

# Supplement to ‘Estimating interactions between individuals from concurrent animal movements’

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*Published in Methods in Ecology and Evolution (2019)*

## Purpose

Test if an individual reacts to an other individual.

## Data and setup

We will need the following packages.

```
library(raster)
library(tidyverse)
library(amt)
```

We start by loading a simulated example data set of two individuals that are attracted to each other.

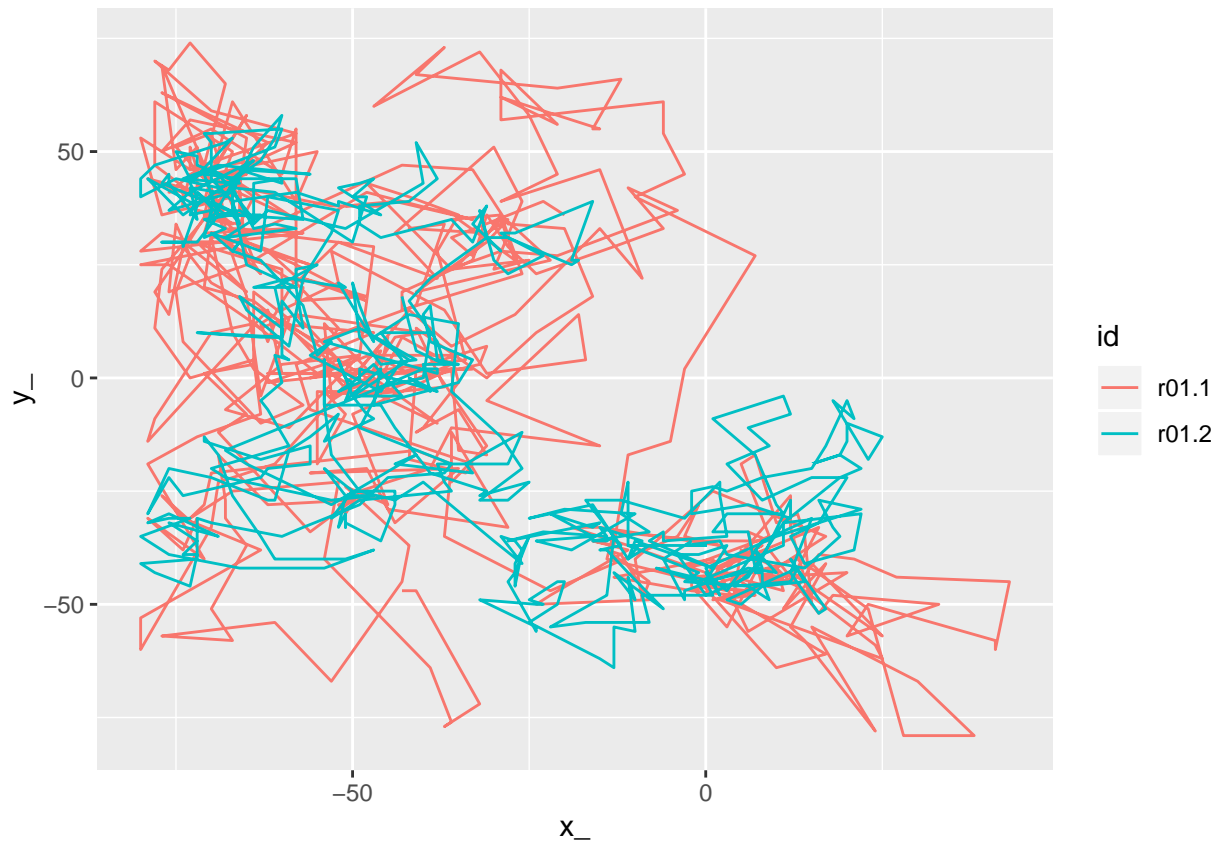
```
dat <- read_rds("example_data.rds")
```

Next we create track,

```
dat1 <- dat %>% make_track(x, y, date, id = id, crs = CRS("+init=epsg:4326"))
```

and can visually inspect the two individuals.

```
dat1 %>% ggplot(aes(x_, y_, col = id)) + geom_path()
```



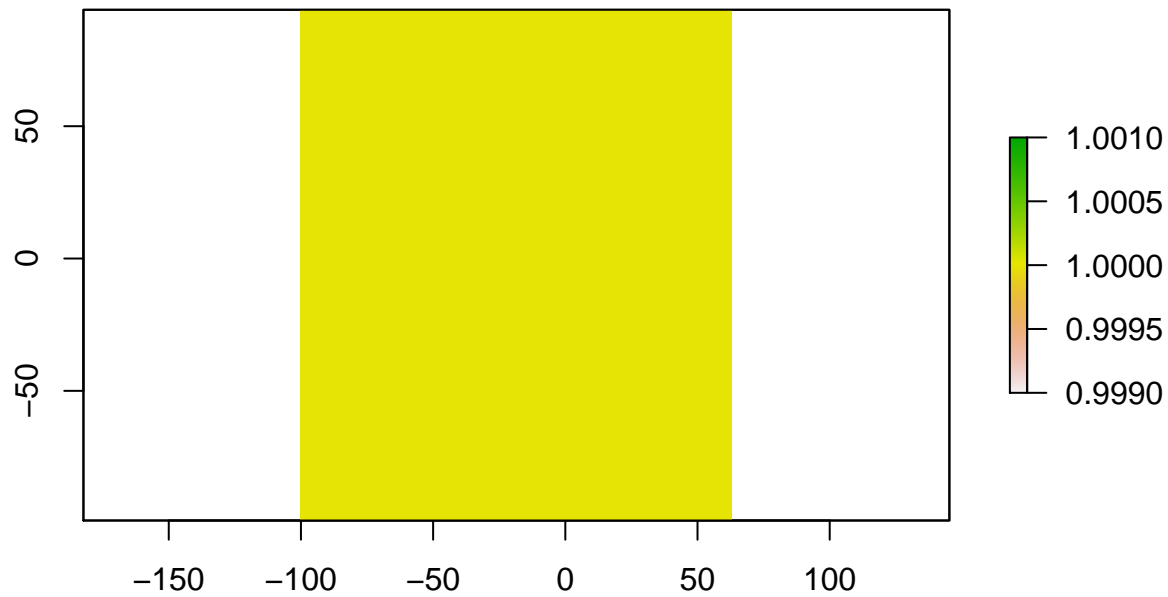
## Estimating the occurrence distribution (OD)

In order to estimate an OD, we will have to provide a template raster (i.e., the raster on which the OD is projected). We use the function `bbox` to create an extent of the template raster and give it a resolution of 1.

```
trast <- raster(amt::bbox(dat1, buffer = 20), res = 1)
```

We can inspect the raster.

```
trast[] <- 1  
plot(trast)
```

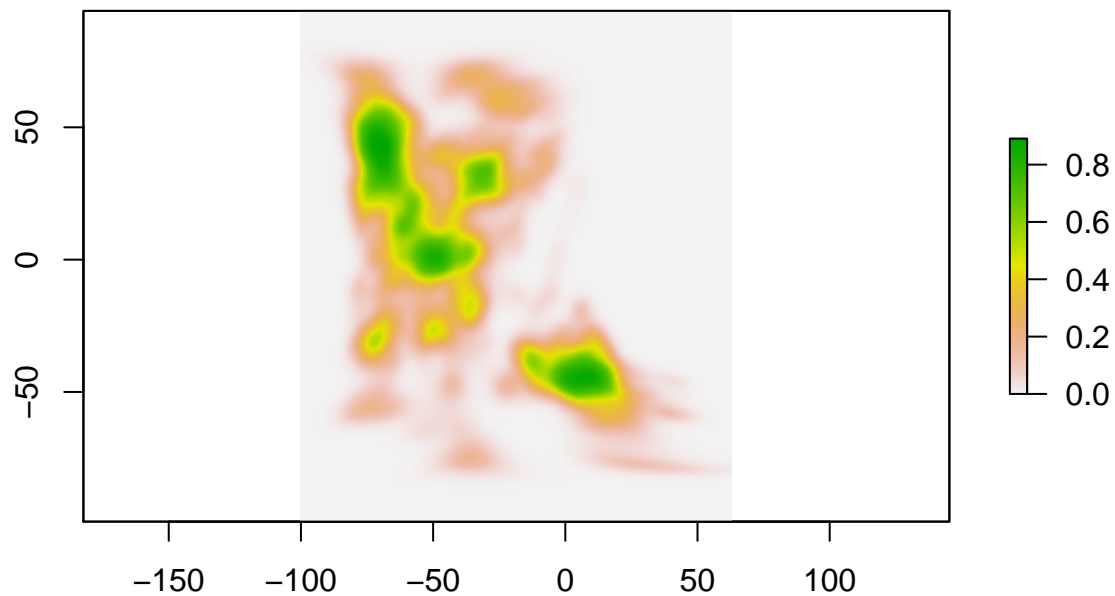


Subset the data such that data of only the first individual is retained (`r01.1`). We want to test if the second individual is attracted to or avoiding this first one.

```
dat2 <- filter(dat1, id == "r01.1")
```

First, we will estimate an overall OD.

```
od1 <- od(dat2, trast)
raster::plot(od1)
```



Next, we want to estimate an OD for a rolling window of 40 time steps and create a raster stack.

```
od_roll <- rolling_od(dat2, trast, n.points=40, show.progress = FALSE)
```

If you are rerunning the code try: `raster::animate(od_roll)` to get an animated version of the rolling OD.

## Fit a Step-Selection Function

We can now use the rolling OD as a predictor for the habitat selection of the other individual (r01.2).

```
m1 <- dat1 %>% filter(id == "r01.2") %>% steps() %>% random_steps() %>%  
  extract_covariates_var_time(od_roll, max_time = minutes(5), when = "before",  
    name_covar = "opponent") %>%  
  filter(!is.na(opponent)) %>% fit_ssf(case_ ~ opponent + strata(step_id_))  
  
summary(m1)
```

```
## Call:  
## coxph(formula = Surv(rep(1, 5060L), case_) ~ opponent + strata(step_id_),  
##       data = data, method = "exact")  
##  
##      n= 5060, number of events= 460  
##  
##              coef exp(coef) se(coef)      z Pr(>|z|)  
## opponent 2.0650    7.8856   0.2853 7.238 4.54e-13 ***  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
##  
##              exp(coef) exp(-coef) lower .95 upper .95  
## opponent    7.886    0.1268    4.508    13.79  
##  
## Concordance= 0.573 (se = 0.015 )  
## Rsquare= 0.011 (max possible= 0.353 )  
## Likelihood ratio test= 54.28 on 1 df,  p=2e-13  
## Wald test = 52.39 on 1 df,  p=5e-13  
## Score (logrank) test = 54.08 on 1 df,  p=2e-13
```

As expected, there is a significant positive selection for the opponent.

## Session

```
sessionInfo()  
  
## R version 3.5.1 (2018-07-02)  
## Platform: x86_64-apple-darwin15.6.0 (64-bit)  
## Running under: macOS 10.14.3  
##  
## Matrix products: default  
## BLAS: /Library/Frameworks/R.framework/Versions/3.5/Resources/lib/libRblas.0.dylib  
## LAPACK: /Library/Frameworks/R.framework/Versions/3.5/Resources/lib/libRlapack.dylib  
##  
## locale:  
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8  
##  
## attached base packages:  
## [1] stats      graphics  grDevices  utils      datasets  methods   base  
##  
## other attached packages:  
## [1] bindrcpp_0.2.2  amt_0.0.6      forcats_0.3.0  stringr_1.3.1  
## [5] dplyr_0.7.8     purrr_0.2.5    readr_1.3.1    tidyr_0.8.2
```

```

## [9] tibble_1.4.2      ggplot2_3.1.0    tidyverse_1.2.1 raster_2.8-4
## [13] sp_1.3-1
##
## loaded via a namespace (and not attached):
## [1] httr_1.4.0          jsonlite_1.6       splines_3.5.1
## [4] lsei_1.2-0          modelr_0.1.2       fasttime_1.0-2
## [7] assertthat_0.2.0    highr_0.7          cellranger_1.1.0
## [10] yaml_2.2.0          robustbase_0.93-3  pillar_1.3.1
## [13] backports_1.1.3     lattice_0.20-38    glue_1.3.0
## [16] digest_0.6.18       rvest_0.3.2        colorspace_1.3-2
## [19] htmltools_0.3.6     Matrix_1.2-15      plyr_1.8.4
## [22] pkgconfig_2.0.2     broom_0.5.1        haven_2.0.0
## [25] mvtnorm_1.0-8       scales_1.0.0       RSpecra_0.13-1
## [28] generics_0.0.2      withr_2.1.2        lazyeval_0.2.1
## [31] cli_1.0.1           survival_2.43-3    magrittr_1.5
## [34] crayon_1.3.4        readxl_1.2.0       evaluate_0.12
## [37] nlme_3.1-137        MASS_7.3-51.1      xml2_1.2.0
## [40] class_7.3-14        tools_3.5.1        fitdistrplus_1.0-11
## [43] hms_0.4.2           Gmedian_1.2.4      munsell_0.5.0
## [46] ctm_0.5.6           compiler_3.5.1     e1071_1.7-0
## [49] rlang_0.3.0.1       classInt_0.3-1     units_0.6-2
## [52] grid_3.5.1          rstudioapi_0.8     circular_0.4-93
## [55] labeling_0.3         rmarkdown_1.11     boot_1.3-20
## [58] npsurv_0.4-0        gtable_0.2.0       codetools_0.2-16
## [61] DBI_1.0.0           R6_2.3.0           lubridate_1.7.4
## [64] knitr_1.21          rgdal_1.3-6        bindr_0.1.1
## [67] stringi_1.2.4       parallel_3.5.1     Rcpp_1.0.0
## [70] sf_0.7-2            DEoptimR_1.0-8     tidyselect_0.2.5
## [73] xfun_0.4

```