Analyse fulmars from the seabirds-at-sea data

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This vignette gives an example of modelling data from a seabirds-at-sea survey using the `dsm` package. The data here are for fulmars and were collected using a line transect for birds on the water and strip transect for flying birds.

```
library(Distance)
```

```
## Loading required package: mrds

## This is mrds 2.2.4
## Built: R 4.0.2; ; 2020-11-30 17:31:53 UTC; unix

##
## Attaching package: 'Distance'

## The following object is masked from 'package:mrds':
##
##     create.bins
```

```
library(dsm)
```

```
## Loading required package: mgcv

## Loading required package: nlme

## This is mgcv 1.8-34. For overview type 'help("mgcv-package")'.

## Loading required package: numDeriv

## This is dsm 2.3.1
## Built: R 4.0.2; ; 2021-03-23 21:16:18 UTC; unix
```

```
library(tidyr)
library(dplyr)
```

```
##
## Attaching package: 'dplyr'

## The following object is masked from 'package:nlme':
##
##     collapse

## The following objects are masked from 'package:stats':
##
##     filter, lag

## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
library(ggplot2)
library(patchwork)
library(sf)
```

```
## Linking to GEOS 3.8.1, GDAL 3.1.4, PROJ 6.3.1
```

Then load the data, already in `dsm` format. See the vignette to Miller et al., (2013), the `?"dsm-data"` manual page and this guide for more details on this data format.

```
load("RData/fulmars.RData")
ls()
```

```
## [1] "dists_fly"  "dists_swim" "obs"        "pred"       "pred_sf"
## [6] "segs"
```

A summary of the loaded objects

`dists_swim`

Distance data for the fulmars on the water, used to fit the detection function.

```
head(dists_swim)
```

```
##     object    Sample.Label size distance precip2 vis
## 215   1437 AA150617_03_004    1      250       1 0.5
## 223   1476 AA150617_06_005    1      150       1 0.5
## 224   1481 AA150617_07_003    1      150       1 0.5
## 226   1483 AA150617_07_003    1       25       1 0.5
## 227   1487 AA150617_07_004    4       75       1 0.5
## 229   1491 AA150617_07_005    1      150       1 0.5
```

`dists_fly`

The "distance" data for the flying fulmars, the `distance` column is not used but the data is used to set up a dummy detection function:

```
head(dists_fly)
```

```
##     object    Sample.Label size distance
## 199   1344 AA140617_07_003    1        0
## 218   1448 AA150617_04_004    1        0
## 225   1482 AA150617_07_003    1        0
## 233   1516 AA150617_09_001    1        0
## 240   1531 AA150617_09_004    1        0
## 241   1532 AA150617_09_004    1        0
```

`obs`

The observation `data.frame` that matches the `dists_` data to the sample units (transect segments) in `segs`.

```
head(obs)
```

```
##     object    Sample.Label size distance FlySwim
## 199   1344 AA140617_07_003    1       25       F
## 215   1437 AA150617_03_004    1      250       W
## 218   1448 AA150617_04_004    1      150       F
## 223   1476 AA150617_06_005    1      150       W
## 224   1481 AA150617_07_003    1      150       W
## 225   1482 AA150617_07_003    1       75       F
```

segs

The segment data, giving each sample location that was visited, the effort expended and the observation covariates collected at the segment level.

```
head(segs)
```

```
##            x         y    Sample.Label Effort precip2 vis
## 479 518947.9 -498769.8 AA130617_01_001   1494       0  10
## 480 518292.1 -497006.2 AA130617_01_002   1803       0  10
## 481 517222.0 -494920.7 AA130617_02_001   1860       0  10
## 482 516175.0 -493500.6 AA130617_02_002   1273       0  10
## 483 515335.1 -491547.0 AA130617_02_003   2557       0  10
## 484 514402.7 -488919.9 AA130617_02_004   2561       0  10
```

pred

The prediction grid with covariates as in `segs`:

```
head(pred)
```

```
##           x         y      area   off.set
## 1 -528819.5 -549250.9 117631586 117631586
## 2 -518193.3 -550130.9 117631586 117631586
## 3 -507565.3 -550992.9 117631586 117631586
## 4 -496935.7 -551837.1 117631586 117631586
## 5 -486304.4 -552663.4 117631586 117631586
## 6 -475671.4 -553471.8 117631586 117631586
```

pred_sf

The prediction grid in R `sf` format, for nicer printing (not essential).

```
head(pred_sf)
```

```
## Geometry set for 6 features
## Geometry type: POLYGON
## Dimension:     XY
## Bounding box:  xmin: -573026.7 ymin: -721675.4 xmax: -508720.5 ymax: -705027.2
## CRS:           +proj=ortho +datum=WGS84 +lon_0=-35 +lat_0=50
## First 5 geometries:

## POLYGON ((-573026.7 -715965.5, -562455.2 -71696...

## POLYGON ((-562455.2 -716963.7, -551880.6 -71794...

## POLYGON ((-551880.6 -717943.2, -541303.2 -71890...

## POLYGON ((-541303.2 -718904.2, -530722.9 -71984...

## POLYGON ((-530722.9 -719846.5, -520139.8 -72077...
```

Detection function analysis

First setting up the data for the swimming birds. Data are collected in bins, so we first need to set up the distance bins:

```
dbins <- c(0, 50, 100, 200, 300)
```

We can now fit detection functions for birds on the water:

```
df_swim_hn <- ds(dists_swim, key='hn', formula=~precip2+vis, adjustment=NULL,
                 cutpoints=dbins)
```

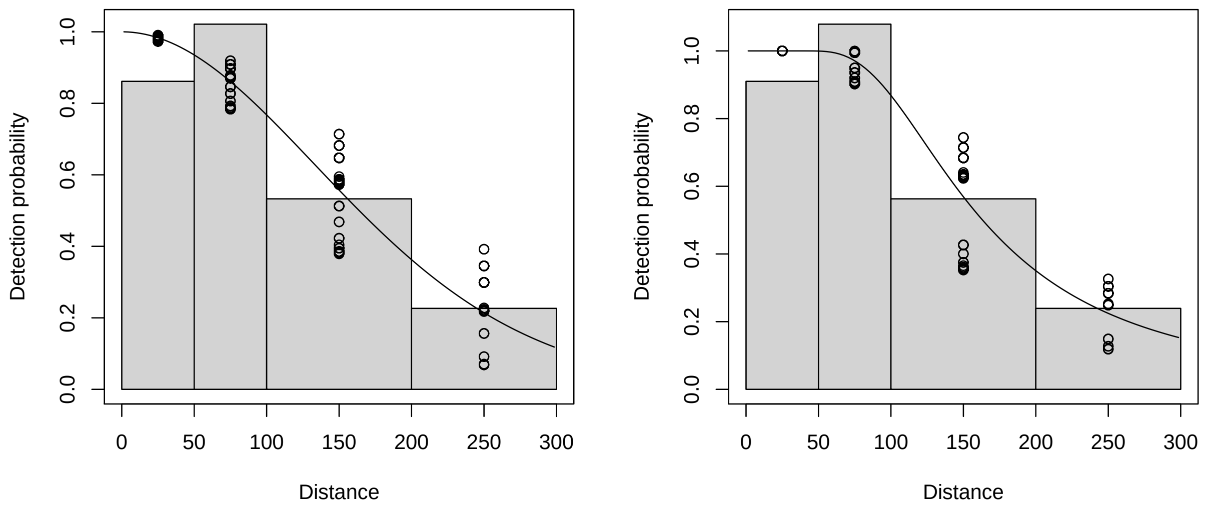
```
## Fitting half-normal key function

## AIC= 1030.036

## No survey area information supplied, only estimating detection function.
```

```
df_swim_hr <- ds(dists_swim, key='hr', formula=~precip2+vis, adjustment=NULL,
                 cutpoints=dbins)
```

```
## Fitting hazard-rate key function

## AIC= 1031.668

## No survey area information supplied, only estimating detection function.
```

We can plot the fitted detection functions:

```
par(mfrow=c(1,2))
plot(df_swim_hn)
plot(df_swim_hr)
```



Comparing models by AIC, we see the half-normal is preferred (but not by much):

```
AIC(df_swim_hn, df_swim_hr)
```

```
##            df      AIC
## df_swim_hn  3 1030.036
## df_swim_hr  4 1031.668
```

(Note we are not able to do a χ^2 goodness-of-fit test as we do not have enough degrees of freedom, as the data were binned at time of collection.)

We can look at the summary of that model:

```
summary(df_swim_hn)
```

```
##
```

```
## Summary for distance analysis
## Number of observations :  383
## Distance range         :  0  -  300
##
## Model : Half-normal key function
## AIC   : 1030.036
##
## Detection function parameters
## Scale coefficient(s):
##                estimate         se
## (Intercept)  4.95362188 0.10566336
## precip21    -0.27832397 0.11724187
## vis          0.01269992 0.01012255
##
##                         Estimate          SE         CV
## Average p              0.5668975  0.02649756 0.04674136
## N in covered region 675.6071023 39.04742187 0.05779605
```

We now construct the dummy detection function to incorporate birds on the water:

```
df_fly <- dummy_ddf(object=dists_fly$object, size=dists_fly$size, width=300)
```

We can use `summary` to check that the model is set-up correctly (at least the number of observations and truncation are correct):

```
summary(df_fly)
```

```
##
## Summary for dummy ds object
## Number of observations :  460
## Distance range         :  0  -  300
##
## Model : No detection function, strip transect
##
## AIC   : NA
```

Setup data

Now we need to setup the segment data to use the multi-platform approach. The first part of this consists of duplicating the segment data to have a set of segments for flying birds and another for birds on the water. We also need to create a column indicating which detection function will be used for a given segment (`ddfobj`) and ensure that the `Sample.Label` is unique.

```
# first duplicate the segment table
segs2 <- rbind(segs, segs)

# create a ddfobj field to keep track of which detection function to use
segs2$ddfobj <- c(rep(1, nrow(segs)), rep(2, nrow(segs)))

# create a flying vs swimming factor, which has the same information as ddfobj
# but has a friendlier name for modelling
segs2$FlySwim <- factor(c(rep("swim", nrow(segs)),
                          rep("fly", nrow(segs))),
                        c("swim", "fly"))

# ensure that that Sample.Labels are unique, concatenating the current
# label with the ddfobj value
segs2$Sample.Label[segs2$ddfobj == 1] <- paste0(segs2$Sample.Label[segs2$ddfobj == 1],
                                                "-1")
segs2$Sample.Label[segs2$ddfobj == 2] <- paste0(segs2$Sample.Label[segs2$ddfobj == 2],
                                                "-2")
```

`dsm` assumes that both sides of the transect were observed, this was not the case for this survey, so we now need to half the effort (this is unrelated to duplicating the effort above):

```
segs2$Effort <- segs2$Effort/2
```

Our next task is to re-write the observation table to ensure that the `Sample.Label`s match those in the segment table and include the `ddfobj` column as for the segment data.

```
obs$Sample.Label[obs$FlySwim == "W"] <- paste0(obs$Sample.Label[obs$FlySwim == "W"], "-1")
obs$Sample.Label[obs$FlySwim == "F"] <- paste0(obs$Sample.Label[obs$FlySwim == "F"], "-2")

# add ddfobj column
obs$ddfobj <- c(1,2)[(obs$FlySwim=="F") + 1]

# simplify columns
obs <- obs[, c("ddfobj", "Sample.Label", "size", "distance", "object")]
```

Now we have the data setup, we can start to fit models.

Fitting the spatial model

We start with the model with no extra terms accounting for platform:

```
dsm_nofactor <- dsm(count~s(x, y, k=100, bs="ts"),
                    ddf.obj=list(df_swim_hn, df_fly),
                    segment.data=segs2, observation.data=obs, family=nb())
summary(dsm_nofactor)
```

```
##
## Family: Negative Binomial(1.475)
## Link function: log
##
## Formula:
## count ~ s(x, y, k = 100, bs = "ts") + offset(off.set)
##
## Parametric coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -16.7064     0.4614  -36.21   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##          edf Ref.df Chi.sq p-value
## s(x,y) 38.79     99    569  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.402   Deviance explained = 63.2%
## -REML = 1307.8  Scale est. = 1         n = 1932
```

Note here that we include a `list` of detection functions. The order of the list relates to the `ddfobj` column in the data (`df_swim_hn` is `ddfobj==1` and `df_fly` is `ddfobj==2`).

Now with a factor for on water/flying:

```
dsm_factor <- dsm(count~ FlySwim + s(x, y, k=100, bs="ts"),
                  ddf.obj=list(df_swim_hn, df_fly),
                  segment.data=segs2, observation.data=obs, family=nb())
summary(dsm_factor)
```

```
##
## Family: Negative Binomial(1.664)
## Link function: log
##
## Formula:
## count ~ FlySwim + s(x, y, k = 100, bs = "ts") + offset(off.set)
##
## Parametric coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -16.42569    0.46707 -35.168  < 2e-16 ***
## FlySwimfly   -0.52787    0.08727  -6.049 1.46e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##          edf Ref.df Chi.sq p-value
## s(x,y) 39.28     99  571.3  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.429   Deviance explained = 64.6%
## -REML = 1291.9  Scale est. = 1         n = 1932
```

And finally the factor-smooth interaction

```
dsm_factorsmooth <- dsm(count~ s(x, y, FlySwim, bs="fs", k=100),
                        ddf.obj=list(df_swim_hn, df_fly),
                        segment.data=segs2, observation.data=obs, family=nb())
summary(dsm_factorsmooth)
```

```
##
## Family: Negative Binomial(1.863)
## Link function: log
##
## Formula:
## count ~ s(x, y, FlySwim, bs = "fs", k = 100) + offset(off.set)
##
## Parametric coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)   -2.732     22.511  -0.121    0.903
##
## Approximate significance of smooth terms:
##                  edf Ref.df Chi.sq p-value
## s(x,y,FlySwim) 65.43    199  630.2  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## R-sq.(adj) =  0.449   Deviance explained = 66.9%
## -REML = 1296.6  Scale est. = 1         n = 1932
```

Propagate uncertainty

We can now use the `dsm_varprop` function to propagate the variance from the detection function through to the spatial model using the method of Bravington et al. (2021). The returned object has a `$refit` element which is a density surface model with a covariance matrix including the uncertainty from the detection function. We don't supply any data (which prompts a warning from `dsm_varprop`) since we are only interested in the refitted model.

```
vp_nofactor <- dsm_varprop(dsm_nofactor)
```

```
## Warning in dsm_varprop(dsm_nofactor): No newdata provided, no predictions
## returned.
```

```
vp_factor <- dsm_varprop(dsm_factor)
```

```
## Warning in dsm_varprop(dsm_factor): No newdata provided, no predictions
## returned.
```

```
vp_fs <- dsm_varprop(dsm_factorsmooth)
```

```
## Warning in dsm_varprop(dsm_factorsmooth): No newdata provided, no predictions
## returned.
```

We can now look at comparing the observed versus the expected values and plot them in a table:

```
knitr::kable(cbind(t(obs_exp(vp_nofactor$refit, "FlySwim")),
                   t(obs_exp(vp_factor$refit, "FlySwim"))[, 2, drop=FALSE],
                   t(obs_exp(vp_fs$refit, "FlySwim"))[, 2, drop=FALSE]),
             format="latex", digits=0,
             col.names=c("Observed", "Null",
                         "Factor", "Factor-smooth"))
```

	Observed	Null	Factor	Factor-smooth
swim	501	405	501	490
fly	533	632	516	517

We can also compare AIC of these models:

```
AIC(vp_nofactor$refit, vp_factor$refit, vp_fs$refit)
```

```
##                         df      AIC
## vp_nofactor$refit 42.60790 2517.002
## vp_factor$refit   43.76449 2495.230
## vp_fs$refit       69.30821 2483.713
```

So by AIC we prefer the factor-smooth model.

Prediction

Now we can make predictions for each of these models. This code is a little complex as it involved binding the predictions onto `pred_sf` which is a spatial object with projection information. We create a `data.frame` that includes flying and swimming abundances combined and individually for the factor and factor-smooth models.

```
# create an extra column to account for the variance propagation model
# the variance propagation adds a random effect covariate named "XX"
# which we can safely give the value 0 now the variance has been propagated.
pred$XX <- matrix(0, nrow=nrow(pred), ncol=3)

# nofactor model
pred_nofactor <- pred
pred_nofactor$Nhat <- predict(vp_nofactor$refit, newdata=pred_nofactor,
                              off.set=pred_nofactor$area)
pred_nofactor$model <- "No factor"
pred_nofactor$subset <- "Combined"

# bind on the spatial data
pred_nofactor_plots <- st_sf(pred_sf, pred_nofactor[,c("model","subset","Nhat")])


# factor model
pred_factor <- rbind(pred, pred)
pred_factor$FlySwim <- factor(rep(c("fly", "swim"), c(nrow(pred), nrow(pred))),
                              c("swim", "fly"))
pred_factor$Nhat <- predict(vp_factor$refit, newdata=pred_factor,
                            off.set=pred_factor$area)
pred_factor$model <- "Factor"
pred_factor$subset <- as.character(pred_factor$FlySwim)

# bind on the spatial data
pred_factor_plots <- st_sf(pred_sf, pred_factor[, c("model", "subset", "Nhat")])
```

```
## Warning in data.frame(..., check.names = FALSE): row names were found from a
## short variable and have been discarded
```

```
# prepare the combined/difference columns
pred_factor_plots2 <- pred_factor_plots
pred_factor_plots2$subset <- rep(c("Combined", "Difference"),
                                 c(nrow(pred), nrow(pred)))
# combined estimate
pred_factor_plots2$Nhat[pred_factor_plots2$subset=="Combined"] <-
  (pred_factor_plots$Nhat[1:nrow(pred)] +
   pred_factor_plots$Nhat[(nrow(pred)+1):(2*nrow(pred))])/2
# difference in estimates
pred_factor_plots2$Nhat[pred_factor_plots2$subset=="Difference"] <-
  pred_factor_plots$Nhat[1:nrow(pred)] -
   pred_factor_plots$Nhat[(nrow(pred)+1):(2*nrow(pred))]

# bind them together
pred_factor_plots <- rbind(pred_factor_plots, pred_factor_plots2)


# factor-smooth model
pred_fs <- pred_factor
pred_fs$Nhat <- predict(vp_fs$refit, newdata=pred_fs,
                        off.set=pred_factor$area)
pred_fs$model <- "Factor-smooth"
pred_fs$subset <- as.character(pred_fs$FlySwim)
```

```r
# bind on the spatial data
pred_fs_plots <- st_sf(pred_sf, pred_fs[,c("model", "subset", "Nhat")])
```

```
## Warning in data.frame(..., check.names = FALSE): row names were found from a
## short variable and have been discarded
```

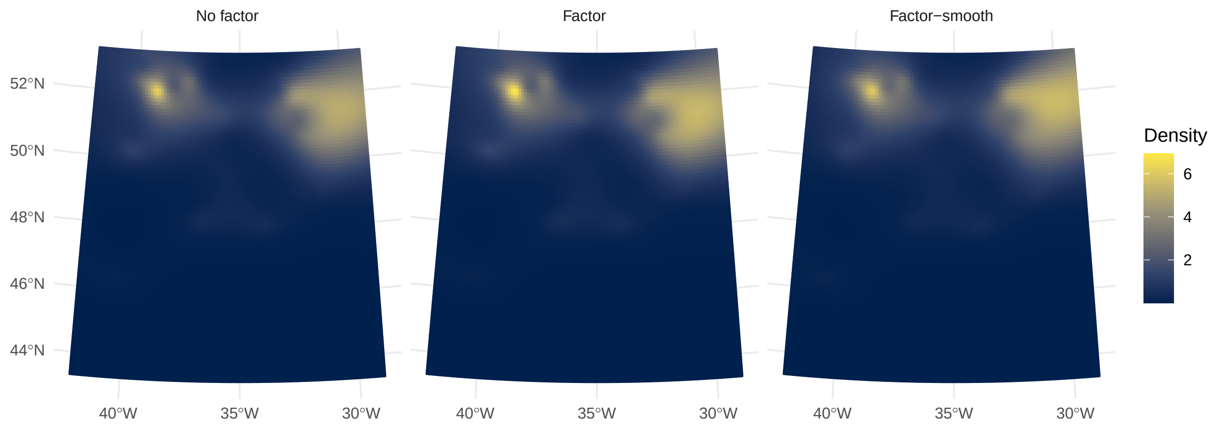
```r
# prepare the combined/difference columns
pred_fs_plots2 <- pred_fs_plots
pred_fs_plots2$subset <- rep(c("Combined", "Difference"),
                             c(nrow(pred), nrow(pred)))

# combined estimate
pred_fs_plots2$Nhat[pred_fs_plots2$subset=="Combined"] <-
  (pred_fs_plots$Nhat[1:nrow(pred)] +
   pred_fs_plots$Nhat[(nrow(pred)+1):(2*nrow(pred))])/2
# difference in estimates
pred_fs_plots2$Nhat[pred_fs_plots2$subset=="Difference"] <-
  pred_fs_plots$Nhat[1:nrow(pred)] -
   pred_fs_plots$Nhat[(nrow(pred)+1):(2*nrow(pred))]

# bind them together
pred_fs_plots <- rbind(pred_fs_plots, pred_fs_plots2)
```

Once we've put all this together, we calculate a density for plotting by dividing by grid cell area

```r
# concatenate everything
all_Nhats <- rbind(pred_nofactor_plots, pred_factor_plots, pred_fs_plots)
# convert abundance to density
# note that st_area will give the area in metres and we want density per km^2
all_Nhats$Density <- all_Nhats$Nhat/(as.numeric(st_area(all_Nhats)) / 1000^2)

# reorder rows to give preferred plotting order
all_Nhats$model <- factor(all_Nhats$model,
                          c("No factor", "Factor", "Factor-smooth"))
```

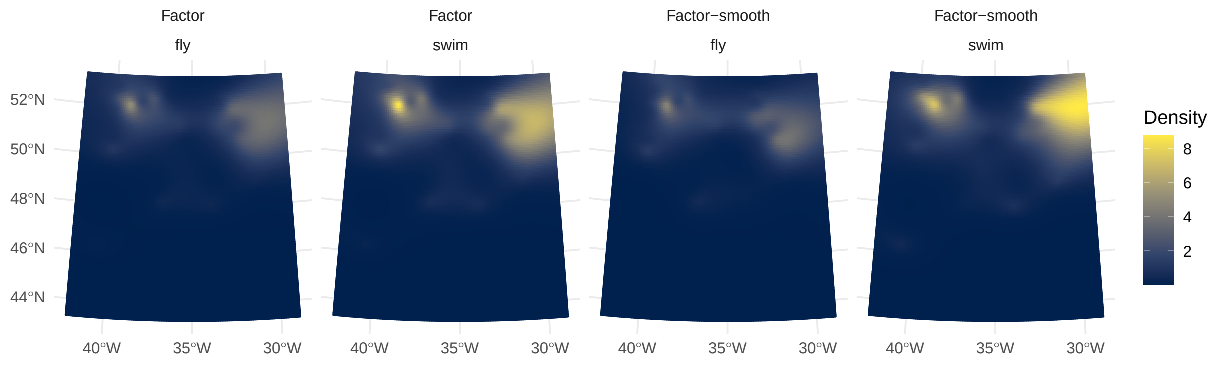
We can now plot of the combined results:

```r
combined_data <- subset(all_Nhats, subset=="Combined")

combined_plot <- ggplot() +
  geom_sf(data=combined_data, aes(colour=Density, fill=Density)) +
  facet_wrap(~model, drop=TRUE, nrow=1) +
  labs(x="", y="", fill="Density") +
  theme_minimal() +
  scale_colour_viridis_c(option="E") +
  scale_fill_viridis_c(option="E")
combined_plot
```



And the uncombined predictions:

```
uncombined_data <- subset(all_Nhats, subset %in% c("swim", "fly"))

uncombined_plot <- ggplot() +
  geom_sf(data=uncombined_data, aes(colour=Density, fill=Density)) +
  facet_wrap(model~subset, drop=TRUE, nrow=1) +
  labs(x="", y="", fill="Density") +
  theme_minimal() +
  scale_colour_viridis_c(option="E") +
  scale_fill_viridis_c(option="E")
uncombined_plot
```



Estimating variance

To estimate variance of the predictions we first need to construct the matrix that maps the parameters to the predictions on the linear predictor scale, $\mathbf{X}_p$.

```
lp_nofactor <- predict(vp_nofactor$refit, newdata=pred, type="lpmatrix")
lp_factor <- predict(vp_factor$refit, newdata=pred_factor, type="lpmatrix")
lp_fs <- predict(vp_fs$refit, newdata=pred_factor, type="lpmatrix")
```

We can then generate parameter samples using the Metropolis-Hasting sampler in `mgcv`. We need to use tools from `https://github.com/dill/GAMsampling` to ensure that the sampling works for the variance-propagated DSM.

```
# load additional code
source("likelihood_tools.R")
source("gam.mh_fix.R")
source("ttools.R")
samples_nofactor <- gam.mh(vp_nofactor$refit, ns=10000, burn=1000, t.df=20,
                           rw.scale=.05, thin=10)
samples_factor <- gam.mh(vp_factor$refit, ns=10000, burn=1000, t.df=20,
                         rw.scale=.05, thin=10)
samples_fs <- gam.mh(vp_fs$refit, ns=10000, burn=1000, t.df=20,
                     rw.scale=.025, thin=10)
```

We can now make grids of abundance estimates per cell per posterior sample:

```
nofactor_Ngrid <- pred_nofactor$area * exp(lp_nofactor %*% t(samples_nofactor$bs))
factor_Ngrid <- pred_factor$area * exp(lp_factor %*% t(samples_factor$bs))
fs_Ngrid <- pred_factor$area * exp(lp_fs %*% t(samples_fs$bs))
```

Once we have the estimates for each grid cell for each sample, we can build the data for plotting. This involves taking the empirical variance of these predictions over the samples.

```
all_Nhats$var <- NA
all_Nhats$var[all_Nhats$model == "No factor" &
              all_Nhats$subset == "Combined"] <- apply(nofactor_Ngrid, 1, var)

# for the factor model, we have the first 10000 entries for the first level
# of the factor and the second 10000 for the second level, we need a variance
# for each of those subsets
all_Nhats$var[all_Nhats$model == "Factor" &
              all_Nhats$subset == "fly"] <- apply(factor_Ngrid[1:10000,],
                                                  1, var)
all_Nhats$var[all_Nhats$model == "Factor" &
              all_Nhats$subset == "swim"] <- apply(factor_Ngrid[10001:20000,],
                                                   1, var)
all_Nhats$var[all_Nhats$model == "Factor" &
              all_Nhats$subset == "Combined"] <-  apply(factor_Ngrid[1:10000,] +
                               factor_Ngrid[10001:20000,], 1, var)
all_Nhats$var[all_Nhats$model == "Factor" &
              all_Nhats$subset == "Difference"] <-
  sqrt(all_Nhats$var[all_Nhats$model == "Factor" &
                     all_Nhats$subset == "fly"])-
  sqrt(all_Nhats$var[all_Nhats$model == "Factor" &
                     all_Nhats$subset == "swim"])

# same with the factor-smooth model
```

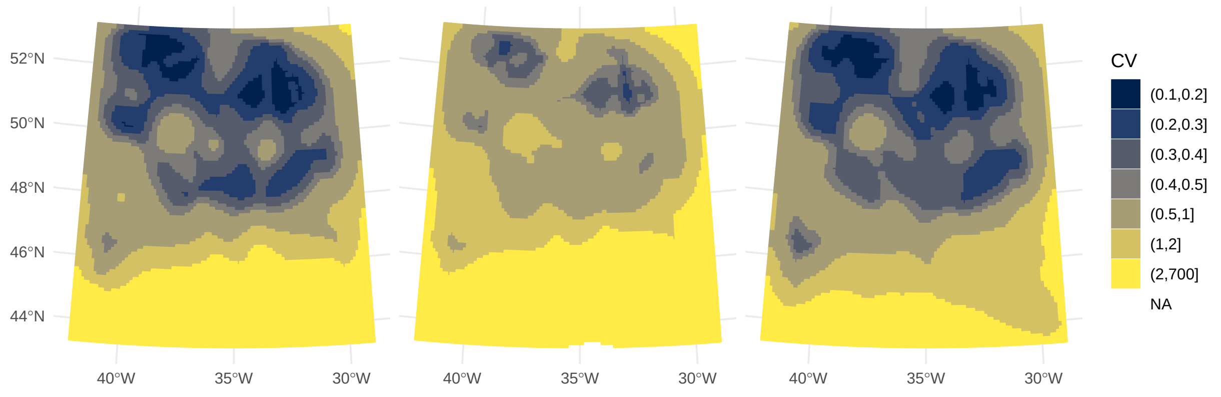
```
all_Nhats$var[all_Nhats$model == "Factor-smooth" &
              all_Nhats$subset == "fly"] <- apply(factor_Ngrid[1:10000,],
                                                  1, var)
all_Nhats$var[all_Nhats$model == "Factor-smooth" &
              all_Nhats$subset == "swim"] <- apply(factor_Ngrid[10001:20000,],
                                                   1, var)
all_Nhats$var[all_Nhats$model == "Factor-smooth" &
              all_Nhats$subset == "Combined"] <-  apply((factor_Ngrid[1:10000,] +
                              factor_Ngrid[10001:20000,])/2, 1, var)
all_Nhats$var[all_Nhats$model == "Factor-smooth" &
              all_Nhats$subset == "Difference"] <-
  sqrt(all_Nhats$var[all_Nhats$model == "Factor-smooth" &
                     all_Nhats$subset == "fly"])-
  sqrt(all_Nhats$var[all_Nhats$model == "Factor-smooth" &
                     all_Nhats$subset == "swim"])

# make a CV column
all_Nhats$CV <- (sqrt(all_Nhats$var))/all_Nhats$Nhat
```

```
## Warning in sqrt(all_Nhats$var): NaNs produced
```

```
# discretize
all_Nhats$CV_d <- cut(all_Nhats$CV,
                      c(0, 0.05, 0.1, 0.2, 0.3, 0.4, 0.5, 1, 2, 700))
```

Now we can make a plot of the combined effects

```
combined_CV_data <- subset(all_Nhats, subset=="Combined")

combined_CV_plot <- ggplot() +
  geom_sf(data=combined_CV_data, aes(fill=CV_d, colour=CV_d)) +
  facet_wrap(~model, drop=TRUE, nrow=1) +
  labs(x="", y="", fill="CV", colour="CV") +
  theme_minimal() +
  theme(strip.text.x = element_blank()) +
  scale_fill_viridis_d(option="E") +
  scale_colour_viridis_d(option="E")
combined_CV_plot
```



```r
# write out the plot for the paper
# (here using patchwork to put the plots ontop of each other)
ggsave(combined_plot / combined_CV_plot, file="figures/fulmar_combined.pdf",
       width=13, height=9)
```

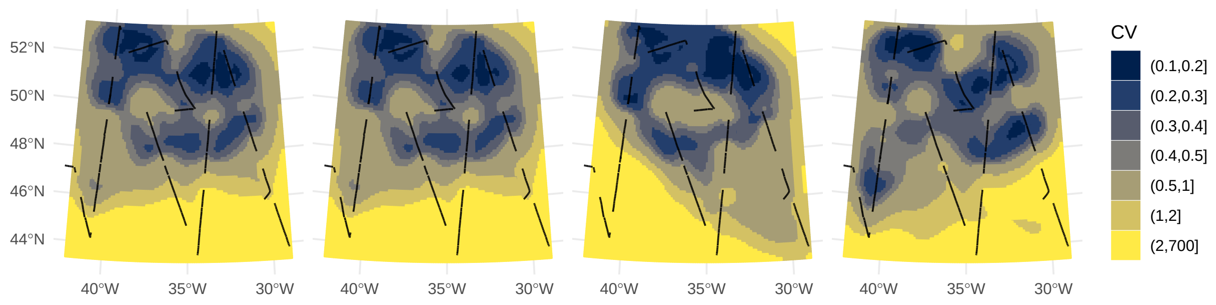
And the uncombined CV plots:

```r
# load track to overplot
load("RData/track_sf.RData")
track_sf <- st_transform(track_sf, st_crs(pred_sf))
track_sf <- st_crop(track_sf, pred_sf)
```

```
## Warning: attribute variables are assumed to be spatially constant throughout all
## geometries
```

```r
uncombined_CV_data <- subset(all_Nhats, subset %in% c("swim", "fly"))

uncombined_CV_plot <- ggplot() +
  geom_sf(data=uncombined_CV_data, aes(fill=CV_d, colour=CV_d)) +
  geom_sf(data=track_sf) +
  facet_wrap(model~subset, drop=TRUE, nrow=1) +
  labs(x="", y="", fill="CV", colour="CV") +
  theme_minimal() +
  theme(strip.text.x=element_blank()) +
  scale_fill_viridis_d(option="E") +
  scale_colour_viridis_d(option="E")
uncombined_CV_plot
```

```
## Warning in strip_mat[panel_pos] <- unlist(unname(strips), recursive = FALSE)
## [[params$strip.position]]: number of items to replace is not a multiple of
## replacement length
```

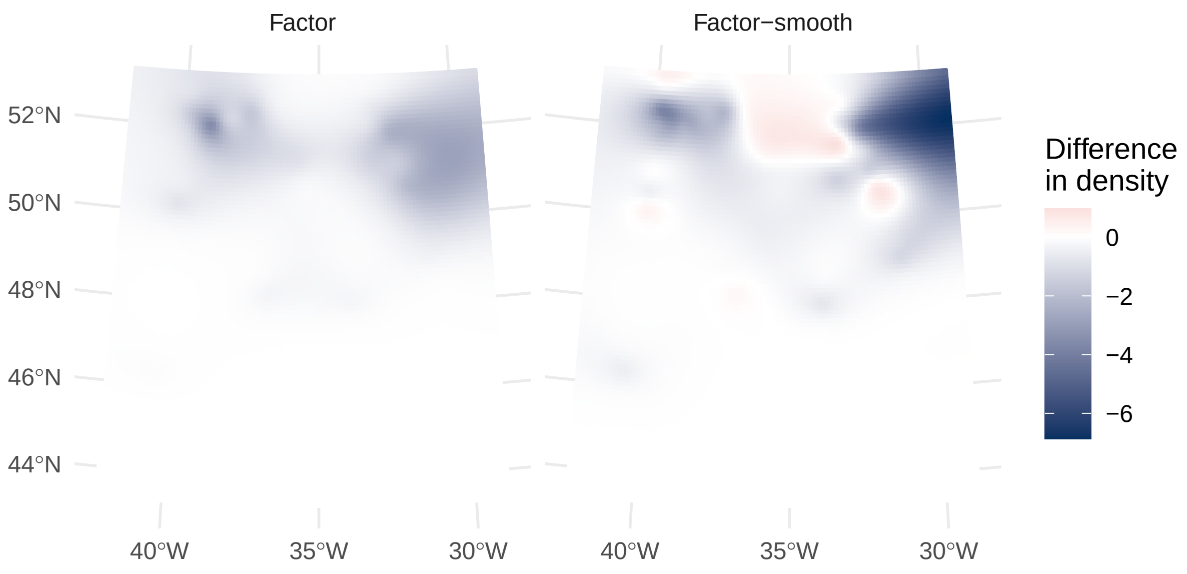


```
# write out the plot for the paper
# (again using patchwork to put the plots ontop of each other)
ggsave(uncombined_plot / uncombined_CV_plot, file="figures/fulmar_uncombined.pdf",
       width=13, height=7.5)
```

```
## Warning in strip_mat[panel_pos] <- unlist(unname(strips), recursive = FALSE)
## [[params$strip.position]]: number of items to replace is not a multiple of
## replacement length
```

Finally we can plot the differences between the platforms within each model:

```
diff_data <- subset(all_Nhats, subset=="Difference")

diff_plot <- ggplot() +
  geom_sf(data=diff_data, aes(fill=Nhat/10^2, colour=Nhat/10^2)) +
  facet_wrap(~model, drop=TRUE, nrow=1) +
  labs(x="", y="", fill="Difference\nin density", colour="Difference\nin density") +
  theme_minimal() +
  scale_fill_gradient2(low="#053061", high="#b2182b") +
  scale_colour_gradient2(low="#053061", high="#b2182b")
diff_plot
```



```r
# write out the plot for the paper
ggsave(diff_plot, file="figures/fulmar_diff.pdf", width=13, height=7.5)
```