

Calculation and application of the Species Synanthropy Index: additional example

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This second tutorial demonstrates the applicability of the SSI function to larger datasets, such as GBIF data.

We load necessary packages

```
library(SynAnthrop)
library(dplyr)
library(magrittr)
library(ggplot2)
```

Species Synanthropy Index: an example with GBIF data of amphibian populations in France

Setup

The raster map used here is extracted from the French Naturalness Map, developed by Guetté et al.(2021). This raster layer is not loaded with the `Synanthrop` package and can be downloaded here and must be put in the `data/amphibiansGBIF` folder of this project under the name `Naturalness_France.tif`.

```
ras_raw <- raster::raster(file.path(here::here(), "data", "amphibiansGBIF", "Naturalness_France.tif"))
rast_to_plot <- terra::rast(ras_raw)
```

Next, we load the occurrence data to be evaluated and check for missing coordinates.

```
sp0cc <- read.csv(file.path(here::here(),
                             "data",
                             "amphibiansGBIF",
                             "amphibiansOccurrencesGBIF.csv"),
                  sep = ";", h=T, na.strings=c("(vide)"))

# eliminate points with missing coordinates
missingcoord <- dim(sp0cc %>% filter(is.na(Y) | !is.na(Y)))[1]
sp0cc %>% filter(!is.na(Y) | !is.na(Y))
cat(paste(missingcoord, "point(s) were eliminated because of missing coordinates"))
```

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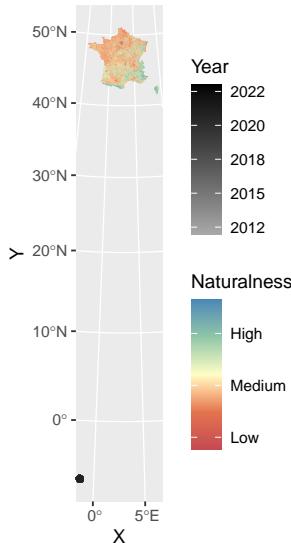
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```
## 1 point(s) were eliminated because of missing coordinates
```

We plot the data to make sure the two datasets use the same coordinate system and everything looks as expected.

```
ggplot() +
  tidyterra::geom_spatraster(data = rast_to_plot) +
  geom_point(data = sp0cc, aes(x = X, y = Y, color = Year)) +
  scale_colour_gradient(labels = function(x) sprintf("%.0f", x),
                        low = "darkgray", high = "black") +
  tidyterra::scale_fill_whitebox_c(palette = "muted", direction = -1,
                                   breaks = c(100, 325, 550),
                                   labels = c("Low", "Medium", "High"),
                                   name = "Naturalness")
```

```
## SpatRaster resampled to ncells = 500588
```

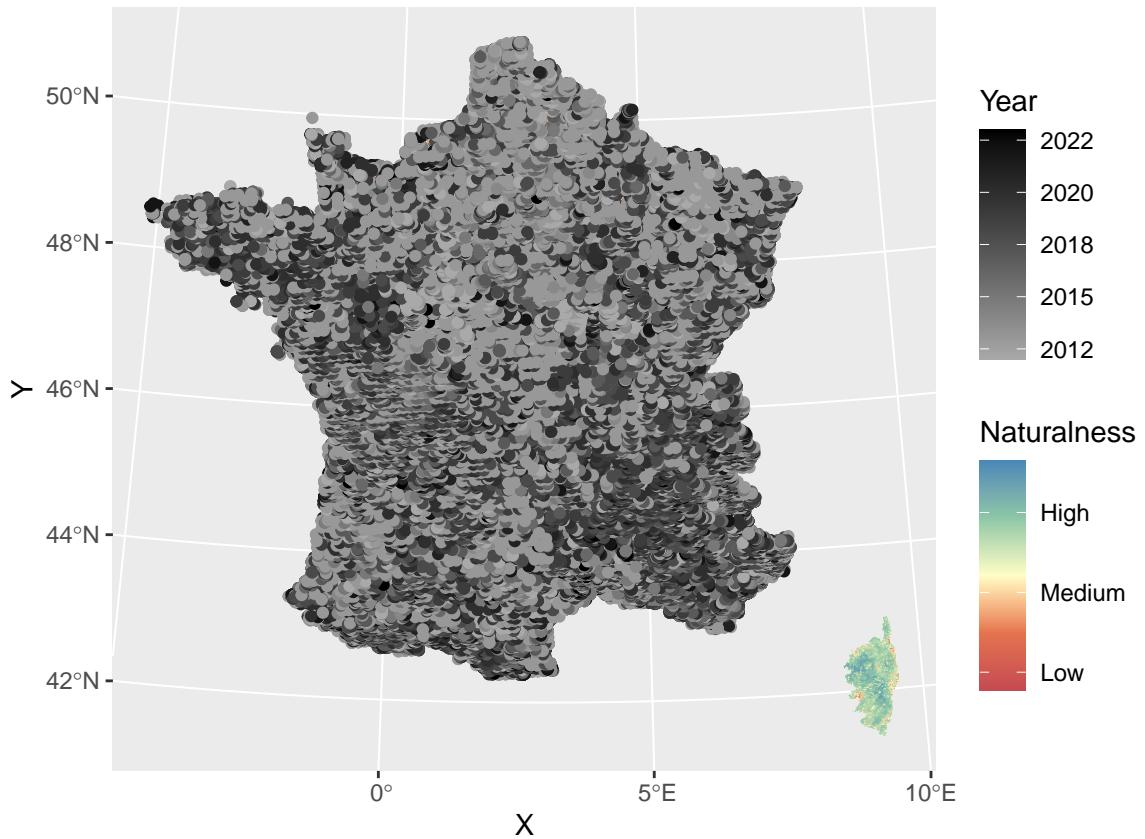


Coordinates seem to be from different coordinate systems. We convert the occurrence data coordinate system (RGF93) to match that of the raster file (WGS84) and check if coordinates now match.

```
sp_map <- sf::st_as_sf(sp0cc, coords = c("X", "Y"), crs = 4326)
LCCcoord <- data.frame(sp_map %>%
  sf::st_transform(crs = sf::st_crs(ras_raw)) %>%
  sf::st_coordinates())
sp0cc %>% mutate(X = LCCcoord$X,
                   Y = LCCcoord$Y)

ggplot() +
  tidyterra::geom_spatraster(data = rast_to_plot) +
  geom_point(data = sp0cc, aes(x = X, y = Y, color = Year)) +
  scale_colour_gradient(labels = function(x) sprintf("%.0f", x),
                        low = "darkgray", high = "black") +
  tidyterra::scale_fill_whitebox_c(palette = "muted", direction = -1,
                                   breaks = c(100, 325, 550),
                                   labels = c("Low", "Medium", "High"),
                                   name = "Naturalness")
```

```
## SpatRaster resampled to ncells = 500588
```



SSI calculation

Here, we execute the function for 2 resolutions (500, 1000), with 500 simulations each. Each species must have been found in a minimum of 1000 cells to be evaluated (threshold argument). You will be prompted to validate the species list detected in the dataset.

```
ssi_results <- ssi(r = ras_raw,
                     resolution = c(1000, 500),
                     data = spOcc,
                     sim = 500,
                     threshold = 1000)
```

```
## 2023-08-18 09:34:39 - Aggregate naturalness raster cells at resolution 1000 (this step may take a few minutes)
## 1 observation(s) were eliminated because of mismatch with the raster file
```

```
## Warning in ks.defaults(x = x, w = w, binned = binned, bgridsize = bgridsize, : Weights don't sum to zero, so they were scaled down by 0.0001000000000002
## Species that will be evaluated are:
## Alytes obstetricans
## Bufo bufo
## Lissotriton helveticus
## Rana dalmatina
```

```

## Rana temporaria
## Salamandra salamandra
## 2023-08-18 10:07:18 - Generating null distributions for:
## 2023-08-18 10:07:18 Alytes obstetricans (1/6)
## Simulation 1/500... 100/500... 200/500... 300/500... 400/500... 500/500
## 2023-08-18 10:07:41 Bufo bufo (2/6)
## Simulation 1/500... 100/500... 200/500... 300/500... 400/500... 500/500
## 2023-08-18 10:08:00 Lissotriton helveticus (3/6)
## Simulation 1/500... 100/500... 200/500... 300/500... 400/500... 500/500
## 2023-08-18 10:08:23 Rana dalmatina (4/6)
## Simulation 1/500... 100/500... 200/500... 300/500... 400/500... 500/500
## 2023-08-18 10:08:45 Rana temporaria (5/6)
## Simulation 1/500... 100/500... 200/500... 300/500... 400/500... 500/500
## 2023-08-18 10:09:07 Salamandra salamandra (6/6)
## Simulation 1/500... 100/500... 200/500... 300/500... 400/500... 500/500
## 2023-08-18 10:09:32 - Calculating effect sizes...
## Simulation 1/500... 100/500... 200/500... 300/500... 400/500... 500/500
## 2023-08-18 10:14:37 Analysis finished for resolution 1000
## 2023-08-18 10:14:37 - Aggregate naturalness raster cells at resolution 500 (this step may take a few
## 1 observation(s) were eliminated because of mismatch with the raster file

## Warning in ks.defaults(x = x, w = w, binned = binned, bgridsize = bgridsize, : Weights don't sum to 1

## Species that will be evaluated are:
## Alytes obstetricans
## Bombina variegata
## Bufo bufo
## Bufo spinosus
## Epidalea calamita
## Hyla arborea
## Hyla meridionalis
## Ichthyosaura alpestris
## Lissotriton helveticus
## Pelodytes punctatus
## Pelophylax ridibundus
## Rana dalmatina
## Rana temporaria
## Salamandra salamandra
## Triturus cristatus
## Triturus marmoratus
## 2023-08-18 10:42:21 - Generating null distributions for:
## 2023-08-18 10:42:21 Alytes obstetricans (1/16)
## Simulation 1/500... 100/500... 200/500... 300/500... 400/500... 500/500
## 2023-08-18 10:43:17 Bombina variegata (2/16)
## Simulation 1/500... 100/500... 200/500... 300/500... 400/500... 500/500
## 2023-08-18 10:43:41 Bufo bufo (3/16)
## Simulation 1/500... 100/500... 200/500... 300/500... 400/500... 500/500
## 2023-08-18 10:44:27 Bufo spinosus (4/16)
## Simulation 1/500... 100/500... 200/500... 300/500... 400/500... 500/500
## 2023-08-18 10:45:02 Epidalea calamita (5/16)
## Simulation 1/500... 100/500... 200/500... 300/500... 400/500... 500/500
## 2023-08-18 10:45:41 Hyla arborea (6/16)
## Simulation 1/500... 100/500... 200/500... 300/500... 400/500... 500/500
## 2023-08-18 10:46:21 Hyla meridionalis (7/16)

```

```

## Simulation 1/500... 100/500... 200/500... 300/500... 400/500... 500/500
## 2023-08-18 10:46:45 Ichthyosaura alpestris (8/16)
## Simulation 1/500... 100/500... 200/500... 300/500... 400/500... 500/500
## 2023-08-18 10:47:16 Lissotriton helveticus (9/16)
## Simulation 1/500... 100/500... 200/500... 300/500... 400/500... 500/500
## 2023-08-18 10:48:15 Pelodytes punctatus (10/16)
## Simulation 1/500... 100/500... 200/500... 300/500... 400/500... 500/500
## 2023-08-18 10:48:40 Pelophylax ridibundus (11/16)
## Simulation 1/500... 100/500... 200/500... 300/500... 400/500... 500/500
## 2023-08-18 10:49:20 Rana dalmatina (12/16)
## Simulation 1/500... 100/500... 200/500... 300/500... 400/500... 500/500
## 2023-08-18 10:50:20 Rana temporaria (13/16)
## Simulation 1/500... 100/500... 200/500... 300/500... 400/500... 500/500
## 2023-08-18 10:51:20 Salamandra salamandra (14/16)
## Simulation 1/500... 100/500... 200/500... 300/500... 400/500... 500/500
## 2023-08-18 10:52:21 Triturus cristatus (15/16)
## Simulation 1/500... 100/500... 200/500... 300/500... 400/500... 500/500
## 2023-08-18 10:52:55 Triturus marmoratus (16/16)
## Simulation 1/500... 100/500... 200/500... 300/500... 400/500... 500/500
## 2023-08-18 10:53:33 - Calculating effect sizes...
## Simulation 1/500... 100/500... 200/500... 300/500... 400/500... 500/500
## 2023-08-18 11:12:25 Analysis finished for resolution 500
## 2023-08-18 11:12:25 All done.

```

Visualise and analyse the SSI results

SSI and effect sizes per species

Here we visualize effect sizes and SSI obtained with the resolution 500.

```

sp_ssi <- ssi_results[[1]]
effsize_res <- ssi_results [[2]]

# keep only data for resolution 500
# associate the SSI to the detailed effect sizes
sub_effsize_res <- effsize_res %>%
  filter(Resolution == 500) %>%
  left_join(sp_ssi, by = c("Species", "Resolution"))

# make the score a factor
sub_effsize_res$Index <- as.factor(sub_effsize_res$Index)

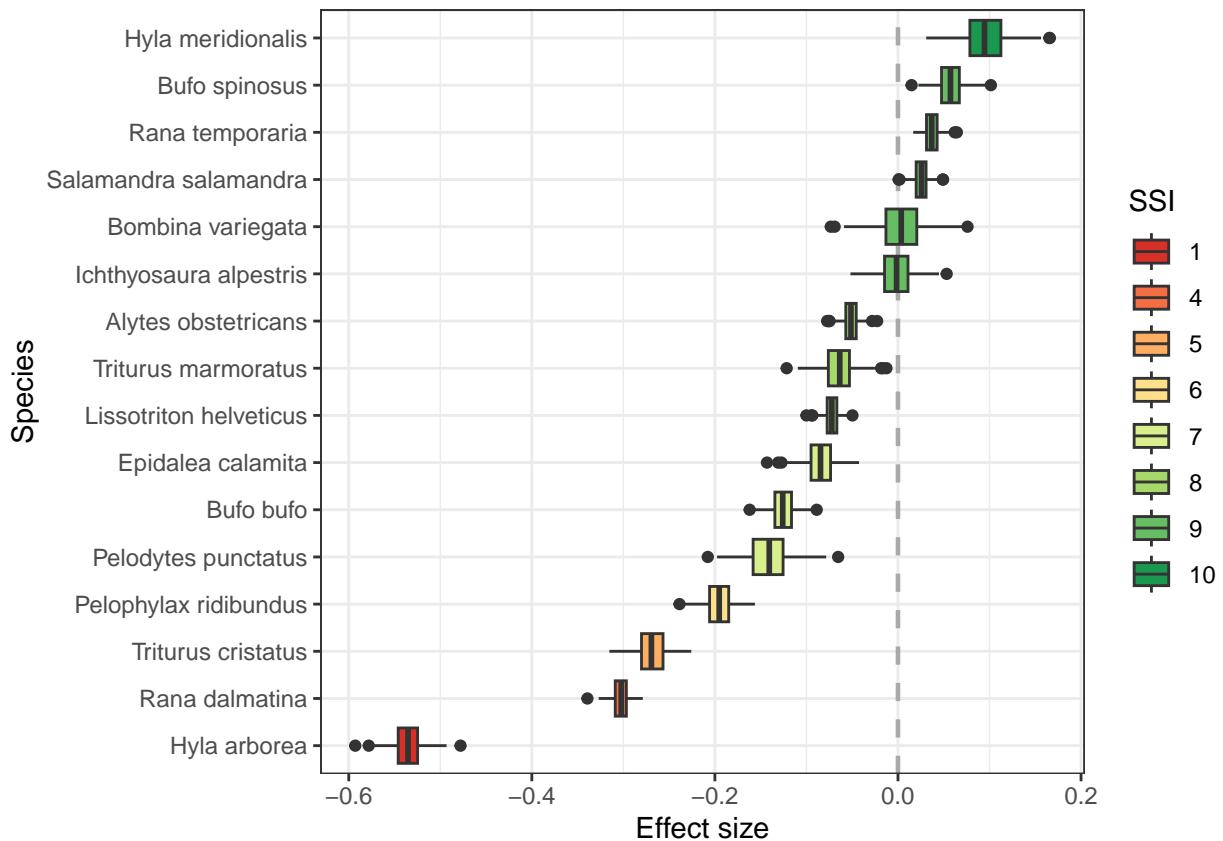
# plot the results
ggplot(sub_effsize_res,
       aes(x = reorder(Species, -effsize),
            y = -effsize, fill = Index)) +
  geom_hline(yintercept = 0.0, color = "darkgrey",
             linewidth = 0.8, linetype = "dashed") +
  geom_boxplot() +
  coord_flip() +
  scale_fill_brewer(name = "SSI", palette = "RdYlGn") +
  ylab("Effect size") +
  xlab("Species") +

```

```

theme(axis.title.y = element_blank()) +
theme(legend.position = c(0.9, 0.2)) +
theme_bw()

```



Resolution comparison

```

sp_ssi$Resolution <- as.factor(sp_ssi$Resolution)

CGPfunctions::newggslopegraph(dataframe = sp_ssi,
  Resolution,
  Index,
  Grouping = Species,
  Title = "Synanthropy scores for amphibian species in western France",
  SubTitle = NULL,
  Caption = NULL)

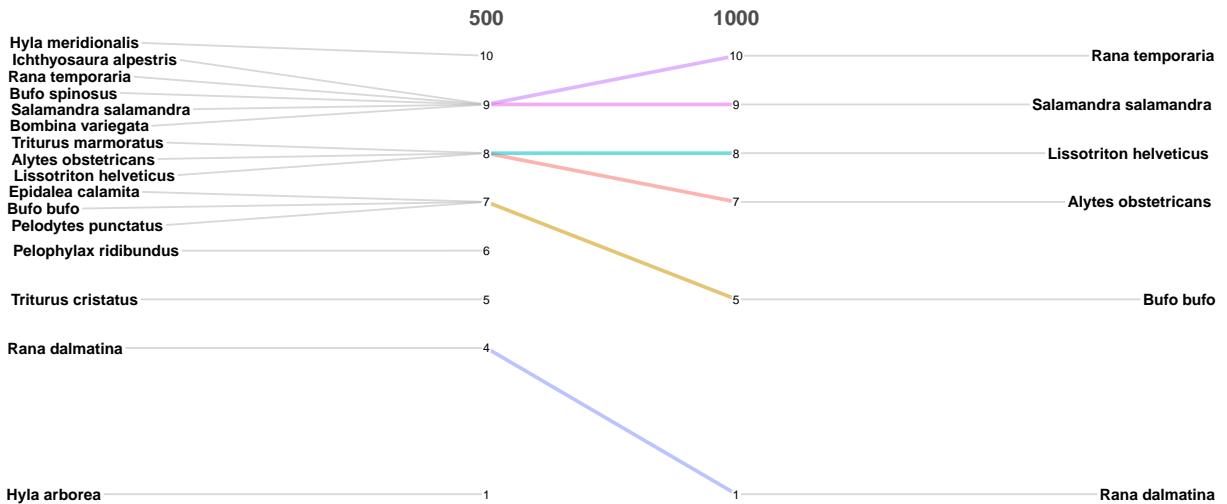
```

```

## 
## Converting 'Resolution' to an ordered factor

```

Synanthropy scores for amphibian species in western France



Distribution map

```

points <- ssi_results[[3]]

# we select one resolution, one set of simulated points, and the observed points
sub_points <- points %>% filter(Resolution == "1000",
                                simulation %in% c(1, "no"))

ggplot() +
  geom_point(data = sub_points, aes(x = x, y = y, color = variable),
             size = 1.5, alpha = 0.5) +
  scale_color_manual(values = c("#ff6600", "#660099")) +
  theme(axis.title.x = element_blank(),
        axis.title.y = element_blank()) +
  guides(color = guide_legend(title = "Points")) +
  facet_wrap(. ~ Species) +
  theme_void()

```

