Relational Event Models 2.0

Mixed effect additive REMs - Tutorial Section: Sheet

Boschi, Martina

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Mixed Effect Additive REMs: Application to Alien Species Invasions

0. Preparatory Steps: Introducing Alien Species Invasions

0.1. Installing libraries

In the following section, we will install the necessary packages for this tutorial. The provided code ensures that the packages are installed only if they are not already present on your system.

```
if (!require("mgcv", quietly = TRUE)) {
  # If not installed, install it
  install.packages("mgcv")
  # Load the package
  library("mgcv")
} else {
  if (!require("splines", quietly = TRUE)) {
    install.packages("splines")
    library("splines")
  } else {
    if (!require("ggplot2", quietly = TRUE)) {
      install.packages("ggplot2")
      library("ggplot2")
    } else {
      if (!require("tidyverse", quietly = TRUE)) {
        install.packages("tidyverse")
        library("tidyverse")
      } else {
        if (!require("RColorBrewer", quietly = TRUE)){
          install.packages("RColorBrewer")
        } else {
          if (!require("mgcViz", quietly = TRUE)){
            install.packages("mgcViz")
          } else {
            library("mgcv")
            library("splines")
            library("ggplot2")
            library("tidyverse")
            library("RColorBrewer")
            library("mgcViz")
          }
        }
      }
```

```
    }
  }
}
```

During the tutorial, we will refer to the following color palettes to improve the visualization of the results.

```
pal.blue <- brewer.pal(9, "Blues")
pal.rose <- brewer.pal(9, "RdPu")
colors <- c("#E69F00", "#56B4E9", "#009E73", "#F0E442", "#0072B2",
            "#D55E00", "#CC79A7", "#999999", "#66C2A5", "#FC8D62")
```

0.2. Introducing alien species invasions

Demo 1:

D1.1: Load the input data "input00.RData".

```
load(file="01-Data/01-Inputs/input00.RData")
```

D1.2: Inspect the original data contained in the object `FR`. Have a look at the columns: `"LifeForm"`, `"Taxon"`, `"Region"`, `"FirstRecord"`, `"Source"`.

```
head(FR[,c("LifeForm", "Taxon",
           "Region", "FirstRecord",
           "Source")])
```

```
##   LifeForm                     Taxon          Region FirstRecord
## 1    Algae    Acanthophora muscoides          Turkey        1986
## 2    Algae Acanthophora nayadiformis          Cyprus        1997
```

```
## 3    Algae Acanthophora nayadiformis           Turkey        1970
## 4    Algae    Acanthophora spicifera Hawaiian Islands        1952
## 5    Algae    Acetabularia caliculus           Israel        1943
## 6    Algae    Acetabularia caliculus            Spain        1957
##                      Source
## 1      Cinar et al. (2005)
## 2                    DAISIE
## 3      Cinar et al. (2005)
## 4 Carlton & Eldrege (2009)
## 5                    DAISIE
## 6                    DAISIE
```

D1.3 : Interpret this data as a relational event network. Define sender set, receiver set, and time-window.

D1.4 : Inspect the object `native`. A species' native range (NR) is the collection of areas where it is indigenous. How would you relate this concept to that of risk set?

```
head(native)
```

```
##               species      region sp.num r.num
## 994830 Adelges piceae      Turkey     12     1
## 994831 Adelges piceae Switzerland     12    90
## 994832 Adelges piceae      Greece     12    28
## 994833 Adelges piceae     Romania     12     7
## 994834 Adelges piceae      Serbia     12   232
## 994835 Adelges piceae     Germany     12    15
```

D1.5 : Inspect the object `first_records`. Describe this relational event network and identify why it can be considered a subset of the previous one.

```
head(first_records[,c("year","lf",
           "species",
           "region")])
```

```
##       year      lf                species        region
## 9337  1880 Insects  Adelges nordmannianae   Switzerland
## 15937 1881 Insects   Pheidole megacephala        France
## 16225 1884 Insects             Pineus pini   New Zealand
## 12792 1886 Insects       Eulachnus rileyi United States
## 14019 1887 Insects     Linepithema humile      Portugal
## 11797 1889 Insects Ctenarytaina eucalypti   New Zealand
```

D1.6 : Read the commented function `invaded.regions` that allows computing which regions the species invaded before the current year. Which type of covariates does this function allow to compute: exogenous, endogenous, or global?

```
invaded.regions <- function(sp.n, r.n, y, native, first_records){

  # Convert input arguments to numeric type if not already
  sp.n <- as.numeric(sp.n)
  r.n <- as.numeric(r.n)
  y <- as.numeric(y)

  # Get unique combinations of species number and region number from native data
  t <- unique(as.vector(subset(native, sp.num == sp.n, r.num)))

  # Get region numbers from first records data where species number matches
  pr <- as.vector(subset(first_records, sp.num == sp.n, r.num))
```

```
  # If the invasion is both present in first records data and in native range
  # consider the former as actual piece of information
  t <- setdiff(t, pr)

  # Find indices of first records occurring before end date for the species
  set.sp <- which(first_records$sp.num == sp.n & first_records$year < y)

  # Combine regions in native range with regions in first records before date
  t <- na.omit(c(t, first_records$r.num[set.sp]))

  # Do not consider the involved region
  inv <- unlist(setdiff(t, r.n))

  # Return invaded regions
  return(inv)
}
```

0.3. Building the Case-Control Dataset

Demo 2 :

D2.1 : Consider the smaller relational event network described by the data in `first_records`. Begin by defining the sender set and storing it in `spec`, followed by defining the receiver set and storing it in `reg.lf`.

```
# Define sender set - species
spec <- unique(first_records$species)
(s <- length(spec))
```

```
## [1] 114
```

```
# Define receiver set - regions
reg.lf <- unique(first_records$region)
(r <- length(reg.lf))
```

```
## [1] 159
```

The dynamic network of FRs consists of two sets of nodes: the set of species and the set of regions. Additionally, in the dataset, we refer to a numerical formulation of species and regions, which correspond to the set of unique observed species in the data and the set of regions reported in the matrix of geographical distances, respectively.

```
reg <- colnames(data_distance)
```

D2.2 : Review the commented function `creating_case_control_dataset`, which utilizes information from the relational event network, noting that the relational event is non-recurrent.

```
creating_case_control_dataset <- function(first_records,
                                  spec, reg.lf, reg,
                                  seed=1234
                                  ){

  reg.lf.num <- match(reg.lf, reg)
  s <- length(spec)
  r <- length(reg.lf)

  ## POSSIBLE (S,R) INTERACTIONS ####
  # Initialize a vector to keep track of the risk set size over time
```

```
at.risk <- NULL
# Create a matrix to indicate possible (species, region) interactions
alien.occ <- matrix(0, nrow = s, ncol = r)
rownames(alien.occ) <- spec
colnames(alien.occ) <- reg.lf
for (n.sp in 1:s){
  # Identify native regions for each species
  nat.id <- unique(native$r.num[native$sp.num == n.sp])
  # Identify regions where the species is not native
  possible.to <- setdiff(reg.lf.num,nat.id)
  # Mark these regions as possible invasion sites for the species
  alien.occ[n.sp,reg[possible.to]] <- 1
}

## COLLECTING INFORMATION ####
dat.gam <- data.frame(matrix(NA, nrow=nrow(first_records),ncol=6))
colnames(dat.gam) <- c("y", "year",
                       "sp1", "r1",
                       "sp2", "r2")
# The response is fixed and equal to 1
dat.gam[,1] <- rep(1, nrow(first_records))

set.seed(seed)
# For each FR:
for (i in 1:nrow(first_records)){

  ### INFORMATION CONCERNING THE EVENT ####
  # year of the invasion event
  dat.gam[i,2] <- year <- first_records[i,"year"]
  # invading species
  dat.gam[i,3] <- s.ev <- first_records[i,"species"]
  # invaded country
  dat.gam[i,4] <- r.ev <- first_records[i,"region"]

  ### POSSIBLE EVENTS ####
  # Events occurred at the same time of the considered event
  # are removed from the risk set
  sub_stp <- first_records[first_records$year==year,
                           c("species", "region")]
  ni <- nrow(sub_stp)
  for (j in 1:ni){
    # Mark these (species, region) pairs as not at risk
    alien.occ[sub_stp[j,1],sub_stp[j,2]] <- 0
  }
  at.risk <- c(at.risk, sum(alien.occ==1))

  ### SAMPLING THE NON-EVENT ####
  sr.nv<-sample(which(alien.occ!=0),1)
  # species non-event
  dat.gam[i,5] <- s.nv <- spec[(sr.nv-1)%%s+1]
  # region non-event
  dat.gam[i,6] <- r.nv <- reg.lf[(sr.nv-1)%/%s+1]
}
```

```
  return(dat.gam)
}
```

D2.3: Use the function `creating_case_control_dataset` with `first_records` and generate the case-control dataset. Additionally, determine the numerical codification of species and regions.

```
dat.gam <- creating_case_control_dataset(first_records,
                                         spec, reg.lf, reg)
```

```
dat.gam$sp1.num <- match(dat.gam$sp1, spec)
dat.gam$r1.num <- match(dat.gam$r1, reg)
dat.gam$sp2.num <- match(dat.gam$sp2, spec)
dat.gam$r2.num <- match(dat.gam$r2, reg)
```

```
head(dat.gam[c("year","sp1", "r1","sp2", "r2")])
```

```
##   year                    sp1           r1                       sp2
## 1 1880  Adelges nordmannianae   Switzerland      Epiphyas postvittana
## 2 1881   Pheidole megacephala        France        Chilo suppressalis
## 3 1884            Pineus pini   New Zealand Coccinella septempunctata
## 4 1886       Eulachnus rileyi United States       Agrilus planipennis
## 5 1887     Linepithema humile      Portugal        Tremex fuscicornis
## 6 1889 Ctenarytaina eucalypti   New Zealand       Xyleborus glabratus
##                 r2
## 1        Venezuela
## 2            Benin
## 3           Gambia
## 4            Benin
## 5    Guinea-Bissau
## 6 Hawaiian Islands
```

```
head(dat.gam[c("year","sp1.num", "r1.num","sp2.num", "r2.num")])
```

```
##   year sp1.num r1.num sp2.num r2.num
## 1 1880       1     90      22     77
## 2 1881       2     11      34    195
## 3 1884       3     31      66    208
## 4 1886       4     37     106    195
## 5 1887       5     25     103    211
## 6 1889       6     31     108      3
```

1. Time-Varying Effect of Trade on Species Invasions

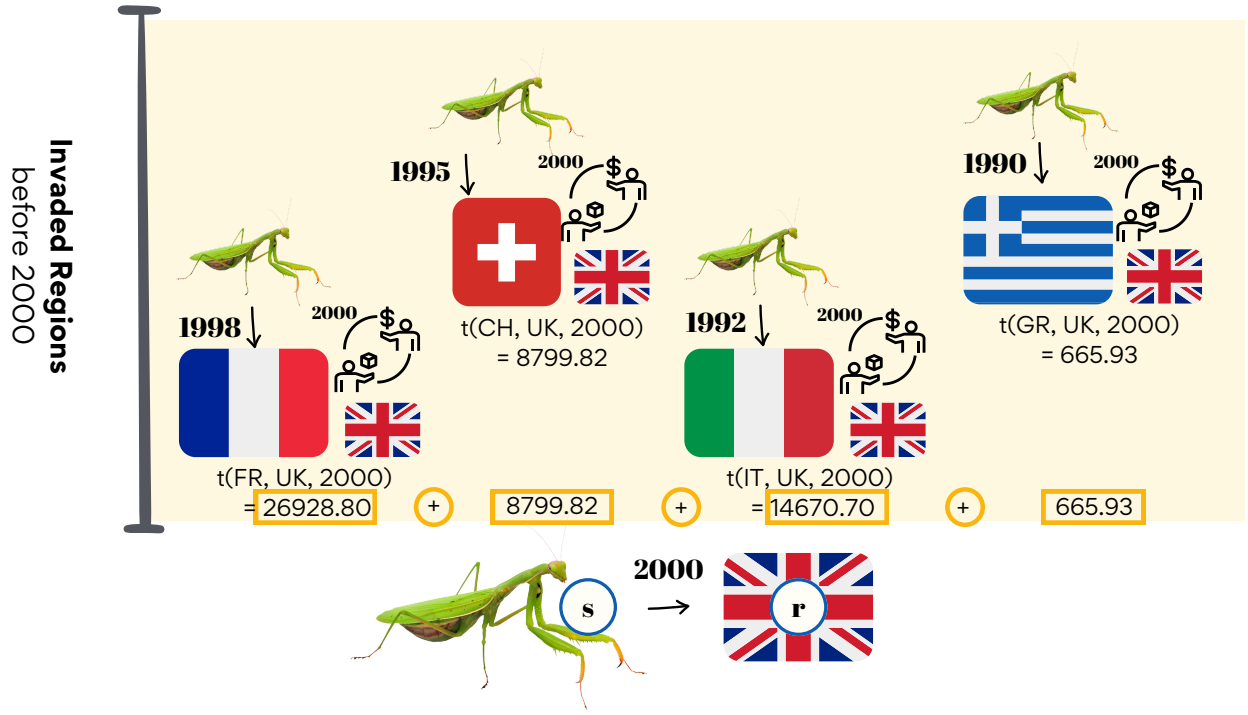
1.1. Trade: Covariate Computation

Demo 3:

D3.1: Load the input data "input01.RData".

```
load("01-Data/01-Inputs/input01.RData")
```

D3.2: Write a function `log_trade` that, given a relational event (and all the relevant information required), computes the annual trade between the involved region and the previously invaded regions by the species. Apply the function to the events and the sampled non-events, and compute the difference. Refer to the figure in the following slide to understand how the covariate is computed.




```
t <- which(data_trade$transfer < 0)
data_trade$transfer[t] <- 0
```

```
trade.funct <- function(inv, r.n, y, reg, data_trade){

  # Convert input arguments to numeric type if not already
  r.n <- as.numeric(r.n)
  y <- as.numeric(y)

  # Check if there are already invaded countries
  if(length(inv)!=0){

    # Find rows that involve invaded countries as sending trade
    u <- which(data_trade$FromRegion %in% reg[inv])
    # Find rows that involve region of interest as receiving trade
    v <- which(data_trade$ToRegion == reg[r.n])
    # Find the intersection of the two sets
    w <- intersect(u,v)
    x <- data_trade[w,]
    # Consider the trade instances occurred before or at the time of interest
    x <- x[x$year<=y,]
    trade_value <- NULL
    # If there are rows in the filtered dataset
    if(nrow(x)>0){
      # For each invaded country, the maximum year is recorded
      o <- aggregate(x$year, list(x$FromRegion), FUN=max)
      # For each of them, the corresponding transfer is stored
      for (o.i in 1:nrow(o)){
        trade_value <- c(trade_value,
                         x$transfer[x$FromRegion==o[o.i,1] &
                                    x$year==o[o.i,2]])}
```

```
    }
  } else {
  # If there are not already invaded countries, trade is set equal to 0
    trade_value <- 0
  }
  # Compute the log-transformed sum of trade values (with an added constant 1)
  log_trade.value <- ifelse(length(trade_value)>0,
                            log(sum(trade_value, na.rm =T)+1),0)

  # Return the computed log-transformed trade value
  return(log_trade.value)
}
```

```
log_trade <- function(sp.n, r.n, y, native, first_records, reg, data_trade){

  inv <- invaded.regions(sp.n = sp.n,
                         r.n = r.n,
                         y = y,
                         native = native,
                         first_records = first_records)

  log_trade.value <- ifelse(r.n==match("USACanada", reg),
                            mean(trade.funct(inv = inv,
                                             r.n = match("United States",reg),
                                             y = y,
                                             reg = reg,
                                             data_trade = data_trade),
                                 trade.funct(inv = inv,
                                             r.n = match("Canada",reg),
                                             y = y,
                                             reg = reg,
                                             data_trade = data_trade)),
                            trade.funct(inv = inv,
                                        r.n = r.n,
                                        y = y,
                                        reg = reg,
                                        data_trade = data_trade))

  return(log_trade.value)
}
```

```
dat.gam$tr1 <- apply(dat.gam[,c("sp1.num", "r1.num", "year")], 1,
                            function(x) log_trade(sp.n = x[1],
                                                  r.n = x[2],
                                                  y = x[3],
                                                  native = native,
                                                  first_records =
                                                    first_records,
                                                  reg = reg,
                                                  data_trade = data_trade))
dat.gam$tr2 <- apply(dat.gam[,c("sp2.num", "r2.num", "year")], 1,
                            function(x) log_trade(x[1], x[2], x[3],
                                                  native = native,
                                                     first_records =
```

```
                                                    first_records,
                                                reg = reg,
                                                data_trade = data_trade))
dat.gam$tr = dat.gam$tr1 - dat.gam$tr2
```

D3.3: Inspect the nature of the covariate. Is it a monadic or dyadic covariate?

D3.4: Is it an endogenous or exogenous covariate?

1.2. Effect of Trade as Spline function of Time

D4.0 Choose the basis-dimension q.

```
q = 10
```

D4.1 Select the **spline basis functions types**

```
bspline <- function(x, k, i, m = 2) {
  # ith B-spline basis function of order m at the values in x
  # given knot locations in k

  if (m == -1) {
    # Base case of the recursion:
    # when m is -1, we are at the lowest order basis function
    res <- as.numeric(x < k[i + 1] & x >= k[i])
    # Returns 1 if x is within the interval [k[i], k[i+1])

  } else {

    # Recursive case:
    # B-spline basis function from lower order basis functions
    # Calculate the first term's coefficient
    z0 <- (x - k[i]) / (k[i + m + 1] - k[i])
    # Calculate the second term's coefficient
    z1 <- (k[i + m + 2] - x) / (k[i + m + 2] - k[i + 1])

    # Recursive calls to the lower order basis functions
    res <- z0 * bspline(x, k, i, m - 1) + z1 * bspline(x, k, i + 1, m - 1)
  }
  return(res)  # Return the evaluated B-spline basis function
}
```

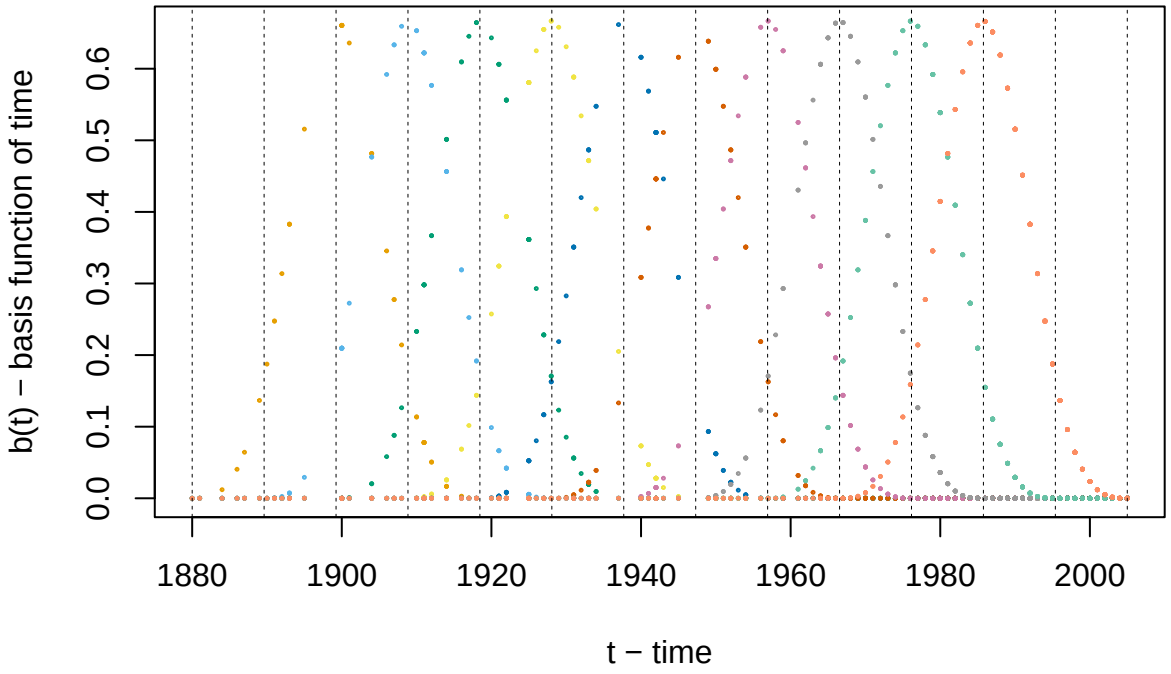
D4.2 Given **range of the variable**, select the **basis evaluation points**.

```
# Equally spaced knots from 1880 to 2005
n_knots = 14.
knots = seq(from = min(dat.gam$year),
            to = max(dat.gam$year),
            length.out = n_knots)
```

D4.3 Evaluate the q **basis functions** of time $b_l(t)$.

```
m = 2
basis = matrix(0, nrow = length(dat.gam$year), ncol = q)
for (j in 1:q) {
  basis[, j] = bspline(dat.gam$year, k = knots, i = j)
}
```

```r
plot(y = basis[, 1],
     x = dat.gam$year,
     ylab = 'b(t) - basis function of time', xlab = 't - time',
     col = 0,
     cex = 0.2)
for (j in 1:10) {
  points(y = basis[, j],
         x = dat.gam$year,
         cex = 0.2,
         col = colors[j])
}
for (k in knots) {
  abline(v=k, lty=2, lwd=0.5)
}
```



1.3. Determine Trade's Contribution

- To the log-hazard of an interaction}

$$f_{sr} = ... + \sum_{j=1}^{q} \theta_l b_j(t) tr_{sr}(t) + ...$$

- To the sampled likelihood function}

$$PL(\theta) = \prod_{i=1}^{n} \frac{e^{\left[\sum_{j=1}^{q} \theta_j b_j(t)\right] \Delta tr_i}}{1 + e^{\left[\sum_{j=1}^{q} \theta_j b_j(t)\right] \Delta tr_i}}$$

1.4. Estimate the Coefficients of the Spline

Demo 5 :

D5.1 :Let `x.ev` and `x.nv` be $n \times 1$ vectors of covariate evaluated for events & non-events. Then: `x = x.ev - x.nv`;

```
x.ev <- dat.gam$tr1
x.nv <- dat.gam$tr2
x <- x.ev - x.nv
```

D5.2 Let `stp` be $n \times 1$ vector of event-times.

```
stp <- dat.gam$year
```

D5.3 Fit the model incorporating a time-varying effect for `x`.

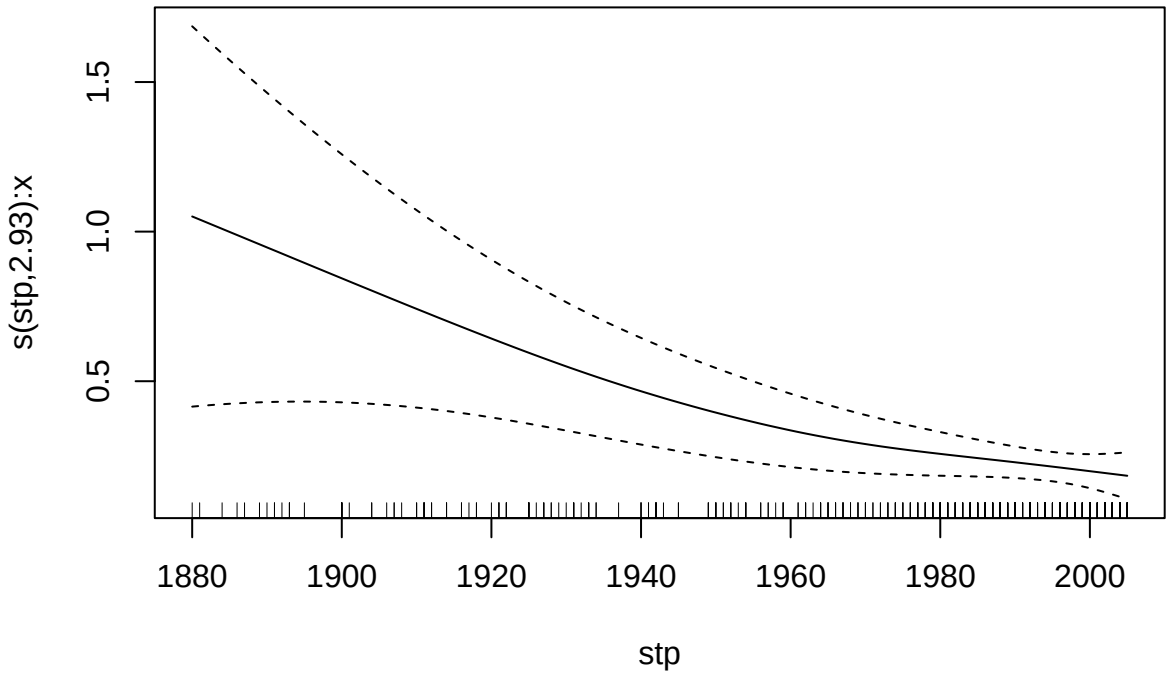
REMARK: default spline's type for `gam` in `mgcv` consists of thin plate regression spline.

```
gam_tr.only <- gam(y ~ s(stp, by=x) - 1,
    family="binomial"(link = 'logit'),
    method="REML", data=dat.gam)
```

1.5. Interpreting Trade's Effect

Demo 6

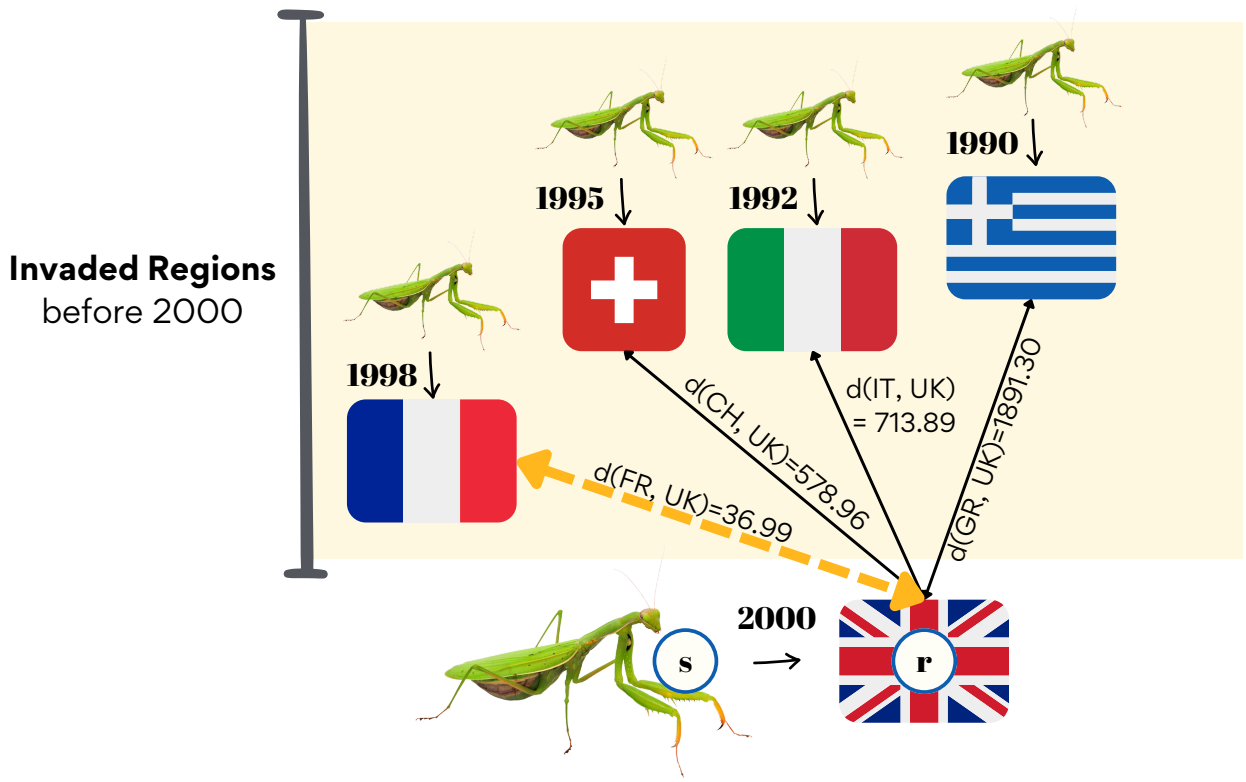
```
plot(gam_tr.only)
```



2. Non-Linear Effect of Distance on Species Invasions

2.1. Distance: Covariate Computation

Supplementary 2



2.2. Effect: Spline function of Distance

Supplementary 3

2.3. Determine Distance's Contribution

- To the **log-hazard of an interaction**}

$$f_{sr} = ... + \sum_{j=1}^{q} \theta_j b_j[d_{sr}(t)] + ...$$

- To the **sampled likelihood function**}

$$PL(\theta) = \prod_{i=1}^{n} \frac{e^{\left[\sum_{j=1}^{q} \theta_j b_j[d_{s_i r_i}(t_i)] - b_j[d_{s_i^* r_i^*}(t_i)]\right]}}{1 + e^{\left[\sum_{j=1}^{q} \theta_j b_j[d_{s_i r_i}(t_i)] - b_j[d_{s_i^* r_i^*}(t_i)]\right]}}$$

2.4. Estimate the Coefficients of the Spline

Exercise 1 :

E1.1 : Load the input data "input02.RData".

E1.2 : Let `x.ev` and `x.nv` be $n \times 1$ vectors of covariate evaluated for events & non-events.

E1.2 : Let `unit` be $n \times 1$ unit vector.

E1.3 : Define `X`, combining `x.ev` and `x.nv` and `I` combining `unit` and `-unit`.

E1.4 Fit the model incorporating a non-linear effect.

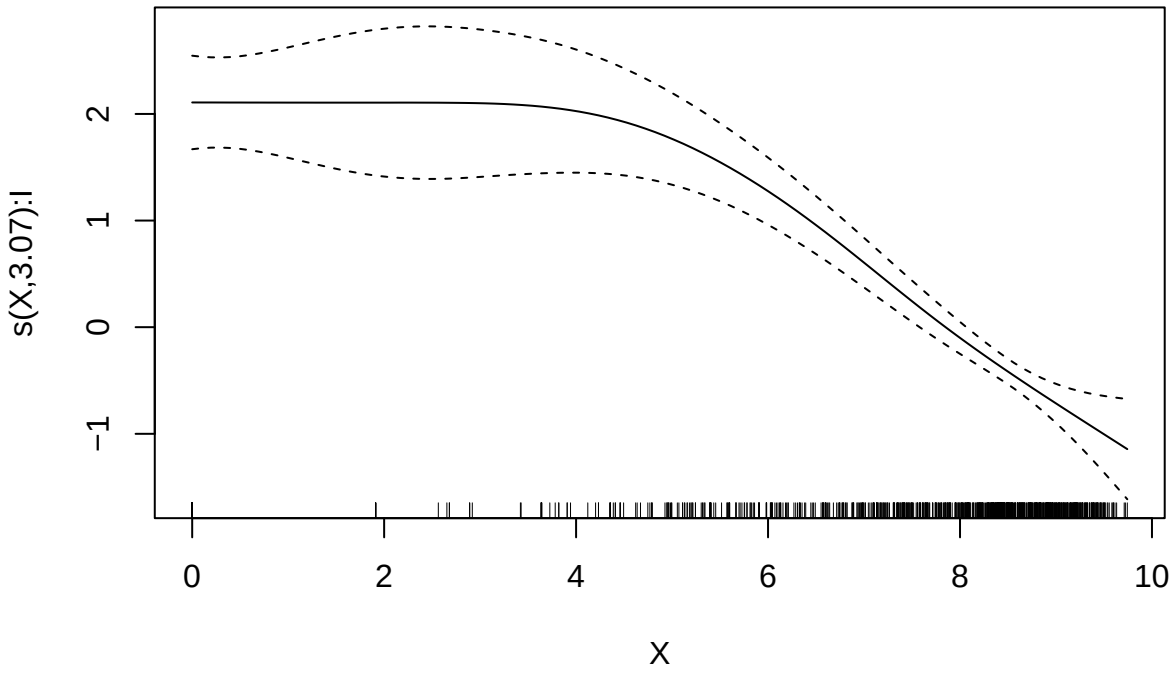
REMARK: default spline's type for `gam` in `mgcv` consists of thin plate regression spline.

2.5. Interpreting Distance's Effect

Demo 7

```
load(file="01-Data/02-Gam-Fits/gam_d.only.RData")
```

```
plot(gam_d.only)
```



3. Species Invasiveness Random Effect

3.1. Species Invasiveness: Covariate Computation

Demo 8:

D8.1: Load the input data "input03.RData".

```
load("01-Data/01-Inputs/input03.RData")
```

D8.2: Define the covariate: $z_s(t)$: involvement of species s in first record occurring at t. Create a $n \times 2$ matrix `sp` containing in the fist column `spec` levels related to species involved in the events and in the second those involved in the non-events.

```
sp1 <- dat.gam$sp1
sp2 <- dat.gam$sp2
sp <- factor(c(sp1,sp2))
dim(sp) <- c(length(sp1),2)
```

D7.3: Inspect the nature of the covariate. Is it a monadic or dyadic covariate? It is just reporting the label of species involved s, so the covariate $z_s(t)$ is monadic.

3.2. Random Effects as Smooths

$$\gamma' z_s(t) = \sum_{s' \in \mathcal{S}} \gamma_{s'} 1\{s = s'\}$$

3.3. Species Invasiveness' Contribution

- To the **log-hazard of an interaction**}

$$f_{sr} = ... + \sum_{s' \in \mathcal{S}} \gamma_{s'} 1\{s = s'\} + ...$$

- To the **sampled likelihood function**}

$$PL(\gamma) = \prod_{i=1}^{n} \frac{e^{\gamma_{s_i} - \gamma_{s_i^*}}}{1 + e^{\gamma_{s_i} - \gamma_{s_i^*}}} - \frac{1}{2\sigma_{\text{sp}}^2} \gamma^T \gamma$$

3.4. Estimate the Coefficients of the Spline

Exercise 3 :

E3.1 : Let `unit` be $n \times 1$ unit vector. Define `I` combining `unit` and `-unit`.

E3.2 Fit the model incorporating a random effect.

REMARK: default spline's type for `gam` in `mgcv` consists of thin plate regression spline. Instead, we need to specify that we aim to fit a random effect.

3.5. Interpreting Species Invasiveness Random Effects

Demo 8 :

```
load(file="01-Data/02-Gam-Fits/gam_sp.only.RData")
```

```
re.species <- coefficients(gam_sp.only)
names(re.species) <- levels(sp)
```

```
sort(re.species, decreasing = TRUE)[1:5]
```

```
## Frankliniella occidentalis           Aphis spiraecola
##                   2.411066                   1.848464
##            Cinara cupressi       Phenacoccus manihoti
##                   1.789825                   1.749139
##             Apis mellifera
##                   1.571748
```

```
sort(re.species)[1:5]
```

```
##  Xylosandrus compactus    Solenopsis richteri    Scolytus schevyrewi
##             -1.5031237             -1.2676923             -1.0597829
## Archips fuscocupreanus    Agrilus planipennis
##             -1.0562797             -0.9503508
```

4. Fit a model with all the components included

Exercise 4 :

E4.1 : Load the input data "input04.RData".

```
load("01-Data/01-Inputs/input04.RData")
```

```
load(file="01-Data/02-Gam-Fits/gam_dt.only.RData")
load(file="01-Data/02-Gam-Fits/gam_tr.only.RData")
load(file="01-Data/02-Gam-Fits/gam_d.only.RData")
load(file="01-Data/02-Gam-Fits/gam_sp.only.RData")
```

```
AIC(gam_dt.only)
```

Model Selection

```
## [1] 742.7089
```

```
AIC(gam_tr.only)
```

```
## [1] 630.9921
```

```
AIC(gam_d.only)
```

```
## [1] 550.0876
```

```
AIC(gam_sp.only)
```

```
## [1] 642.3556
```

```
# sort(re.species, decreasing = TRUE)[1:5]
# sort(re.species)[1:5]
```

```
# re.species_complete <- coefficients(gam_complete)[21:length(coefficients(gam_complete))]
# names(re.species_complete) <- levels(sp)
# sort(re.species_complete, decreasing = TRUE)[1:5]
# sort(re.species_complete)[1:5]
```

```
# sort(re.species)[1:3]
# sort(re.species_complete)[1:3]
```

Changes in random effect predictions