# Supplemental material

## S1. Code to reproduce the examples

# Installing the package (only at first instance)
# devtools::install\_github("OnofriAndreaPG/drcte")

# Loading the package
library(drcte)

# Example 1
filePath <- "https://www.casaonofri.it/\_datasets/alfalfa3.csv"
dataset <- read.csv(filePath, header = T)
head(dataset)

mod <- drmte(nSeeds ~ timeBef + timeAf, fct = W1.3(),
 data = dataset)
coef(mod)

# Example 2
rm(list = ls())
filePath <- "https://www.casaonofri.it/\_datasets/TwoFlushes.csv"
dataset <- read.csv(filePath, header = T)
head(dataset)

mod <- drmte(nEmerg ~ timeBef + timeAf, data = dataset,
 fct = NPMLE())

plot(mod, ylim = c(0, 1), xlim = c(0, 35),
 xlab = "Time (d)",
 ylab = "Cumulative proportion of emerged seedlings")

mod2 <- drmte(nEmerg ~ timeBef + timeAf, fct = KDE(),
 data = dataset)
mod3 <- drmte(nEmerg ~ timeBef + timeAf, data = dataset,
 fct = KDE(bw = "boot"))
mod4 <- drmte(nEmerg ~ timeBef + timeAf, data = dataset,
 fct = loglogistic())

plot(mod2, ylim = c(0, 1), xlim = c(0, 35),
 xlab = "Time (d)", ylab = "Cumulative proportion
 of emerged seedlings")
points(mod3$curve[[1]][[1]](1:30) ~ c(1:30),
 type = "l", lty = 2)
points(as.numeric(mod4$curve[[1]](1:30)) ~ c(1:30),
 type = "l", lty = 3)

# Example 3
rm(list = ls())
data(verbascum)
head(verbascum)
modVerb <- drmte(nSeeds ~ timeBef + timeAf, curveid = Species,
 fct = NPMLE(), data = verbascum)

plot(modVerb, legendPos = c(12, 0.6), legendText = c("V. arcturus", "V. blattaria",
 "V. creticum"),
 ylab = "Cumulative proportion of germinated seeds",
 xlab = "Time (d)")
test <- compCDF(modVerb, units = verbascum$Dish)
test

tab <- predict(modVerb, newdata = c(5, 10), se.fit = T, units = verbascum$Dish)
tab

probsList <- c(0.1, 0.5)
GR <- lapply(probsList, function(x) quantile(modVerb,
 probs = x, restricted = F, rate = T,
 interval = "boot", units = verbascum$Dish,
 display = F))
GR <- do.call(rbind, GR)
GR

# Example 4
rm(list = ls())
data(rape)
head(rape, 20)
modTE <- drmte(nSeeds ~ timeBef + timeAf + Psi,
 data = rape, fct = HTLL())
# modNLS <- drm(propCum ~ timeAf + Psi,
# data = rape, fct = HTLL())
coef(modTE)
summary(modTE)
summary(modTE, units = rape$Dish)

# Example 5
rm(list = ls())
path <- "https://www.casaonofri.it/\_datasets/Lactuca.csv"
lactuca <- read.csv(path, header = T)
head(lactuca)
mod <- drmte(nSeeds ~ timeBef + timeAf,
 data = lactuca,
 fct = lognormal())
plot(mod)
tab1 <- summary(mod)
tab1
tab2 <- summary(mod, units = lactuca$dish)
tab2