

Consider all species and treatments together

```
# 23.08.2021
# In this analysis, we take all the species and treatments together

if ( ! require(runjags) ) { install.packages("runjags" ); library(runjags) }
if ( ! require(rjags) ) { install.packages("rjags" ); library(rjags) }
if ( ! require(bbmle) ) { install.packages("bbmle" ); library(bbmle) }
if ( ! require(ggpubr) ) { install.packages("ggpubr" ); library(ggpubr) }
if ( ! require(reshape2) ) { install.packages("reshape2"); library(reshape2) }
if ( ! require(IDPmisc) ) { install.packages("IDPmisc" ); library(IDPmisc) }

dd <- readRDS("Dataset/extinction.week.Rdata")

## Just for some plotting, not for analysis
## Add 0.5 to get approx. extinction time
dd$week.persist <- dd$week.persist + 0.5

## Set the extant populations to an extinction time of 20 weeks
dd <- transform(dd, dd.fm=ifelse(week.persist==8.5, 20, week.persist))

## For potential survival analysis
## Make binary (0 or 1) variables for temperature and energy treatments
dd <- transform(dd, temp.var=ifelse(temp==15, 0, 1))
dd <- transform(dd, energy.var=ifelse(energy==0.275, 0, 1))

## Define day1 (the last week at which the species was observed)
## Define day2 (the first week when the species was not observed)
dd <- transform(dd, day1=week.persist-0.5)
dd <- transform(dd, day2=week.persist+0.5)

## Set a censored observation to Inf
dd$day2 <- ifelse(dd$day2==9, Inf, dd$day2)

#####
## Let's check the dataset after this first transformation
head(dd)

## define a JAGS object for our model
file.jags.model <- "survival.jags"

## define the number of iterations of the Markov Chain
samsize <- 10000

## transform the data to get the counts of the extinction events
data.survival.frame <- data.frame(matrix(ncol=3,nrow=8,0))
```

```

colnames(data.survival.frame) <- c("var","t","data")

#### We consider all the species and treatments together
spp.dd <- dd

#### count the extinction events during the different weeks
ww <- 1
for(ww in 1:8){
  data.survival.frame[ww,"var"] <-paste("Extinction ",ww,sep="")
  data.survival.frame[ww,"t"] <-ww
  data.survival.frame[ww,"data"]<-length(which(spp.dd$day2==ww))
}

## compile the data
## nuber of replicates
N <- 200
## count of ectinction events
# y <- c(data.survival.frame$data,N-sum(data.survival.frame$data))

y <- c(data.survival.frame$data,dim(dd)[1]-sum(data.survival.frame$data))

## time intervals
## note that we set t=1000 for the replicates where the species survived
t <- c(0,data.survival.frame$t,1000)

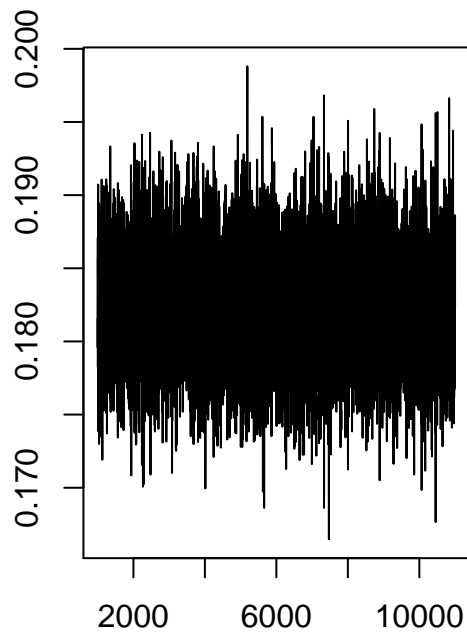
## write JAGS model definition file:
cat("model {\n",
    "  mulog_lambda <- log(mu_lambda)-0.5*sdlog_lambda^2\n",
    "  sdlog_lambda <- sqrt(log(1+sd_lambda^2/mu_lambda^2))\n",
    "  lambda ~ dlnorm(mulog_lambda,1/sdlog_lambda^2)\n",
    "  for ( i in 1:n ) {\n",
    "    p[i] <- exp(-lambda*t[i])-exp(-lambda*t[i+1])\n",
    "  }\n",
    "  y ~ dmulti(p,N)\n",
    "}\n",
    sep="",
    file=file.jags.model)

## run JAGS:
jags.obj <- jags.model(file.jags.model,
                      data=list(mu_lambda = 0.2, ### mean of the prior
                                sd_lambda = 0.2, ### standard deviation of the prior
                                n = nrow(data.survival.frame)+1,
                                N = sum(y),
                                t = t,
                                y = y))

## extract and plot results:
jags.res <- coda.samples(jags.obj,c("lambda"),sampsiz)
plot(jags.res)

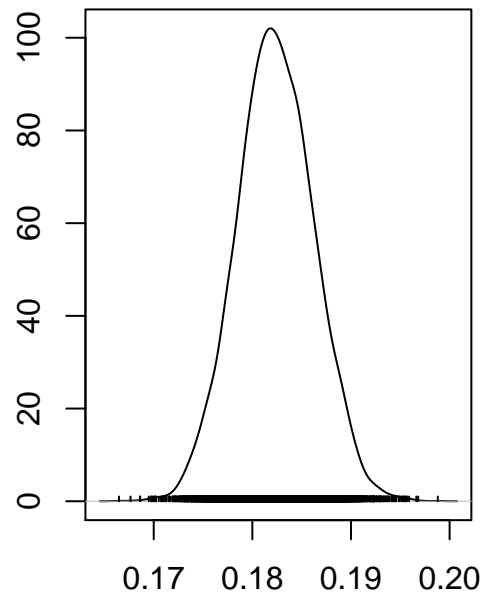
```

Trace of lambda



Iterations

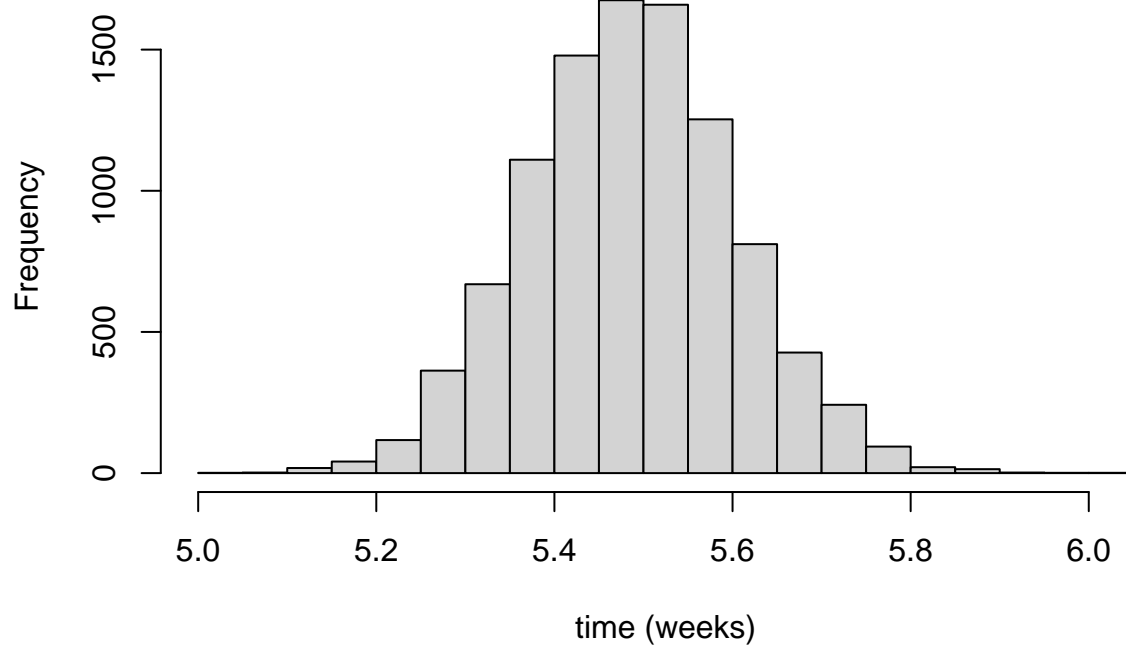
Density of lambda



N = 10000 Bandwidth = 0.0006521

```
## compute and plot the distribution of the inferred Mean time to extinction
MTE <- 1/as.matrix(jags.res)
hist(MTE,main="MTE",xlab="time (weeks)")
```

MTE



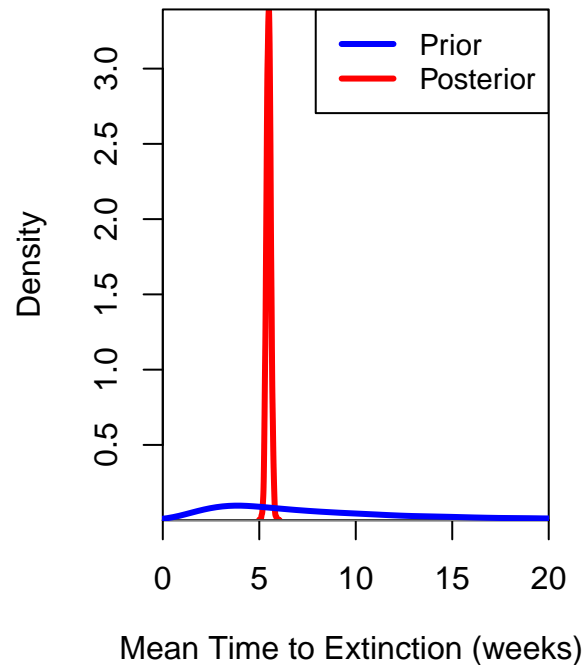
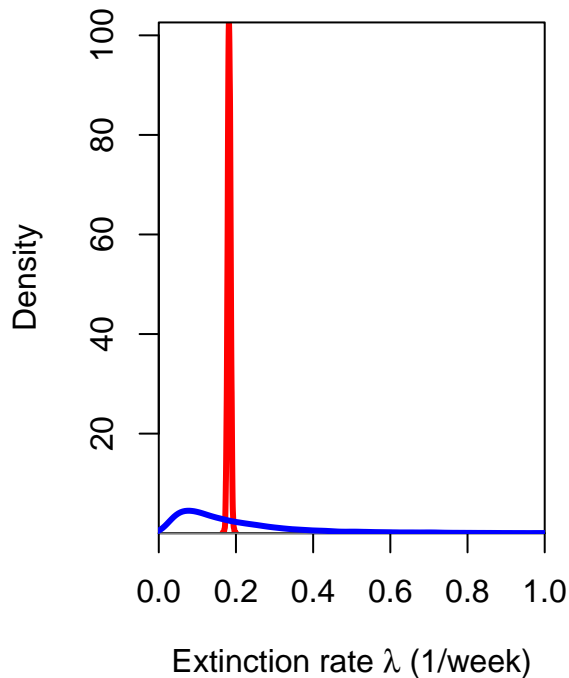
```

## COMPARE THIS RESULT WITH THE PLOTS OBTAINED BEFORE
## WHAT CAN YOU TELL ABOUT THE OBSERVED EXTINCTION TIME?
## TRY TO CHANGE THE PRIORS PARAMETERS, AND SEE HOW THIS AFFECTS THE MTE.
### first attempt to make a DENSITY PLOT to compare prior and posterior DOUBLE CHECK!!
## conversion functions that give the mean and sd of associated normal (to put into R)
mfun <- function(m,s){log(m)-log(1+s^2/m^2)/2}
sdfun <- function(m,s){sqrt(log(1+(s/m)^2))}
mu_lambda <- 0.2
sd_lambda <- 0.2
### get the mean and sd in log scale
mul_lambda <- mfun(mu_lambda,sd_lambda)
sdl_lambda <- sdfun(mu_lambda,sd_lambda)
### sample from R
prior_lambda <- rlnorm(sampsize,mul_lambda,sdl_lambda)
prior_MTE <- 1/prior_lambda
### posteriors from JAGS output
posterior_lambda <- as.matrix(jags.res)
posterior_MTE <- 1/posterior_lambda

### some simple plots
par(mfrow=c(1,2))
### prior posterior plots of extinction rates
plot(density(posterior_lambda), col="red",
     lwd=3,lty=1,xaxs="i",yaxs="i",
     main="",
     xlab=expression(paste("Extinction rate ", lambda , " (1/week)",sep="")),
     #xaxt="n",
     #ylim=c(0,MAX_DENSITY),
     xlim=c(0,1)
)
lines(density(prior_lambda), col="blue",lwd=3,lty=1)

### prior posterior plots of MTE
plot(density(posterior_MTE), col="red",
     lwd=3,lty=1,xaxs="i",yaxs="i",
     main="",
     xlab=expression(paste("Mean Time to Extinction (weeks) ",sep="")),
     #xaxt="n",
     #ylim=c(0,MAX_DENSITY),
     xlim=c(0,20)
)
lines(density(prior_MTE), col="blue",lwd=3,lty=1)
legend("topright",legend=c("Prior","Posterior"),lwd=3,cex=0.9,col=c("blue","red"))

```



```
# Vary the mean and sd of normal distribution but keeping the mean equal to the sd
mu_lambda_all <- c(0.2, 0.3, 0.4)
sd_lambda_all <- mu_lambda_all
N <- length(mu_lambda_all)

df <- data.frame(prior_lambda = double(), posterior_lambda = double(),
                 prior_MTE = double(), posterior_MTE = double(),
                 mean = factor())

for(i in 1:N){

  mu_lambda <- mu_lambda_all[i]
  sd_lambda <- sd_lambda_all[i]

  ### get the mean and sd in log scale
  mul_lambda <- mfun(mu_lambda, sd_lambda)
  sdl_lambda <- sdfun(mu_lambda, sd_lambda)
  ### sample from R
  prior_lambda <- rlnorm(sampsize, mul_lambda, sdl_lambda)
  prior_MTE <- 1/prior_lambda

  ## run JAGS:
  jags.obj <- jags.model(file.jags.model,
                        data=list(mu_lambda = mu_lambda, ### mean of the prior
                                sd_lambda = sd_lambda, ### standard deviation of the prior
                                n = nrow(data.survival.frame)+1,
                                N = sum(y),
                                t = t,
                                y = y))

  ## extract and plot results:
  jags.res <- coda.samples(jags.obj, c("lambda"), sampsize)
```

```

### posteriors from JAGS output
posterior_lambda <- as.matrix(jags.res)
posterior_MTE <- 1/posterior_lambda

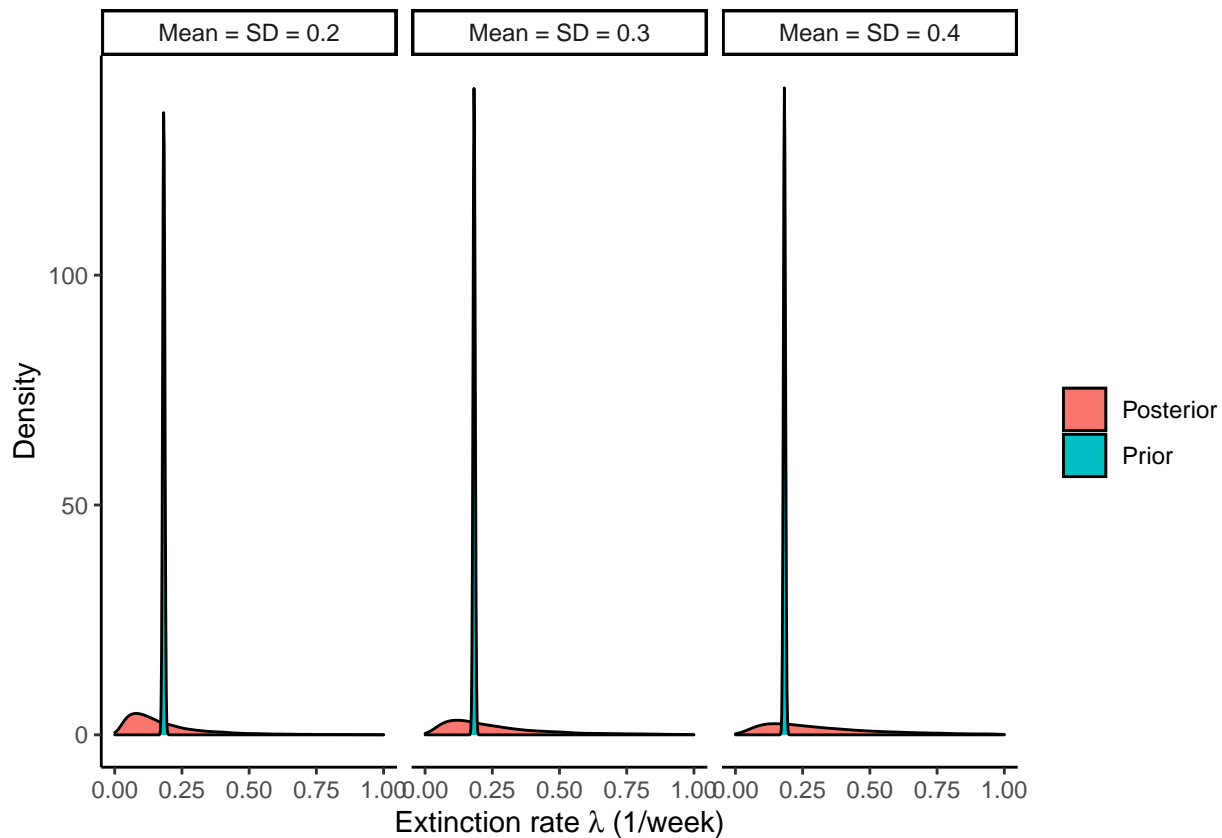
df <- rbind(df,
  data.frame(prior_lambda = prior_lambda, posterior_lambda = as.numeric(posterior_lambda),
    prior_MTE = prior_MTE, posterior_MTE = as.numeric(posterior_MTE),
    mean = as.factor(mu_lambda))
)

}

ggplot(df) +
  geom_density(aes(x = prior_lambda, fill = "blue"), position = "identity") +
  geom_density(aes(x = posterior_lambda, fill = "red"), position = "identity") +
  facet_wrap(~mean, labeller = as_labeller(c("0.2" = "Mean = SD = 0.2",
    "0.3" = "Mean = SD = 0.3",
    "0.4" = "Mean = SD = 0.4")))) +

  theme_classic() +
  xlim(c(0,1)) +
  xlab(expression(paste("Extinction rate ", lambda, " (1/week)", sep=""))) +
  scale_fill_discrete(name = "", labels = c("blue" = "Posterior", "red" = "Prior")) +
  ylab("Density")

```



Next, we investigate how the week persist vary with the bodysize. Points are jittered.

```
library(dplyr)

dd_old <- readRDS("Dataset/extinction.week.Rdata")

bodysize <- read.csv("Dataset/sizes.csv")

dd <- bodysize %>%
  select(species = spp.names2, mass) %>%
  right_join(dd_old, by = "species")

ggplot(dd) +
  geom_point(aes(x = mass, y = week.persist),
             position = position_jitter()) +
  theme_bw() +
  xlab("Bodysize (mg)") +
  ylab("Week persist") +
  scale_x_log10()
```

