# 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

# The first line (highlighted in blue) downloads the example data from a website.

# But when you use your own data, you need to reference the path to the file on your

# computer. The data need to be formatted and labeled exactly like the example,

# or you need to change the code. The Excel file should be saved as a CSV.   
filePath <- <https://www.casaonofri.it/_datasets/alfalfa3.csv>

#OR

filePath <- C:\Users\greta.gramig\Documents\Projects\example\_1.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

First, install R, version 4.2.0:

https://cran.r-project.org/bin/windows/base/

The installation of drcte package fails because of a missing dependency: kedd. This package is not available for the latest version of R. To install it from the archives, do the following:

Install the devtools package, from R

Install R Tools https://cran.r-project.org/bin/windows/Rtools/rtools42/rtools.html

Install kedd from archives:

Run this code in R:

require(devtools)

install\_version("kedd", version = "1.0.3", repos = "http://cran.us.r-project.org")