Yampolsky et al. (2014) Adaptive phenotypic plasticity and local adaptation for temperature tolerance in freshwater zooplankton

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Contents

Introduction

```r
# find all csv files in data directory, and read files in as list elements
data <- lapply(paste('../data/', dir('../data', '\\.csv'), sep=''), read.csv,
               stringsAsFactors=FALSE)
# make colnames consistent
colnames(data[[2]])[1] <- 'Clone'

names(data) <- c('HbPublic', 'SuppTable1', 'DmagnaPublic')
```

Data preprocessing

Clone names are not conserved across datasets. Also, `Clone` and `CloneID` are two columns that pertain to the same information. Also, clone names don't sync up, which may be the reason for the lack of reproducibility for Tables 2 and 4.

```r
data[[3]][which(data[[3]][,'Clone'] == 'Xinb3'),'Clone'] <- 'Xinb-3'
data[[3]][which(data[[3]][,'Clone'] == 'Iinb1'),'Clone'] <- 'Iinb-1'
```

Figure 1

```r
getFig1 <- function(data, useExisting = TRUE){

  if(useExisting == FALSE){
   require(dplyr)
   hotData <- data[[3]][which(data[[3]][['AccT']] == 28),]
   coldData <- data[[3]][which(data[[3]][['AccT']] == 20),]
   hotRet <- as.data.frame(hotData %>%
                          group_by(Clone) %>%
                          summarize(mn = mean(logTimm),
                                   se = sd(logTimm)/sqrt(length(logTimm))))
   coldRet <- as.data.frame(coldData %>%
                           group_by(Clone) %>%
                           summarize(mn = mean(logTimm),
                                    se = sd(logTimm)/sqrt(length(logTimm))))
   aht <- c(23, 25, 20,  NA, NA, 21, 21, 27, 23, 21, 24, 31, 30, 30,
           24, 20, 17, 17, 23, 25, 21, 25, 20)

   names(aht) <- c("BE-OM-2", "CH-H-149", "EL-75-69", "ELNA-1", "F1", "FAT-1-6",
                  "FHS-2-11-8", "FRC-1-1", "FSP-1-16-2", "FUT-1-2-1", "Iinb-1",
                  "IR-1-7", "ISR-1-8", "Israel-8", "Mu-11", "N-47-20", "RBol-1-1",
                  "RKOR-1-1", "RMZ-009", "RYAK", "SE-G1-9", "WR-G1-9", "Xinb-3")
   plot(aht, coldRet[,2], pch=21, las=1, ylim=c(3.5, 5.5), tck=0.01, bg = 'white',
        ylab= expression(paste('log(T'[imm],')')),
        xlab=expression(paste('warmest month average high, T (', ~degree ,'C)')))

   segments(x0 = aht, y0 = coldRet[,2] + coldRet[,3], y1 = coldRet[,2] - coldRet[,3])
   abline(lm(coldRet[,2] ~ aht), lwd=2, lty=2 )
   points(aht, coldRet[,2], pch = 21, bg='white')

   points(aht, hotRet[,2], pch = 16)
   segments(x0 = aht, y0 = hotRet[,2] + hotRet[,3], y1 = hotRet[,2] - hotRet[,3])
   abline(lm(hotRet[,2] ~ aht), lwd=2)
  }

  if(useExisting){
   aht <- data[[2]][,6]
   logTimm <- data[[2]][,16]
   plot(aht, logTimm, pch=21, las=1, ylim=c(3.5, 5.5), tck=0.01, bg = 'white',
        ylab= expression(paste('log(T'[imm],')')),
        xlab=expression(paste('warmest month average high, T (', ~degree ,'C)')))

   segments(x0 = aht, y0 = logTimm + data[[2]][,18], y1 = logTimm - data[[2]][,18])
   abline(lm(logTimm ~ aht), lwd=2, lty=2 )
   points(aht, logTimm, pch = 21, bg='white')

   logTimmH <- data[[2]][,17]
   points(aht, logTimmH, pch = 16)
   segments(x0 = aht, y0 = logTimmH + data[[2]][,19], y1 = logTimmH - data[[2]][,19])
   abline(lm(logTimmH ~ aht), lwd=2)}
}
```

```
# this is using the data from the supplied data[[2]] data.frame
getFig1(data)
```
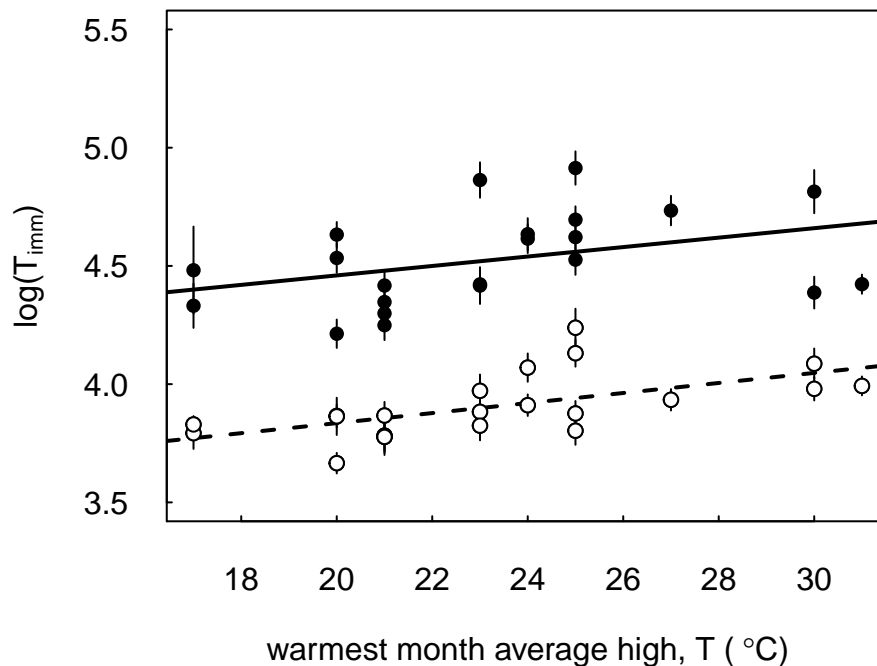

Figure 1: Time until immobilization as a function of the warmest month average high.

```
# this is attempting to calculate means from the data in data[[3]]. I'm missing something.
getFig1(data, useExisting = FALSE)
```

```
## Loading required package: dplyr
##
## Attaching package: 'dplyr'
##
## The following object is masked from 'package:stats':
##
##     filter
##
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
# excluding data not from the "Main" experiment makes the results look more similar.
test <- data
test[[3]] <- test[[3]][-which(test[[3]]$Experiment != 'Main'),]
getFig1(test, useExisting=FALSE)
```
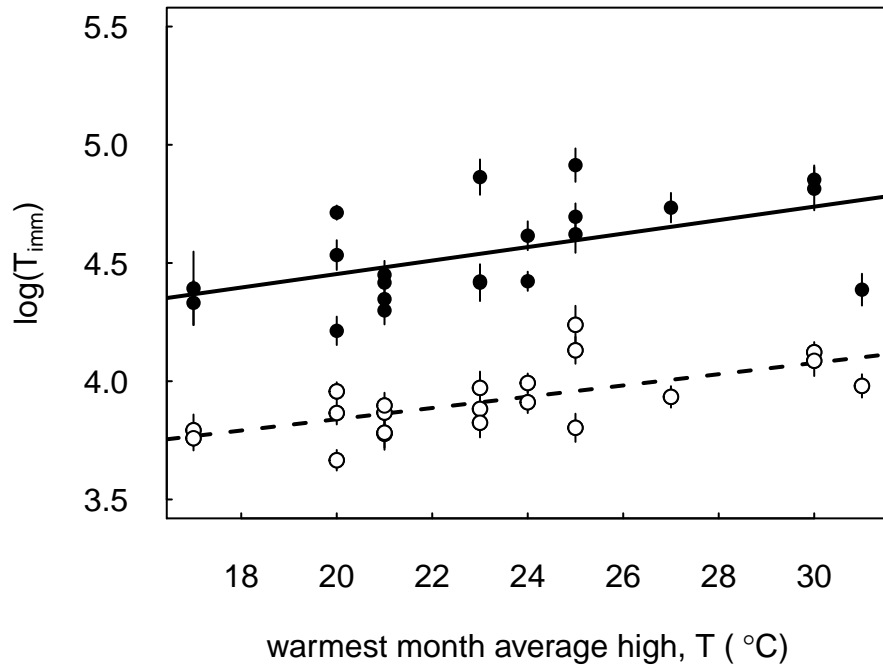
Figure 2: Time until immobilization as a function of the warmest month average high.
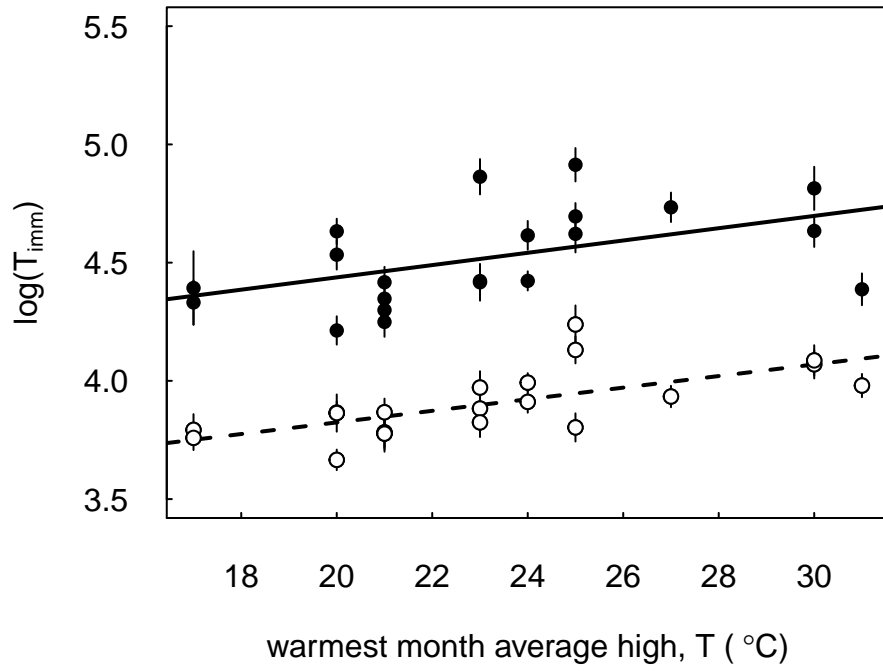

Figure 3: Time until immobilization as a function of the warmest month average high.

Table 2

```
library(xtable)
glmTimm <- aov(lm(c(data[[2]][,16], data[[2]][,17]) ~ rep(data[[2]][,6],2) *
                c(rep(20,nrow(data[[2]])), rep(28, nrow(data[[2]])))))
glmTimmTable <- matrix(unlist(summary(glmTimm)), ncol=5)

rownames(glmTimmTable) <- c("AHT_warmest", "AccT", "Acct * AHT_warmest", "Residuals")
colnames(glmTimmTable) <- c('df', 'SS', 'MS', 'F', 'p-value')

print(xtable(glmTimmTable), floating.placement='!', type='latex', include.rownames=FALSE)
```

% latex table generated in R 3.1.1 by xtable 1.7-4 package % Thu Sep 10 18:07:47 2015

df	SS	MS	F	p-value
1.00	0.26	0.26	11.08	0.00
1.00	4.23	4.23	179.02	0.00
1.00	0.00	0.00	0.01	0.92
40.00	0.95	0.02		

Figure 2

I took a few liberties and added some pretty colors instead of the cross hatch black and white from the original paper.

```r
getFig2 <- function(data, color = rainbow(4),  ...){
 require(dplyr)
 short <- data[[3]][which(data[[3]][,'Experiment'] == 'Short-term feeding'),]
 long  <- data[[3]][which(data[[3]][,'Experiment'] == 'Long-term feeding'),]

 shBarData <- short %>%
   group_by(Treatment, AccT) %>%
   summarize(mean(logTimm), sd(logTimm)/sqrt(length(logTimm)))

 lgBarData <- long %>%
   group_by(Treatment, AccT) %>%
   summarize(mean(logTimm), sd(logTimm)/sqrt(length(logTimm)))

 layout(matrix(c(1,2),ncol=2))
 shBar <- barplot(shBarData[[3]][c(3,1,4,2)], space = c(0.2, 0, 1, 0),
                  las=1, tck=0.01, col=color, ylab=expression(paste('log(T'[imm],')')),
                  xlab=expression(paste('acclimitization temperature (', ~degree ,'C)')),
                  ...)
 legend('topright', expression(italic('a')), bty='n', cex=1.25)
 axis(1, labels=c('20', '28'), at = c(1.2, 4.6), tck=0.01)

 segments(x0 = shBar,
          y0 = shBarData[[3]][c(3,1,4,2)] + shBarData[[4]][c(3,1,4,2)],
          y1 = shBarData[[3]][c(3,1,4,2)] - shBarData[[4]][c(3,1,4,2)])

 lgBar <- barplot(lgBarData[[3]][c(3,1,4,2)], space = c(0.2, 0, 1, 0),
                  las=1, tck=0.01, col=color, ylab='',
                  xlab=expression(paste('acclimitization temperature (', ~degree ,'C)')),
                  ...)
 legend('topright', expression(italic('b')), bty='n', cex=1.25)
 axis(1, labels=c('20', '28'), at = c(1.2, 4.6), tck=0.01)

 segments(x0 = lgBar,
          y0 = lgBarData[[3]][c(3,1,4,2)] + lgBarData[[4]][c(3,1,4,2)],
          y1 = lgBarData[[3]][c(3,1,4,2)] - lgBarData[[4]][c(3,1,4,2)])

}

prettyColors <- c('#dbed9f', '#a5cd26', '#ed9fdb', '#cd26a5')
getFig2(data, color = prettyColors, xpd=FALSE, ylim=c(3,5.5))
```
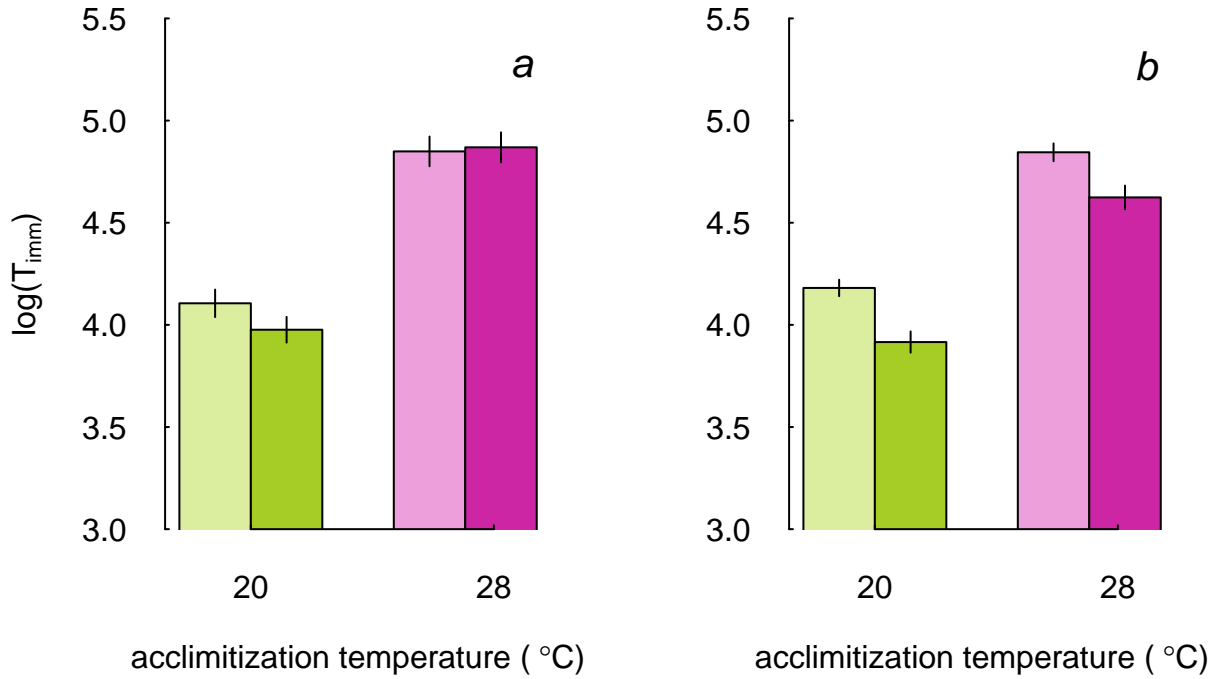
Figure 4: Time until immobilization as a function of acclimization temperature (20 or 28 C) under both high (darker bars) and limited (lighter bars) food resource levels for both short-term (8h; panel *a*) and long-term (1 generation; panel *b*) nutritional manipulation treatments.

Table 3

```
getTable3 <- function(data, type='html'){
  require(xtable)
  datS <- data[[3]][which(data[[3]]$Experiment == 'Short-term feeding'),]
  datL <- data[[3]][which(data[[3]]$Experiment == 'Long-term feeding'),]

  glmS <- aov(glm(datS$logTimm ~ datS$AccT * datS$Treatment))
  glmS2 <- matrix(unlist(summary(glmS)), ncol=5)
  rownames(glmS2)<- c("AccT", "food", "Acct * food", "Residuals")
  colnames(glmS2)<- c('df', 'SS', 'MS', 'F', 'p-value')

  glmL <- aov(glm(datL$logTimm ~ datL$AccT * datL$Treatment))
  glmL2 <- matrix(unlist(summary(glmL)), ncol=5)
  rownames(glmL2)<- c("AccT ", "food ", "Acct * food ", "Residuals ")
  colnames(glmL2)<- c('df', 'SS', 'MS', 'F', 'p-value')

  glmTable <- rbind(rep(NA, 5), glmS2, rep(NA, 5), glmL2)

  rownames(glmTable)[c(1,6)] <- c("short-term food manipulation treatment",
                                  "long-term food manipulation treatment")

  print(xtable(glmTable), floating.placement='!',
        comment = FALSE, digits = 2, type=type)
}
```

```
getTable3(data, type='latex')
```

	df	SS	MS	F	p-value
short-term food manipulation treatment					
AccT	1.00	8.03	8.03	138.92	0.00
food	1.00	0.04	0.04	0.62	0.43
Acct * food	1.00	0.07	0.07	1.16	0.29
Residuals	44.00	2.54	0.06		
long-term food manipulation treatment					
AccT	1.00	5.65	5.65	195.40	0.00
food	1.00	0.71	0.71	24.50	0.00
Acct * food	1.00	0.01	0.01	0.20	0.66
Residuals	44.00	1.27	0.03		

Figure 3

Still not quite there. Need the `aht` values that sync up nicely with their respective clone.

```r
getFig3 <- function(data, aht, plotIt=TRUE, ...){
  require(dplyr)
  hotData <- data[[3]][which(data[[3]][['AccT']] == 28),]
  coldData <- data[[3]][which(data[[3]][['AccT']] == 20),]
  retHot <- as.data.frame(hotData %>%
                          group_by(Clone) %>%
                          summarize(mn = mean(logTimm),
                                    se = sd(logTimm)/sqrt(length(logTimm))))

  retCold <- as.data.frame(coldData %>%
                           group_by(Clone) %>%
                           summarize(mn = mean(logTimm),
                                     se = sd(logTimm)/sqrt(length(logTimm))))
  hotData1 <- data[[1]][which(data[[1]][['AccT']] == 28),]
  coldData1 <- data[[1]][which(data[[1]][['AccT']] == 20),]

  h576Hot <-  as.data.frame(hotData1 %>%
                            group_by(Clone) %>%
                            summarize(mn = mean(dA576normTProt,na.rm=TRUE),
                                      se = sd(dA576normTProt,na.rm=TRUE)
                                      /sqrt(length(na.omit(dA576normTProt)))))

  h576Cold <-  as.data.frame(coldData1 %>%
                             group_by(Clone) %>%
                             summarize(mn = mean(dA576normTProt,na.rm=TRUE),
                                       se = sd(dA576normTProt,na.rm=TRUE)
                                       /sqrt(length(na.omit(dA576normTProt)))))

  #lifted from manuscript text (where is this in the data?)
  aht <- c(23, 25, 20,  NA, NA, 21, 21, 27, 23, 21, 24, 31, 30, 30,
           24, 20, 17, 17, 23, 25, 21, 25, 20)

  names(aht) <- c("BE-OM-2", "CH-H-149", "EL-75-69", "ELNA-1", "F1", "FAT-1-6",
                  "FHS-2-11-8", "FRC-1-1", "FSP-1-16-2", "FUT-1-2-1", "Iinb-1",
                  "IR-1-7", "ISR-1-8", "Israel-8", "Mu-11", "N-47-20", "RBol-1-1",
                  "RKOR-1-1", "RMZ-009", "RYAK", "SE-G1-9", "WR-G1-9", "Xinb-3")
  if(plotIt == TRUE){
    #Time to make the mega-plot
    layout(matrix(c(1,2,3), ncol=1))
    par(mar=c(6,4,0,0))
    #panel a
    plot(h576Hot[,2], retHot[,2], pch=21, las=1, xlim=c(0,0.1), ylim=c(3.5, 5.5),
         tck=0.01, bg = 'white',
         ylab= expression(paste('log(T'[imm],')')),
         xlab= expression(paste('H'[576])))
    segments(x0 = h576Hot[,2], y0 = retHot[,2]+retHot[,3], y1 = retHot[,2] - retHot[,3])
    segments(x0 = h576Hot[,2]+h576Hot[,3], y0 = retHot[,2], x1 = h576Hot[,2]-h576Hot[,3])
    points(h576Hot[,2], retHot[,2], pch = 21, bg='white')

    points(h576Cold[,2], retCold[,2], pch = 16)
```

```r
    segments(x0 = h576Cold[,2], y0 = retCold[,2]+retCold[,3],
            y1 = retCold[,2] - retCold[,3])

    segments(x0 = h576Cold[,2] + h576Cold[,3], y0 = retCold[,2],
            x1 = h576Cold[,2]-h576Cold[,3])
    legend('topright', expression(italic('a')), bty='n', cex=1.25)


    #panel b
    plot(aht, h576Hot[,2] - h576Cold[,2], pch=21, las=1, tck=0.01, ylim=c(-0.01, 0.1),
        bg = 'white', ylab= expression(paste(Delta, 'H'[576])),
        xlab=expression(paste('AHT_warmest (', ~degree ,'C)')), ...)
    abline(lm((h576Hot[,2] - h576Cold[,2]) ~ aht))
    legend('topright', expression(italic('b')), bty='n', cex=1.25)


    #panel c
    plot(aht, h576Hot[,2], pch=21, las=1, tck=0.01, bg = 'white', ylim=c(-0.01, 0.1),
        ylab = expression(paste('H'[576])),
        xlab = expression(paste('AHT_warmest (', ~degree ,'C)')), ...)
    segments(x0 = aht, y0 = h576Hot[,2] + h576Hot[,3],
            y1 = h576Hot[,2] - h576Hot[,3])
    points(aht, h576Hot[,2], pch = 21, bg='white')

    points(aht, h576Cold[,2], pch = 16)
    segments(x0 = aht, y0 = h576Cold[,2] + h576Cold[,3],
            y1 = h576Cold[,2] - h576Cold[,3])
    legend('topright', expression(italic('c')), bty='n', cex=1.25)
  }

  if(plotIt == FALSE){
    ret  <- rbind(retHot, retCold)
    h576 <- rbind(h576Hot, h576Cold)
    acct <- c(rep(28, nrow(retHot)), rep(20,nrow(retCold)))
    return(list(Timm=ret, h576=h576, AccT=acct, aht = aht))
  }
}

getFig3(data, aht)
```
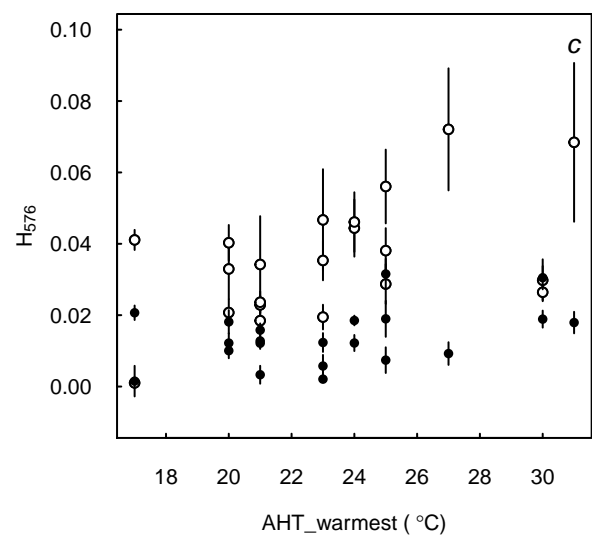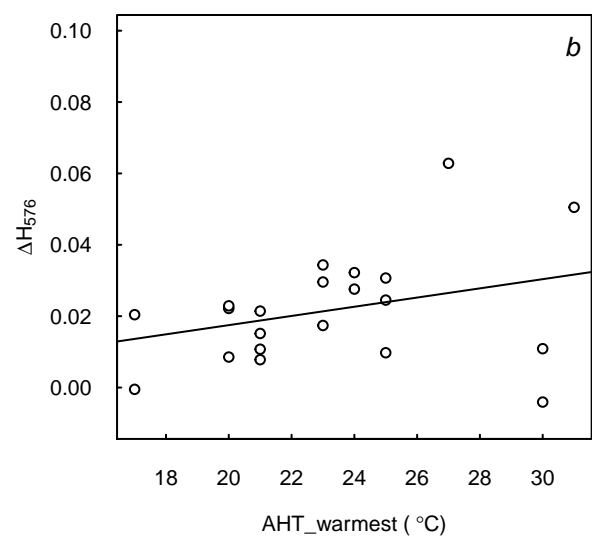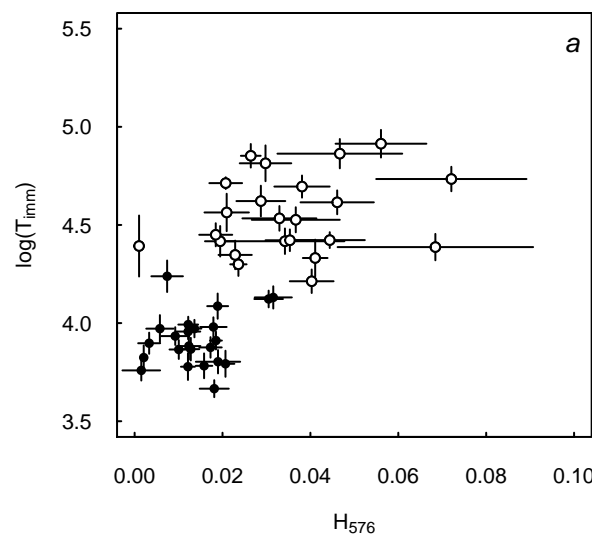
Figure 5:

Table 4

Wrong.

```
getTable4 <- function(data, type='html'){
  require(xtable)
  raw <- getFig3(data, aht, plotIt = FALSE)
  glmH576 <- aov(glm(log(raw[['h576']][,2]) ~ rep(raw[['aht']],2) * raw[['AccT']]))
  glmH576Table <- matrix(unlist(summary(glmH576)), ncol=5)
  rownames(glmH576Table) <- c("AHT_warmest", "AccT", "Acct * AHT_warmest", "Residuals")
  colnames(glmH576Table) <- c('df', 'SS', 'MS', 'F', 'p-value')
  print(xtable(glmH576Table), floating.placement='!', comment=FALSE, type=type)
}

getTable4(data, type='latex')
```

	df	SS	MS	F	p-value
AHT_warmest	1.00	5.27	5.27	8.96	0.00
AccT	1.00	9.97	9.97	16.94	0.00
Acct * AHT_warmest	1.00	0.08	0.08	0.13	0.72
Residuals	38.00	22.37	0.59		