

Text 1 Supplementary Material

Several shades of gray: Combining land use, animal behavior, and urban zoning to assess landscape permeability in (growing) urban areas

Tulaci Bhakti, João Carlos de Castro Pena, Bernardo Brandão Niebuhr, Juliana Sampaio, Fernando F. Goulart, Cristiano Schetini de Azevedo, Milton Cezar Ribeiro, Yasmine Antonini

Landscape and Urban Planning

Rationale

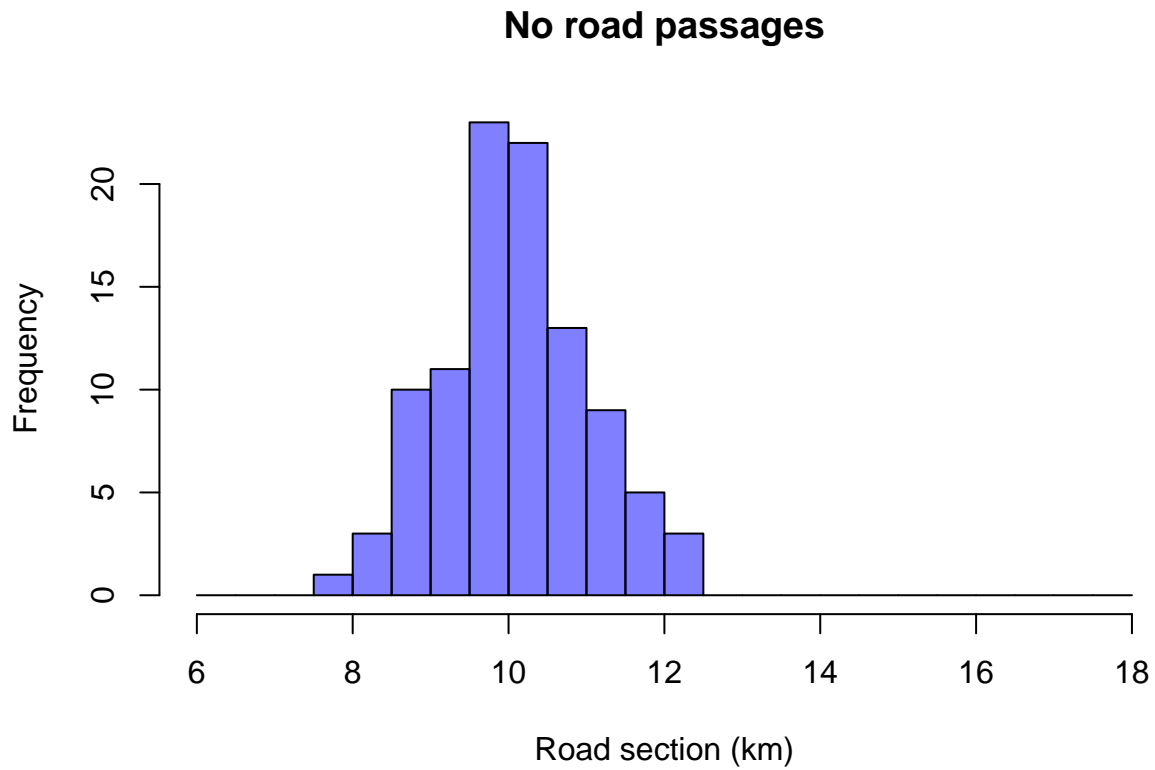
Here we introduce the method used to calculate the overlap between ecological corridors in different simulation scenarios and for distinct species. The general idea is that one has two maps of corridors - e.g. maps for the same species in different scenarios or for the different species in the same scenario - and we want to measure how much the corridors overlap between each other. This includes not only whether the corridors overlap, but also how many corridors from each map cross pixels where there is overlap.

A simple example

First, we give a 1 dimensional example. Imagine that, instead of corridor simulations in a two dimensional space, we have the number of animals that cross a given section of a road (so, a 1-dimensional problem). It is still an issue of landscape permeability, but simplified for illustration purposes. Let's say the number of animals in a given scenario (e.g., with no road passages) is given by a Gaussian distribution with $\mu = 10$ and $\sigma = 1$. We'll sample 100 points where animals crossed this road section. This mean most animals tend to cross the road at the kilometer 10, but there is some variation and animals also crossing at other places. One possibility of explanation of this pattern may be that, at the kilometer 10, there are habitat patches contiguous to both sides of the road, so animals are prone to approach and cross the road at this place. Below we show this distribution:

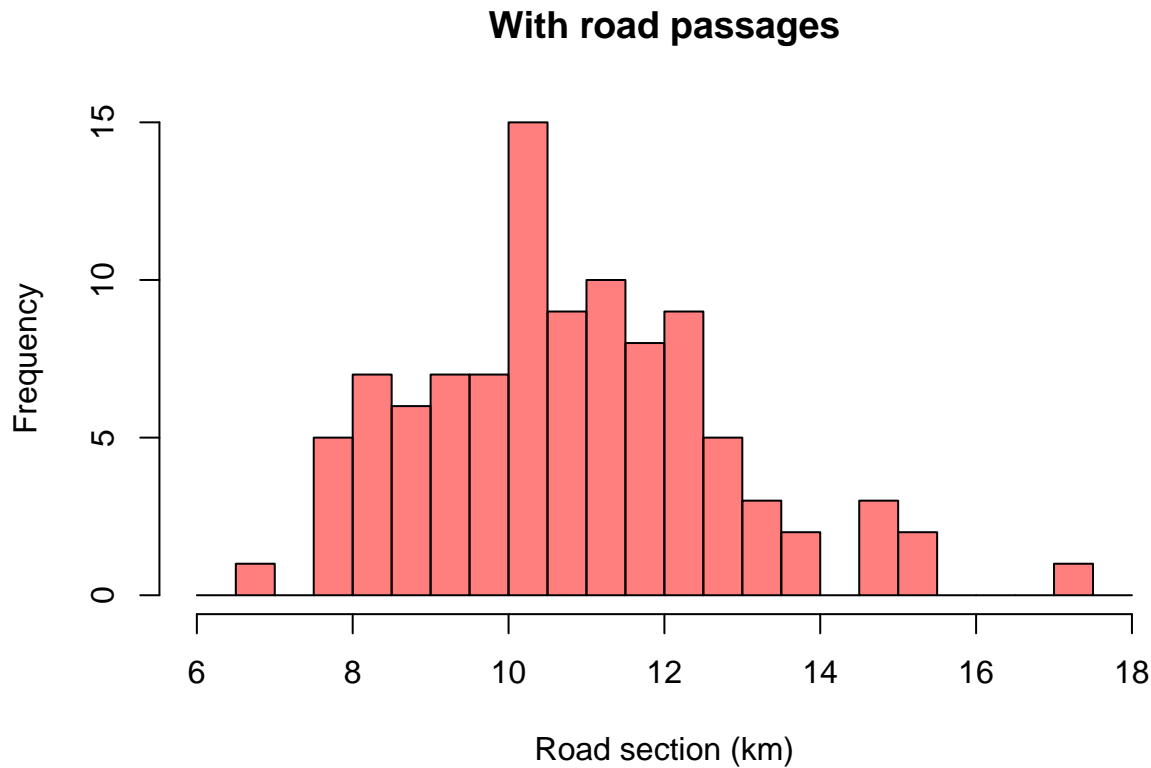
```
# seed to keep the random numbers fixed
set.seed(123)

no.passages <- rnorm(100, 0, 1) + 10
breaks <- seq(6, 18, 0.5)
hist(no.passages, breaks = breaks, col = rgb(0, 0, 1, alpha = 0.5),
     xlab = 'Road section (km)', main = 'No road passages')
```



Now We'll do the same after a road passage is built at the kilometer 11 (so we'll assume most animals will start to cross the road at this new point, but again with the some variation).

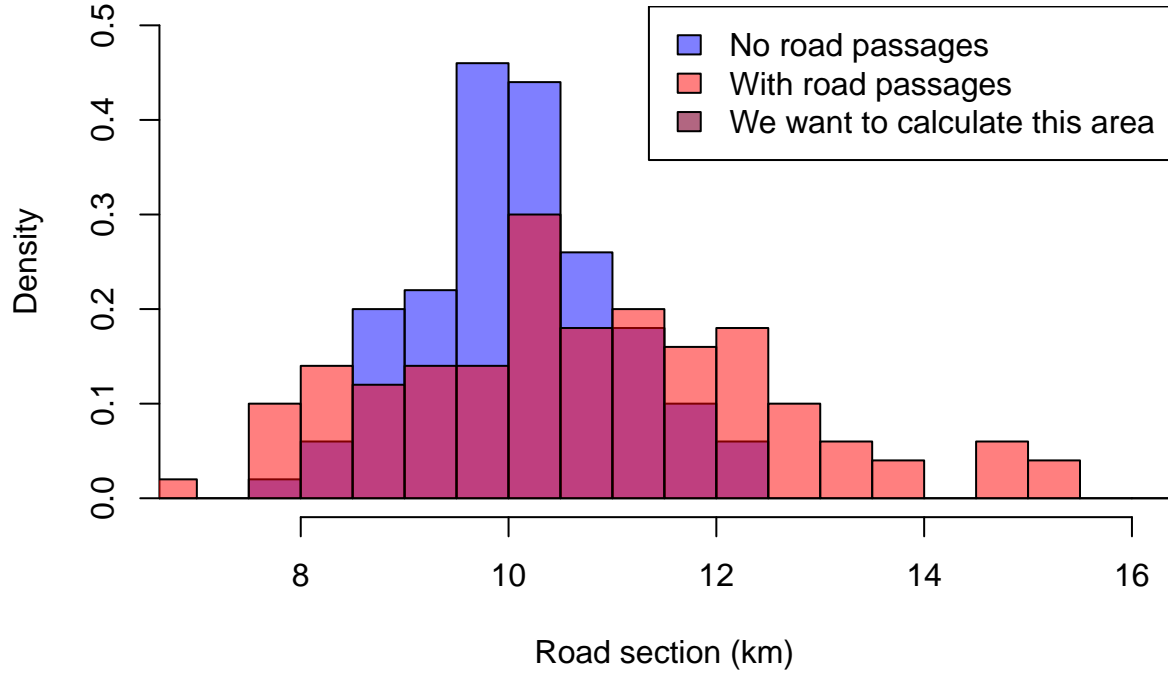
```
passages <- rnorm(100, 0, 2) + 11
hist(passages, breaks = breaks, col = rgb(1, 0, 0, alpha = 0.5),
      xlab = 'Road section (km)', main = 'With road passages')
```



Let's compare both now. But, instead of showing the absolute frequency of records at each location, we'll present the relative frequency of records at each location. This means that, if we multiply the width and the height of each bar in this histogram, we'll get the probability of observing an animal crossing the road at each section. The probability density in the y axis is then the probability of crossing per unit of length of the road section.

What we want, at the end, is to calculate the area under both curves, where there is an overlap between both probability curves. This will tell us how much consistency there is between the two scenarios (without and with road passages), a value between 0 (no overlap at all) and 1 (complete overlap, the number of crossing animals in each road section is exactly the same in both scenarios).

```
hist(no.passages, breaks = breaks, col = rgb(0, 0, 1, alpha = 0.5), prob = T,
     xlab = 'Road section (km)', main = '',
     ylim = c(0, 0.5), xlim = c(7,16))
hist(passages, breaks = breaks, col = rgb(1, 0, 0, alpha = 0.5), prob = T, add = T)
legend('topright',
      legend = c('No road passages', 'With road passages', 'We want to calculate this area'),
      fill = c(rgb(0, 0, 1, alpha = 0.5), rgb(1, 0, 0, alpha = 0.5),
               rgb(0.5, 0, 0.18, alpha = 0.6)))
```



If we would calculate the overlap between continuous probability distributions, we would calculate the area that falls below both curves, using the formula:

$$\int_x \min(p_1(x), p_2(x)) dx \quad (1)$$

where $p_1(x)$ and $p_2(x)$ are the two probability functions. As we're using samples of a distribution, we can approximate that for:

$$\sum_x \min(p_1(x), p_2(x)) \Delta x \quad (2)$$

and Δ can be as small as one wants. We'll do that for our case.

First, we'll count the number of crossing records at each road section (here, road sections of 0.5 km) and each scenario.

```
breaks <- seq(6, 18, 0.5)
(np.tab <- cut(no.passages, breaks) %>% table)
```

```
## .
## (6,6.5] (6.5,7] (7,7.5] (7.5,8] (8,8.5] (8.5,9] (9,9.5]
##      0      0      0      1      3     10     11
## (9.5,10] (10,10.5] (10.5,11] (11,11.5] (11.5,12] (12,12.5] (12.5,13]
##     23     22     13      9      5      3      0
## (13,13.5] (13.5,14] (14,14.5] (14.5,15] (15,15.5] (15.5,16] (16,16.5]
##      0      0      0      0      0      0      0
```

```
## (16.5,17] (17,17.5] (17.5,18]
##          0          0          0
```

```
(p.tab <- cut(passages, breaks) %>% table)
```

```
## .
## (6,6.5] (6.5,7] (7,7.5] (7.5,8] (8,8.5] (8.5,9] (9,9.5]
##      0      1      0      5      7      6      7
## (9.5,10] (10,10.5] (10.5,11] (11,11.5] (11.5,12] (12,12.5] (12.5,13]
##      7      15      9      10      8      9      5
## (13,13.5] (13.5,14] (14,14.5] (14.5,15] (15,15.5] (15.5,16] (16,16.5]
##      3      2      0      3      2      0      0
## (16.5,17] (17,17.5] (17.5,18]
##      0      1      0
```

Now we'll combine both counts in a `data.frame`, calculate the probability of crossing at each road section, and the calculus of $\min(p_1(x), p_2(x))$ (as in eq. 2 above) for each road section.

```
(df <- data.frame(cbind(np.tab, p.tab)) %>%
  mutate(np.prob = np.tab/sum(np.tab),
         p.prob = p.tab/sum(p.tab),
         overlap_per_road_section = pmin(np.prob, p.prob)))
```

##	np.tab	p.tab	np.prob	p.prob	overlap_per_road_section
## 1	0	0	0.00	0.00	0.00
## 2	0	1	0.00	0.01	0.00
## 3	0	0	0.00	0.00	0.00
## 4	1	5	0.01	0.05	0.01
## 5	3	7	0.03	0.07	0.03
## 6	10	6	0.10	0.06	0.06
## 7	11	7	0.11	0.07	0.07
## 8	23	7	0.23	0.07	0.07
## 9	22	15	0.22	0.15	0.15
## 10	13	9	0.13	0.09	0.09
## 11	9	10	0.09	0.10	0.09
## 12	5	8	0.05	0.08	0.05
## 13	3	9	0.03	0.09	0.03
## 14	0	5	0.00	0.05	0.00
## 15	0	3	0.00	0.03	0.00
## 16	0	2	0.00	0.02	0.00
## 17	0	0	0.00	0.00	0.00
## 18	0	3	0.00	0.03	0.00
## 19	0	2	0.00	0.02	0.00
## 20	0	0	0.00	0.00	0.00
## 21	0	0	0.00	0.00	0.00
## 22	0	0	0.00	0.00	0.00
## 23	0	1	0.00	0.01	0.00
## 24	0	0	0.00	0.00	0.00

Finally, we calculate the total overlap (the are below both curves) summing the overlap column to get the sum in eq (2):

```
sum(df$overlap_per_road_section)
```

```
## [1] 0.65
```

Overlap between ecological corridors simulated in different scenarios

Now we're going to extend this approach to a two dimensional example, using an data from this manuscript. We simulated ecological corridors in two scenarios (considering (a) land use only and (b) land use + urban zoning) to define the permeability of animals moving throughout the landscape. We use the Route Selection Frequency Index of each scenario (RSFI), which measures the number of corridors crossing each pixel in space, and is therefore a proxy for the frequency distribution in 1D shown above. We'll transform this RSFI map into a map of probability of movement (specifically, a probability per unit of area) by dividing the RSFI by the sum of all RSFI pixel values. Then, we'll proceed with the same calculus of eq. 2, but applied to the 2-dimensional space.

Let's first load the RSFI maps.

```
# Corridors without urban zoning
files <- list.files('simulated_corridors/RSFI/', pattern = 'nozoning',
                  include.dirs = T, full.names = T)
files_tif <- files[endsWith(files, '.tif')]

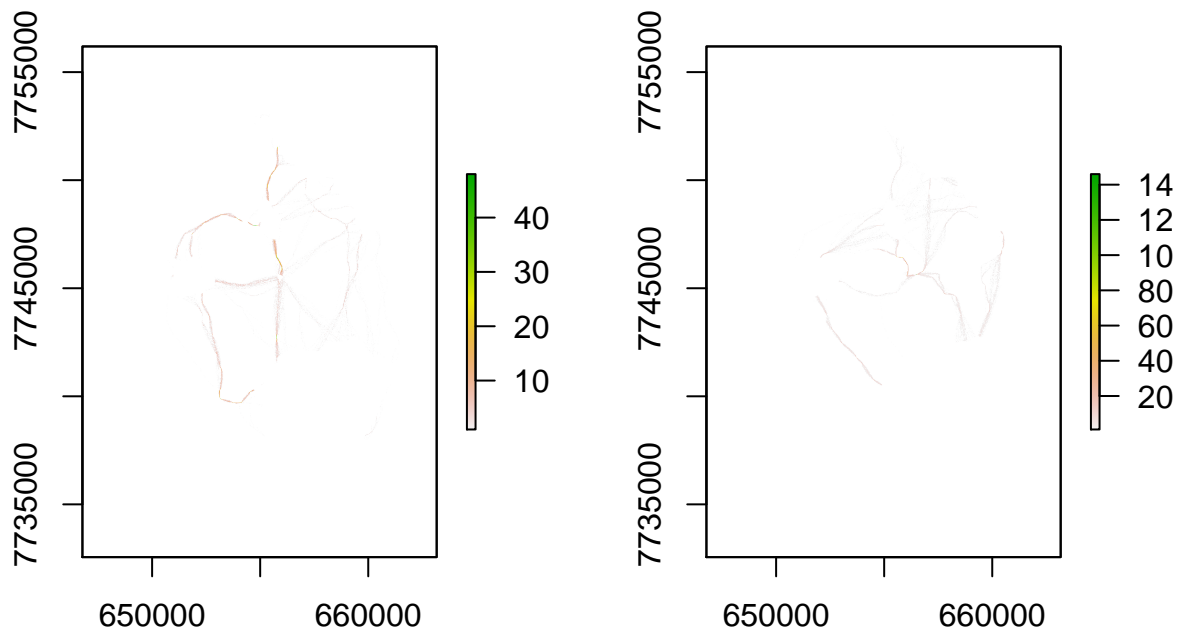
corridors_no_zone <- list()
for(i in 1:length(files_tif)) {
  corridors_no_zone[[i]] <- raster(files_tif[i])
}

# Corridors with urban zoning
files <- list.files('simulated_corridors/RSFI/', pattern = '_zoning',
                  include.dirs = T, full.names = T)
files_tif <- files[endsWith(files, '.tif')]

corridors_zone <- list()
for(i in 1:length(files_tif)) {
  corridors_zone[[i]] <- raster(files_tif[i])
}
```

Let's compare how the corridors look like in both scenarios for one species, **A. leucophthalmus**.

```
par(mfrow = c(1, 2))
plot(corridors_no_zone[[1]])
plot(corridors_zone[[1]])
```



```
par(mfrow = c(1,1))
```

Now we'll transform both maps into movement probability maps, as mentioned above:

```
nz.prob <- corridors_no_zone[[1]]/cellStats(corridors_no_zone[[1]], sum)
sum(nz.prob[], na.rm = T) # ok, sum = 1
```

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

```
# plot(nz.prob)
```

```
z.prob <- corridors_zone[[1]]/cellStats(corridors_zone[[1]], sum)
sum(z.prob[], na.rm = T) # ok, sum = 1
```

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

The next step is to calculate the overlap at each pixel, but before that we have to make sure both maps have exactly the same extent. Finally, we'll sum the values of the overlap layer to get a measure of overlap or consistency between the two scenarios, and we'll also plot that to visualize the locations where there was more overlap.

```
# Force that the no zone probability map has the same extent as the zone map,
# by extending and cropping its extension.
nz.prob2 <- crop(extend(nz.prob, z.prob), z.prob)
#plot(nz.prob2)
```

```
# Calculate the overlap at each pixel
overlap <- z.prob
overlap[] <- pmin(nz.prob2[], z.prob[])
```

```
# Total overlap value between scenarios  
cellStats(overlap, sum)
```

```
## [1] 0.09913602
```

```
# Plot overlap layer in log scale, since the probability values per unit area are  
# too small.
```

```
plot(log(overlap))
```

