

# Vector model

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## Vector model dynamics

In this code we will integrate the vector model:

$$\frac{dL}{dt} = afA^{(h)} \left(1 - \frac{L}{K}\right) - d_L L - \delta_L L \quad (1)$$

$$\frac{dA}{dt} = -\rho(A)H + d_L L - \delta_A A \quad (2)$$

$$\frac{dA^{(h)}}{dt} = \rho(A)H - aA^{(h)} - \delta_A A^{(h)} \quad (3)$$

with the forcing impose by the citizen science model,  $\rho(M)$ , the number of mosquitoes encounter per human:

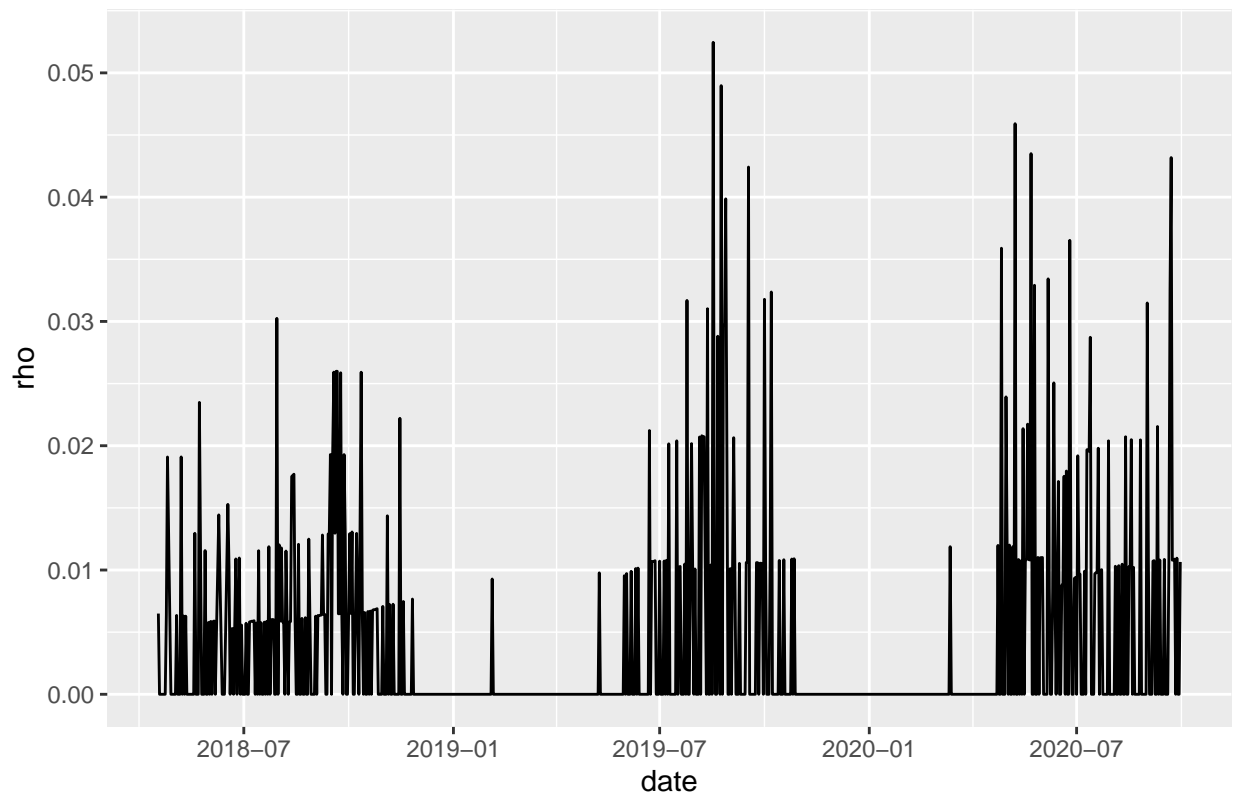
$$\rho(M, \Delta t) = \frac{1}{\sum_{i=0}^n p_i(R|e)P_i(\Delta t)} \frac{\Delta R}{\Delta t}, \quad (4)$$

First we set the path and compile the C code with the adult mosquito model.

First, we read the input data:

```
# Rho, mosquito encounter per human capita rate:
Path= "/home/marta/Documentos/PHD/2021/SUR_Model/Code/OUTPUT/df_rho.dat"
df_rho <- data.frame(t(read.table(Path, header=FALSE)))
colnames(df_rho) <- c("time", "rho", "date")
df_rho$date = as.Date(df_rho$date , "%Y-%m-%d")
df_rho$time <- NULL
df_rho$rho <- as.numeric(df_rho$rho)
ggplot(df_rho) +
  geom_line(aes(x = date, y =rho)) +
  ggtitle("Encounter rate computed from Citizen Science model")
```

## Encounter rate computed from Citizen Science model

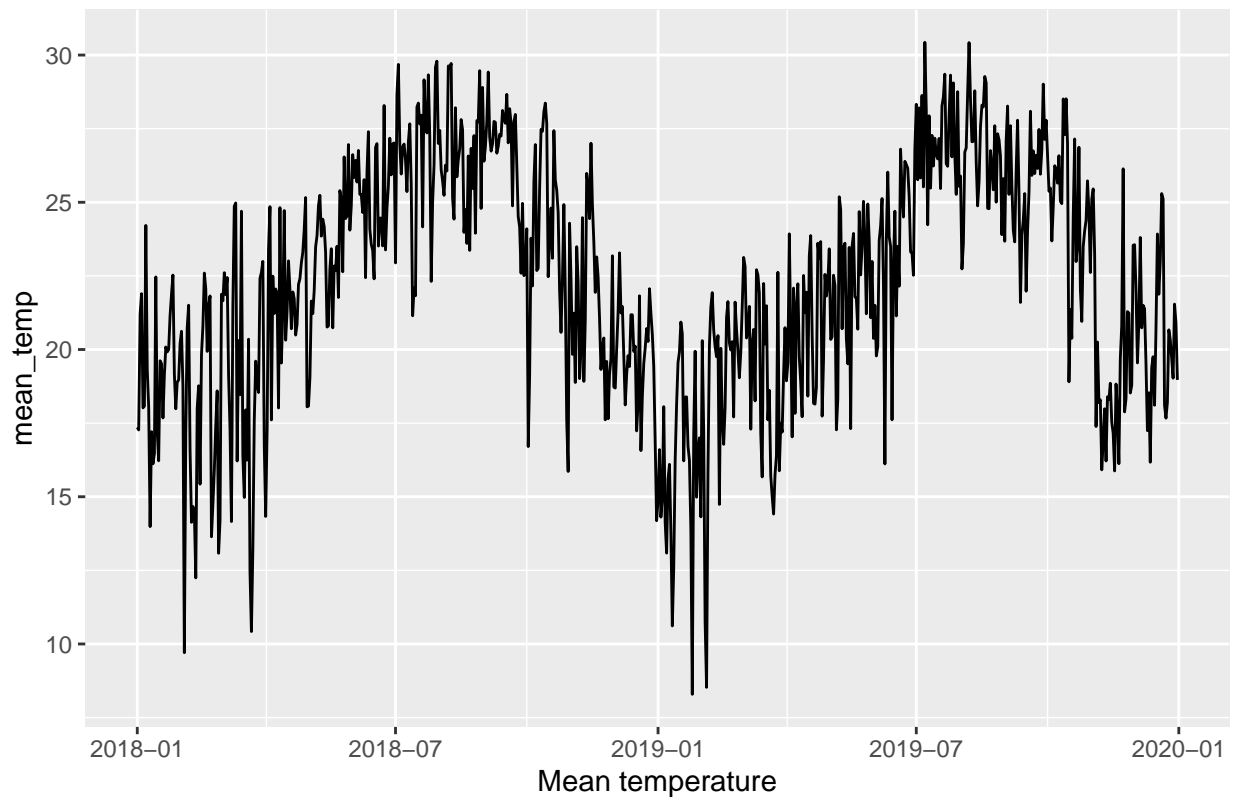


We compute the functional response along the period of computation for the temperatures given in this period. We will set the temperature to the mean temperature between five meteorological station in Barcelona each day.

```
# Temperatures from Barcelona:
Path_temp = "/home/marta/Documentos/PHD/2021/Mosquito_model/data/bcn_weather_daily.Rds"
temp <- read_rds(Path_temp)
temp$date = as.Date(temp$date , "%Y-%m-%d")
temp <- temp %>% group_by(date) %>% summarise(mean_temp = mean(valor))

ggplot(temp) +
  geom_line(aes(date, mean_temp))+
  ggtitle("Mean temperature Barcelona") +
  xlab("Mean temperature")
```

## Mean temperature Barcelona

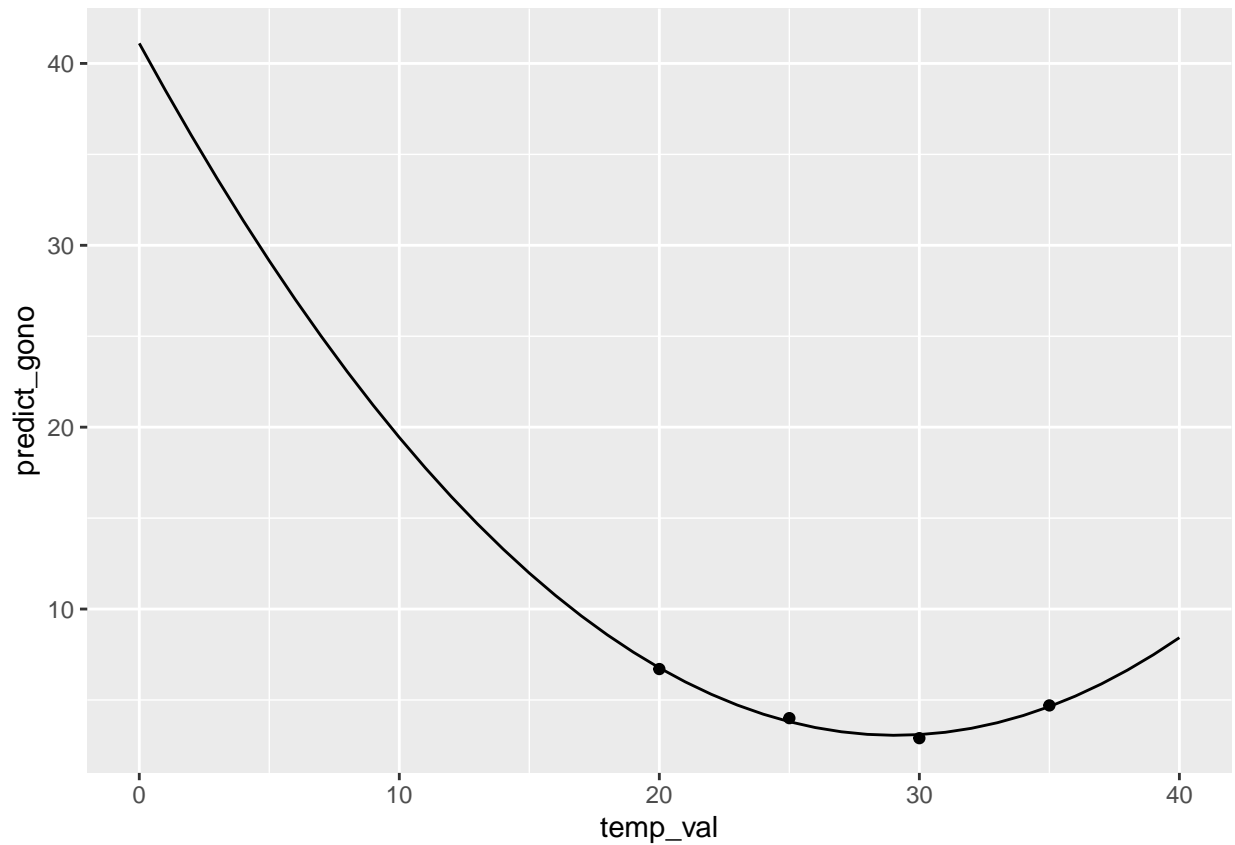


We will do a fit of the gonotrophic cycle, from the data obtain in Delate et al “Influence of Temperature on Immature Development” .

Temperature (°C)	Mean value
20	6.7
25	4
30	2.9
35	4.7

```
temp_vec = c(20,25,30,35)
dur_gono = c(6.7,4,2.9,4.7)
temp_vec2 <- temp_vec^2
quadratic_mod <- lm(dur_gono ~ temp_vec + temp_vec2)
temp_val <- seq(0,40,1)
predict_gono <- predict(quadratic_mod, list(temp_vec=temp_val, temp_vec2=temp_val^2))
df_gono_data <- data.frame(temp_vec, dur_gono)
df_predict <- data.frame(temp_val, predict_gono)

ggplot(df_predict, aes(temp_val, predict_gono)) +
  geom_line()+
  geom_point(data = df_gono_data, aes(x = temp_vec, y =dur_gono))
```



```
int = quadratic_mod$coefficients[1]
beta = quadratic_mod$coefficients[2]
beta2 = quadratic_mod$coefficients[3]
int
```

```
## (Intercept)
##      41.105
```

```
beta
```

```
## temp_vec
##    -2.617
```

```
beta2
```

```
## temp_vec2
##      0.045
```

```
# Gonotrophic cycle
gonot <- function(T){
  a = beta2*T^2+beta*T+int
  val = min(1,1/a)
  return(val)
}
```

```

# Development rate
d_L <- function(T){
  val = 0
  #0.1727*exp(-((T-28.40)/10.20)^2)
  return(val)
}

# Larva mortality rate
delta_L <- function(T){
  a = abs(-0.1305*T^2+3.868*T+30.83)
  val = min(1, 1/a)
  return(val)
}

# Adult mosquito mortality rate
delta_A <- function(T){
  a = abs(-0.1921*T^2+8.147*T-22.98)
  val = min(1, 1/a)
  return(val)
}

```

There are a few parameters on the model depending on temperature, i.e., those parameters are:

1. The duration of the gonotrophic cycle:

$$a = 41.105 - 2.617 * T + 0.045 * T^2$$

2. Larva development rate:

$$d_L = 0.1727 * \exp(-((T - 28.40)/10.20)^2)$$

3. Larva mortality rate:

$$\delta_L = \min \left( 1, \frac{1}{|-0.1305 * T^2 + 3.868 * T + 30.83|} \right)$$

4. Adult mosquito mortality rate:

$$\delta_L = \min \left( 1, \frac{1}{|-0.1921 * T^2 + 8.147 * T - 22.98|} \right)$$

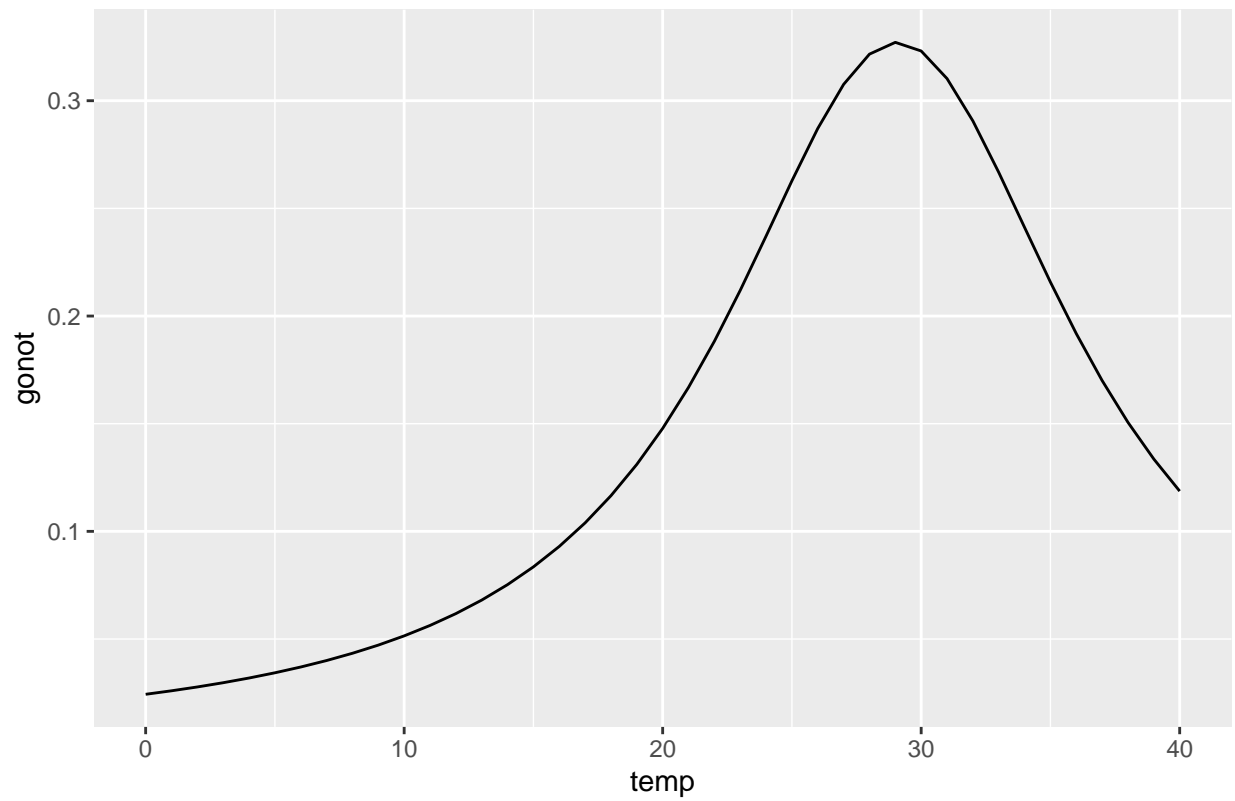
```

vec = seq(0,40,1)
df_gonot_vec <- data.frame(temp = vec, gonot =unlist(lapply(vec,gonot)))
df_dL_vec <- data.frame(temp = vec, dL = unlist(lapply(vec,d_L)))
df_deltaL_vec <- data.frame(temp = vec, deltaL = unlist(lapply(vec,delta_L)))
df_deltaA_vec <- data.frame(temp = vec, deltaA = unlist(lapply(vec,delta_A)))

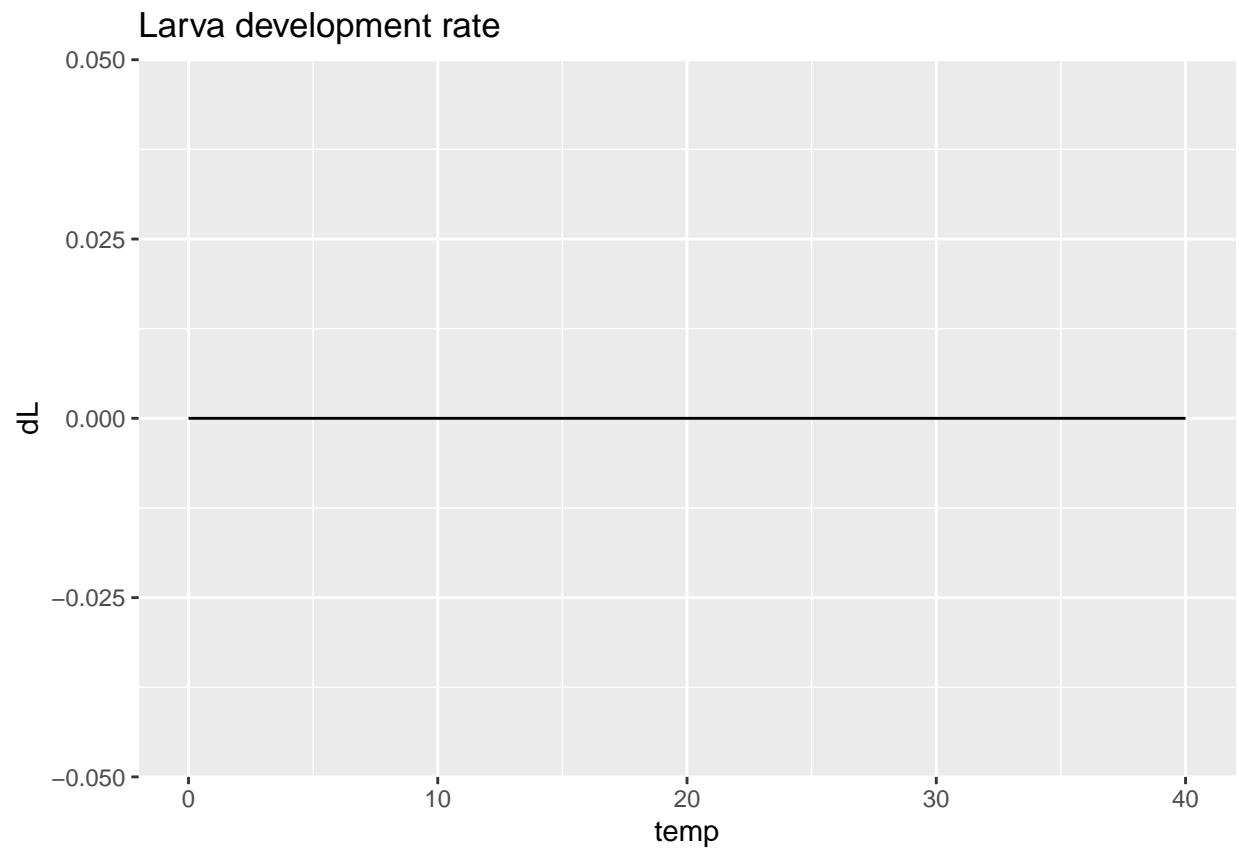
ggplot(df_gonot_vec) + geom_line(aes(temp,gonot)) + ggtitle("Inverse of the Gonotrophic cycle")

```

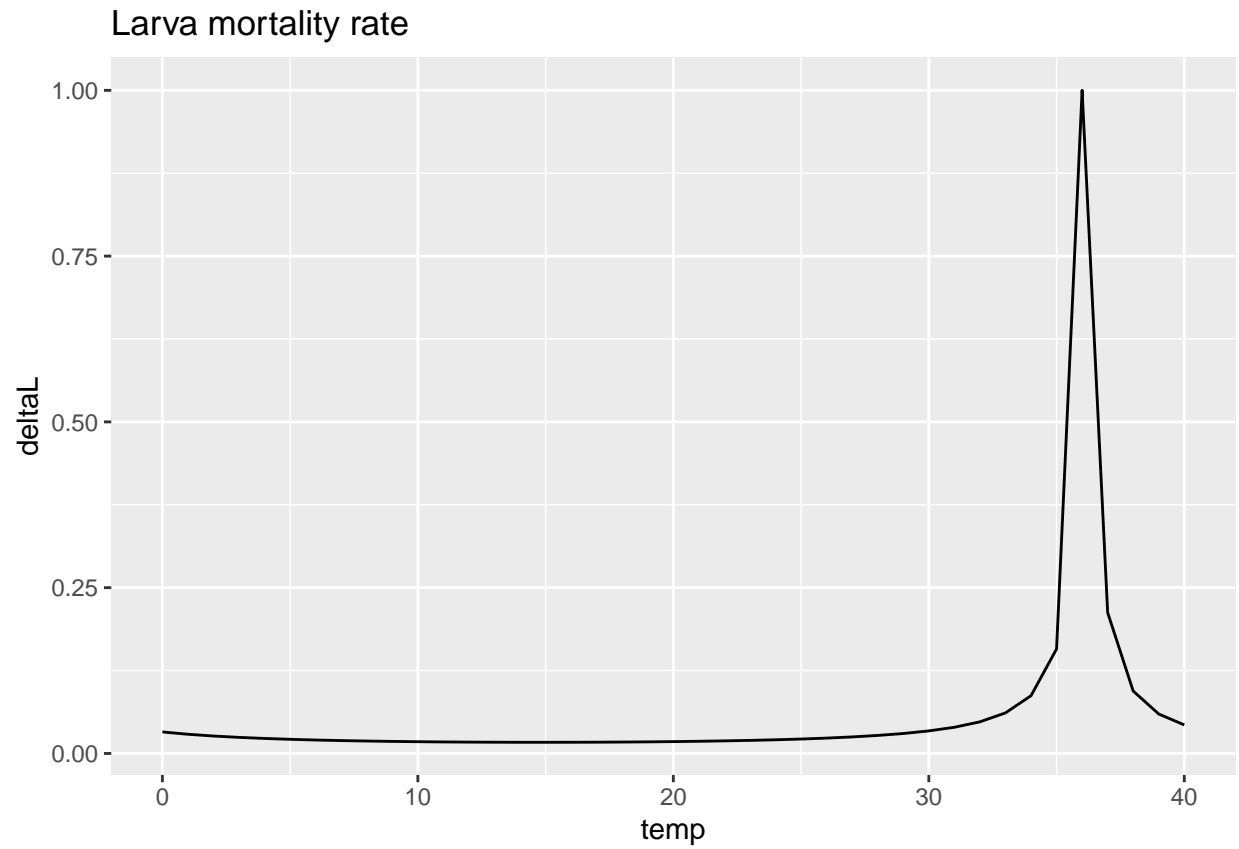
Inverse of the Gonotrophic cycle



```
ggplot(df_dL_vec) + geom_line(aes(temp,dL)) + ggtitle("Larva development rate")
```



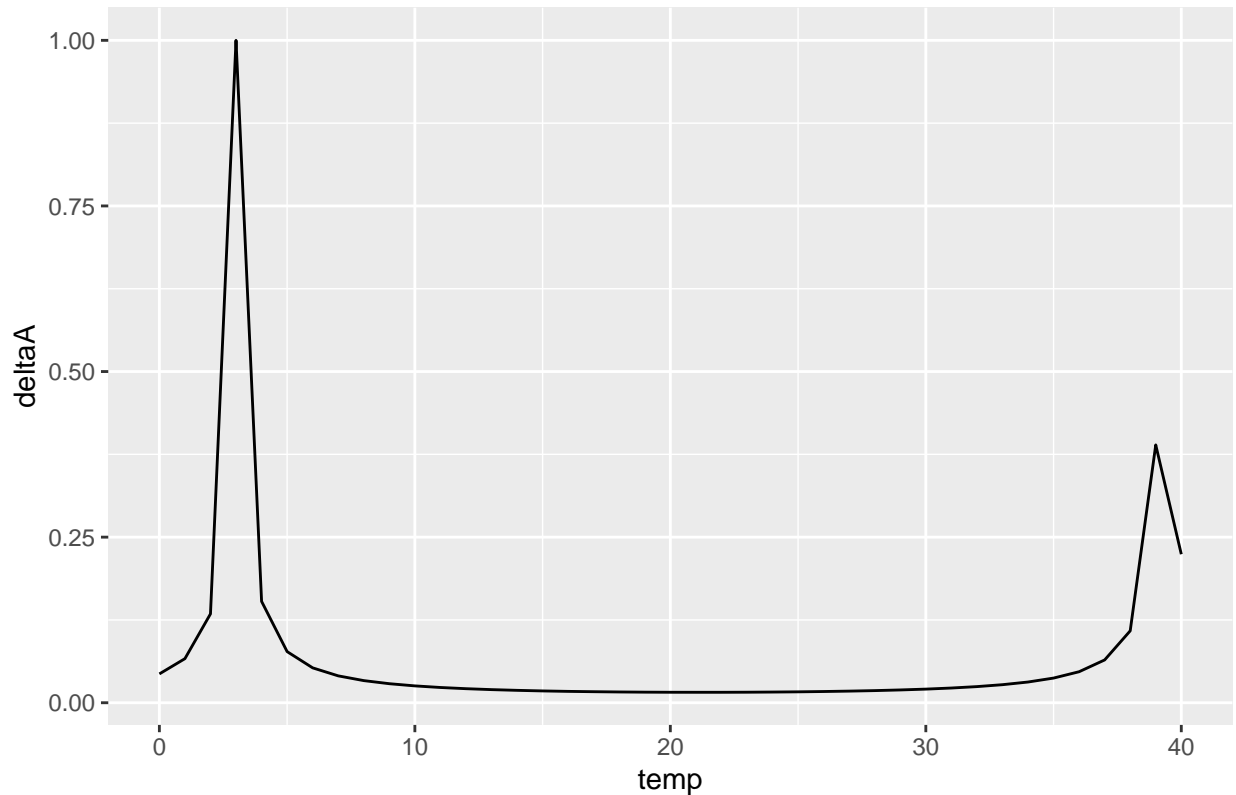
```
ggplot(df_deltaL_vec) + geom_line(aes(temp,deltaL)) + ggtitle("Larva mortality rate")
```



```
ggplot(df_deltaA_vec) + geom_line(aes(temp,deltaA)) + ggtitle("Mosquito adult mortality rate")
```



## Mosquito adult mortality rate



Now we compute the data frames for the functional responses of the mosquito.

```
# Compute the values of the functions/forcings with temp.
# Compute the minimum date of the rho:
min_rho_date <- min(df_rho$date)
# DFs with the date and value of the parameter at that time.
gono = unlist(lapply(temp$mean_temp, gonot))
df_gonot_out <- data.frame(date = temp$date, gono)

ref_date <- max(min(df_rho$date), min(df_gonot_out$date))
df_gonot_out$time = as.numeric(df_gonot_out$date - as.Date(ref_date, "%Y-%m-%d")) , units="days")
df_gonot_out <- df_gonot_out %>% filter( df_gonot_out$time >= 0)

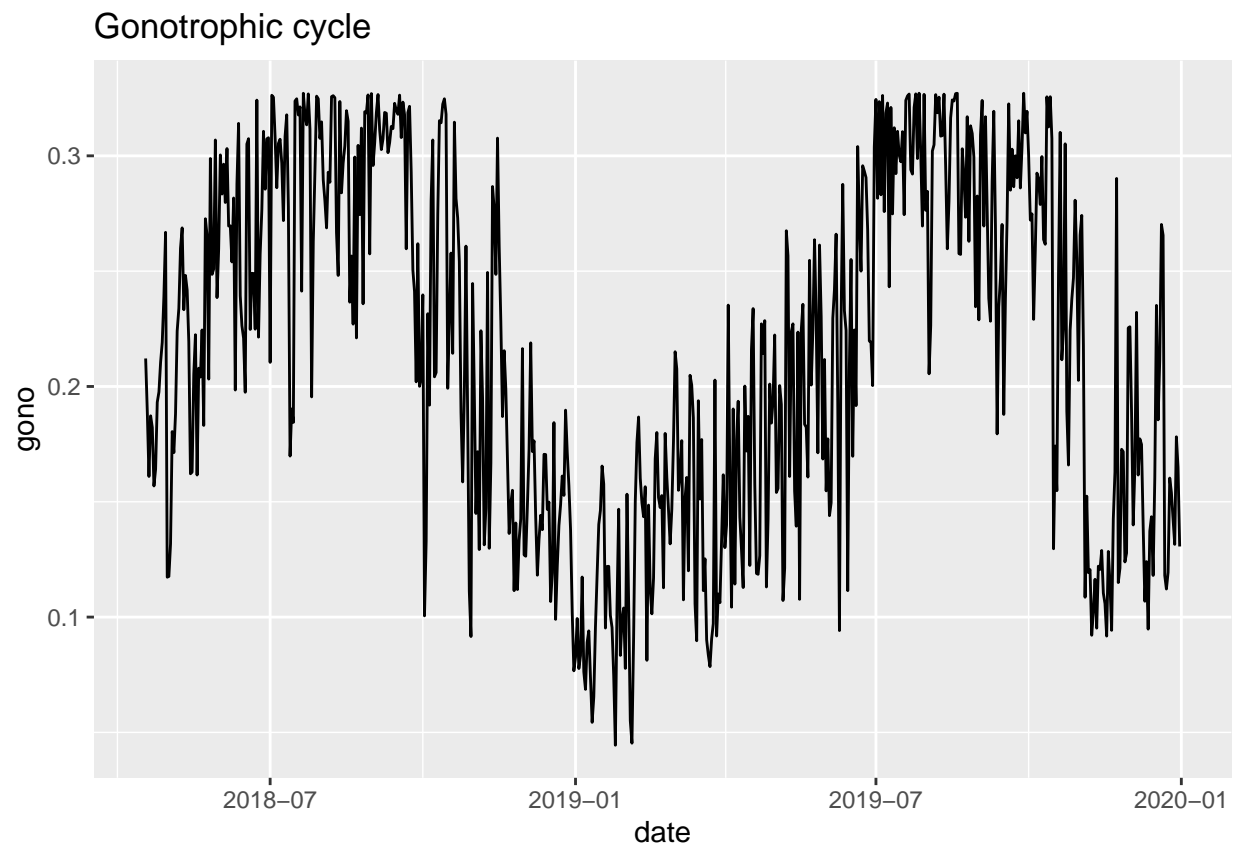
df_dL_out <- data.frame(date = temp$date, dL = unlist(lapply(temp$mean_temp, d_L)))
df_dL_out$time = as.numeric(df_dL_out$date - as.Date(ref_date, "%Y-%m-%d")) , units="days")
df_dL_out <- df_dL_out %>% filter( df_dL_out$time >= 0)

df_deltaL_out <- data.frame(date = temp$date, deltaL = unlist(lapply(temp$mean_temp, delta_L)))
df_deltaL_out$time = as.numeric(df_deltaL_out$date - as.Date(ref_date, "%Y-%m-%d")) , units="days")
df_deltaL_out <- df_deltaL_out %>% filter( df_deltaL_out$time >= 0)

df_deltaA_out <- data.frame(date = temp$date, deltaA = unlist(lapply(temp$mean_temp, delta_A)))
df_deltaA_out$time = as.numeric(df_deltaA_out$date - as.Date(ref_date, "%Y-%m-%d")) , units="days")
df_deltaA_out <- df_deltaA_out %>% filter( df_deltaA_out$time >= 0)

df_rho$time = as.numeric(df_rho$date - as.Date(ref_date, "%Y-%m-%d")) , units="days")
df_rho <- df_rho %>% filter( df_rho$time >= 0)
```

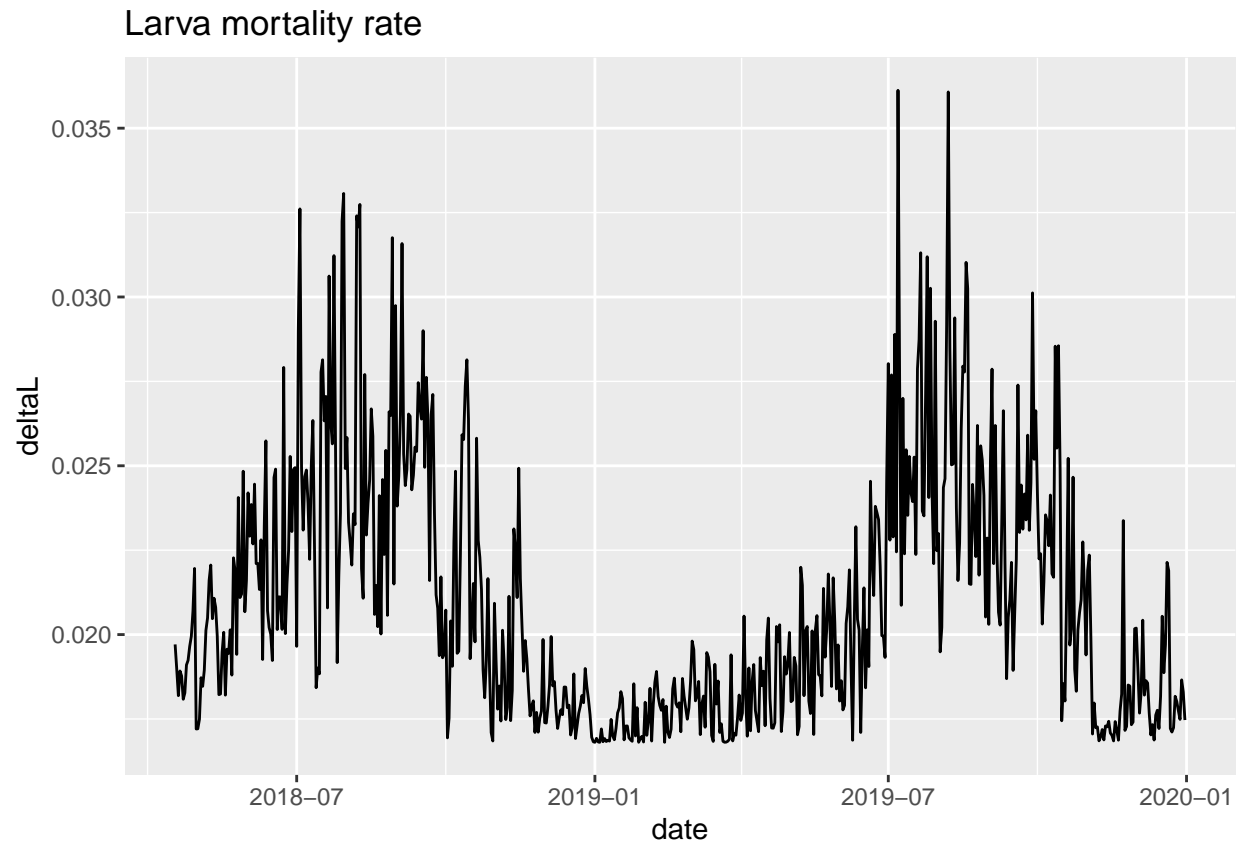
```
ggplot(df_gonot_out) + geom_line(aes(date,gono)) + ggtitle("Gonotrophic cycle")
```



```
ggplot(df_dL_out) + geom_line(aes(date,dL)) + ggtitle("Larva development rate")
```

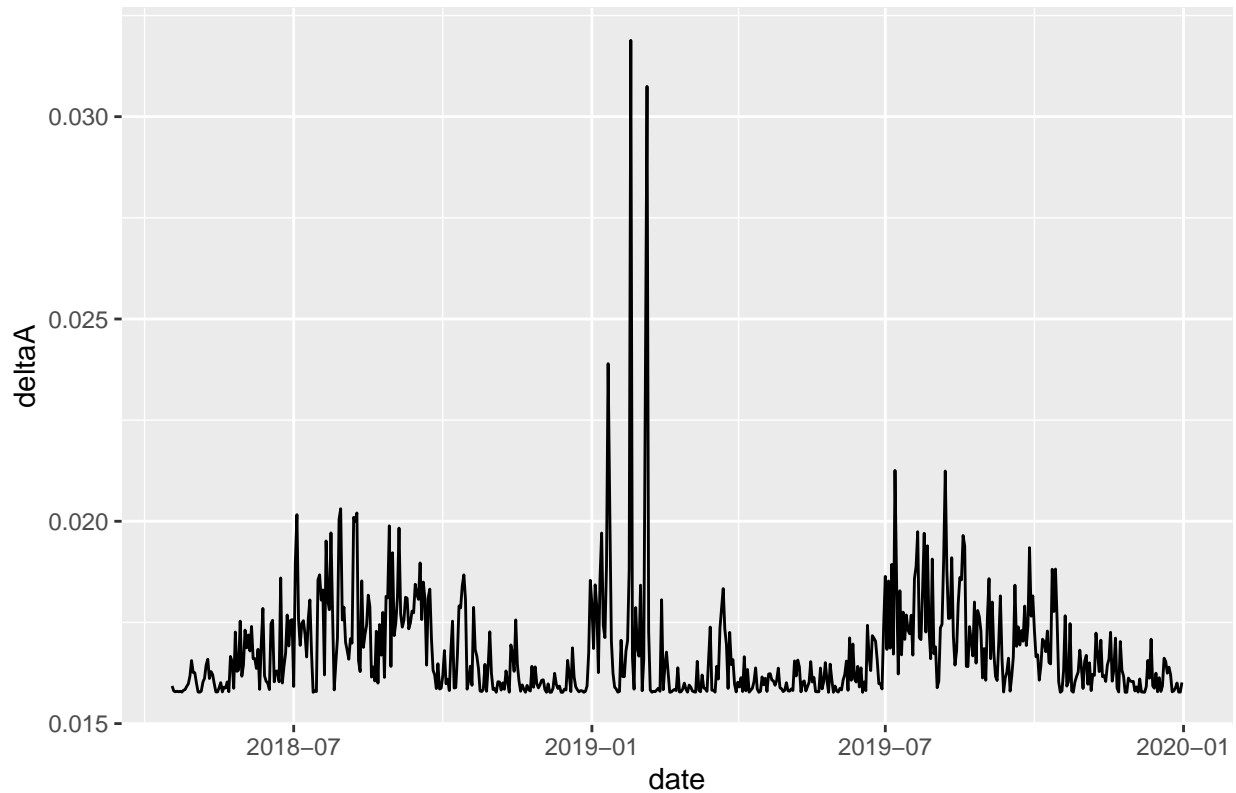


```
ggplot(df_deltaL_out) + geom_line(aes(date,deltaL)) + ggtitle("Larva mortality rate")
```



```
ggplot(df_deltaA_out) + geom_line(aes(date,deltaA)) + ggtitle("Adult mosquito mortality rate")
```

Adult mosquito mortality rate



```
df_gonot_out$date <- NULL
df_gonot_out <- df_gonot_out[,c(2,1)]
df_dL_out$date <- NULL
df_dL_out <- df_dL_out[,c(2,1)]
df_deltaL_out$date <- NULL
df_deltaL_out <- df_deltaL_out[,c(2,1)]
df_deltaA_out$date <- NULL
df_deltaA_out <- df_deltaA_out[,c(2,1)]
df_rho$date <- NULL
df_rho <- df_rho[,c(2,1)]
```

After checking if the functional response for the tiger mosquito does make sense, we use them to integrate the mosquito model. For that we will choose a carrying capacity  $K$  of 250.000 and a fecundity rate equal to one over the number of eggs per oviposition. We will set the number of eggs to 100. Other constant parameter will be the number of people in Barcelona,  $H$ , we will set it to 1600000.

```
f = 100
K = 250000
H = 1600000
# We create a vector with the constant parameters.
parms = c(f,K,H)
# We set the initial conditions to zero.
Y <- c(y1 = 1000.0, y2 = 10.0, y3 = 10.0)
# List with the data frames of the forcings, sort as the c code.
forcs_mat <- list(data.matrix(df_gonot_out),
```

```

      data.matrix(df_dL_out),
      data.matrix(df_deltaL_out),
      data.matrix(df_rho),
      data.matrix(df_deltaA_out))
min_t <- min(df_rho$time)
max_t <- max(df_rho$time)
times <- seq(min_t,max_t, 1)
out <- ode(Y, times, func = "derivs",
          parms = parms, dllname = "model",
          initfunc = "initmod", nout = 1,
          outnames = "Sum", initforc = "forc",
          forcings = forcs_mat, fcontrol = list(method = "constant"))

ode_df <- data.frame(out)
ode_df$Sum <- NULL
df_plot <- reshape2::melt(ode_df, id.vars = c("time"))
#df_plot$value[which(df_plot$variable == "y2")] <- 1
ggplot(df_plot,aes(time, value)) +
  geom_line(aes( colour = variable)) +
  ylab("Counts") +
  ggtitle("Participation dynamics")+
  scale_color_manual(name = "",
                    labels = c("Larva", "Adult mosquito","Handling mosquito"),
                    values=c('#FF00F6','#FF2C00','#00FF5E'))

```

