Calculation and application of the Species Synanthropy Index: tutorial

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This tutorial demonstrates: - the calculation of the Species Synanthropy Index (SSI) and possible subsequent analyses and graphs, based on an example dataset of amphibian populations collected in western France - the application of the SSI at the community scale, the Synanthropy Community Score (SCS) to estimate the overall sensitivity of assemblages to land use change.

We load necessary packages

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

1- Species Synanthropy Index: an example with amphibian populations in western France

Setup

Two types of data are required to run the SSI function: (i) a raster describing the spatial gradient of anthropogenization of the region to be analysed, and (ii) a database of species occurrences, with XY coordinates and corresponding sampling dates.

The raster map used here is extracted from the French Naturalness Map, developed by Guetté et al.(2021) and cropped to the region of interest, Brittany. You can download the cropped map at [url]. Place it in the `data/amphibiansBrittany` folder.

```
# load the raster file
ras_raw <- raster::raster(file.path(here::here(),
                                    "data",
                                    "amphibiansBrittany",
                                    "naturalnessMap.tif"))

# create an object to visualize the raster
rast_to_plot <- terra::rast(ras_raw)
```

Next, we load the occurrence data to be evaluated, and take a look at the structure required for the analysis. Note that sampling years need to correspond to the years used to build the naturalness map for the analysis to make the most sense.

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```r
# load the CSV file
spOcc <- read.csv(file.path(here::here(),
                           "data",
                           "amphibiansBrittany",
                           "amphibianOccurrences.csv"),
                 sep = ";", h=T)

# look at data structure
head(spOcc)
```

```
##                     Species Year Abundance      X       Y
## 1          Bufo spinosus 2015         1 259519 6807029
## 2        Pelophylax spp. 2015         1 259519 6807029
## 3 Salamandra salamandra 2015         1 259519 6807029
## 4          Bufo spinosus 2015         1 259519 6807029
## 5 Salamandra salamandra 2015         1 259519 6807029
## 6        Pelophylax spp. 2015         1 261357 6806526
```

The table contains one row per species, site and year sampled, with a total of 5 columns: species detected, sampling year, abundance detected, and geographic coordinates (X,Y). We make sure that all rows contain geographic coordinates.

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

```
## [1] "0 point(s) were eliminated because of missing coordinates"
```

At this point, it is useful to plot the data to make sure the two datasets use the same coordinate system and everything looks as expected.

```r
ggplot() +
  tidyterra::geom_spatraster(data = rast_to_plot) +
  geom_point(data = spOcc, 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 = 501050
```
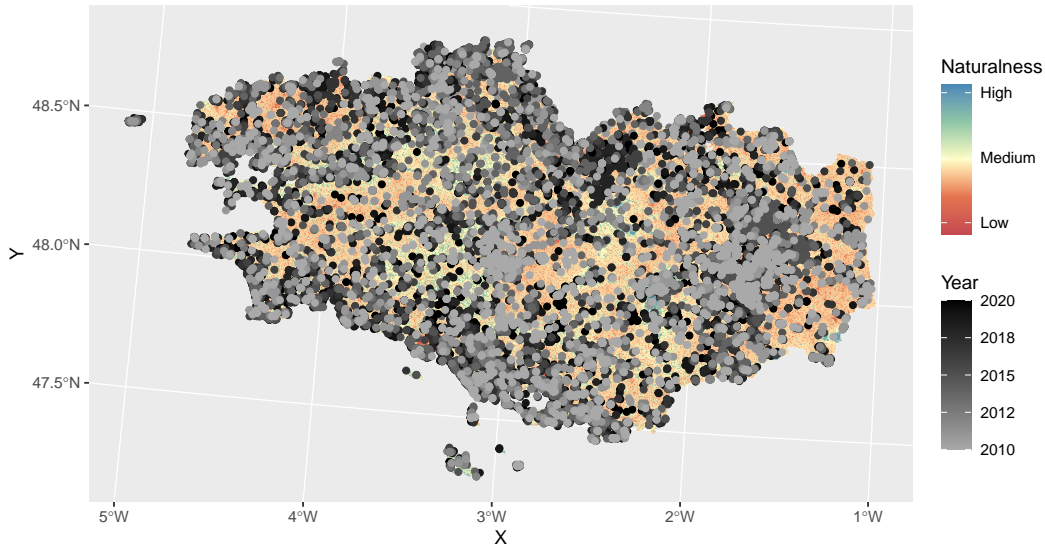
SSI calculation

The function was designed to calculate SSI automatically from a data set (for a taxon, a territory and a period). Several raster resolutions can be evaluated in a row.

A null distribution is generated by randomly selecting sites within the species range. The effect of the studied gradient is measured by the effect size between the simulated and the observed species distributions, repeated n times. A synanthropy score, the SSI is assigned to each species based on the average difference between the null and observed distributions (from 1 to 10).

Here, we execute the function for 3 resolutions (100, 200, 250), with 500 simulations each. Each species must have been found in a minimum of 30 cells to be evaluated (threshold argument). You will be prompted to validate the species list detected in the dataset. Make sure that there are no typos or synonyms, as each species will be considered separately for the analyses. A warning message may pop up but will not influence the process.

```
ssi_results <- ssi(r = ras_raw,
                   resolution = c(100, 200, 250),
                   data = spOcc,
                   sim = 500,
                   threshold = 30)
```

```
## 2023-08-16 17:07:43 - Aggregate naturalness raster cells at resolution 100 (this step may take a few
## 0 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
```

```
## Species that will be evaluated are:
## Alytes obstetricans
## Bufo spinosus
## Epidalea calamita
## Hyla arborea
## Ichthyosaura alpestris
## Lissotriton helveticus
```

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```
## Pelodytes punctatus
## Pelophylax kl. esculentus
## Pelophylax spp.
## Rana dalmatina
## Rana temporaria
## Salamandra salamandra
## Triturus marmoratus
## 2023-08-16 17:10:03 - Generating null distributions for:
## 2023-08-16 17:10:03 Alytes obstetricans (1/13)
## Simulation 1/500...  100/500...  200/500...  300/500...  400/500...  500/500
## 2023-08-16 17:10:17 Bufo spinosus (2/13)
## Simulation 1/500...  100/500...  200/500...  300/500...  400/500...  500/500
## 2023-08-16 17:10:54 Epidalea calamita (3/13)
## Simulation 1/500...  100/500...  200/500...  300/500...  400/500...  500/500
## 2023-08-16 17:11:03 Hyla arborea (4/13)
## Simulation 1/500...  100/500...  200/500...  300/500...  400/500...  500/500
## 2023-08-16 17:11:22 Ichthyosaura alpestris (5/13)
## Simulation 1/500...  100/500...  200/500...  300/500...  400/500...  500/500
## 2023-08-16 17:11:34 Lissotriton helveticus (6/13)
## Simulation 1/500...  100/500...  200/500...  300/500...  400/500...  500/500
## 2023-08-16 17:12:00 Pelodytes punctatus (7/13)
## Simulation 1/500...  100/500...  200/500...  300/500...  400/500...  500/500
## 2023-08-16 17:12:10 Pelophylax kl. esculentus (8/13)
## Simulation 1/500...  100/500...  200/500...  300/500...  400/500...  500/500
## 2023-08-16 17:12:19 Pelophylax spp. (9/13)
## Simulation 1/500...  100/500...  200/500...  300/500...  400/500...  500/500
## 2023-08-16 17:12:43 Rana dalmatina (10/13)
## Simulation 1/500...  100/500...  200/500...  300/500...  400/500...  500/500
## 2023-08-16 17:13:06 Rana temporaria (11/13)
## Simulation 1/500...  100/500...  200/500...  300/500...  400/500...  500/500
## 2023-08-16 17:13:28 Salamandra salamandra (12/13)
## Simulation 1/500...  100/500...  200/500...  300/500...  400/500...  500/500
## 2023-08-16 17:14:00 Triturus marmoratus (13/13)
## Simulation 1/500...  100/500...  200/500...  300/500...  400/500...  500/500
## 2023-08-16 17:14:16 - Calculating effect sizes...
## Simulation 1/500...  100/500...  200/500...  300/500...  400/500...  500/500
## 2023-08-16 17:24:04 Analysis finished for resolution 100
## 2023-08-16 17:24:04 - Aggregate naturalness raster cells at resolution 200 (this step may take a few
## 0 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

## Species that will be evaluated are:
## Alytes obstetricans
## Bufo spinosus
## Epidalea calamita
## Hyla arborea
## Ichthyosaura alpestris
## Lissotriton helveticus
## Pelodytes punctatus
## Pelophylax kl. esculentus
## Pelophylax spp.
## Rana dalmatina
## Rana temporaria
```

```
## Salamandra salamandra
## Triturus marmoratus
## 2023-08-16 17:27:09 - Generating null distributions for:
## 2023-08-16 17:27:09 Alytes obstetricans (1/13)
## Simulation 1/500...  100/500...  200/500...  300/500...  400/500...  500/500
## 2023-08-16 17:27:19 Bufo spinosus (2/13)
## Simulation 1/500...  100/500...  200/500...  300/500...  400/500...  500/500
## 2023-08-16 17:27:42 Epidalea calamita (3/13)
## Simulation 1/500...  100/500...  200/500...  300/500...  400/500...  500/500
## 2023-08-16 17:27:48 Hyla arborea (4/13)
## Simulation 1/500...  100/500...  200/500...  300/500...  400/500...  500/500
## 2023-08-16 17:28:02 Ichthyosaura alpestris (5/13)
## Simulation 1/500...  100/500...  200/500...  300/500...  400/500...  500/500
## 2023-08-16 17:28:11 Lissotriton helveticus (6/13)
## Simulation 1/500...  100/500...  200/500...  300/500...  400/500...  500/500
## 2023-08-16 17:28:28 Pelodytes punctatus (7/13)
## Simulation 1/500...  100/500...  200/500...  300/500...  400/500...  500/500
## 2023-08-16 17:28:34 Pelophylax kl. esculentus (8/13)
## Simulation 1/500...  100/500...  200/500...  300/500...  400/500...  500/500
## 2023-08-16 17:28:42 Pelophylax spp. (9/13)
## Simulation 1/500...  100/500...  200/500...  300/500...  400/500...  500/500
## 2023-08-16 17:28:58 Rana dalmatina (10/13)
## Simulation 1/500...  100/500...  200/500...  300/500...  400/500...  500/500
## 2023-08-16 17:29:14 Rana temporaria (11/13)
## Simulation 1/500...  100/500...  200/500...  300/500...  400/500...  500/500
## 2023-08-16 17:29:29 Salamandra salamandra (12/13)
## Simulation 1/500...  100/500...  200/500...  300/500...  400/500...  500/500
## 2023-08-16 17:29:49 Triturus marmoratus (13/13)
## Simulation 1/500...  100/500...  200/500...  300/500...  400/500...  500/500
## 2023-08-16 17:30:01 - Calculating effect sizes...
## Simulation 1/500...  100/500...  200/500...  300/500...  400/500...  500/500
## 2023-08-16 17:38:55 Analysis finished for resolution 200
## 2023-08-16 17:38:55 - Aggregate naturalness raster cells at resolution 250 (this step may take a few
## 0 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

## Species that will be evaluated are:
## Alytes obstetricans
## Bufo spinosus
## Epidalea calamita
## Hyla arborea
## Ichthyosaura alpestris
## Lissotriton helveticus
## Pelodytes punctatus
## Pelophylax kl. esculentus
## Pelophylax spp.
## Rana dalmatina
## Rana temporaria
## Salamandra salamandra
## Triturus marmoratus
## 2023-08-16 17:42:07 - Generating null distributions for:
## 2023-08-16 17:42:07 Alytes obstetricans (1/13)
## Simulation 1/500...  100/500...  200/500...  300/500...  400/500...  500/500
```

```
## 2023-08-16 17:42:19 Bufo spinosus (2/13)
## Simulation 1/500...  100/500...  200/500...  300/500...  400/500...  500/500
## 2023-08-16 17:42:40 Epidalea calamita (3/13)
## Simulation 1/500...  100/500...  200/500...  300/500...  400/500...  500/500
## 2023-08-16 17:42:47 Hyla arborea (4/13)
## Simulation 1/500...  100/500...  200/500...  300/500...  400/500...  500/500
## 2023-08-16 17:43:02 Ichthyosaura alpestris (5/13)
## Simulation 1/500...  100/500...  200/500...  300/500...  400/500...  500/500
## 2023-08-16 17:43:11 Lissotriton helveticus (6/13)
## Simulation 1/500...  100/500...  200/500...  300/500...  400/500...  500/500
## 2023-08-16 17:43:28 Pelodytes punctatus (7/13)
## Simulation 1/500...  100/500...  200/500...  300/500...  400/500...  500/500
## 2023-08-16 17:43:35 Pelophylax kl. esculentus (8/13)
## Simulation 1/500...  100/500...  200/500...  300/500...  400/500...  500/500
## 2023-08-16 17:43:44 Pelophylax spp. (9/13)
## Simulation 1/500...  100/500...  200/500...  300/500...  400/500...  500/500
## 2023-08-16 17:44:01 Rana dalmatina (10/13)
## Simulation 1/500...  100/500...  200/500...  300/500...  400/500...  500/500
## 2023-08-16 17:44:18 Rana temporaria (11/13)
## Simulation 1/500...  100/500...  200/500...  300/500...  400/500...  500/500
## 2023-08-16 17:44:35 Salamandra salamandra (12/13)
## Simulation 1/500...  100/500...  200/500...  300/500...  400/500...  500/500
## 2023-08-16 17:44:54 Triturus marmoratus (13/13)
## Simulation 1/500...  100/500...  200/500...  300/500...  400/500...  500/500
## 2023-08-16 17:45:07 - Calculating effect sizes...
## Simulation 1/500...  100/500...  200/500...  300/500...  400/500...  500/500
## 2023-08-16 17:53:40 Analysis finished for resolution 250
## 2023-08-16 17:53:40 All done.
```

Visualise and analyse the SSI results

The SSI function produces 3 data frames.

SSI and effect sizes per species

The first table contains the SSI calculated per species and resolution. It is a summary table containing one line per species per resolution, with the mean effect size, the number of simulations, and the SSI (1 to 10).

```
head(sp_ssi <- ssi_results[[1]])
```

```
## # A tibble: 6 x 5
##   Species                 mean  nRun Index Resolution
##   <chr>                  <dbl> <int> <dbl>      <dbl>
## 1 Alytes obstetricans   0.0212   500     2        100
## 2 Bufo spinosus         0.0566   500     1        100
## 3 Epidalea calamita    -0.502    500    10        100
## 4 Hyla arborea          0.0178   500     2        100
## 5 Ichthyosaura alpestris -0.0385  500     3        100
## 6 Lissotriton helveticus -0.0975  500     4        100
```

The second table is a data.frame compiling the effect sizes (effsize) calculated for each comparison of simulated (Null) and observed data, for each species and resolution. The sample sizes for simulated (n1) and observed

6

(n2) data are specified, as well as the magnitude of the effect size (negligible < small < moderate < large) provided by `rstatix::cohens_d`.

```
head(effsize_res <- ssi_results [[2]])
```

```
## # A tibble: 6 x 10
##   .y.   group1 group2    effsize    n1    n2 magnitude  Species     Run Resolution
##   <chr> <chr>  <chr>        <dbl> <int> <int> <ord>      <chr>     <int>      <dbl>
## 1 value Null   Observed  -0.225     385   385 small      Trituru~      1        100
## 2 value Null   Observed  -0.0187   1675  1674 negligible Salaman~      1        100
## 3 value Null   Observed  -0.289     930   930 small      Rana te~      1        100
## 4 value Null   Observed  -0.0276   1031  1031 negligible Rana da~      1        100
## 5 value Null   Observed   0.0270   1087  1087 negligible Pelophy~      1        100
## 6 value Null   Observed   0.0682    134   134 negligible Pelophy~      1        100
```

Here we combine these two tables to visualize effect sizes and SSI obtained with the resolution 100.

```r
# keep only data for resolution 100
# associate the SSI to the detailed effect sizes
sub_effsize_res <- effsize_res %>%
  filter(Resolution == 100) %>%
  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()
```
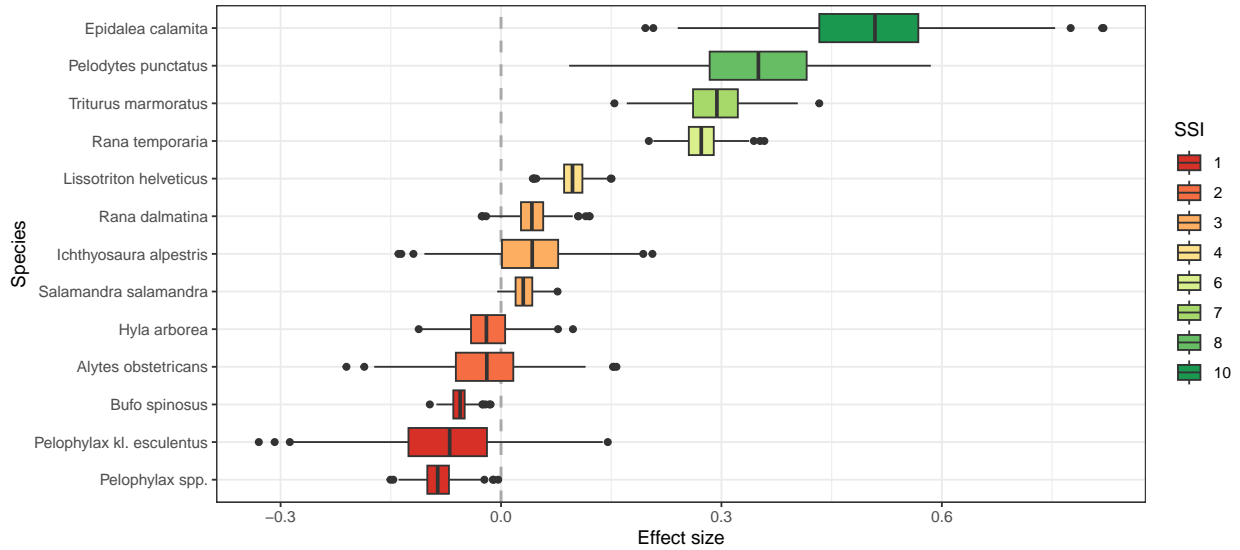
Based on this plot, we observe that species have contrasted SSI. Epidalea calamita shows high affinity for anthropogenic systems (SSI = 10), followed by Pelodytes punctatus, Triturus marmoratus, and Rana temporaria that all have positive effect sizes. On the opposite end of the gradient, green frogs (Pelophylax spp. and Pelophylax kl. esculentus) have low synanthropy scores (SSI = 1), and negative effect sizes along with Bufo spinosus.

Resolution comparison

It is useful to check whether scores are affected by the level of data aggregation operated during the process. We create a graph that allows the comparison of scores and species ranks across data resolutions.

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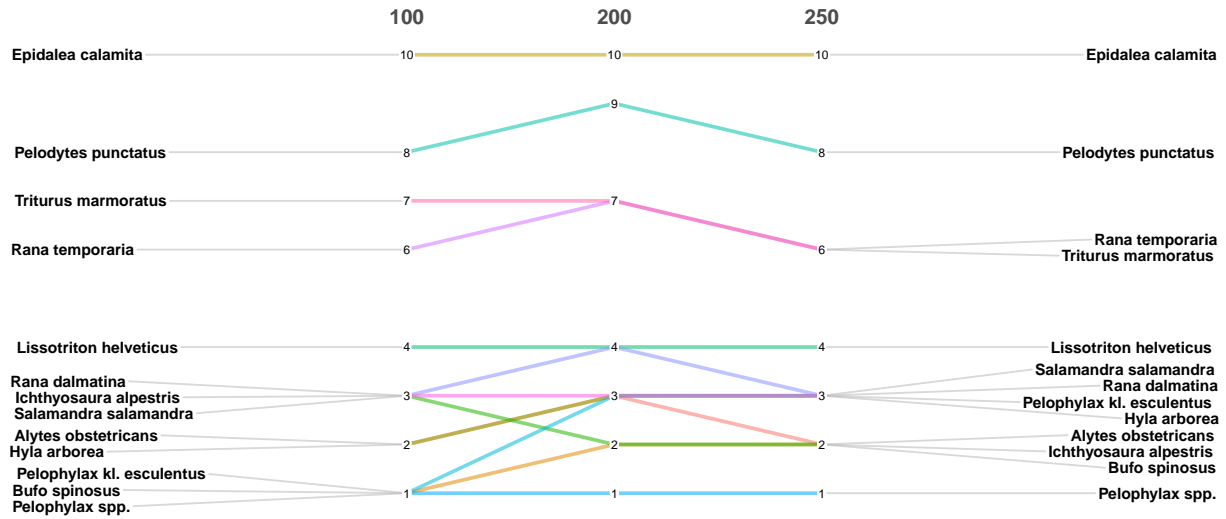
```
##
## Converting 'Resolution' to an ordered factor
```

Synanthropy scores for amphibian species in western France

Interestingly, scores are not affected much by the change in data resolution, with unchanged ranks for species with SSI > 4. This suggests that the evaluation is robust to data aggregation.

Distribution map

Finally, the third table contains all the points simulated and observed.

```
head(points <- ssi_results[[3]])
```

```
##   Cell simulation          Species variable        x        y Resolution
## 1 8802          1 Triturus marmoratus     Null 186047.6 6768984        100
## 2 7697          1 Triturus marmoratus     Null 392047.6 6784984        100
## 3 5192          1 Triturus marmoratus     Null 214047.6 6816984        100
## 4 9735          1 Triturus marmoratus     Null 240047.6 6756984        100
## 5 5209          1 Triturus marmoratus     Null 248047.6 6816984        100
## 6 7023          1 Triturus marmoratus     Null 252047.6 6792984        100
```

We can visualize the locations of observations and of one set of randomly selected sites for each species.

```
# we select one resolution, one set of simulated points, and the observed points
sub_points <- points %>% filter(Resolution == "100",
                                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()
```
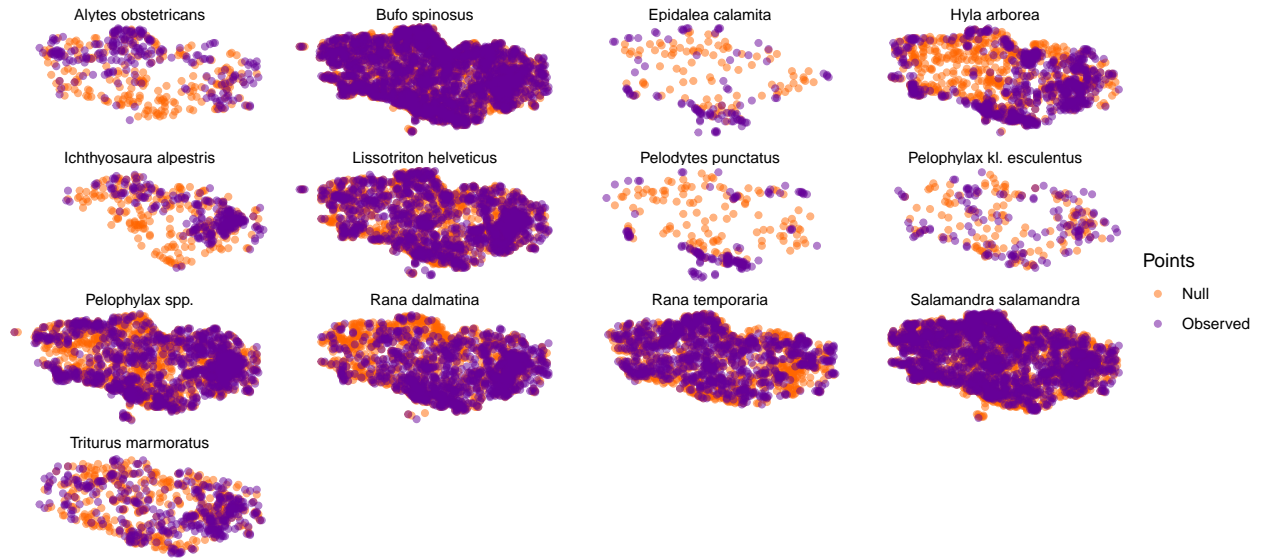
2- Synanthropy Community Score: application of the SSI to amphibian communities in ponds

The scores may then be used at the community scale to estimate the overall sensitivity of assemblages to land use change. These average scores are complementary to anthropisation maps, which must be considered as potential. Indeed, there are cases where the maps present values higher than the scores when sensitive species are not detected, and cases where the maps present values lower than the scores when in reality some populations of sensitive species have maintained themselves locally.

Here we test the scores obtained in the previous section with data of amphibian communities surveyed in western France (around the city of Rennes) between 2000 and 2010.

Setup

We load the dataset and take a look at it. Its structure is similar to that of the previous dataset, with columns for species names, year, and site of sampling, abundance, and XY coordinates.

```
ex_com <- read.table(file.path(here::here(), "data",
                               "amphibiansBrittany",
                               "Amphibian_community_MNIE.csv"), sep=";", h=T)
head(ex_com)
```

```
##                   Species      X       Y Abundance Years     Site
## 1          Bufo spinosus 357337 6783846         1  2010 Site 136
## 2     Pelodytes punctatus 348398 6785920         1  2010  Site 58
## 3         Rana dalmatina 357337 6783846         1  2010 Site 136
## 4  Salamandra salamandra 357337 6783846         1  2010 Site 136
## 5            Hyla arborea 344270 6809372         1  2009  Site 29
## 6  Ichthyosaura alpestris 353382 6782286         1  2006 Site 109
```

Because not all species were attributed a SSI based on the threshold number applied, we need to check whether some species will not have a SSI in this community.

```
# species that are in the community dataset, that are not in the SSI dataset
sub_sp_ssi <- sp_ssi %>% filter(Resolution == "100")
(unevaluated_species <- setdiff(unique(ex_com$Species), unique(sub_sp_ssi$Species)))
```

```
## [1] "Triturus cristatus"   "Lissotriton vulgaris" "Pelophylax lessonae"
```

```
# total number of sites sampled
nsites <- ex_com %>% count(Site) %>% nrow()

# proportion of communities these species are present in
ex_com %>%
  filter(Species %in% unevaluated_species) %>%
  count(Site) %>%
  nrow()/ nsites
```

```
## [1] 0.3463687
```

3 species of the community dataset do not have a SSI and they are present in 34% of the studied communities. Community analyses must be interpreted with this caveat in mind.

We then associate previously calculated SSI at resolution 100 to each species, and calculate for each site the species richness, SCS, i.e. the mean of SSI, and SCS, i.e. the SCS weighted by species abundance.

```
ex_com_evaluated <- ex_com %>% inner_join(sub_sp_ssi %>% select(Species, Index))
```

```
## Joining with `by = join_by(Species)`
```

```
head(ex_com_sites <- ex_com_evaluated %>%
  group_by(Site, Years, X, Y) %>%
  summarise(Richness = n_distinct(Species),
            SCS = round(mean(Index), 2),
            SCSw = round(weighted.mean(Index, Abundance), 2)))
```

```
## `summarise()` has grouped output by 'Site', 'Years', 'X'. You can override
## using the `.groups` argument.
```

```
## # A tibble: 6 x 7
## # Groups:   Site, Years, X [6]
##   Site      Years      X       Y Richness   SCS  SCSw
##   <chr>     <int>  <int>   <int>    <int> <dbl> <dbl>
## 1 Site 1     2010 335076 6788565        3  3.33   3.2
## 2 Site 10    2010 340610 6790480        5  3.4    3.4
## 3 Site 100   2010 351549 6778613        5  3.4    3.67
## 4 Site 101   2010 351550 6778573        3  3.33   3.33
## 5 Site 102   2010 351577 6780908        3  2.67   3.54
## 6 Site 103   2010 351641 6778430        4  2.25   2.84
```

We also calculated the Synanthropy Community Index (SCI), an equivalent of the Floristic Quality Index to account for variation of species richness, using the following formula :

$$SCI = SCS(\sqrt{richness})$$

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```
ex_com_sites %<>% mutate(SCI = round(SCS * sqrt(Richness), 2),
                         SCIw = round(SCSw * sqrt(Richness), 2))

head(ex_com_sites)
```

```
## # A tibble: 6 x 9
## # Groups:   Site, Years, X [6]
##   Site      Years      X       Y Richness   SCS  SCSw   SCI  SCIw
##   <chr>     <int>  <int>   <int>    <int> <dbl> <dbl> <dbl> <dbl>
## 1 Site 1     2010 335076 6788565        3  3.33   3.2  5.77  5.54
## 2 Site 10    2010 340610 6790480        5  3.4    3.4   7.6   7.6
## 3 Site 100   2010 351549 6778613        5  3.4    3.67  7.6   8.21
## 4 Site 101   2010 351550 6778573        3  3.33   3.33  5.77  5.77
## 5 Site 102   2010 351577 6780908        3  2.67   3.54  4.62  6.13
## 6 Site 103   2010 351641 6778430        4  2.25   2.84  4.5   5.68
```

Map the results

We can now visualize our new index.

```
# Create spatial objects
ex_com_map <- sf::st_as_sf(ex_com_sites, coords = c("X", "Y"), crs = 2154)
rast_to_plot2 <- raster::crop(rast_to_plot, ex_com_map)

# Plot the map
ggplot() +
  tidyterra::geom_spatraster(data = rast_to_plot2, alpha = 0.8) +
  geom_sf(data = ex_com_map, aes(color = SCIw, size = Richness)) +
  scale_colour_gradient(low = "yellow", high = "darkgreen") +
  tidyterra::scale_fill_whitebox_c(palette = "muted", direction=-1) +
  ggtitle("Amphibian communities in ponds") +
  theme(legend.position = "bottom")
```

```
## SpatRaster resampled to ncells = 501102
```


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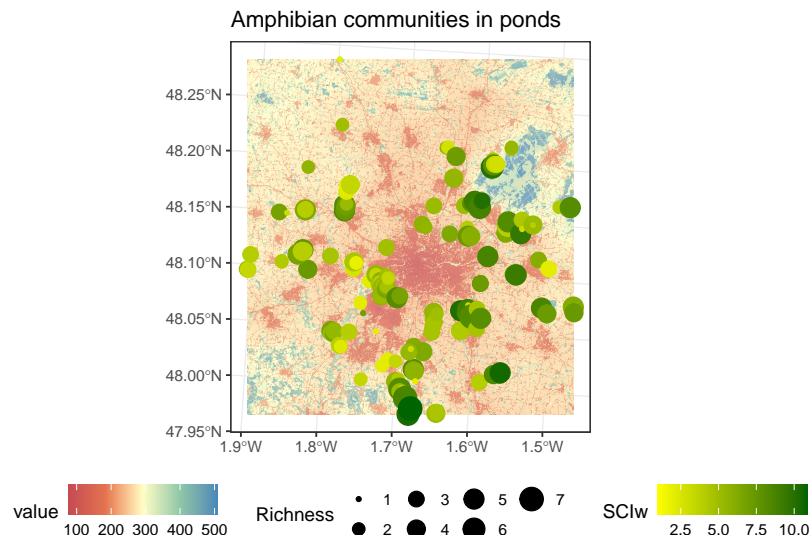
On this map, the background shows the naturalness index with lower (red) values indicating low naturalness and higher (blue) values indicating high naturalness. Point size represents the amphibian community richness. Lighter green points identify the ponds that have less synanthropic assemblages and are therefore potentially more sensitive to urbanisation and intensified land-use. Darker green points distinguish the ponds presenting rather synanthropic assemblages. It is interesting to note that these results contrast in part with the map, with some examples of communities with low SCI scores in areas with low naturalness, illustrating the complementarity of the two approaches.

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