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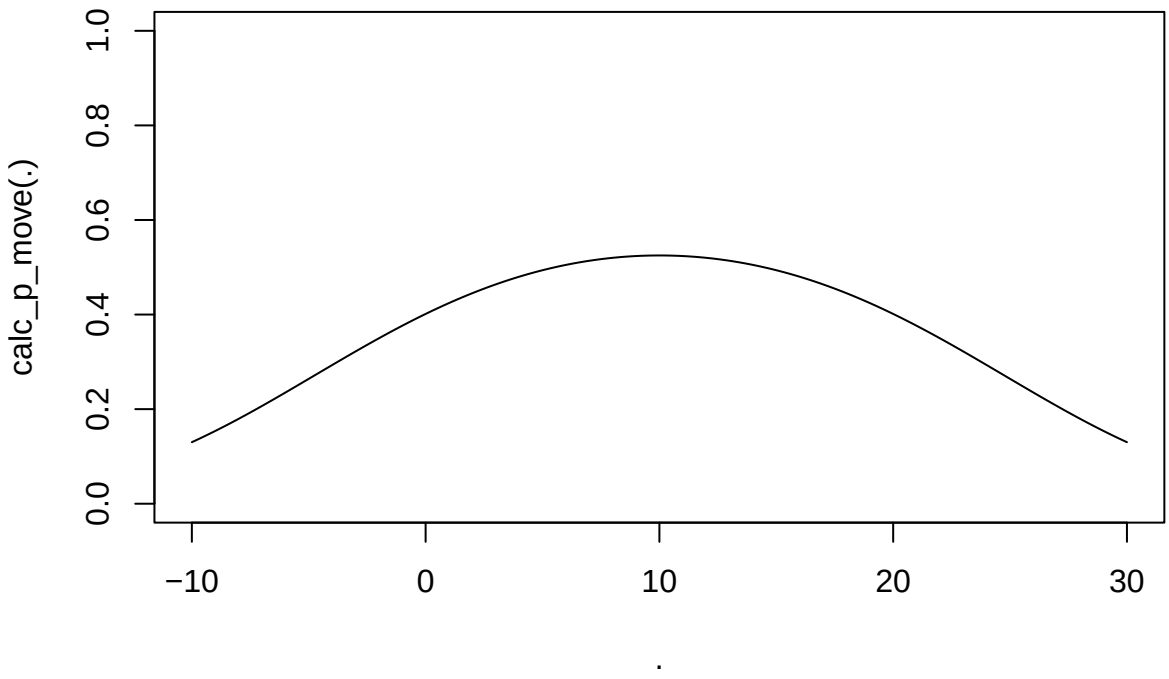
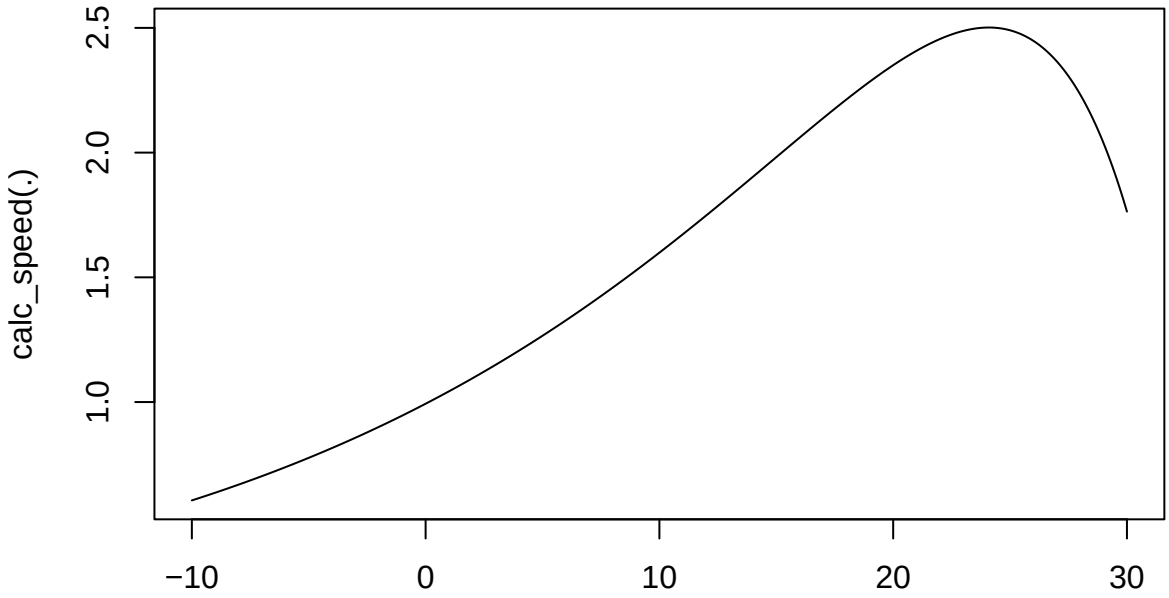
Generating the data

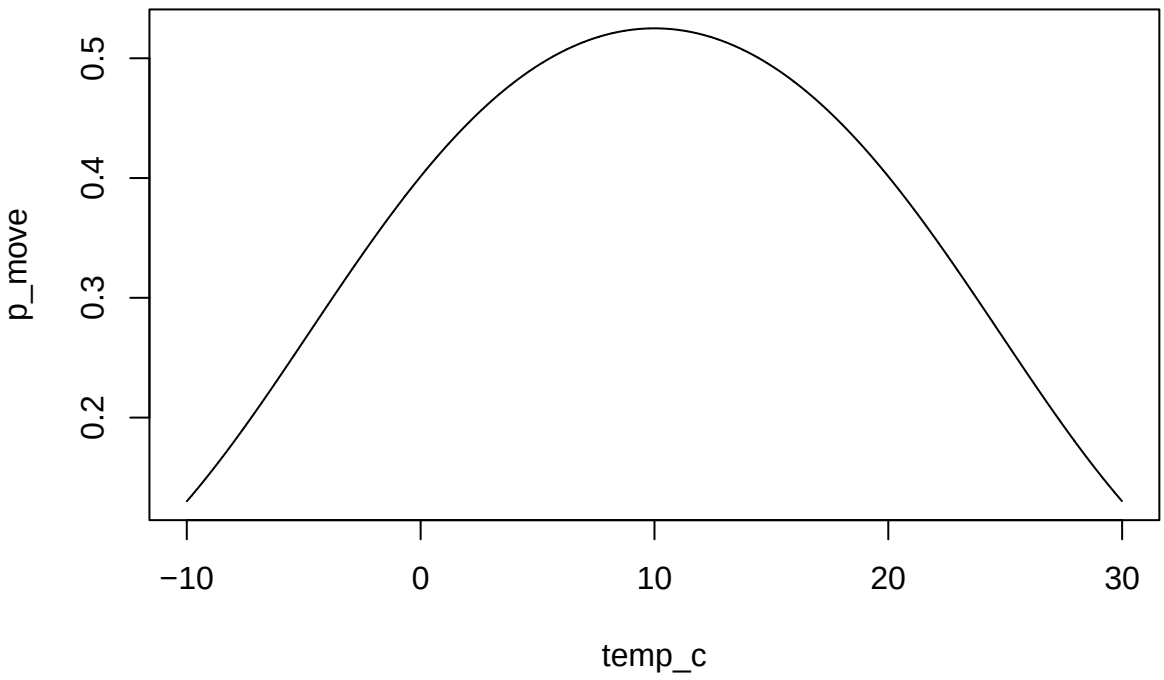
```
library('dplyr') # for data wrangling
library('mgcv')  # for GAMs

calc_p_move <- function(temp_c) {
  brms:::inv_logit(- 0.005 * (temp_c - 10)^2 + 0.1)
}

seq(-10, 30, by = 0.01) %>%
  plot(., calc_p_move(.), type = 'l', ylim = c(0, 1))
```



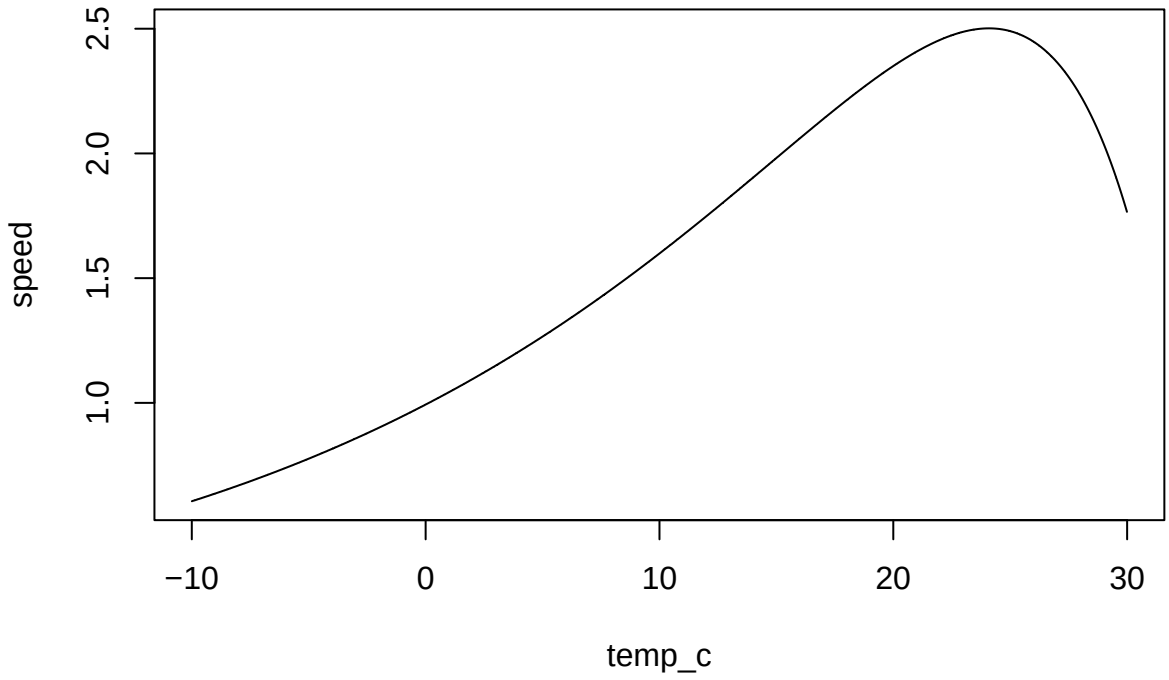
```r
calc_speed <- function(temp_c) {
  exp(0.05 * temp_c) - exp(0.2 * (temp_c - 25))
}

seq(-10, 30, by = 0.01) %>%
  plot(., calc_speed(.), type = 'l')
```



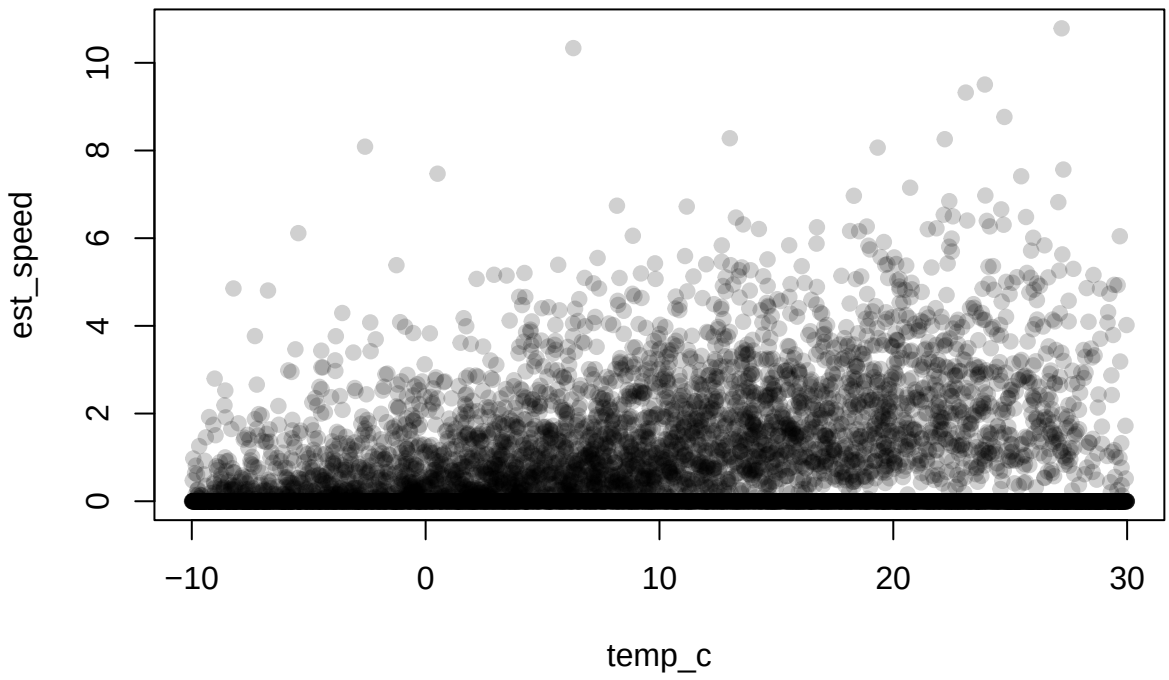

```r
d <-
  tibble(temp_c = runif(n = 1e4, -10, 30),
         p_move = calc_p_move(temp_c),
         speed = calc_speed(temp_c),
         # speed is 0 if not moving and rgamma if moving
         est_speed = rbinom(n = length(temp_c), size = 1, prob = p_move) *
           rgamma(n = length(temp_c), speed)) %>%
  arrange(temp_c)

# check the means and the speed estimates
plot(p_move ~ temp_c, d, type = 'l')
```




```
plot(speed ~ temp_c, d, type = 'l')
```




```
plot(est_speed ~ temp_c, d, pch = 19, col = '#00000030')
```




```
# make a matrix where 1st column contains the response observations and
# the 2nd column indexes the distribution (family) from which it comes.
d2 <-
  bind_rows(
    # binomial data
    mutate(d,
           y = cbind(if_else(est_speed > 0, 1, 0), 1),
           parameter = 'p_moving'),
    # gamma data given that the animal is moving
    d %>%
      filter(est_speed > 0) %>%
      mutate(y = cbind(est_speed, 2),
             parameter = 'speed')) %>%
  mutate(parameter = factor(parameter))
```

Fitting the model

```
m <- gam(formula = y ~ s(temp_c, k = 15, by = parameter),
         family = gfam(list(binomial(link = 'logit'),
                            Gamma(link = 'log'))),
         data = d2,
         method = 'REML')
```

```
layout(matrix(1:4, ncol = 2, byrow = TRUE))
plot(m, scale = 0, scheme = 1)
plot(p_move ~ temp_c, arrange(d, temp_c), type = 'l')
plot(speed ~ temp_c, arrange(d, temp_c), type = 'l')
```