# Calculation of EmT50 values from emergence data for all food-density-combinations using a two-parameter log-logistic model

#setwd("<SET YOUR FILE PATH HERE>")

allemergdata <- read.table("food\_dep\_emerg\_data.csv",sep=",",dec=".",header=T)

library(drc)

# Initialize output vectors

e\_values <- 0

b\_values <- 0

R2\_values <- 0

# Loop through all treatments

for (i in 1:(ncol(allemergdata)-1)){

# Create data structure in correct format for drm function

notNA <- which(!is.na(allemergdata[,i+1]))

emergdata <- matrix(c(allemergdata[notNA,1], allemergdata[notNA,1+i]/max(allemergdata[notNA,1+i])), ncol = 2, byrow = FALSE)

colnames(emergdata) <- c('time','emergence')

emergdata <- as.data.frame(emergdata)

# Fit the drm model (normally used for dose-response curves)

emergdata.m1<-drm(emergence~time, data = emergdata, fct=LL.2(), type="binomial")

# Extract the fitted parameters

e\_values[i] <- emergdata.m1$coefficients[2]

b\_values[i] <- emergdata.m1$coefficients[1]

# Compute R squared

realdata <- emergdata$emergence

simdata <- (1/(1+(emergdata$time/e\_values[i])^b\_values[i]))

R2\_values[i] <- cor(realdata, simdata)^2

# Create plot

nam <- colnames(allemergdata)[i+1]

plot(emergdata.m1,ylab="Emerged fraction",xlab="Time (d)",ylim=c(0,1), log = "", main = nam) # Default plot

# curve(1/(1+(x/e\_values[i])^b\_values[i]), add = TRUE, col = "red", lty = 2) # Curve function for validation that this is the correct equation

# Save plot to file

PlotRecord<-recordPlot()

# Create png with width, height and resolution as input

png(paste(i,"\_",nam,".png", sep = ""), width=4, height=4, units="in", res = 300)

replayPlot(PlotRecord)

dev.off()

}

# Output results in csv file

output <- matrix(c(e\_values,b\_values,R2\_values), ncol = ncol(allemergdata)-1 , byrow=TRUE)

colnames(output) <- colnames(allemergdata)[2:ncol(allemergdata)]

rownames(output) <- c("e","b","Rsqrd")

output <- as.data.frame(output)

write.csv(output, "drc\_par\_summary.csv", row.names=TRUE)