Mesocosm experiment plots

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Contents

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This document can be found at https://github.com/darwinanddavis/UsefulCode

TO DO

How much of the population does the sampling effort capture?

Overview

This document uses the schisto mesocosm 2016 data to explore cercariae production from snail hosts of different body sizes (diameter in mm and mass in mg) over a 14 week period under high and low N/P nutrient conditions. Host reproduction (egg masses) is also calculated.

Install dependencies

Get data

```
wd <- params$dir # working dir is set in yaml header
setwd(paste0(wd,"/"))
f <- "meso1.csv"
f2 <- "meso2.csv"
```

Load data

```
meso1 <- read.table(f,header=T,sep=",", row.names=NULL,stringsAsFactors=FALSE, strip.white=TRUE) # read
meso2 <- read.table(f2,header=T,sep=",",row.names=NULL,stringsAsFactors=FALSE, strip.white=TRUE) # read
colnames(meso2)[2] <- "NP" # fix col names
meso2$Week <- as.integer(meso2$Week)
str(meso2)
```

```
'data.frame':   768 obs. of  9 variables:
 $ Tank   : int  1 2 3 4 5 6 7 8 9 10 ...
 $ NP     : chr  "High" "Low" "Low" "High" ...
 $ Size   : chr  "Small" "Intermediate" "Intermediate" "Small" ...
 $ Schisto: chr  "No" "Yes" "Yes" "Yes" ...
 $ Date   : chr  "24/05/16" "24/05/16" "24/05/16" "24/05/16" ...
 $ Week   : int  1 1 1 1 1 1 1 1 1 1 ...
 $ Eggs   : int  0 0 1 0 0 0 7 10 1 0 ...
 $ Phyto_F: num  2585 1005 1327 1399 2341 ...
 $ Peri_F : num  7301 4711 7253 8212 4293 ...
```

```
meso1[is.na(meso1)] <- 0 ; meso2[is.na(meso2)] <- 0 # remove NAs
mass <- 0.0096*(meso1$Diameter^3) # add mass to df
meso1$Mass <- mass
```

Outlier

```
print("Outlier"); meso1[which(meso1$Mass==max(meso1$Mass)),]
```

```
[1] "Outlier"
```

```
# A tibble: 1 x 9
   Tank Picture_Name Date     Snail Diameter Cercariae  Week Sampling_Effort  Mass
 * <int> <chr>        <chr>    <chr>    <dbl>     <int> <int>           <dbl> <dbl>
 1    38 P1001057     29/06/16 143       50.5         0     6               3 1239.
```

```r
outlier <- 0 # remove outlier from data?
if(outlier==1){meso1 <- subset(meso1,Mass<max(Mass))}
```

Cleaning Snail and Date cols

```r
#unique(meso1$Snail)
#unique(meso1$Date)
sapply(meso1, function(x) sum(nchar(x))) # check number of characters in each col
```

Tank	Picture_Name	Date	Snail	Diameter	Cercariae
84102	367153	358163	86955	239237	46575
Week	Sampling_Effort	Mass			
58976	46116	668838			

Set Cex sizes

```r
cex_cer <- (meso1$Cercariae+1)/1000
cex_sam <- meso1$Sampling_Effort/1.5
cex_diam <- meso1$Diameter/3
```

Set plotting graphics

```r
plot_it <- function(manuscript,bg,cp,alpha,family){ # plotting function (plot for MS or not, set bg col
  graphics.off()
  if(manuscript==0){
    if(bg=="black"){
      colvec<-magma(200,1)
      par(bg = colvec[1],col.axis="white",col.lab="white",col.main="white",fg="white",bty="n",las=1,mar=
      border=adjustcolor("purple",alpha=0.5)
    }else{
      colvec<-bpy.colors(200)
      par(bg = colvec[1],col.axis="white",col.lab="white",col.main="white",fg="white",bty="n",las=1,mar=
      border=adjustcolor("blue",alpha=0.5)
    }
  }else{
#    graphics.off()
    par(bty="n",las=1,family=family)
  }
  # color palettes
  # ifelse(manuscript==1,colvec<-adjustcolor(brewer.pal(9,cp)[9], alpha = alpha),colvec <- adjustcolor(
   # colfunc <<- colorRampPalette(brewer.pal(9,cp),alpha=alpha)
  colfunc <<- adjustcolor(brewer.pal(9,cp),alpha=alpha) # USES <<- OPERATOR
}

# Setting ggplot theme graphics
plot_it_gg <- function(bg){ # bg = colour to plot bg, family = font family
  if(bg=="white"){
    bg <- "white"
    fg <- "black"
  theme_tufte(base_family = "HersheySans") +
    theme(panel.border = element_blank(),panel.grid.major = element_blank(),panel.grid.minor = element_
    theme(axis.line = element_line(color = fg)) +theme(axis.ticks = element_line(color = fg)) + theme(p
}
  }# end gg
```

Set plotting parameters

```
print("1/0, set colour, set colour palette 'display.brewer.all()',set alpha for col,set font")
plot_it(0,"blue","YlOrRd",1,"HersheySans") # set col function params
plot_it_gg("white") # same as above

# set colors you want
col <- "lightblue"
col2 <- "orange"
```

Get only infected snails

```
# get only infected snails
meso1_II <- subset(meso1,subset=Cercariae>0)
meso1_UU <- subset(meso1,subset=Cercariae==0)
```


Mesocosm1 data sheet

Snail size per tank

Shell diameter (mm) per tank

```
par(bty="n", las = 1)
#plot_it(0,"blue","YlOrRd",1,"HersheySans") # set col function params
par(mfrow=c(1,1))
ylim <- round_any(max(meso1$Diameter),10,ceiling)
boxplot(Diameter~Tank, data=meso1,
        ylim=c(0,ylim),
        col = "light blue",
        notch = T,xlab="Tank",ylab="Diameter (mm)",
        main=paste0("Shell diameter (mm) over ",max(meso1$Week)," weeks")
)
abline(h=mean(meso1$Diameter),col="pink",lty=3)
```

Shell diameter (mm) over 14 weeks
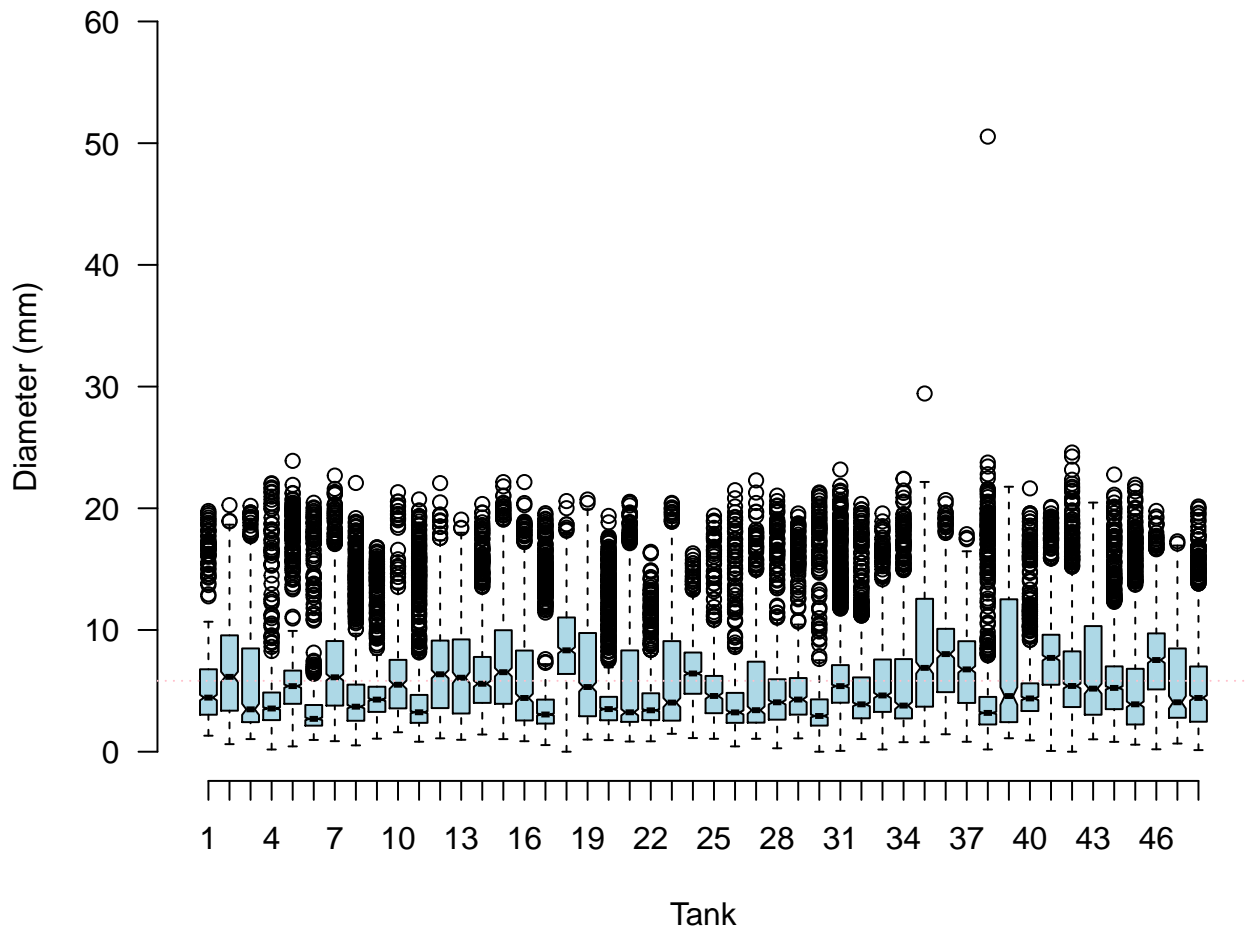

```r
with(meso1,t.test(Diameter,Tank)) # t.test
```

```
	Welch Two Sample t-test

data:  Diameter and Tank
t = -292.62, df = 54631, p-value < 2.2e-16
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -19.45781 -19.19889
sample estimates:
mean of x mean of y
 5.822942 25.151292
```

**Snail diameter (mm) distribution**

```r
par(bty="n", las = 1)
#plot_it(0,"blue","YlOrRd",1,"HersheySans") # set col function params
den <- density(meso1$Diameter)
xlim <- round_any(max(den$x),10,ceiling)
```

```
ylim <- round_any(max(den$y),0.1,ceiling)
plot(den,
     col=adjustcolor(col,alpha=0.5),
     xlim=c(0,xlim),
     ylim=c(0,ylim),
     xlab="Diameter (mm)",
     ylab="Density",
     main=paste0("Overall shell diameter (mm) over ",max(meso1$Week)," weeks"))
polygon(den, col=adjustcolor(col,alpha=0.5),border=col) # fill AUC
abline(v=mean(meso1$Diameter),col=col,lty=3,ylim=c(0,ylim)) # get mean
```

Overall shell diameter (mm) over 14 weeks
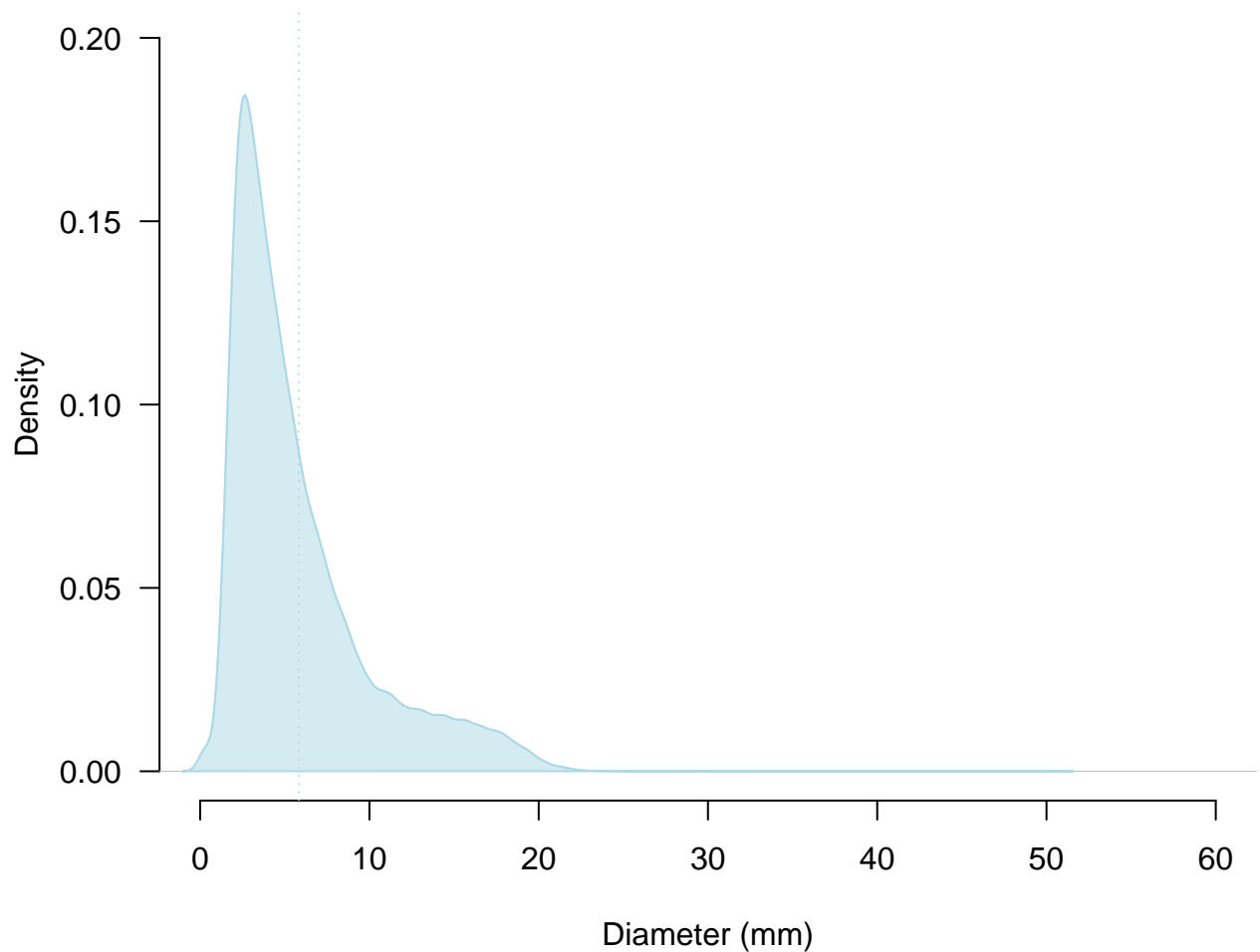

```
# un/infected diameter
# Uninfected
den <- density(meso1_UU$Diameter)
plot(den,
     col=adjustcolor(col,alpha=0.5),
     xlim=c(0,xlim),
     ylim=c(0,ylim),
     xlab="Diameter (mm)",
     ylab="Density",
```

```r
      main=paste0("Shell diameter (mm) over ",max(meso1$Week)," weeks"))
polygon(den, col=adjustcolor(col,alpha=0.5),border=col) # fill AUC
abline(v=mean(meso1_UU$Diameter),col=col,lty=3,ylim=c(0,ylim)) # get mean
par(new=T)
# Infected
den2 <- density(meso1_II$Diameter)
plot(den2,
     col=adjustcolor(col2,alpha=0.5),
     xlim=c(0,xlim),
     ylim=c(0,ylim),
     xlab="",
     ylab="",
     main="")
polygon(den2, col=adjustcolor(col2,alpha=0.5),border=col2) # fill AUC
abline(v=mean(meso1_II$Diameter),col=col2,lty=3,ylim=c(0,ylim)) # get mean
par(family="mono")
legend("right",legend=c("Uninfected","Infected"),col=c(col,col2),
       bty="n",pch=20,pt.cex=1.5,cex=0.7,y.intersp = 0.5, xjust = 0.5,
       title="",title.adj = 0.3,
       # text.font=2,
       trace=T,inset=0.1)
```

Shell diameter (mm) over 14 weeks
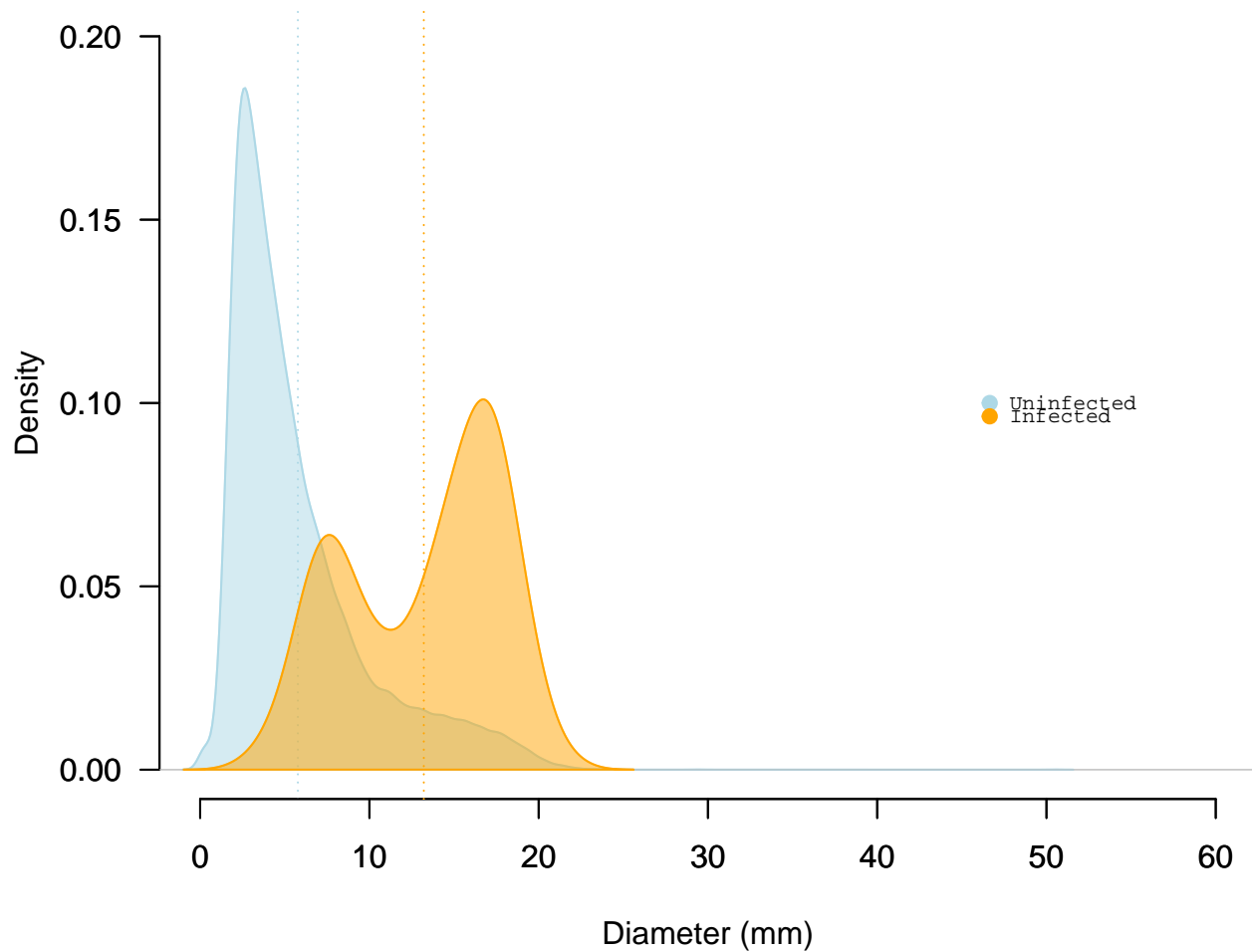

```
xchar= 1.181 ; (yextra,ychar)= -0.003635 0.003635
points2( 46.65 46.65 , 0.1 0.09637 , pch= 20 20 , ...)
```

Snail size over time (weeks)

Shell diameter (mm) over time (weeks)
~1000 eggs inoculated at 0,2,4,6 weeks

```r
par(bty="n", las = 1)
#plot_it(0,"blue","YlOrRd",1,"HersheySans") # set col function params
layout(matrix(c(1,1,2,3), 2, 2, byrow = TRUE)) # plot stacked plots
ylim <- round_any(max(meso1$Diameter),10,ceiling)
boxplot(Diameter~Week, data=meso1,
        # xlim=c(0,max(meso1$Week)),
        ylim=c(0,ylim),
        col = col,
        notch = T,xlab="Week",ylab="Diameter (mm)",
        main=paste0("Shell diameter (mm) over ",max(meso1$Week)," weeks"),
        xaxs = "i", yaxs = "i"
)
```

```r
abline(h=mean(meso1$Diameter),col=col,lty=3)
par(new=T)
points(x=c(1,3,5,7),y=rep(ylim/2,4),pch="~",col="red")# add inoculation points
# un/infected
boxplot(Diameter~Week, data=meso1_UU,
        # xlim=c(0,max(meso1$Week)),
        ylim=c(0,ylim),
        col = col,
        notch = T,xlab="Week",ylab="Diameter (mm)",
        main=paste0("Shell diameter (mm) over ",max(meso1$Week)," weeks \n(uninfected snails)"),
        xaxs = "i", yaxs = "i"
)
abline(h=mean(meso1_UU$Diameter),col=col,lty=3)
par(new=T)
points(x=c(1,3,5,7),y=rep(ylim/2,4),pch="~",col="red")# add inoculation points

# infected
boxplot(Diameter~Week, data=meso1_II,
        # xlim=c(0,max(meso1$Week)),
        ylim=c(0,ylim),
        col = col2,
        notch = T,xlab="Week",ylab="Diameter (mm)",
        main=paste0("Shell diameter (mm) over ",max(meso1$Week)," weeks \n (infected snails)"),
        xaxs = "i", yaxs = "i"
)
abline(h=mean(meso1_II$Diameter),col=col,lty=3)
par(new=T)
points(x=c(1,3),y=rep(ylim/2,2),pch="~",col="red")# add inoculation points
```
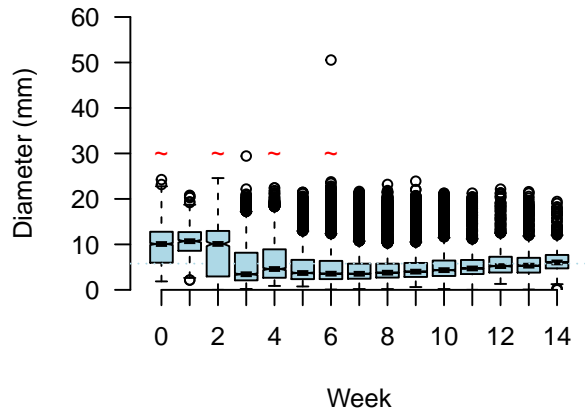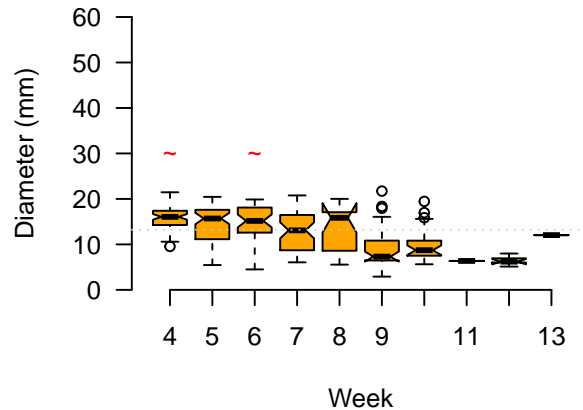
Shell diameter (mm) over 14 weeks
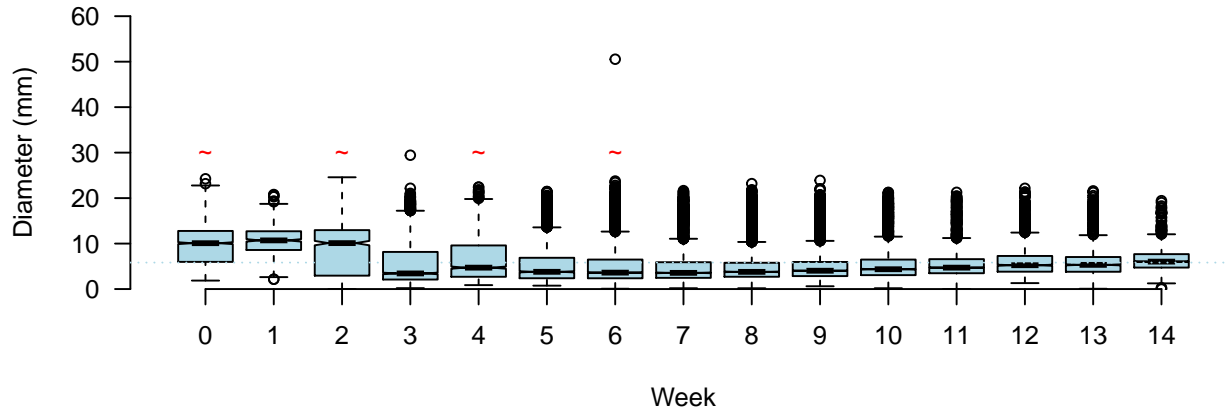
Shell diameter (mm) over 14 weeks (uninfected snails)

Shell diameter (mm) over 14 weeks (infected snails)

Snail size over time (weeks) per tank

Snail size density over time for all tanks (total = 48) have been saved as 'Size_per_tank_over_time.pdf' in /Users/malishev/Documents/Emory/research/mesocosm

~1000 eggs inoculated at 0,2,4,6 weeks

```
#### size dist per tank over time ('Snail size over time (weeks)' but for each tank)
# Plot Tanks with large nutrients at the beginning versus tanks with lower nutrients
# Pick high and low nutrient tanks to compare

# Focus on diameter rather than biomass

# Eight replicates per size class and NP combo: six received schisto, two didn't. (Replication factor)

# Select tank #. Max 48
tank <- 45

par(bty="n", las = 1)
#plot_it(0,"blue","YlOrRd",1,"HersheySans") # set col function params
layout(matrix(c(1,1,2,3), 2, 2, byrow = TRUE)) # plot stacked plots
snail <- subset(meso1,subset=Tank==tank) # get tank level indiviudals
```

```
ggplot(snail, aes(x = Diameter, y = as.factor(Week), fill=..x..)) + # geom_density_ridges()
  # scale = overlap
  geom_density_ridges_gradient(scale = 5, size=0.2,color="black", rel_min_height = 0.01,panel_scaling=T
  geom_density_ridges(scale = 5, size=0.2,color="black", rel_min_height = 0.01,fill="white",alpha=0.2)
  # geom_density_ridges(scale = 5, size=0.2,color="white", rel_min_height = 0.01,fill=col,alpha=0.5) +
  scale_fill_viridis(name = "Diameter", alpha=0.1, option = "magma",direction=-1) + # "magma", "inferno
  xlim(c(0,25)) +
  labs(title = paste0("Snail diameter over ",max(meso1$Week)," weeks for tank ",tank)) +
  xlab("Snail diameter (mm)") +
  ylab("Week") +
  plot_it_gg("white")
```
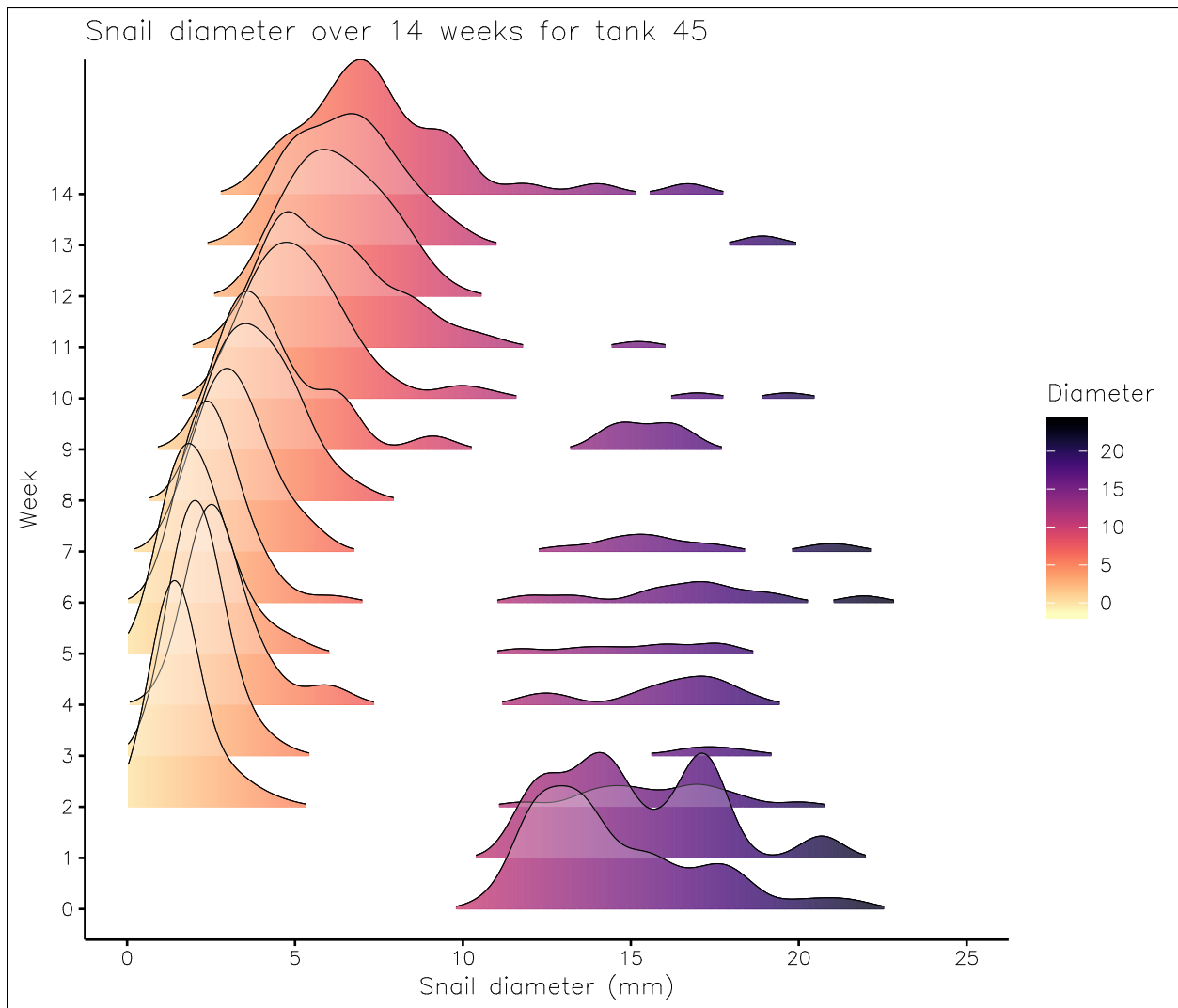

Body mass (mg) over time (weeks)

(Soft tissue dry mass in mg = 0.0096 * Diameter[in mm]^3)
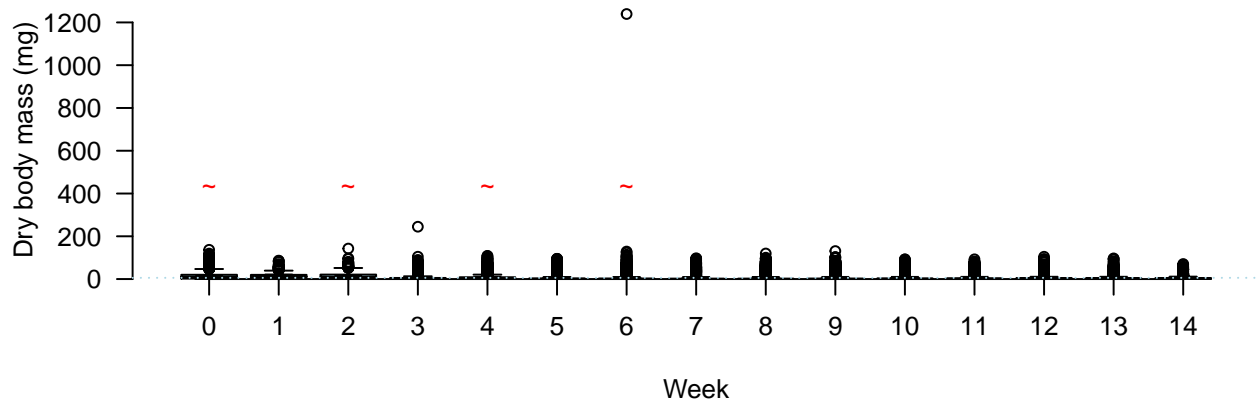~1000 eggs inoculated at 0,2,4,6 weeks

Outer

Outlier

```r
par(bty="n", las = 1)
#plot_it(0,"blue","YlOrRd",1,"HersheySans") # set col function params
layout(matrix(c(1,1,2,3), 2, 2, byrow = TRUE))# plot stacked plots
ylim <- round_any(max(meso1$Mass),100,ceiling)
boxplot(Mass~Week, data=meso1,
        # xlim=c(0,max(meso1$Week)),
        ylim=c(0,ylim),
        col = col,
        notch = T,xlab="Week",ylab="Dry body mass (mg)",
        main=paste0("Body mass (mg) over ",max(meso1$Week)," weeks"),
        xaxs = "i", yaxs = "i"
)
abline(h=mean(meso1$Mass),col=col,lty=3)
points(x=c(1,3,5,7),y=rep(ylim/3,4),pch="~",col="red")# add inoculation points

### uninfected ###
boxplot(Mass~Week, data=meso1_UU,
        # xlim=c(0,max(meso1$Week)),
        ylim=c(0,ylim),
        col = col,
        notch = T,xlab="Week",ylab="Dry body mass (mg)",
        main=paste0("Body mass (mg) over ",max(meso1$Week)," weeks \n(uninfected)"),
        xaxs = "i", yaxs = "i"
)
abline(h=mean(meso1$Mass),col=col,lty=3)
points(x=c(1,3,5,7),y=rep(ylim/3,4),pch="~",col="red")# add inoculation points
### infected ###
ylim <- round_any(max(meso1_II$Mass),100,ceiling)
boxplot(Mass~Week, data=meso1_II,
        # xlim=c(0,max(meso1$Week)),
        ylim=c(0,ylim),
        col = col2,
        notch = F,xlab="Week",ylab="Dry body mass (mg)",
        main=paste0("Body mass (mg) over ",max(meso1$Week)," weeks \n(infected)"),
        xaxs = "i", yaxs = "i"
)
abline(h=mean(meso1$Mass),col=col2,lty=3)
points(x=c(1,3),y=rep(ylim/1.2,2),pch="~",col="red")# add inoculation points
```
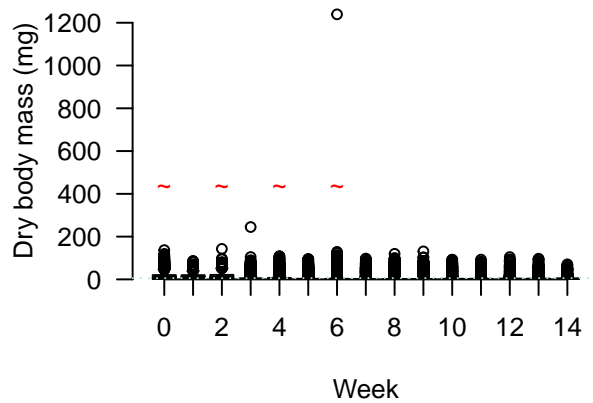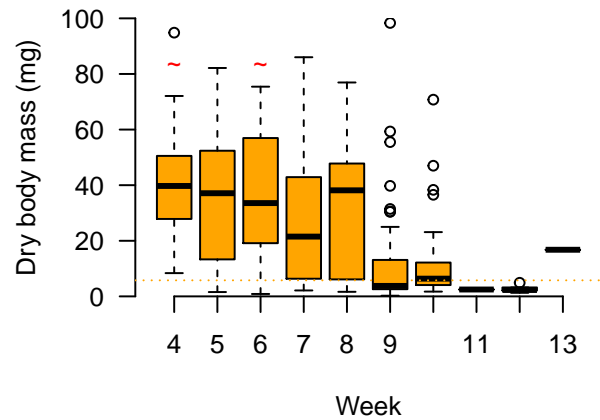
Body mass (mg) over 14 weeks

Body mass (mg) over 14 weeks (uninfected)

Body mass (mg) over 14 weeks (infected)

Without outlier

Outlier

```
outer <- meso1[which(meso1$Mass==max(meso1$Mass)),][,c("Mass","Cercariae")] # identify outlier
outer
```

```
# A tibble: 1 x 2
   Mass Cercariae
* <dbl>     <int>
1 1239.         0
```

```
par(bty="n", las = 1)
#plot_it(0,"blue","YlOrRd",1,"HersheySans") # set col function params
layout(matrix(c(1,1,2,3), 2, 2, byrow = TRUE))# plot stacked plots
ylim <- round_any(max(meso1$Mass),100,ceiling)
boxplot(Mass~Week, data=meso1,
        outline = F,
        # xlim=c(0,max(meso1$Week)),
        ylim=c(0,60),
        col = col,
        notch = T,xlab="Week",ylab="Dry body mass (mg)",
```

```
        main=paste0("Body mass (mg) over ",max(meso1$Week)," weeks without outlier"),
        xaxs = "i", yaxs = "i"
)
abline(h=mean(meso1$Mass),col=col,lty=3)
points(x=c(1,3,5,7),y=rep(ylim/3,4),pch="~",col="red")# add inoculation points

### uninfected ###
boxplot(Mass~Week, data=meso1_UU,outline=F,
        # xlim=c(0,max(meso1$Week)),
        ylim=c(0,60),
        col = col,
        notch = T,xlab="Week",ylab="Dry body mass (mg)",
        main=paste0("Body mass (mg) over ",max(meso1$Week)," weeks  \n(uninfected)"),
        xaxs = "i", yaxs = "i"
)
abline(h=mean(meso1$Mass),col=col,lty=3)
points(x=c(1,3,5,7),y=rep(ylim/3,4),pch="~",col="red")# add inoculation points
### infected ###
ylim <- round_any(max(meso1_II$Mass),100,ceiling)
boxplot(Mass~Week, data=meso1_II,
        # xlim=c(0,max(meso1$Week)),
        ylim=c(0,ylim),
        col = col2,
        notch = F,xlab="Week",ylab="Dry body mass (mg)",
        main=paste0("Body mass (mg) over ",max(meso1$Week)," weeks  \n(infected)"),
        xaxs = "i", yaxs = "i"
)
abline(h=mean(meso1$Mass),col=col2,lty=3)
points(x=c(1,3),y=rep(ylim/1.2,2),pch="~",col="red")# add inoculation points
```
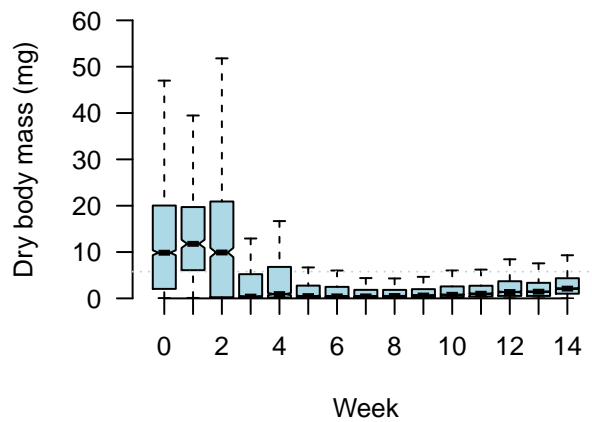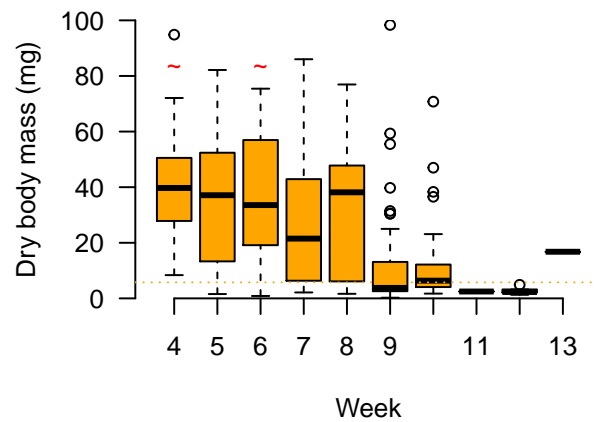
Body mass (mg) over 14 weeks without outlier
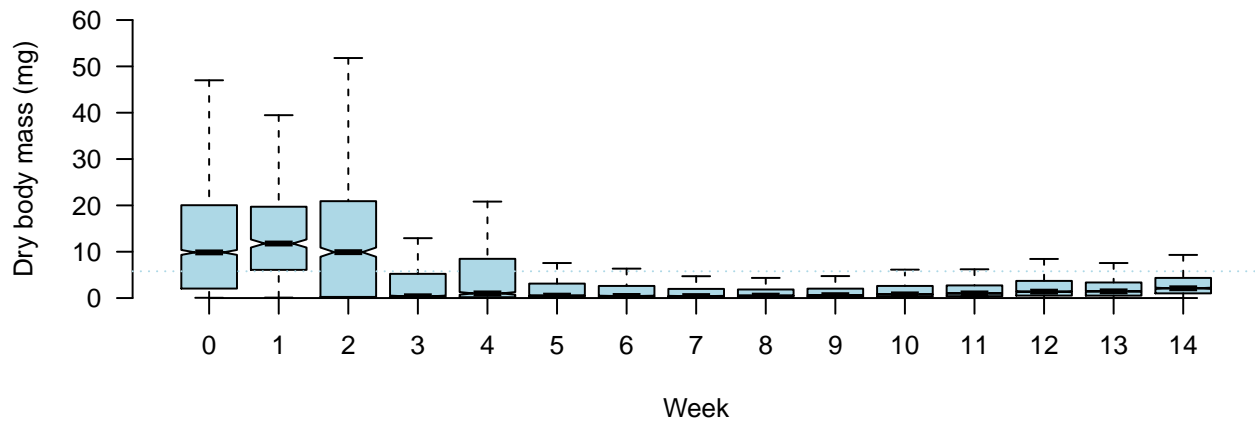
Body mass (mg) over 14 weeks (uninfected)

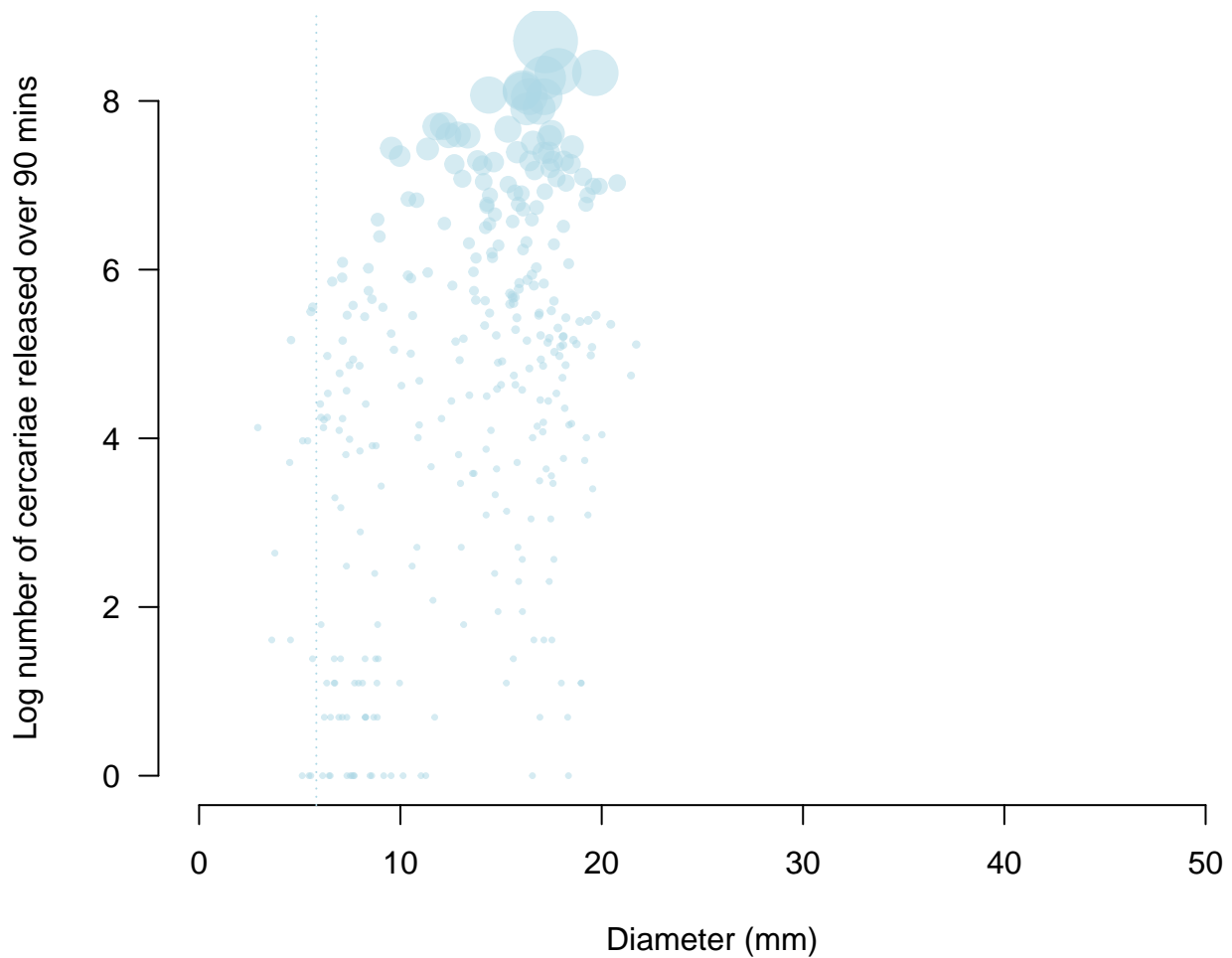## Body mass (mg) over 14 weeks (infected)

Snail size and number of cercariae produced

Point size by cercariae number

```
par(bty="n", las = 1)
#plot_it(0,"blue","YlOrRd",1,"HersheySans") # set col function params
with(meso1,plot(Diameter,log(Cercariae),pch=20,
                col=adjustcolor(col,alpha=0.5),
                cex=cex_cer+0.5,
                ylab="Log number of cercariae released over 90 mins",xlab=" Diameter (mm)"
))
title("Number of cercarie for each snail length (mm)")
abline(v=mean(meso1$Diameter),lty=3,col=col)# mean diameter
points(outer,col="red",pch=20) # plot outlier
```

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# Number of cercarie for each snail length (mm)

Linear log

```
# summary(with(meso1,lm(log(Cercariae)~Diameter))) # linear log
```

Snail mass and cercariae produced (mg)

```r
par(bty="n", las = 1)
#plot_it(0,"blue","YlOrRd",1,"HersheySans") # set col function params
with(meso1,plot(log(Mass),Cercariae,pch=20,
               col=adjustcolor(col,alpha=0.5),
               cex=cex_cer+0.5,
               # cex=1.5,
               ylab="Number of cercariae released over 90 mins",xlab="Log dry body mass (mg)"))
title("Number of cercariae for each log snail mass (mg)")
abline(v=log(mean(meso1$Mass)),lty=3,col=col)# mean diameter
outer <- meso1[which(meso1$Mass==max(meso1$Mass)),][,c("Mass","Cercariae")] # identify outlier
points(outer,col="red",pch=20) # plot outlier
```

Number of cercariae for each log snail mass (mg)
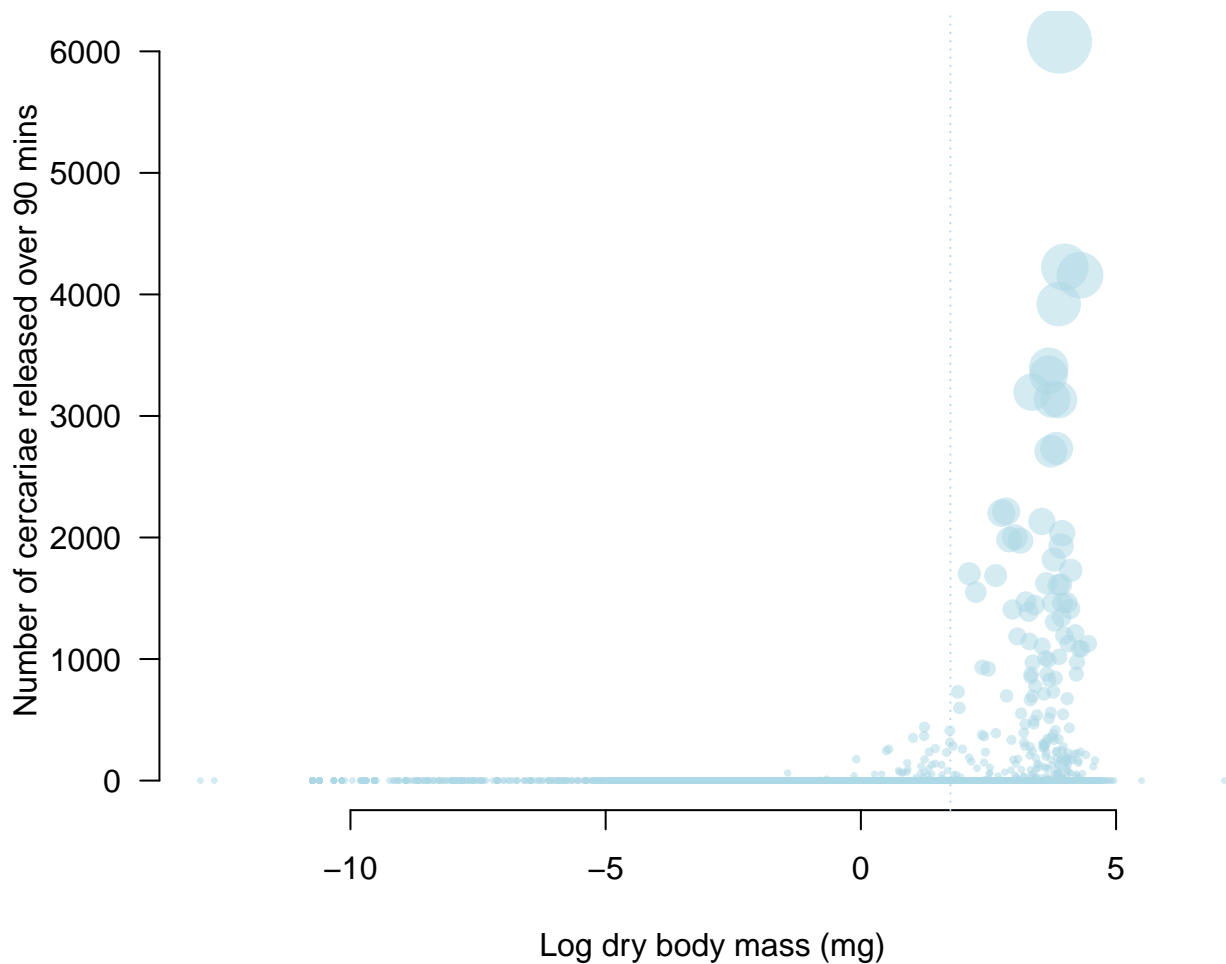
Snail size per tank

Shell diameter (mm)
Select tank #. max 48

```
tank <- 2
```

```r
par(bty="n", las = 1)
#plot_it(0,"blue","YlOrRd",1,"HersheySans") # set col function params
layout(matrix(c(1,1,2,3), 2, 2, byrow = TRUE)) # plot stacked plots
snail <- subset(meso1,subset=Tank==tank) # get tank level indiviudals
diam_total <- 1 # set ylim either to max for tank or max across all tanks (16.8)
den <- density(snail$Diameter) # get diameter density
xlim <- round_any(max(den$x),10,ceiling)
ylim <- round_any(max(den$y),0.05,ceiling)
plot(den,
    col=adjustcolor(col,alpha=0.5),
    xlim=c(0,xlim),ylim=c(0,ylim),
    xlab="",ylab="",main=""
)
```

```r
  polygon(den, col=adjustcolor(col,alpha=0.5),border=col) # fill AUC
  abline(v=mean(snail$Diameter),col=col,lty=3,ylim=c(0,ylim)) # get mean
  title(main=paste0("Shell diameter (mm) distribution for tank #",tank),
        xlab="Shell diameter (mm)")
  title(ylab="Density",line=3.5)


  ### uninfected ###
  snail_UU <- subset(snail,subset=Cercariae==0)
  den <- density(snail_UU$Diameter) # get diameter density
  xlim <- round_any(max(den$x),10,ceiling)
  ylim <- round_any(max(den$y),0.05,ceiling)
  plot(den,
       col=adjustcolor(col,alpha=0.5),
       xlim=c(0,xlim),ylim=c(0,ylim),
       xlab="",ylab="",main=""
  )
  polygon(den, col=adjustcolor(col,alpha=0.5),border=col) # fill AUC
  abline(v=mean(snail_UU$Diameter),col=col,lty=3,ylim=c(0,ylim)) # get mean
  title(main=paste0("Uninfected snails in tank #",tank),
        xlab="Shell diameter (mm)")
  title(ylab="Density",line=3.5)


  ### infected ###
  snail_II <- subset(snail,subset=Cercariae>0)
  if(length(snail_II$Tank)>0){
    den2 <- density(snail_II$Diameter) # get diameter density
    plot(den2,
         col=adjustcolor(col2,alpha=0.5),
         xlim=c(0,xlim),ylim=c(0,ylim),
         xlab="",ylab="",main=""
    )
    polygon(den2, col=adjustcolor(col2,alpha=0.5),border=col2) # fill AUC
    abline(v=mean(snail_II$Diameter),col=col2,lty=3,ylim=c(0,ylim)) # get mean
    title(main=paste0("Infected snails in tank #",tank),
          xlab="Shell diameter (mm)")
  }else{
    plot(0,0,type="n");title(main=paste0("Infected snails in tank #",tank)); text(0,0.5,paste0("No cercari
  }
```
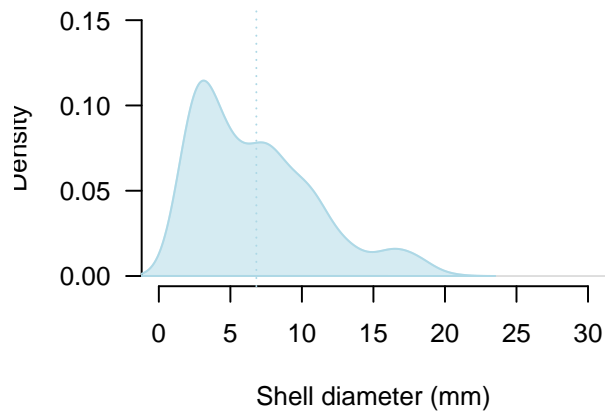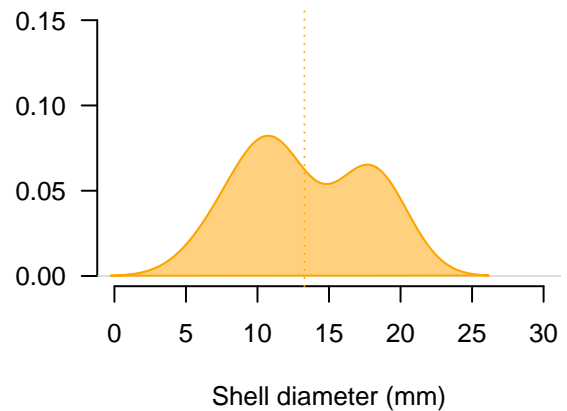
Shell diameter (mm) distribution for tank #2
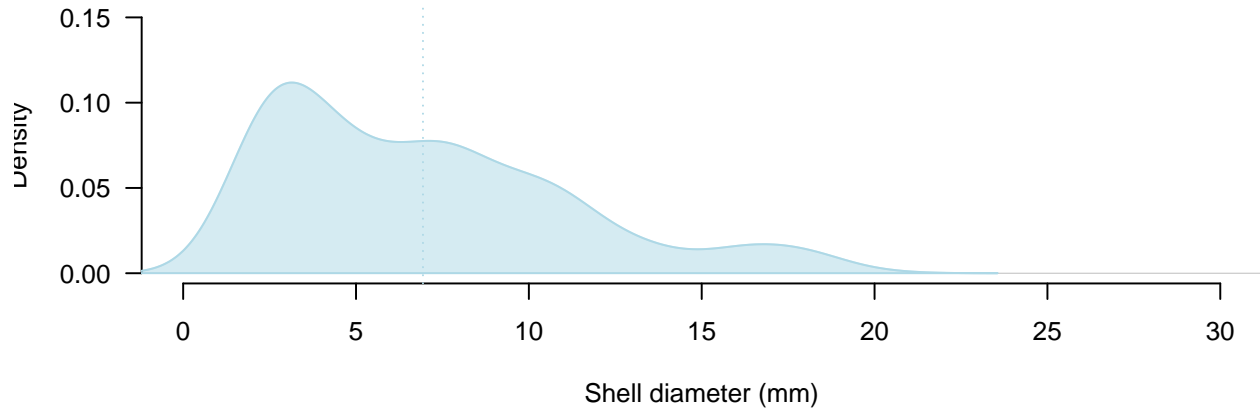
Uninfected snails in tank #2

Infected snails in tank #2

Cercariae production over time

Cercariae shed over 90 mins per week
~1000 eggs inoculated at 0,2,4,6 weeks
Snail abundance over time (weeks)

```r
par(bty="n", las = 1)
#plot_it(0,"blue","YlOrRd",1,"HersheySans") # set col function params
xlim <- max(meso1$Week) # uses total num of weeks
ylim <- round_any(max(meso1$Cercariae),100,ceiling)
with(meso1,plot(Cercariae~Week,
                col=adjustcolor(col,alpha=0.5),
                type="h",
                lwd=5,
                xlim=c(0,xlim),ylim=c(0,ylim),
                xlab="",ylab="",main=""
))
abline(h=mean(meso1$Cercariae),col=col,lty=3,ylim=c(0,ylim)) # get mean
title(main=paste0("Cercariae production over ",max(meso1$Week)," weeks"),
      xlab="Week")
```

```
title(ylab="Number of cercariae shed in 90 mins",line=3.5)
```

Cercariae production over 14 weeks

Y-axis: Number of cercariae shed in 90 mins

X-axis: Week
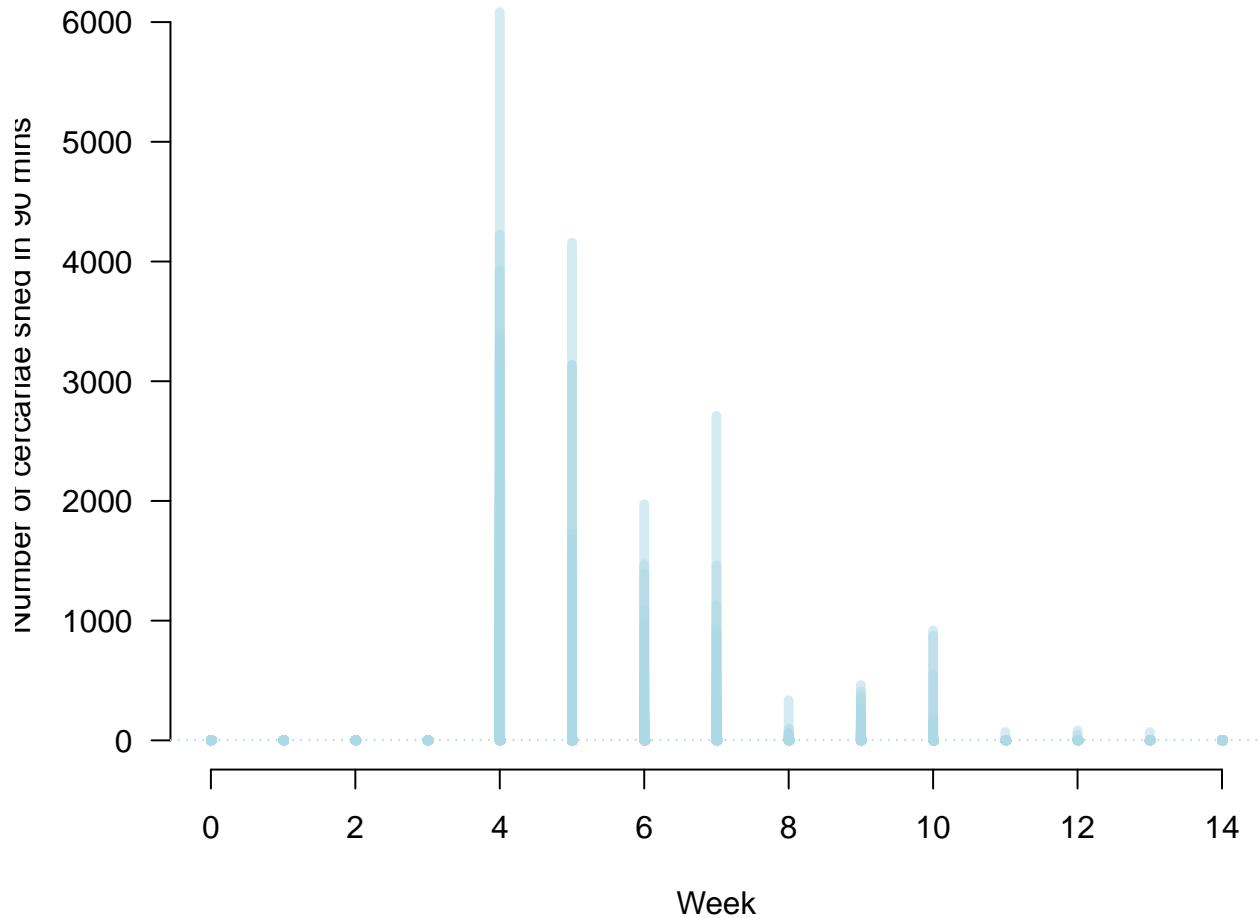
Tank cercariae production over time per tank

Select tank #. max 48

```
tank <- 9
```

```
par(bty="n", las = 1)
#plot_it(0,"blue","YlOrRd",1,"HersheySans") # set col function params
cer_total <- 0 # set ylim either to max for tank (1) or max across all tanks (6100)

snail <- subset(meso1,subset=Tank==tank) # get tank level individuals
snail <- subset(snail,subset=Cercariae>0) # get only cercariae
xlim <- max(meso1$Week) # uses total num of weeks
ylim <- round_any(max(snail$Cercariae),100,ceiling)
ifelse(cer_total==1,ylim <- round_any(max(meso1$Cercariae),100,ceiling),ylim <- round_any(max(snail$Cerc
```

```
[1] 400
```
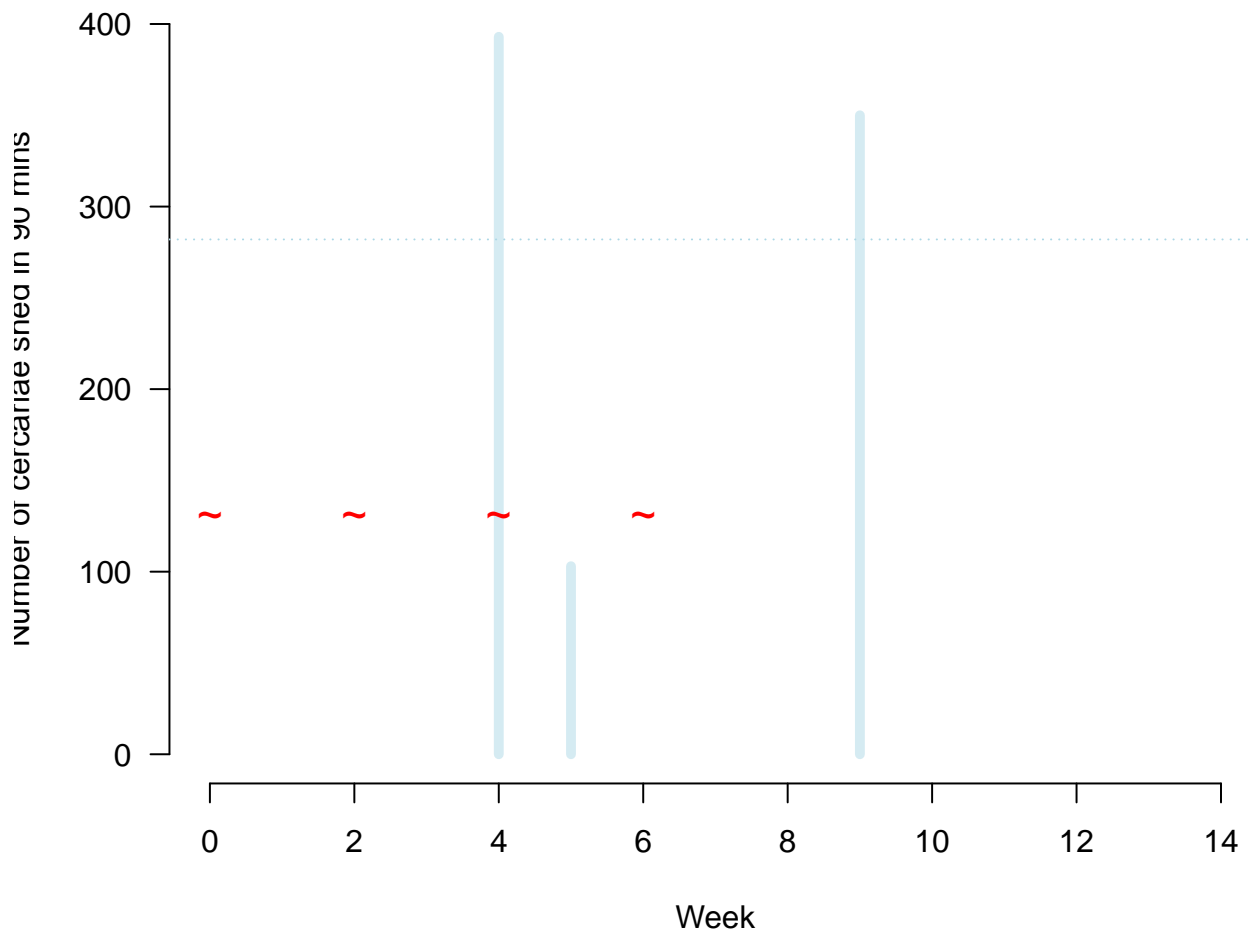
```
par(mfrow=c(1,1))
if(length(snail$Cercariae)>0){
  with(snail,plot(Cercariae~Week,
                  col=adjustcolor(col,alpha=0.5),
                  type="h",
                  lwd=5,
                  xlim=c(0,xlim),ylim=c(0,ylim),
                  xlab="",ylab="",main=""
  ))
  abline(h=mean(snail$Cercariae),col=col,lty=3,ylim=c(0,ylim)) # get mean
  title(main=paste0("Cercariae production for tank ",tank," over ",max(meso1$Week)," weeks"),
        xlab="Week")
  title(ylab="Number of cercariae shed in 90 mins",line=3.5)
  par(new=T)
  points(x=c(0,2,4,6),y=rep(max(snail$Cercariae)/3,4),pch="~",cex=1.5,col="red")# add inoculation point
}else{print(paste0("No cercariae in tank #",tank))}
```

Cercariae production for tank 9 over 14 weeks


```
#####

###########################################################################################
###########################################################################################
```

```
######################################################################################
```

Mesocosm 2 data sheet

Clean data

```r
meso2$Schisto <- as.integer(as.factor(meso2$Schisto))-1# convert Y/N in Schisto col to 1/0
# convert size to integers
meso2$Size <- gsub("Intermediate","2Intermediate",meso2$Size)
meso2$Size <- gsub("Small","1Small",meso2$Size)
meso2$Size <- gsub("Large","3Large",meso2$Size)
meso2$Size <- as.integer(as.factor(meso2$Size))

### get snails with egg masses
#### First get presence of schisto
meso2_UU <-  subset(meso2,Schisto==0)
meso2_II <- subset(meso2,Schisto==1)

# get uninfected snails with egg masses
eggs_UU <- subset(meso2_UU,Eggs>0)
# get infected snails with egg masses
eggs_II <- subset(meso2_II,Eggs>0)

# get size classes
small <- subset(meso2,Size==1) #small
int <- subset(meso2,Size==2) #intermediate
large <- subset(meso2,Size==3) #large

# get NP conc
high <- subset(meso2,NP=="High") # high NP conc
low <- subset(meso2,NP=="Low") # low NP conc
```

Egg mass distribution

```r
par(bty="n", las = 1)
#plot_it(0,"blue","YlOrRd",1,"HersheySans") # set col function params
den <- density(meso2$Eggs[meso2$Eggs>0]) # get only snails with eggs
xlim <- round_any(max(den$x),50,ceiling)
ylim <- round_any(max(den$y),0.01,ceiling)
plot(den,
     col=adjustcolor(col,alpha=0.5),
     xlim=c(0,xlim),
     ylim=c(0,ylim),
     xlab="Number of egg masses",
     ylab="Density",
     main=paste0("Distribution of number of egg masses over ",max(meso1$Week)," weeks"))
polygon(den, col=adjustcolor(col,alpha=0.5),border=col) # fill AUC
abline(v=mean(meso2$Eggs),col=col,lty=3,ylim=c(0,ylim)) # get mean
```

Distribution of number of egg masses over 14 weeks
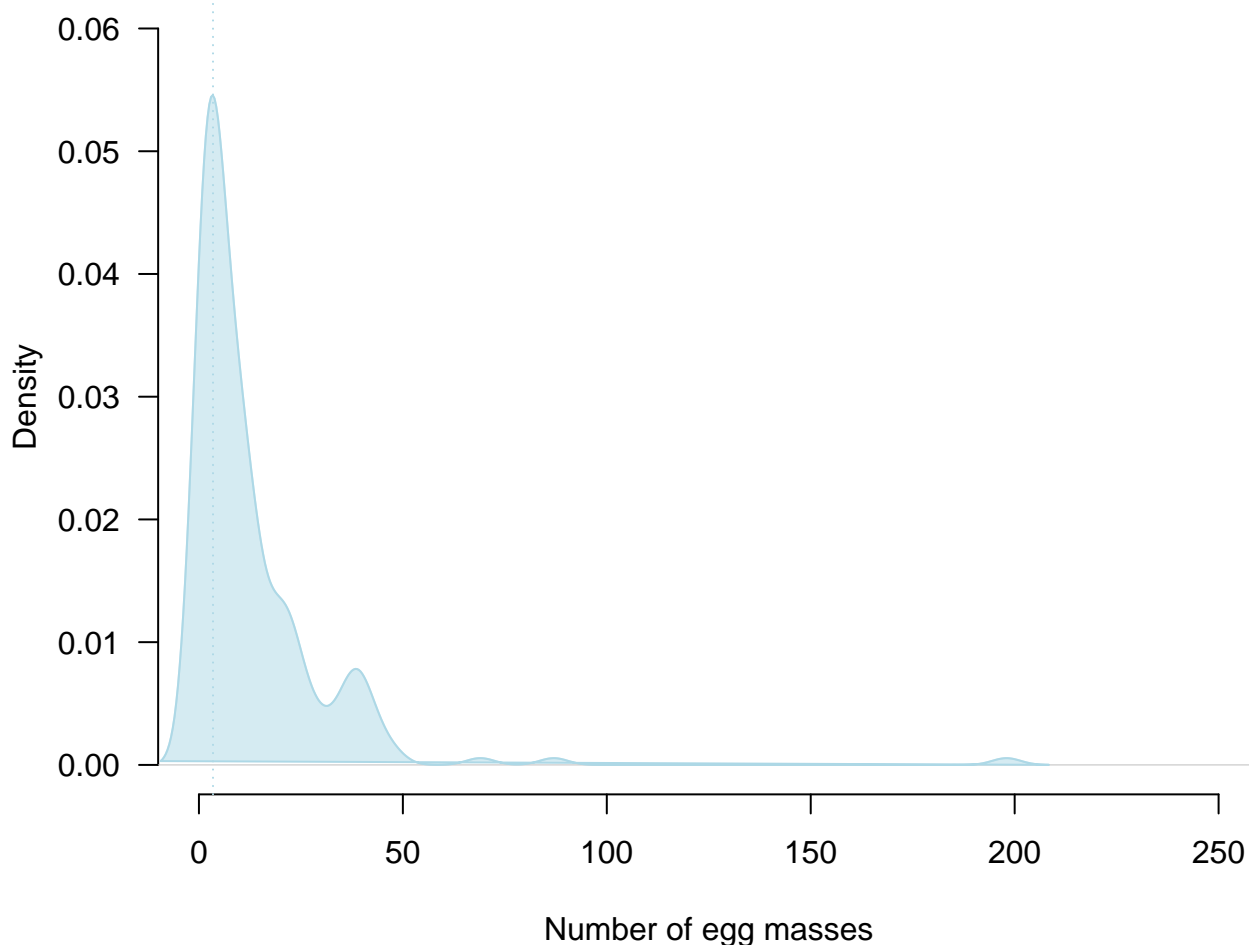
N/P concentration v egg mass

```r
par(bty="n", las = 1)
#plot_it(0,"blue","YlOrRd",1,"HersheySans") # set col function params
layout(matrix(c(1,1,2,3), 2, 2, byrow = TRUE)) # plot stacked plots
ylim=round_any(max(meso2$Eggs),10)
with(meso2,stripchart(Eggs~NP,
                      method="jitter", jitter=0.1,
                      pch=20,cex=2,
                      # cex=cex_diam,
                      col=adjustcolor(col,alpha=0.3),
                      vertical=T,
                      ylim=c(0,ylim),
                      group.names=c("High","Low"),
                      xlab="",ylab="",main="")
)
abline(h=mean(meso2$Eggs),col=col,lty=3)
title(main=paste0("Number of egg masses for high and low N/P levels over ",max(meso1$Week)," weeks"),
      xlab="N/P level")
```

```r
title(ylab="Number of egg masses",line=3.5)

### uninfected ###
with(eggs_UU,stripchart(Eggs~NP,
                        method="jitter", jitter=0.1,
                        pch=20,cex=2,
                        col=adjustcolor(col,alpha=0.3),
                        vertical=T,
                        ylim=c(0,ylim),
                        group.names=c("High","Low"),
                        xlab="",ylab="",main="")
)
abline(h=mean(eggs_UU$Eggs),col=col,lty=3)
title(main=paste0("Uninfected snails"),
      xlab="N/P level")
title(ylab="Number of egg masses",line=3.5)

### infected ###
with(eggs_II,stripchart(Eggs~NP,
                        method="jitter", jitter=0.1,
                        pch=20,cex=2,
                        col=adjustcolor(col2,alpha=0.3),
                        vertical=T,
                        ylim=c(0,ylim),
                        group.names=c("High","Low"),
                        xlab="",ylab="",main="")
)
abline(h=mean(eggs_II$Eggs),col=col2,lty=3)
title(main=paste0("Infected snails"),
      xlab="N/P level")
```
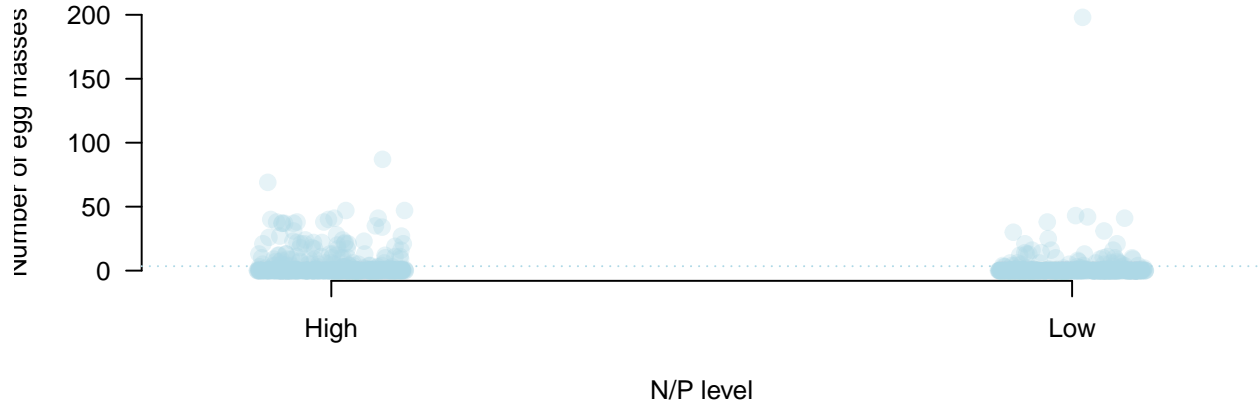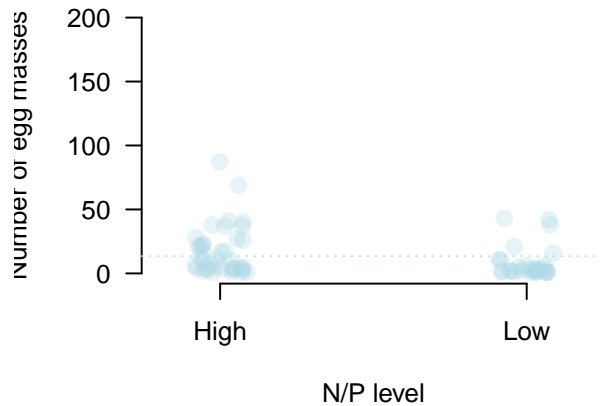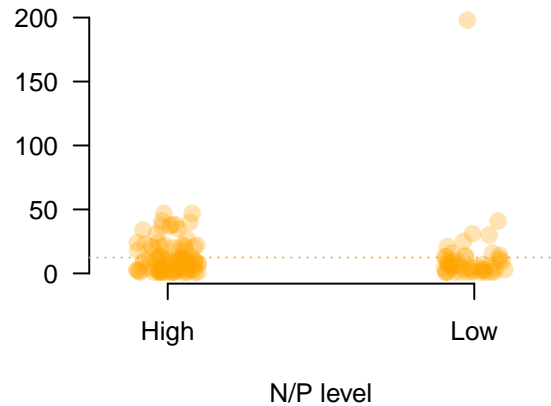
Number of egg masses for high and low N/P levels over 14 weeks

Uninfected snails

Infected snails

Phyto and Peri Distribution

phyto = flourescence units
peri = flourescence per 2 weeks / 3.5 inch^2 tile (gross productivity biomass rate)

```r
par(bty="n", las = 1)
par(mfrow=c(1,1))
#plot_it(0,"blue","YlOrRd",1,"HersheySans") # set col function params
den <- density(meso2$Phyto_F)
xlim <- round_any(max(den$x),10000,ceiling)
ylim <- round_any(max(den$y),0.0001,ceiling)
plot(den,
     col=adjustcolor(col,alpha=0.5),
     xlim=c(0,xlim),
     ylim=c(0,ylim),
     xlab="",ylab="",main=""
)
polygon(den, col=adjustcolor(col,alpha=0.5),border=col) # fill AUC
abline(v=mean(meso2$Phyto_F),col=col,lty=3,ylim=c(0,ylim)) # get mean
par(new=T) # add periphyton concentration
```

```
den2 <- density(meso2$Peri_F)
plot(den2,
     col=adjustcolor(col2,alpha=0.5),
     xlim=c(0,xlim), # uses xy lims from phyto
     ylim=c(0,ylim),
     xlab="",ylab="",main=""
)
polygon(den2, col=adjustcolor(col2,alpha=0.5),border=col2) # fill AUC
abline(v=mean(meso2$Peri_F),col=col2,lty=3,ylim=c(0,ylim)) # get mean
title(main=paste0("Resource concentration over ",max(meso1$Week)," weeks"),
      xlab="Resource concentration")
title(ylab="Density",line=3.5)
par(family='mono')
legend("topright",legend=c("Phytoplankton","Periphyton"),title="Resource type",
       border="white",pch=19,ncol=1,bty="n",
       cex=0.75,
       xjust=0.5,yjust=0.5,x.intersp = 0.5,y.intersp = 0.5,
       col=c(col,col2)
)
```


Resource concentration over 14 weeks
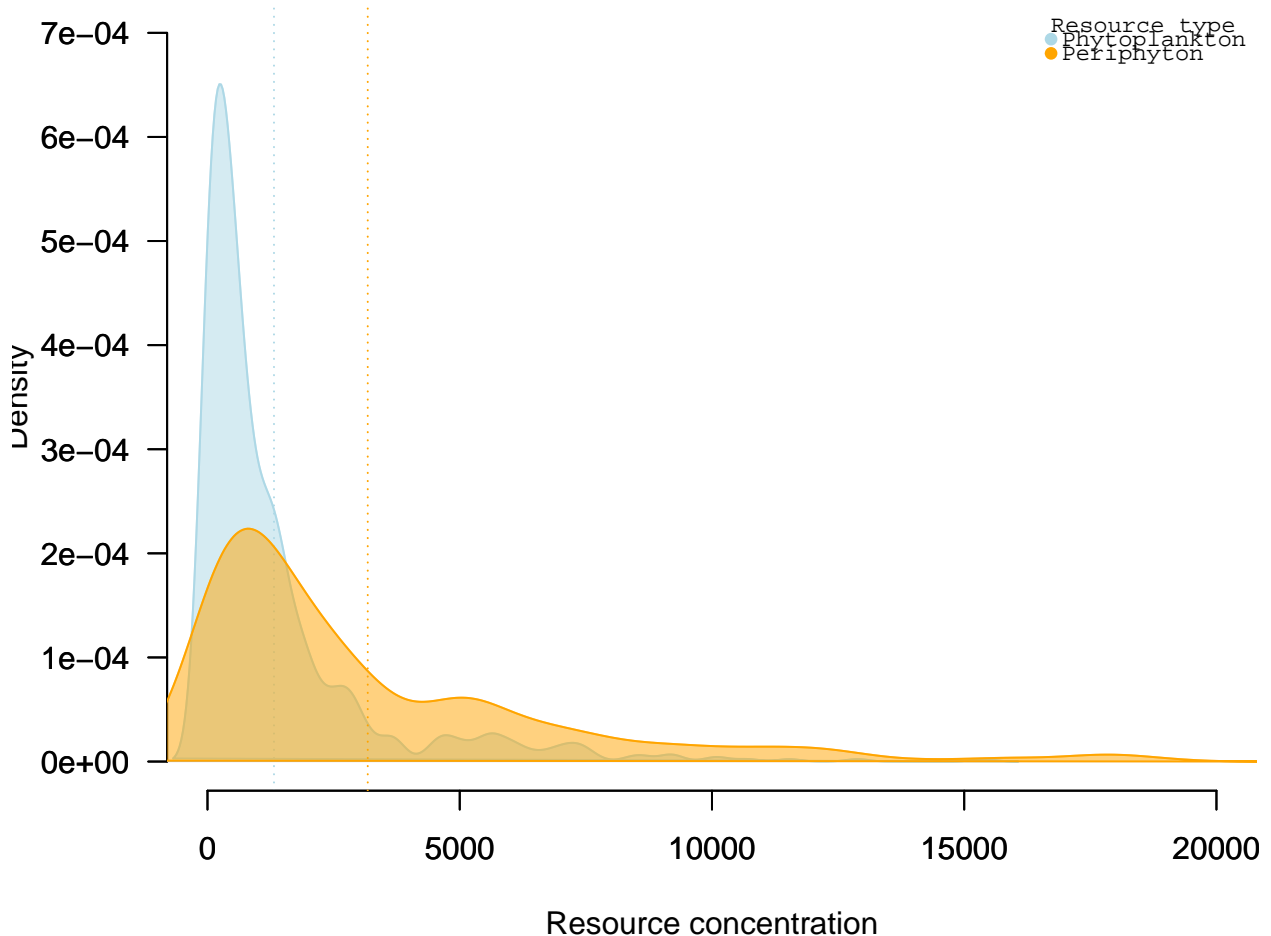
Egg Mass over time v presence of schisto
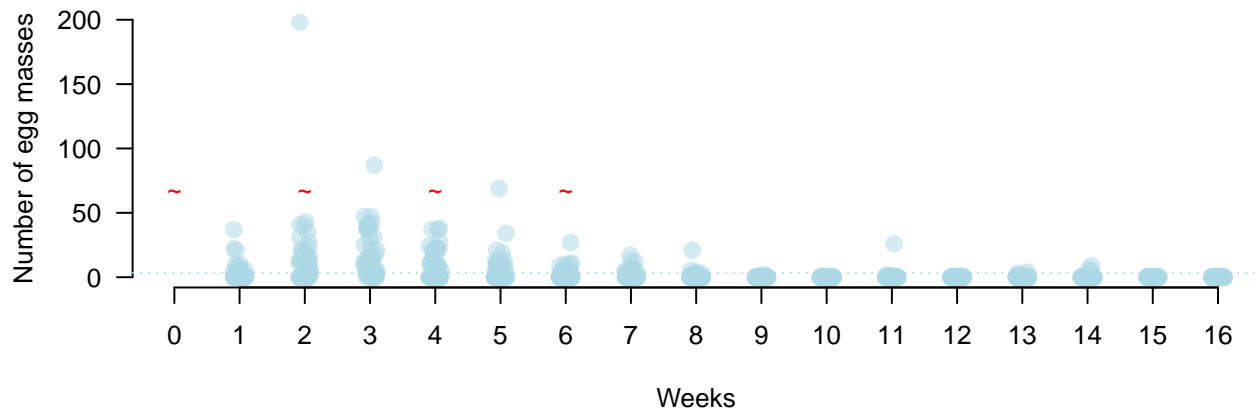
~1000 eggs inoculated at 0,2,4,6 weeks

```r
par(bty="n", las = 1)
#plot_it(0,"blue","YlOrRd",1,"HersheySans") # set col function params
layout(matrix(c(1,1,2,3), 2, 2, byrow = TRUE)) # plot stacked plots
meso2$Week <- as.integer(meso2$Week)
xlim <- max(meso2$Week)
ylim <- round_any(max(meso2$Eggs),10)
with(meso2,stripchart(Eggs~Week,
                      method="jitter", jitter=0.1,
                      pch=20,cex=2,
                      col=adjustcolor(col,alpha=0.5),
                      vertical=T,
                      xlim=c(0,xlim), ylim=c(0,ylim),
                      group.names=unique(meso2$Week),
                      xlab="Weeks",
                      ylab="Number of egg masses",
                      main=paste0("Number of egg masses over ",xlim," weeks")
))
abline(h=mean(meso2$Eggs),col=col,lty=3)
par(new=T)
points(x=c(0,2,4,6),y=rep(max(ylim)/3,4),pch="~",cex=1,col="red")# add inoculation points
axis(1,at=c(0,xlim),labels=c("0",""))# bookending axis tick marks

### uninfected ###
with(eggs_UU, stripchart(Eggs~Week,
                         method="jitter", jitter=0.1,
                         pch=20,cex=2,
                         col=adjustcolor(col,alpha=0.3),
                         vertical=T,
                         xlim=c(0,xlim),ylim=c(0,ylim),
                         group.names=unique(eggs_UU$Week),
                         xlab="Weeks",
                         ylab="Number of egg masses",
                         main="Uninfected")
)
par(new=T)
points(x=c(0,2,4,6),y=rep(max(ylim)/3,4),pch="~",cex=1,col="red")# add inoculation points
axis(1,at=c(0,xlim),labels=c("0","16"))# bookending axis tick marks

### infected ###
with(eggs_II, stripchart(Eggs~Week,
                         method="jitter", jitter=0.1,
                         pch=20,cex=2,
                         col=adjustcolor(col2,alpha=0.3),
                         vertical=T,
                         xlim=c(0,xlim),ylim=c(0,ylim),
                         group.names=unique(eggs_II$Week),
                         xlab="Weeks",
                         ylab="Number of egg masses",
                         main="Infected")
)
```
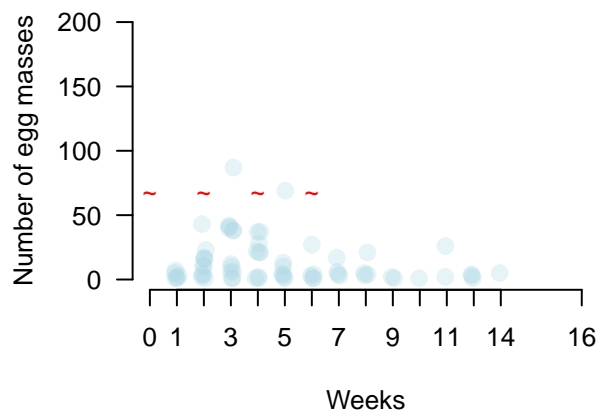
```
par(new=T)
points(x=c(0,2,4,6),y=rep(max(ylim)/3,4),pch="~",cex=1,col="red")# add inoculation points
axis(1,at=c(0,xlim),labels=c("0","16"))# bookending axis tick marks
```
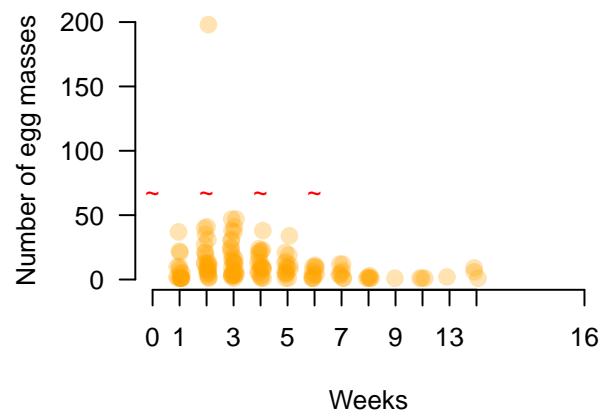
Number of egg masses over 16 weeks

Uninfected

Infected


```
### Size class vs peri
#~1000 eggs inoculated at 0,2,4,6 weeks
```

Size class vs Egg mass (with schisto)

```
par(bty="n", las = 1)
#### Egg masses > 0
den <- density(small$Eggs[small$Eggs>0])
den2 <- density(int$Eggs[int$Eggs>0])
den3 <- density(large$Eggs[large$Eggs>0])
xlim <- round_any(max(den2$x),100) #den2 xlim
ylim <- round_any(max(den2$y),0.01,ceiling) # den2 ylim

colvec <- c(4,6,9) # index for colfunc color palette in plot_it function
par(mfrow=c(1,1))
```

```r
plot(den,
     col=adjustcolor(colfunc[colvec[1]],alpha=0.5),
     xlim=c(0,xlim),
     ylim=c(0,ylim),
     # type="h",# fills density
     xlab="Number of egg masses",
     ylab="Density",
     main="Number of egg masses for each snail size class"
)
lines(den2,col=adjustcolor(colfunc[colvec[2]])) # den2
lines(den3,col=adjustcolor(colfunc[colvec[3]])) # den3
# fill densities
polygon(den, col=adjustcolor(colfunc[colvec[1]],alpha=0.5),border=colfunc[colvec[1]]) # fill AUC
polygon(den2, col=adjustcolor(colfunc[colvec[2]],alpha=0.5),border=colfunc[colvec[2]]) # fill AUC
polygon(den3, col=adjustcolor(colfunc[colvec[3]],alpha=0.5),border=colfunc[colvec[3]]) # fill AUC
# means
abline(v=mean(small$Eggs),col=adjustcolor(colfunc[colvec[1]]),lty=3,ylim=c(0,ylim)) # get mean
abline(v=mean(int$Eggs),col=adjustcolor(colfunc[colvec[2]]),lty=3,ylim=c(0,ylim)) # get mean
abline(v=mean(large$Eggs),col=adjustcolor(colfunc[colvec[3]]),lty=3,ylim=c(0,ylim)) # get mean

par(family="mono")
legend("right",legend=c("Small","Intermediate","Large"),col=c(colfunc[colvec[1:3]]),
       bty="n",pch=20,pt.cex=1.5,cex=0.7,y.intersp = 0.5, xjust = 0.5,
       title="Snail size class",title.adj = 0.3,text.font=2,
       trace=T,inset=0.1)
```

Number of egg masses for each snail size class
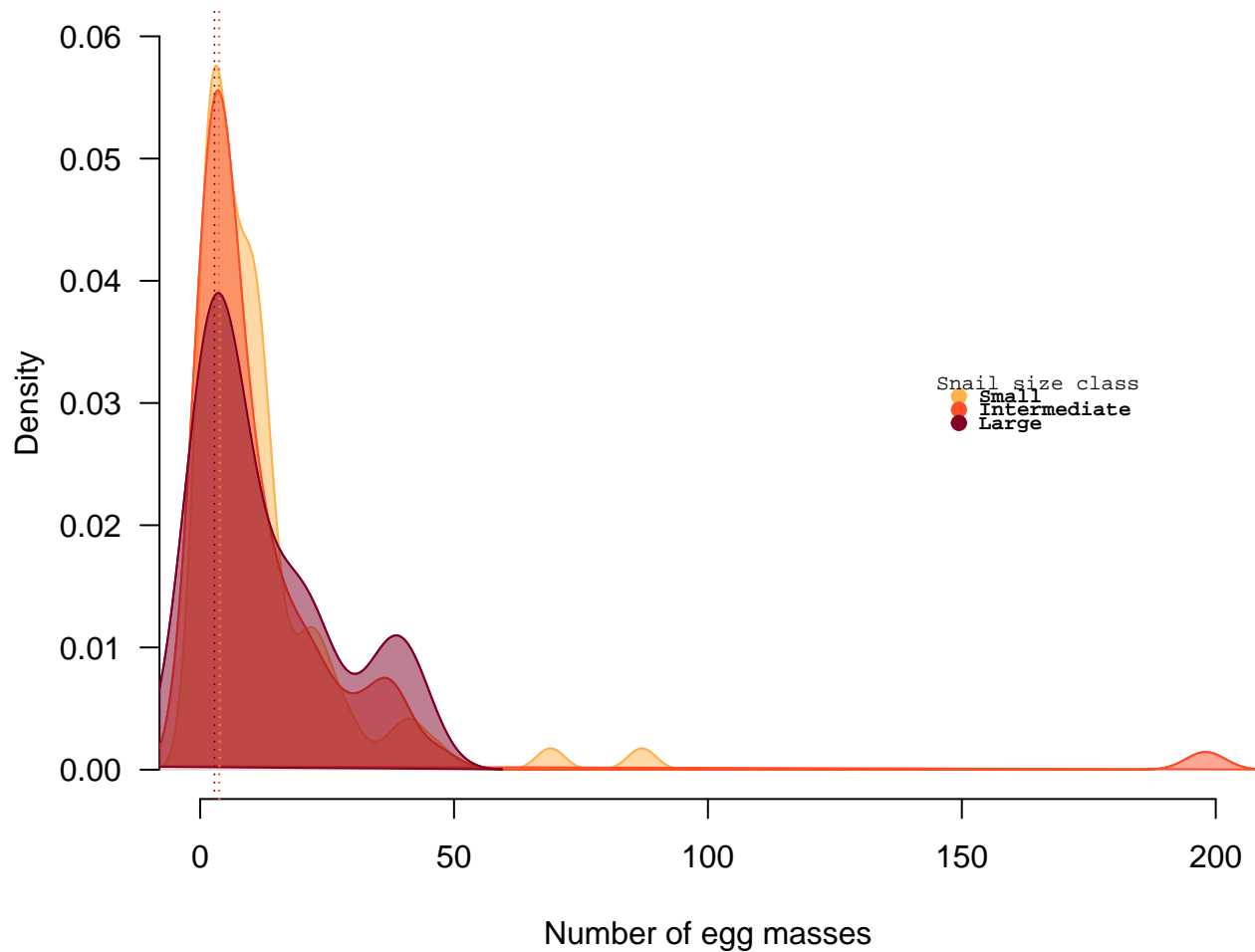

```
xchar= 3.937 ; (yextra,ychar)= -0.00109 0.00109
points2( 149.4 149.4 149.4 , 0.03055 0.02945 0.02836 , pch= 20 20 20 , ...)
```

```r
### Uninfected
small_UU <- subset(small,Schisto==0)
int_UU <- subset(int,Schisto==0)
large_UU <- subset(large,Schisto==0)
### Infected
small_II <- subset(small,Schisto==1)
int_II <- subset(int,Schisto==1)
large_II <- subset(large,Schisto==1)
```

Egg Mass per Week

~1000 eggs inoculated at 0,2,4,6 weeks

```r
par(bty="n", las = 1)
# set data to appropriate class
meso2$Eggs <- as.numeric(meso2$Eggs)
d <- meso2
ggplot(meso2, aes(x = Eggs, y = as.factor(Week), fill=..x..)) + # geom_density_ridges()
```

```
# geom_density_ridges_gradient(scale = 2, size=0.25, rel_min_height = 0.01,panel_scaling=T) +# scale
# scale_fill_viridis(name = "Eggs", alpha=0.5, option = "magma",direction=-1) + # "magma", "inferno",
geom_density_ridges(scale = 3, size=0.2,color="black", rel_min_height = 0.01,fill=col,alpha=0.5) +
labs(title = paste0("Number of egg masses per week ")) +
xlab("Number of egg masses") +
ylab("Week") +
# theme_ridges(grid=F,center_axis_labels = T)
plot_it_gg("white")
```
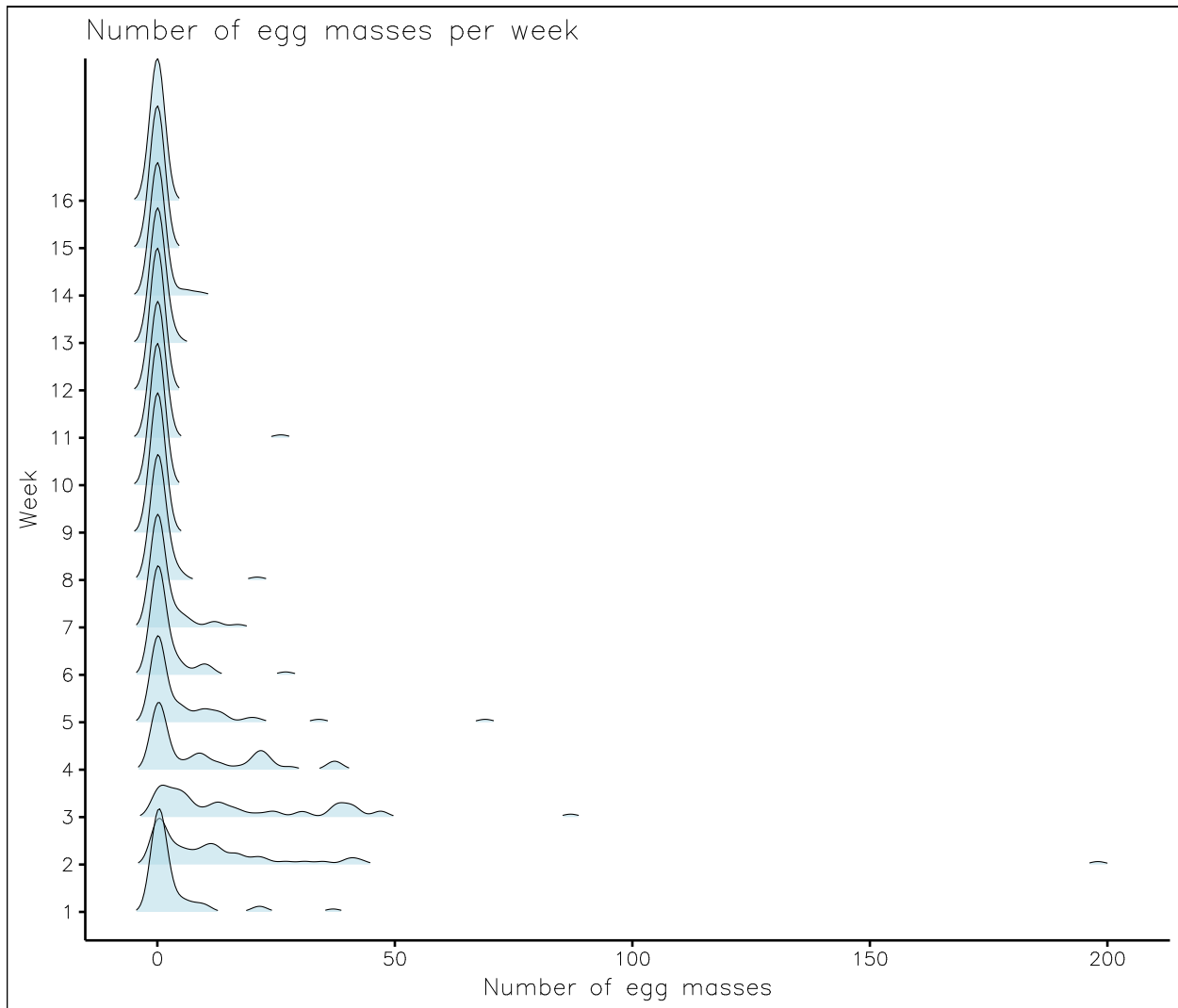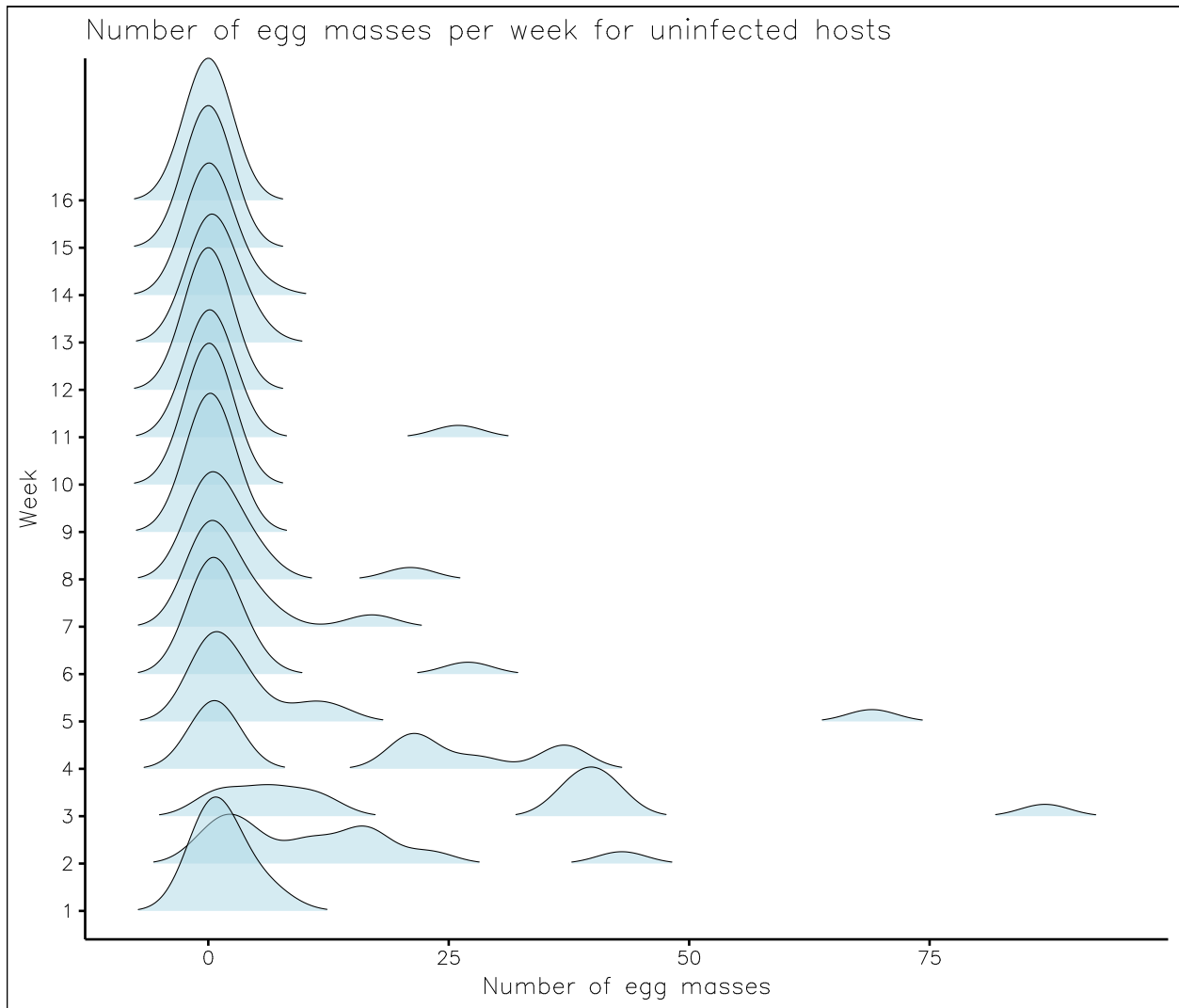


```
#### uninfected ####
par(bty="n", las = 1)
ggplot(meso2_UU, aes(x = Eggs, y = as.factor(Week), fill=..x..)) + # geom_density_ridges()
  # geom_density_ridges_gradient(scale = 2, size=0.25, rel_min_height = 0.01,panel_scaling=T) +# scale
  # scale_fill_viridis(name = "Eggs", alpha=0.5, option = "magma",direction=-1) + # "magma", "inferno",
  geom_density_ridges(scale = 3, size=0.2,color="black", rel_min_height = 0.01,fill=col,alpha=0.5) +
  labs(title = paste0("Number of egg masses per week for uninfected hosts")) +
  xlab("Number of egg masses") +
  ylab("Week") +
  # theme_ridges(grid=F,center_axis_labels = T)
```

```
plot_it_gg("white")
```


Number of egg masses per week for uninfected hosts

```
#### infected ####
par(bty="n", las = 1)
ggplot(meso2_II, aes(x = Eggs, y = as.factor(Week), fill=..x..)) + # geom_density_ridges()
  # geom_density_ridges_gradient(scale = 2, size=0.25, rel_min_height = 0.01,panel_scaling=T) +# scale
  # scale_fill_viridis(name = "Eggs", alpha=0.5, option = "magma",direction=-1) + # "magma", "inferno",
  geom_density_ridges(scale = 3, size=0.2,color="black", rel_min_height = 0.01,fill=col2,alpha=0.5) +
  labs(title = paste0("Number of egg masses per week for infected hosts")) +
  xlab("Number of egg masses") +
  ylab("Week") +
  # theme_ridges(grid=F,center_axis_labels = T)
  plot_it_gg("white")
```

Number of egg masses per week for infected hosts