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

Question

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?

0.1.4 Areal model predictions

We now look at the predictions over space.

Task

Complete the code below to produce:

1. prediction of the linear predictor η_i
2. The risk rate λ_i
3. The expected cases $E_i \exp(\lambda_i)$ over the whole space of interest.

Plot the mean and sd of the resulting surfaces.

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

See Solution

```
# 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

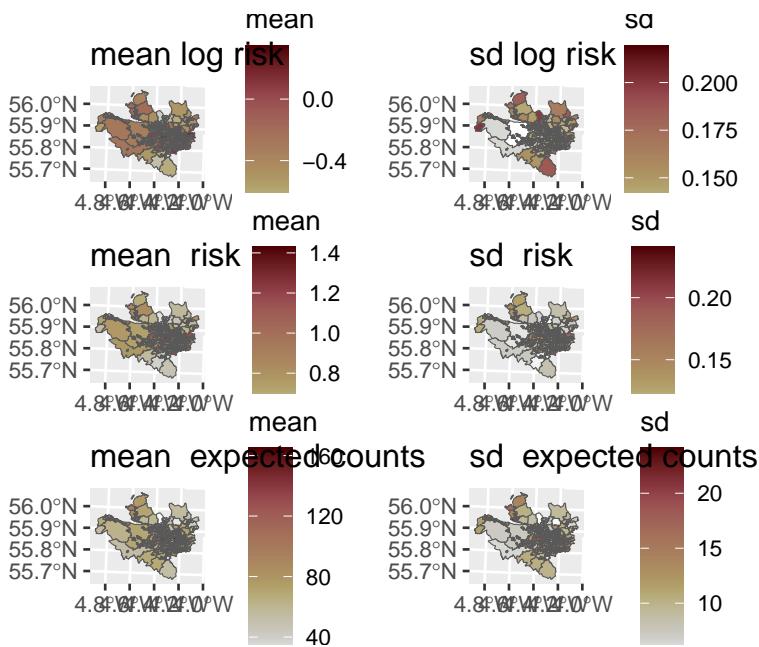
p1 = ggplot() +
  geom_sf(data = pred$log_risk, aes(fill = mean)) + scale_fill_scico(direction = -1) +
  ggtitle("mean log risk")
p2 = ggplot() +
  geom_sf(data = pred$log_risk, aes(fill = sd)) + scale_fill_scico(direction = -1) +
  ggtitle("sd log risk")

p3 = ggplot() +
  geom_sf(data = pred$risk, aes(fill = mean)) + scale_fill_scico(direction = -1) +
  ggtitle("mean risk")

p4 = ggplot() +
  geom_sf(data = pred$risk, aes(fill = sd)) +
  scale_fill_scico(direction = -1) +
  ggtitle("sd risk")

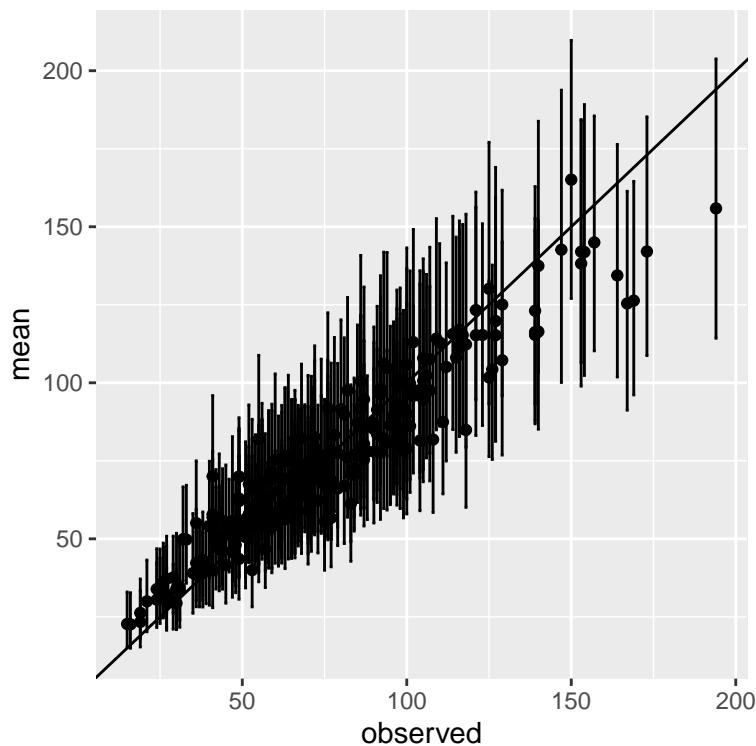
p5 = ggplot() + geom_sf(data = pred$cases, aes(fill = mean)) + scale_fill_scico(direction =
  ggtitle("mean expected counts"))
p6 = ggplot() + geom_sf(data = pred$cases, aes(fill = sd)) + scale_fill_scico(direction =
  ggtitle("sd expected counts"))

p1 + p2 + p3 + p4 + p5 + p6 + plot_layout(ncol=2)
```



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)
```



Here we are predicting the *mean* of counts, not the counts. Predicting the counts is beyond the scope of this short course but you can check the supplementary material below.

Supplementary Material

Posterior predictive distributions, i.e., $\pi(y_i^{\text{new}}|\mathbf{y})$ 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:

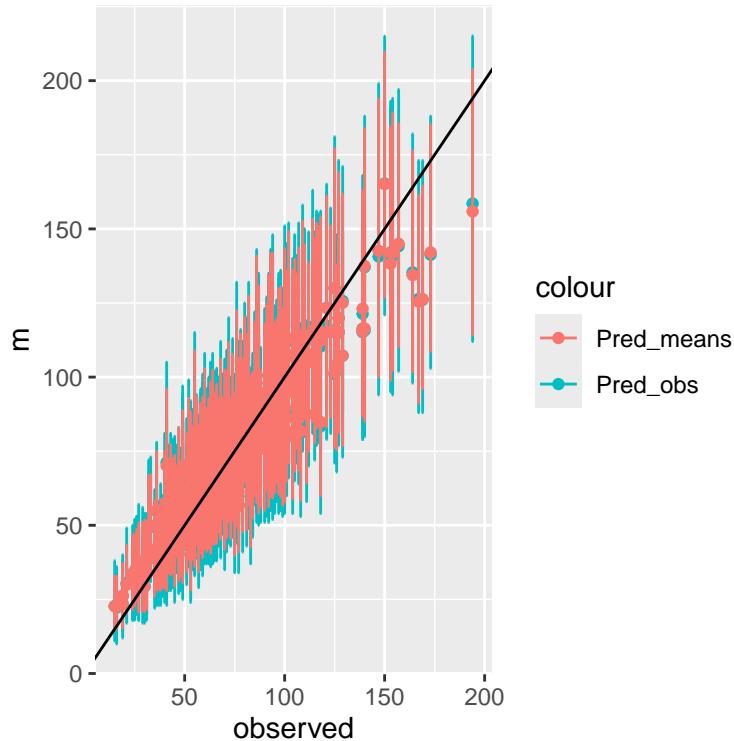
1. Simulate n replicates of $g^k = E_i\lambda_i$ for $k = 1, \dots, n$ using the function `generate()` which takes the same input as `predict()`
2. For each of the k replicates simulate a new value y_i^{new} using the function `rpois()`
3. Summarise the n samples of y_i^{new} using, for example the mean and the 0.025 and 0.975 quantiles.
- 4.

```
# 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)
)
# Plot the observations against the predicted new counts and the predicted expected counts

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)
```



0 Geostatistical data

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

- Explore tools for geostatistical spatial data wrangling and visualization.
- Learn how to fit a geostatistical model in `inlabru`
- Learn how to add spatial covariates to the model
- Learn how to do predictions

Geostatistical data are the most common form of spatial data found in environmental setting. In these data we regularly take measurements of a spatial ecological or environmental process at a set of fixed locations. This could be data from transects (e.g, where the height of trees is recorded), samples taken across a region (e.g., water depth in a lake) or from monitoring stations as part of a network (e.g., air pollution). In each of these cases, our goal is to estimate the value of our variable across the entire space.

Let D be our two-dimensional region of interest. In principle, there are infinite locations within D , each of which can be represented by mathematical coordinates (e.g., latitude and longitude). We then can identify any individual location as $s_i = (x_i, y_i)$, where x_i and y_i are their coordinates.

We can treat our variable of interest as a random variable, Z which can be observed at any location as $Z(s_i)$.

Our geostatistical process can therefore be written as:

$$\{Z(s); s \in D\}$$

In practice, our data are observed at a finite number of locations, m , and can be denoted as:

$$z = \{z(\mathbf{s}_1), \dots z(\mathbf{s}_m)\}$$

In the next example, 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 survey. The `qcs_grid` data contain the depth values stored as 2×2 km grid for Queen Charlotte Sound.

0.2.1 Exploring and visualizing species distribution data

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:

```
library(terra)
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 load also the `tidyterra` library.

```
library(tidyterra)
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("")
```



0.2.2 Fitting a spatial geostatistical species distribution 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!!

0.2.3 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

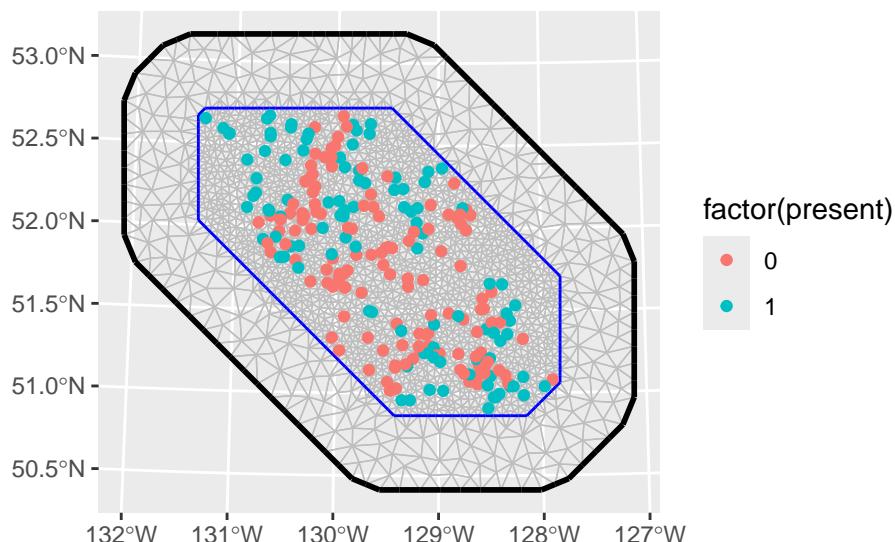
4. Define the observation model using the `bru_obs()` function
5. Run the model using the `bru()` function

0.2.3.1 Step 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
                  cutoff = 2,
                  max.edge = c(7,20),      # 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))) +
  xlab("") + ylab("")
```



Task

Look at the documentation for the `fm_mesh_2d` function typing

```
?fm_mesh_2d
```

Experiment with the different options and create different meshes (see [here](#) for further details on mesh construction).

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 artifact in the estimated variance.

0.2.3.2 Step 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 parameters ρ_0 and p_ρ such that you believe it is reasonable that

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

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

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

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))
```

Question

Considering the `pcod_sf` spatial extension and type of the data, which of the previous choices is more reasonable?

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

Take hint

You can use the `summary()` function to check the coordinate range of an `sf` object.

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

- (C) spde_model3

0.2.3.3 Step 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 data frame we use (pcod_sf) is an sf object the input in the space() component is the geometry of the dataset.

0.2.3.4 Step 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")
```

0.2.3.5 Step 5. Run the model Finally we are ready to run the model

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

0.2.4 Model results

0.2.4.1 Hyperparameters

Task

What are the posterior for the range ρ and the standard deviation σ ? Plot the posterior together with the prior for both parameters.

Take hint

The `spde.posterior()` can be used to calculate the posterior distribution of the range and variance of a model's SPDE component. (type `?spde.posterior` for further details)

[Click here to see the solution](#)

```
# Extract marginal for the range

library(patchwork)
spde.posterior(fit1, "space", what = "range") %>% plot() +
  spde.posterior(fit1, "space", what = "log.variance") %>% plot()
```

0.2.5 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_pixel()` which creates a regular grid of points covering the mesh

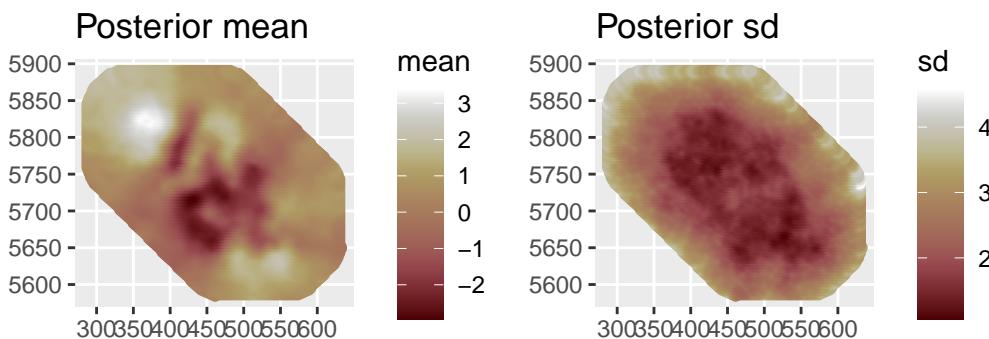
```
pxl = fm_pixels(mesh)
```

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

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

Finally, we can plot the maps

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

0.2.6 An alternative model (including spatial covariates)

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

The `pcod_sf` object already contains the `depth_scaled` containing the squared depth values at each location. However, `inlabru` also allows to specify a raster object directly in the model components. If your raster contains multiple layers, then the desired layer can be called using the `$` symbol (e.g., `my_raster$layer_1`).

[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")

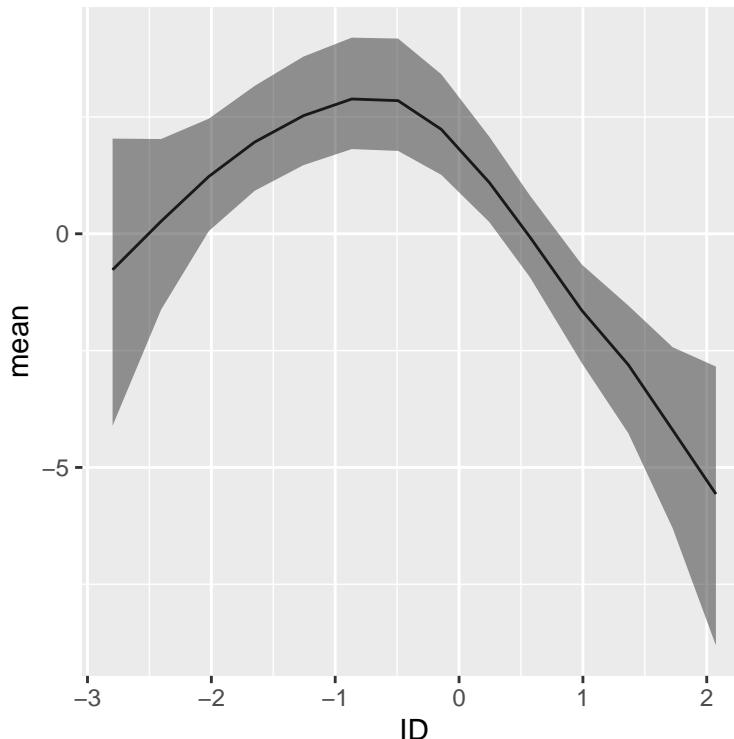
formula = present ~ Intercept + space + covariate

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)
```



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(crdz(depth_r),
                  as.data.frame(depth_r$depth)) %>%
  filter(!is.na(depth)) %>%
  st_as_sf(coords = c("x", "y")) %>% dplyr::select(-depth)
```

Task

Create a map of predicted *probability* from Model 3 by predicting prediction over `pxl1`. 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](#)

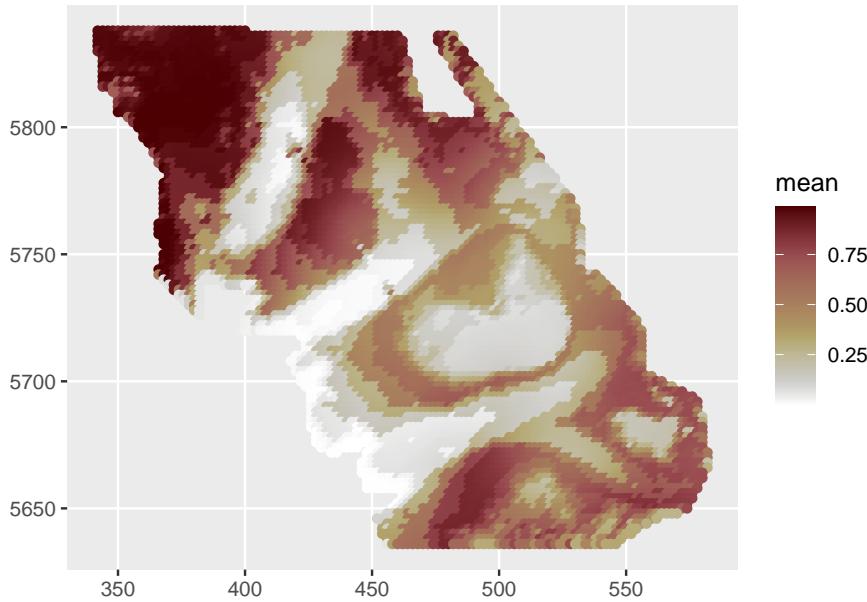
```

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



0 Point process data

In this practical we are going to fit a log Gaussian Cox Proces (LGCP) model to point-referenced data. We will:

- Learn how to fit a LGCP model in inlabru
- Learn how to add spatial covariates to the model
- Learn how to do predictions

In **point processes** we measure the locations where events occur (e.g. trees in a forest, earthquakes) and the coordinates of such occurrences are our data. A spatial point process is a random variable operating in continuous space, and we observe realisations of this variable as point patterns across space.

Consider a fixed geographical region A . The set of locations at which events occur are denoted $\mathbf{s} = s_1, \dots, s_n$. We let $N(A)$ be the random variable which represents the number of events in region A .

We typically assume that a spatial point pattern is generated by an unique point process over the whole study area. This means that the delimitation of the study area will affect the observed point patters.

We can define the intensity of a point process as the expected number of events per unit area. This can also be thought of as a measure of the density of our points. In some cases,

the intensity will be constant over space (homogeneous), while in other cases it can vary by location (inhomogeneous or heterogenous).

In the next example we will be looking at butterflies occurrence records obtained from the *Butterflies for the New Millennium* (BNM) monitoring scheme. The data set consists of Ringlet butterfly's presence-only records collected by volunteers in Scotland's Cairngorms National Park (CNP).

0.3.1 Point-referenced data visualization

Let's begin by loading the data which can be downloaded below:

```
# load data files (set the correct path to where the data are stored)
load("datasets/ringlett_CNP.RData")
elev_rast = terra::rast("datasets/elev_CNP.tif")
```

Then, we load the geographical region of interest which can be downloaded [here](#) (i.e., CNP boundaries). We can use the st_read function from the sf library to load the .shp file by specifying the directory where you downloaded the files. For example,

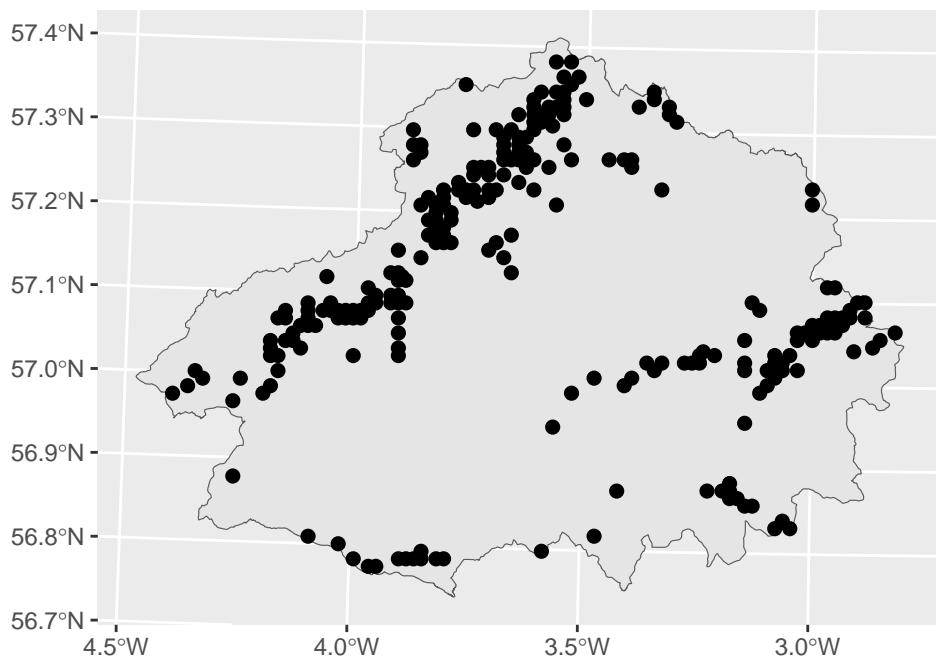
```
shp_SGC <- st_read("datasets/SG_CairngormsNationalPark/SG_CairngormsNationalPark_2010.shp",
```

We need to set an appropriate CRS for our shapefile:

```
shp_SGC <- shp_SGC %>% st_transform(crs = 27700)
shp_SGC <- st_transform(shp_SGC,gsub("units=m","units=km",st_crs(shp_SGC)$proj4string))
```

We can then visually verify the projections by plotting the observation records against the spatial domain of interest as follows:

```
ggplot()+
  geom_sf(data=shp_SGC)+
  geom_sf(data=ringlett_CNP,size=2)
```



Task

Using `tidyterra` and `ggplot`, produce a map of the elevation profile in the CNP and overlay the spatial point pattern of the Ringlet butterfly occurrence records. Use an appropriate colouring scheme for the elevation values. Do you see any pattern?

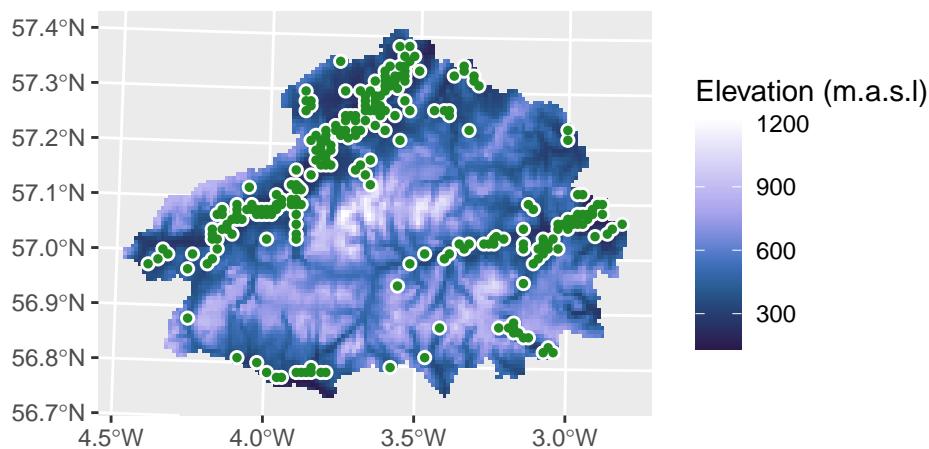
Take hint

You can use the `geom_spatraster()` to add a raster layer to a `ggplot` object. Furthermore the `scico` library contains a nice range of coloring palettes you can choose, type `scico_palette_show()` to see the color palettes that are available.

[Click here to see the solution](#)

```
library(ggplot2)
library(tidyterra)
library(scico)

ggplot()+
  tidyterra::geom_spatraster(data=elev_rast)+
  geom_sf(data=ringlett_CNP,color="white",size=2)+
  geom_sf(data=ringlett_CNP,color="forestgreen",size=1)+
  scale_fill_scico(name = "Elevation (m.a.s.l)",
                  palette = "devon",
                  na.value = "transparent" )
```



0.3.2 Workflow for Fitting a LGCP model

The procedure for fitting a point process model in `inlabru`, specifically a log-Gaussian Cox process, follows a similar workflow to that of a geostatistical model, these are:

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 observational model
5. Run the Model

0.3.2.1 Step 1. Building the mesh for a LGCP First, we need to create the mesh used to approximate the random field. When analyzing point patterns, mesh nodes (integration points) are not typically placed at point locations. Instead, a mesh is created using the `fm_mesh_2d()` function from the `fmesher` library with boundary being our study area.

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.

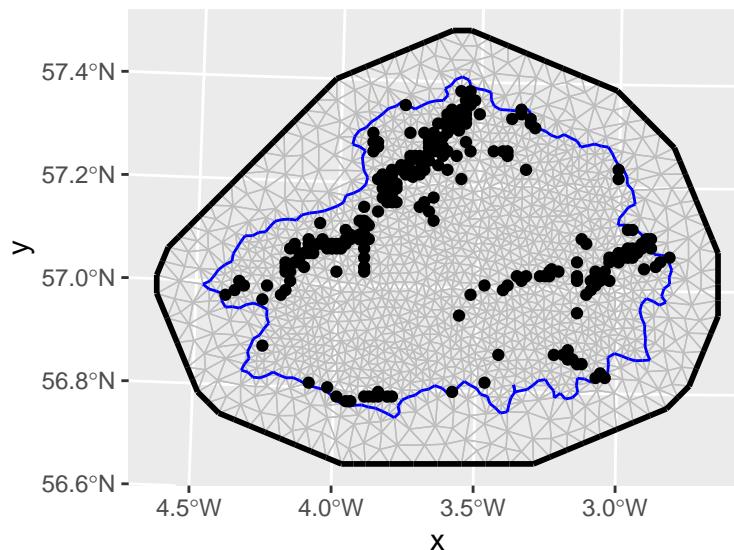
i Note**General guidelines for creating the mesh**

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.

```
# mesh options
max.edge = 2
bound.outer = 10

mesh <- fm_mesh_2d(boundary = shp_SGC,
                     max.edge = c(1,3)*max.edge,
                     offset=c(max.edge, bound.outer),
                     cutoff = 1.5,
                     crs=st_crs(shp_SGC))

ggplot() + gg(mesh) + geom_sf(data=ringlett_CNP)
```



0.3.2.2 Step 2. Defining the SPDE model We can now define our SPDE model using the `inla.spde2.pcmatern` function. To help us chose some sensible model parameters it is

often useful to consider the spatial extension of our study.

```
st_area(shp_SGC)
```

4528.099 [km²]

We can use PC-priors for the range ρ and the standard deviation σ of the Matérn process

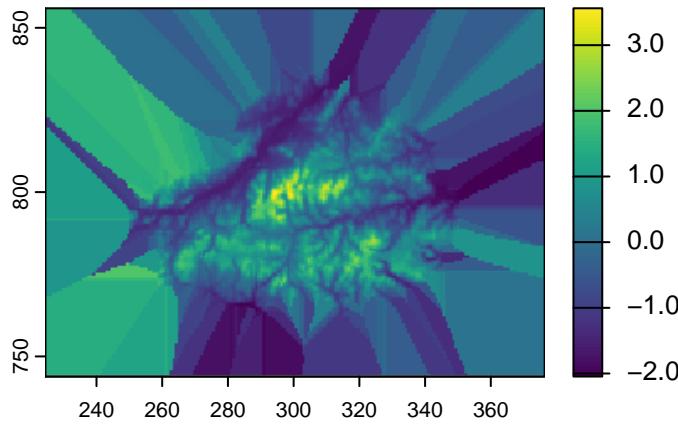
- Define the prior for the range $\text{prior.range} = (\text{range0}, \text{Prange})$ $\text{Prob}(\rho < \rho_0) = p_\rho$
- Define the prior for the range $\text{prior.sigma} = (\text{sigma0}, \text{Psigma})$ $\text{Prob}(\sigma > \sigma_0) = p_\sigma$

```
matern <- inla.spde2.pcmatern(mesh,
                                 prior.range = c(20, 0.5), # P(range < 20) = 0.5
                                 prior.sigma = c(1, 0.5)) # P(sigma > 1) = 0.5
```

Now, for a point process models, the spatial covariates (i.e., the elevation raster) has to be also projected outside the outer mesh for computational purposes. We can achieve this using the following code:

```
library(stars)

# Standardize the raster
elev_rast <- scale(elev_rast)
# Extend raster ext by a factor of 1.5
re <- extend(elev_rast, ext(elev_rast)*1.5)
# Convert to spatial object
re_df <- re %>% stars::st_as_stars() %>% st_as_sf(na.rm=F)
# fill in missing values using the original raster
re_df$GBR_elv_msk <- bru_fill_missing(elev_rast,re_df,re_df$GBR_elv_msk)
# rasterize
elev_rast_p <- stars::st_rasterize(re_df) %>% rast()
# visualize
plot(elev_rast_p)
```



0.3.2.3 Step 3. Defining model components **Stage 1** Model for the response

The total number of points in the study region is a Poisson random variable with a spatially varying intensity and log-likelihood given by :

$$l(\beta; s) = \sum_{i=1}^m \log[\lambda(s_i)] - \int_A \lambda(s) ds.$$

The integral in this expression can be interpreted as the expected number of points in the whole study region. However, the integral of the intensity function has no close form solution and thus we need to approximate it using numerical integration. Luckily, LGCPs are latent Gaussian models and they may be fitted using INLA.

Stage 2 Latent field model

We will model the Ringlet distribution as a point process whose intensity function $\lambda(s)$ is additive on the log-scale:

$$\eta(s) = \log(\lambda(s)) = \beta_0 + \mathbf{x}'(s)\beta + \omega(s),$$

Here, $\mathbf{x}(s)$ is a set of covariates detected at location s with linear fixed effects β to be estimated, and $\omega(s)$ is the Matérn Gaussian field capturing the spatial structure of all the locations where species have been observed (The location where a species occur are assumed to be independent given the Gaussian field).

In this exercise, we will use elevation as our covariate as it seems to be closely related to the distribution of the Ringlet butterfly.

Stage 3 Hyperparameters

The hyperparameters of the model are ρ and σ corresponding to

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

NOTE In this case the linear predictor $\eta(s)$ consists of three components.

After the mesh and a SPDE representation of the spatial GF have been defined, the model components can be specified using the formula syntax (recall that this allows users to choose meaningful names for model components).

```
cmp_lgcp <- geometry ~ Intercept(1) +
  elevation(elev_rast_p, model = "linear") +
  grf(geometry, model = matern)
```

Here the labels Intercept, elevation (elevation effect) and grf (an abbreviation of Gaussian random field) are used to name the components of the model but they equally well could be something else.

Now, notice that we have called the elev_rast_p raster data within the elevation component. Recall that inlabru provides support for sf and terra data structures, allowing it to extract information from spatial data objects. This is particularly relevant for LGCP, as spatial covariates (e.g., the elevation raster) must be available across the whole study area (including the outer mesh).

```
formula = geometry ~ Intercept + elevation + grf
```

Recall that in an sf object, the geo-referenced information of our points is stored in the geometry column, and hence we specify this as our response

0.3.2.4 Step 4. Defining the observational model inlabru has support for latent Gaussian Cox processes through the cp likelihood family:

```
lik = bru_obs(formula = formula,
               data = ringlett_CNP,
               family = "cp",
               samplers = shp_SGC,
               domain = list(geometry = mesh))
```

Notice that we have supplied an sf object as our data. LGCPs can be fitted using an sf points object to describe the locations of the observed points and an sf polygon object to define the observation window (samplers in the code above).

0.3.3 Step 5. Run the model

Finally, we can fit the model as usual

```
fit_lgcp = bru(cmp_lgcp, lik)
```

Posterior summaries of fixed effects and hyper parameters can be obtained using the summary() function.

```
summary(fit_lgcp)
```

| mean | sd | 0.025quant | 0.5quant | 0.975quant | mode |
|-------|-------|------------|----------|------------|-------|
| -4.72 | 0.31 | -5.37 | -4.71 | -4.14 | -4.71 |
| -2.21 | 0.16 | -2.52 | -2.21 | -1.90 | -2.21 |
| 22.12 | 10.69 | 8.76 | 19.75 | 49.63 | 15.86 |
| 0.48 | 0.13 | 0.27 | 0.47 | 0.76 | 0.45 |

0.3.4 Model predictions

Model predictions can be computed using the `predict` function by supplying the coordinates where the covariate is defined. We can do this by defining a `sf` object using coordinates in our original raster data.

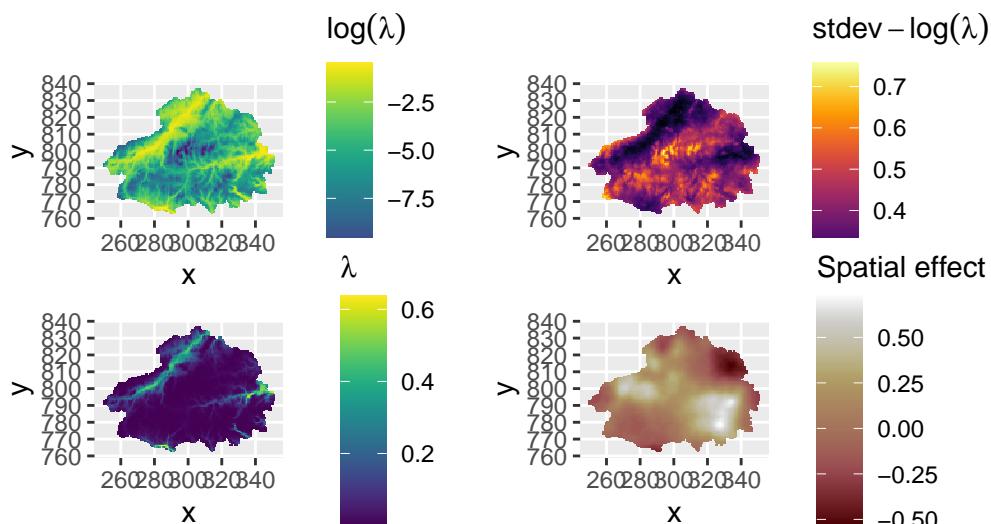
```
pxl1 = data.frame(crds(elev_rast),
                  as.data.frame(elev_rast$GBR_elv_msk)) %>%
  filter(!is.na(GBR_elv_msk)) %>%
  st_as_sf(coords = c("x", "y")) %>%
  dplyr::select(-GBR_elv_msk)
```

The formula object for the prediction can be a generic R expression that references model components using the user-defined names.

The `predict()` method returns an object in the same data format as was used in the `predict` call which, in this case, is an `sf` points object.

Support for plotting `sf` data objects is available in the `ggplot2` package.

1 Model predictions



2 R Code

```
lgcp_pred <- predict(
  fit_lgcp,
  pxl1,
  ~ data.frame(
    lambda = exp(Intercept + elevation + grf), # intensity
    loglambda = Intercept + elevation +grf,  #log-intensity
    GF = grf # matern field
  )
)

# predicted log intensity
ggplot() + gg(lgcp_pred$loglambda, geom = "tile")
# standard deviation of the predicted log intensity
ggplot() + gg(lgcp_pred$loglambda, geom = "tile",aes(fill=sd))
# predicted intensity
ggplot() + gg(lgcp_pred$lambda, geom = "tile")
# spatial field
ggplot() + gg(lgcp_pred$GF, geom = "tile")
```