Model fitting, prediction and plotting

Supporting information for 'The Point Process Framework for Integrated Modelling of Biodiversity Data'

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Loading packages:

```
#devtools::install_github("PhilipMostert/PointedSDMs")
library(PointedSDMs) # model fitting
library(ggplot2)     # plotting
library(raster)      # ???? Model fitting fails if I exclude this
library(mapproj)     # map options for plotting
library(INLA)        # functions for specifying mesh
library(dplyr)       # data handling
library(sf)          # spatial stuff
library(showtext)    # font for plot
library(patchwork)   # combining figures
```

Some plot settings:

```
showtext_auto()
f1 <- "Open sans"
font_add_google(f1, f1)
```

1 Downloading data

Before you run this file, make sure you have the following files:

- `data/artsobs_clean_new.rds`
- `data/survey_clean_new.rds`
- `data/environmental_covariates.rds`
- `data/Norwegian_lakes.rds`

This model may take quite a while to run (approx. 6 hours with the final settings that were used for the paper). To run a faster version, it is possible to use less integration points in the mesh, this is described below. Alternatively, the run-time can be reduced by including less than the full four fish species, you can choose which fish species to include in the chunk below. (OBS: You will also need to remove any species you don't want in the chunk where we use "changeComponents" for specific species fields)

```
fishes <- c("Esox_lucius", "Perca_fluviatilis", "Salmo_trutta", "Salvelinus_alpinus")
```

2 Loading Norway map and making mesh

We begin by making a spatial mesh out of a map of Norway.

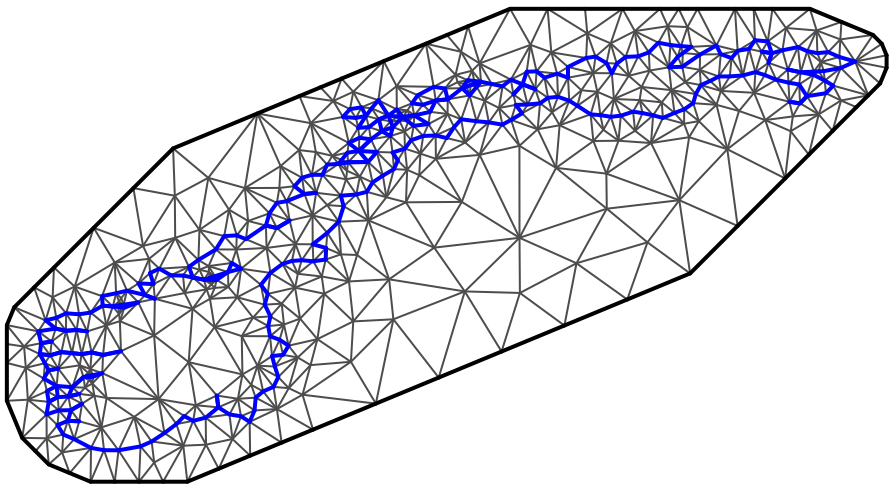
```
#norway <- ggplot2::map_data("world", region = "Norway(?!:Svalbard)")
#norway <- setdiff(norway, dplyr::filter(norway, subregion == "Jan Mayen"))
#norway_sf <- st_as_sf(norway, coords = c("long", "lat"), crs = proj)

proj <- '+proj=utm +zone=32 +datum=WGS84 +units=m +no_defs'
norwayfill <- maps::map("world", "norway", fill=TRUE, plot=FALSE,
                  ylim=c(58,72), xlim=c(4,32))
IDs <- sapply(strsplit(norwayfill$names, ":"), function(x) x[1])
norway.poly <- maptools::map2SpatialPolygons(norwayfill, IDs = IDs,
                                             proj4string = CRS(proj))
```

```
## Please note that 'maptools' will be retired during October 2023,
## plan transition at your earliest convenience (see
## https://r-spatial.org/r/2023/05/15/evolution4.html and earlier blogs
## for guidance);some functionality will be moved to 'sp'.
##  Checking rgeos availability: FALSE
```

Adjusting the mesh to be coarser is the easiest way to decrease the run-time for the model. With the following mesh, the model fitting takes just about 1 hour for us, but feel free to change the `max.edge` or `cutoff` to get a coarser mesh.

```
mesh <- inla.mesh.2d(boundary = inla.sp2segment(norway.poly),
                     cutoff = 0.3, # smallest allowed distance between points
                     max.edge = c(6, 3), # decrease this for more int. points
                     #max.edge = c(3, 1),
                     offset = c(1, 1),
                     crs = st_crs(proj))
plot(mesh)
```



3 Setting up covariate data

Next we load the environmental data, which will be used as covariates.

```
covariates_raw <- readRDS("data/environmental_covariates.RDS")

covariates <- covariates_raw %>%
```

```
  # Log-transform area of lake
  dplyr::mutate(log_area = log(area_km2)) %>%
  # Remove some uninformative variables
  dplyr::select(-c(ebint, no_vatn_lnr, eb_waterregionID))

# Choose from
# "decimalLatitude", "decimalLongitude",
# "log_area", "perimeter_m", "distance_to_road",
# "eurolst_bio10", "catchment_area_km2", "SCI", "HFP"

Use <- c("log_area", "eurolst_bio10", "SCI")

cov_pixel <- SpatialPixelsDataFrame(
  points = covariates[,c("decimalLongitude","decimalLatitude")],
  data = covariates[,Use],
  proj4string = CRS(proj),
  tol = 0.340571)

# Scale covariates and convert to terra::rast
cov_raster <- scale(terra::rast(cov_pixel))
```

4 Observation data

For this model, we have two observation sets, one which is downloaded from GBIF and one that is a survey dataset (see separate document for download instructions).

```
survey <- readRDS("data/survey_clean_new.rds") %>%
  filter(species %in% fishes)
artsobs <- readRDS("data/artsobs_clean_new.rds") %>%
  filter(species %in% fishes)
```

We can plot the observed data points:

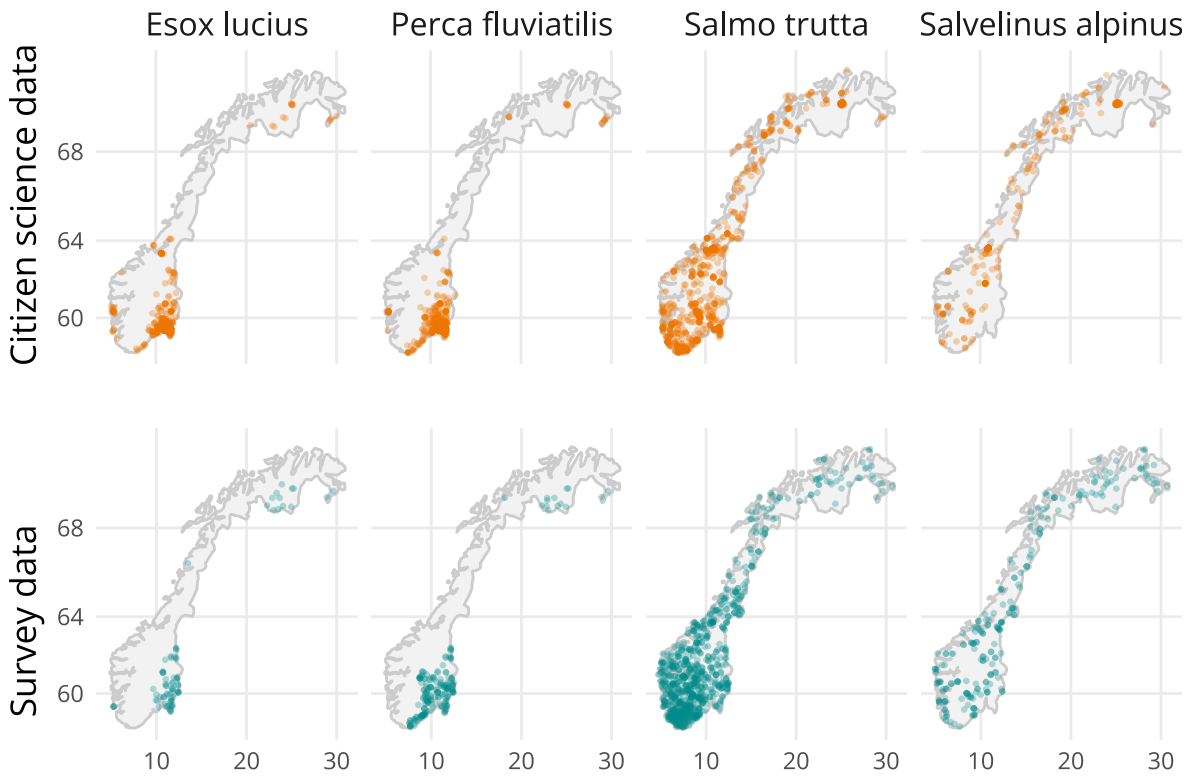
```
norway <- ggplot2::map_data("world", region = "Norway(?!:Svalbard)")
norway <- setdiff(norway, dplyr::filter(norway, subregion == "Jan Mayen"))

p_artsobs <- ggplot(artsobs, aes(x = decimalLongitude, y = decimalLatitude)) +
  geom_polygon(data = norway, aes(long, lat, group = group),
               color="grey80", fill = "grey95") +
  geom_point(color = "darkorange2", size = 0.5, alpha = 0.3) +
  facet_wrap(~species, nrow = 1,
             labeller = labeller(species = function(string) sub("_", " ", string))) +
  coord_map() +
  labs(tag = "Citizen science data") +
  theme_minimal() +
  theme(text = element_text(family = f1),
        strip.text = element_text(family = f1, size = 12),
        plot.tag = element_text(angle = 90, hjust = 0.5),
        plot.tag.position = c(-0.03, 0.45),
        legend.position = "none",
        axis.title = element_blank(),
        axis.text.x = element_blank())

p_survey <- ggplot(survey %>% filter(occurrenceStatus == 1),
```

```
      aes(x = decimalLongitude, y = decimalLatitude)) +
  geom_polygon(data = norway, aes(long, lat, group = group),
               color="grey80", fill = "grey95") +
  geom_jitter(color = "darkcyan", size = 0.5, alpha = 0.3) +
  facet_wrap(~species, nrow = 1) +
  coord_map() +
  xlab("Longitude") +
  ylab("Latitude") +
  labs(tag = "Survey data") +
  theme_minimal() +
  theme(text = element_text(family = f1),
        plot.tag = element_text(angle = 90, hjust = 0.5),
        plot.tag.position = c(-0.03, 0.45),
        legend.position = "none",
        axis.title = element_blank(),
        strip.text = element_blank(),
        plot.margin = margin(l = 30))

p_artsobs / p_survey
```




```
ggsave("figures/presence_points.pdf", height = 5, width = 8)
```

5 Joint model for four fish species

For the presence/absence survey data, we use a Bernoulli distribution, where the presence probability for species $j \in \{$*Salmo trutta, Perca fluvatilis, Esox lucius, Salvelinus alpinus*$\}$ depends on some covariates $x(s)$, along with a spatial field $\xi_j(s)$:

$$Y_{PA,j}(s_i) \sim \text{Bernoulli}(p_{PA,j}(s_i))$$
$$\text{cloglog}(p_{PA,j}(s_i)) = \alpha_{PA,j} + x(s_i)^T\beta_j + \xi_j(s_i).$$

The presence-only data is fitted with a Poisson point process model, where the intensity depends on the same covariates $x(s)$ and the same spatial field $\xi_j(s)$, plus an additional spatial field $\xi_{\text{bias}}(s)$ that is unique to the citizen science data, but shared across all fish species:

$$Y_{PO,j}(s_i) \sim \text{Poisson}(e^{\eta_{PO,j}(s_i)})$$
$$\eta_{PO,j}(s_i) = \alpha_{PO,j} + x(s)^T\beta_j + \xi_j(s_i) + \xi_{\text{bias}}(s_i).$$

So in summary, for this model we have:

- one bias field, based on CS data and common across all species
- four shared fields, shared across the data sets (survey/citizen science), but separate for each fish species.

Since we have two data sets and four species, that means that we in total have eight sub-models.

We first prepare the model using the `intModel` function.

```
fish_model_setup <- intModel(
  survey,                                 # Survey data
  artsobs,                                # Citizen science data
  spatialCovariates = cov_raster,         # Covariates
  speciesName = "species",                # The column containing species name
  speciesSpatial = "copy",                # Copy species fields across data
  Coordinates = c("decimalLongitude", "decimalLatitude"), # Name of coords
  responsePA = "occurrenceStatus",        # Name of response column
  pointsSpatial = NULL,                   # NULL since we use speciesSpatial
  Mesh = mesh,                            # inla mesh object
  Projection = proj)                      # CRS for points and covariates
```

This model has the species specific spatial fields, but we also want a bias field that is shared across the species. We add this using `$addBias`.

```
fish_model_setup$addBias("artsobs")
```

For the species specific fields, the default in PointedSDMs is that these are allowed to be different up to a scaling factor (named beta in INLA) across the data sets. That means that for instance the trout-specific spatial field for the citizen science data set is equal to beta times the trout-specific spatial field for the survey data. In practice, this has to do with the copy-option in INLA. But in our model we want them to be the same, not to vary by a factor. So we manually change this using the `$changeComponents` function, by setting `hyper = list(beta = list(fixed = TRUE))` for each of the four citizen science fields.

```
fish_model_setup$changeComponents(
  ~ Perca_fluviatilis_artsobs_spatial(
      main = geometry,
      copy = "Perca_fluviatilis_survey_spatial",
      hyper = list(beta = list(fixed = TRUE))) +
    Salmo_trutta_artsobs_spatial(
      main = geometry,
      copy = "Salmo_trutta_survey_spatial",
      hyper = list(beta = list(fixed = TRUE))) +
    Salvelinus_alpinus_artsobs_spatial(
      main = geometry,
      copy = "Salvelinus_alpinus_survey_spatial",
      hyper = list(beta = list(fixed = TRUE))) +
    Esox_lucius_artsobs_spatial(
```

```
      main = geometry,
      copy = "Esox_lucius_survey_spatial",
      hyper = list(beta = list(fixed = TRUE))))
```

```
## Components:
## ~-1 + Perca_fluviatilis_survey_spatial(main = geometry, model = Perca_fluviatilis_survey_field) +
##     Salmo_trutta_survey_spatial(main = geometry, model = Salmo_trutta_survey_field) +
##     Salvelinus_alpinus_survey_spatial(main = geometry, model = Salvelinus_alpinus_survey_field) +
##     Esox_lucius_survey_spatial(main = geometry, model = Esox_lucius_survey_field) +
##     Salmo_trutta_artsobs_spatial(main = geometry, copy = "Salmo_trutta_survey_spatial",
##         hyper = list(beta = list(fixed = FALSE))) + Salvelinus_alpinus_artsobs_spatial(main = geometi
##     copy = "Salvelinus_alpinus_survey_spatial", hyper = list(beta = list(fixed = FALSE))) +
##     Esox_lucius_artsobs_spatial(main = geometry, copy = "Esox_lucius_survey_spatial",
##         hyper = list(beta = list(fixed = FALSE))) + Perca_fluviatilis_log_area(main = Perca_fluviatil
##     model = "linear") + Salmo_trutta_log_area(main = Salmo_trutta_log_area,
##     model = "linear") + Salvelinus_alpinus_log_area(main = Salvelinus_alpinus_log_area,
##     model = "linear") + Esox_lucius_log_area(main = Esox_lucius_log_area,
##     model = "linear") + Perca_fluviatilis_eurolst_bio10(main = Perca_fluviatilis_eurolst_bio10,
##     model = "linear") + Salmo_trutta_eurolst_bio10(main = Salmo_trutta_eurolst_bio10,
##     model = "linear") + Salvelinus_alpinus_eurolst_bio10(main = Salvelinus_alpinus_eurolst_bio10,
##     model = "linear") + Esox_lucius_eurolst_bio10(main = Esox_lucius_eurolst_bio10,
##     model = "linear") + Perca_fluviatilis_SCI(main = Perca_fluviatilis_SCI,
##     model = "linear") + Salmo_trutta_SCI(main = Salmo_trutta_SCI,
##     model = "linear") + Salvelinus_alpinus_SCI(main = Salvelinus_alpinus_SCI,
##     model = "linear") + Esox_lucius_SCI(main = Esox_lucius_SCI,
##     model = "linear") + Perca_fluviatilis_intercept(1) + Salmo_trutta_intercept(1) +
##     Salvelinus_alpinus_intercept(1) + Esox_lucius_intercept(1) +
##     artsobs_biasField(main = geometry, model = artsobs_bias_field) +
##     Perca_fluviatilis_artsobs_spatial(main = geometry, copy = "Perca_fluviatilis_survey_spatial",
##         hyper = list(beta = list(fixed = TRUE))) + Salmo_trutta_artsobs_spatial(main = geometry,
##     copy = "Salmo_trutta_survey_spatial", hyper = list(beta = list(fixed = TRUE))) +
##     Salvelinus_alpinus_artsobs_spatial(main = geometry, copy = "Salvelinus_alpinus_survey_spatial",
##         hyper = list(beta = list(fixed = TRUE))) + Esox_lucius_artsobs_spatial(main = geometry,
##     copy = "Esox_lucius_survey_spatial", hyper = list(beta = list(fixed = TRUE)))
## <environment: 0x7f7a961d37b8>
```

We may look at which terms are included in each of the eight sub-models by calling `$updateFormula` with the data sets as the arguments.

```
fish_model_setup$updateFormula(datasetName = "survey")
```

```
## $Perca_fluviatilis
## occurrenceStatus ~ Perca_fluviatilis_log_area + Perca_fluviatilis_eurolst_bio10 +
##     Perca_fluviatilis_SCI + Perca_fluviatilis_intercept + Perca_fluviatilis_survey_spatial
## <environment: 0x7f7a9678ef60>
##
## $Salmo_trutta
## occurrenceStatus ~ Salmo_trutta_log_area + Salmo_trutta_eurolst_bio10 +
##     Salmo_trutta_SCI + Salmo_trutta_intercept + Salmo_trutta_survey_spatial
## <environment: 0x7f7a9678ef60>
##
## $Salvelinus_alpinus
## occurrenceStatus ~ Salvelinus_alpinus_log_area + Salvelinus_alpinus_eurolst_bio10 +
##     Salvelinus_alpinus_SCI + Salvelinus_alpinus_intercept + Salvelinus_alpinus_survey_spatial
## <environment: 0x7f7a9678ef60>
```

```
##
## $Esox_lucius
## occurrenceStatus ~ Esox_lucius_log_area + Esox_lucius_eurolst_bio10 +
##     Esox_lucius_SCI + Esox_lucius_intercept + Esox_lucius_survey_spatial
## <environment: 0x7f7a9678ef60>
```

```
fish_model_setup$updateFormula(datasetName = "artsobs")
```

```
## $Salvelinus_alpinus
## geometry ~ Salvelinus_alpinus_log_area + Salvelinus_alpinus_eurolst_bio10 +
##     Salvelinus_alpinus_SCI + Salvelinus_alpinus_intercept + Salvelinus_alpinus_artsobs_spatial +
##     artsobs_biasField
## <environment: 0x7f7a9678ef60>
##
## $Esox_lucius
## geometry ~ Esox_lucius_log_area + Esox_lucius_eurolst_bio10 +
##     Esox_lucius_SCI + Esox_lucius_intercept + Esox_lucius_artsobs_spatial +
##     artsobs_biasField
## <environment: 0x7f7a9678ef60>
##
## $Salmo_trutta
## geometry ~ Salmo_trutta_log_area + Salmo_trutta_eurolst_bio10 +
##     Salmo_trutta_SCI + Salmo_trutta_intercept + Salmo_trutta_artsobs_spatial +
##     artsobs_biasField
## <environment: 0x7f7a9678ef60>
##
## $Perca_fluviatilis
## geometry ~ Perca_fluviatilis_log_area + Perca_fluviatilis_eurolst_bio10 +
##     Perca_fluviatilis_SCI + Perca_fluviatilis_intercept + Perca_fluviatilis_artsobs_spatial +
##     artsobs_biasField
## <environment: 0x7f7a9678ef60>
```

Finally, we actually fit the model using `fitISDM`.

```
fish_model <- fitISDM(fish_model_setup,
                      options = list(
                        control.inla = list(int.strategy = 'eb', cmin = 0),
                        safe = TRUE,
                        inla.mode = 'experimental'))
```

We may then examine the model summary and save the model for future use.

```
summary(fish_model)

saveRDS(fish_model, "results/fish_model.rds")
```

6 Predictions and plots

Once the model has been fit, we can look at the predictions from the species-specific shared fields and the bias field.

We define a function that will do species-specific predictions, and save the species predictions, since these take a little time to compute.

```
predict_species <- function(model, species, mask, mesh){
  sharedfield <- predict(model,
                         mesh = mesh,
```

```
                          mask = mask,
                          format = 'sp',
                          spatial = TRUE,
                          fun = 'linear',
                          species = species,
                          n.samples = 1000)
  file_name <- paste0("results/sharedfield_", species, ".rds")
  saveRDS(sharedfield, file_name)
  return(sharedfield)
}
```

```
prediction_list <- list()
for(fish in fishes) {
  prediction_list[[fish]] <- predict_species(
    model = fish_model,
    mesh = mesh,
    mask = norway.poly,
    species = fish
  )
}
```

Once we have the predictions, we can make some plots. We similarly define a function that makes a plot for one species, and then run this for all four species.

```
plot_preferences <- list(scale_fill_distiller(palette = "BrBG", direction = 1),
                          coord_map(),
                          xlab(""), ylab(""), labs(fill = ""),
                          theme_minimal(),
                          theme(text = element_text(family = f1),
                                title = element_text(family = f1, size = 10),
                                legend.key.height = unit(0.3, "cm"),
                                legend.position = "bottom",
                                plot.margin = margin(10, 10, 0, 10, "points"))
)

plot_species <- function(predictions, species_to_plot, plot_preferences){
  p <- ggplot() +
    geom_polygon(data = norway, aes(long, lat, group = group),
                 color="grey80", fill = "grey95") +
    gg(predictions$speciesPredictions[[species_to_plot]]) +
    labs(title = sub("_", " ", species_to_plot)) +
    plot_preferences
  return(p)
}
```

```
plot_list <- list()
for(fish in fishes) {
  plot_list[[fish]] <- plot_species(
    predictions = readRDS(paste0("results/sharedfield_", fish, ".rds")),
    species = fish,
    plot_preferences = plot_preferences)
}

patchwork::wrap_plots(plot_list, nrow = 1)
ggsave("figures/fishplot_four_species.pdf", height = 2, width = 8)
```

And finally we predict and plot the bias field, which is shared between all the fish, as it describes the human sampling more than the distribution of the fish.

```
fish_biasfield <- predict(fish_model,
                          mesh = mesh,
                          mask = norway.poly,
                          format = 'sp',
                          biasfield = TRUE,
                          fun = 'linear',
                          n.samples = 1000) # Should "spatial" be false here?

saveRDS(fish_biasfield, "results/fish_biasfield.rds")
fish_biasfield <- readRDS("results/fish_biasfield.rds")

ggplot() +
  geom_polygon(data = norway, aes(long, lat, group = group),
               color="grey80", fill = "grey95") +
  gg(fish_biasfield$biasFields$artsobs) +
  labs(title = "Bias field") +
  plot_preferences

ggsave("figures/fishplot_biasfield.pdf", width = 3, height = 3)
```

This document took 0.01 hours to compile.