Appendix S1. *A priori* models considered as predictors of mean adult body size (SVL) and frequency in mixed models

Model Name	Parameters
Global	Days since soaking rain, Julian day, Julian day^2
Rain + Date	Days since soaking rain, Julian day
Rain	Days since soaking rain
Date^2	Julian day, Julian day^2
Date	Julian day
Null	Intercept only

The best supported model predicting mean SVL was the **Global** model.

Parameter	β	SE	Lower CI	Upper CI
Intercept	59.128	0.523	58.076	60.223
Dry days	-1.363	0.356	-2.060	-0.629
Julian day	-0.924	0.392	-1.805	-0.132
Julian day^2	-1.236	0.418	-2.046	-0.356

The best supported model predicting the number of adults encountered was the **Rain + Date** model.

Parameter	β	SE	Lower CI	Upper CI
Intercept	2.324	0.036	2.242	2.406
Dry days	-0.407	0.049	-0.507	-0.313
Julian day	-0.176	0.036	-0.247	-0.106

Appendix S2: Additional details on the analysis of the mixture, growth and Cormack-Jolly-Seber models, prior specification and R code.

Mixture Analysis

We fit the normal mixture model using Markov chain Monte Carlo (MCMC) simulation with the program JAGS (Plummer 2003), executed using the R2jags package (Su and Yajima 2014) in program R (R Development Core Team 2012). We assigned uninformative priors to all model parameters. The mixture weights, ω_c, were assumed to follow a symmetric Dirichlet prior (1,1,1) and gamma priors were assigned (1.0^{-4}, 1.0^{-4}) to the precision of each normal distribution ($1/\sqrt{\sigma_c}$). We chose a normal (0, 1.0^{-6}) prior for μ_1 and calculated μ_2 as ($\mu_1 + \theta_1, where \, \theta_1 >$ 0). Similarly, μ_3 was calculated as ($\mu_2 + \theta_2, where \, \theta_2 > 0$). This parameterization ensures that body size observations are appropriately divided among the three distinct components of the mixture when vague priors are used to define the distribution means. The parameters θ_1 and θ_2 were assigned half-normal priors (0, 1.0^{-6})I(0,∞). We generated posterior summaries from 20,000 MCMC iterations of three parallel chains that we thinned 1/10 following a burn-in of 10,000 iterations. This resulted in adequate convergence of all model parameters ($\hat{R}$<1.01; Gelman and Hill, 2007).

Growth Analysis

We fit von Bertalanffy growth curves to *P. shermani* recapture data using a hierarchical model that accounts for both measurement error and inter-individual variation in growth (Eaton and Link 2011). We also introduced a log-link function to allow the von Bertalanffy growth rate parameter, k, to vary in relation to weather covariates. We supplied body size (SVL) data in full

capture history format (Individual x Survey) and fit the model using Markov chain Monte Carlo

(MCMC) simulation with the program JAGS (Plummer 2003), executed using the R2jags

package (Su and Yajima 2014) in program R (R Development Core Team 2012). We assigned

uninformative priors to all model parameters. We assigned uniform priors to the parameters for

asymptotic size, a (40, 100), the parameter associated with individual variation in growth, λ

(0.001, 20), the parameter for measurement error, τ (0.001, 10), and the coefficients for the

logarithm of the growth rate parameter, k (-5, 5). For predicting size-at-age, we used the mean

size of hatchlings observed in the month of May (18.08 mm) as the starting size (age 0) of the

growth curve. We generated posterior summaries for model parameters from 75,000 iterations of

three parallel Markov chains following a burn-in of 50,000. Posterior samples were then thinned

at a rate of 1/25 and convergence was assessed using the Gelman-Rubin statistic (Gelman & Hill

2007). All parameters showed adequate convergence (R-hat=1.18 for a, <1.02 for all other

parameters).

Survival Analysis

We used a state-space representation of the Cormack-Jolly-Seber model (Schwarz and

Arnason 1996, Lunn et al. 2009) to estimate survival and detection probabilities of *P. shermani*.

In the current analysis, we estimate a constant survival probability and use a logit-link function

to introduce covariates for body size at last capture (SVL) and days since a soaking rain event on

individual detection probability. We also consider an interaction between body size and days

since rain, which would indicate a difference between large and small individuals in their

responses to rainfall. We considered just adults for this analysis, using a size threshold of 45mm,

which is the size at which males often exhibit the secondary sex characteristic of mental gland

development. We fit the model with Markov chain Monte Carlo (MCMC) simulation using the program JAGS (Plummer 2003), executed using the R2jags package (Su and Yajima 2014) in program R (R Development Core Team 2012). We assigned uninformative uniform priors to all model parameters; (0, 1) for survival probability, φ, and (-10, 10) for all detection coefficients. We assessed convergence using the Gelman-Rubin statistic (R-hat < 1.05 for all parameters; Gelman & Hill 2007).

```
###############################################################################
# Bayesian Mixture Analysis
# 16 January, 2014
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# University of Missouri
###############################################################################

# Libraries
require(mixtools)
require(R2jags)

# Simulate Some Data (based on P. shermani results)
set.seed(101)
NIND <- 1000     # sample size
prob1 <- .23     # probability that an individual is in the 1st age/size class
prob2 <- .39     # probability that an individual is in the 2nd age/size class
prob3 <- .38     # probability that an individual is in the 3rd age/size class
meansizes <- c(24,40,55) # mean size for each class
sdsizes <- c(3.4,4.4,5.4) # sd for each distribution

y1 <- rnorm(n=prob1*NIND,mean=meansizes[1],sd=sdsizes[1]) # random sizes of age 1 individuals
y2 <- rnorm(n=prob2*NIND,mean=meansizes[2],sd=sdsizes[2]) # random sizes of age 2 individuals
y3 <- rnorm(n=prob3*NIND,mean=meansizes[3],sd=sdsizes[3]) # random sizes of age 3 individuals
y <- c(y1,y2,y3)

hist(y,breaks=30)  # Examine simulated size distribution

# Mixture analysis using Mixtools
mixmod <- normalmixEM(y,k=3)
(PROBS <- mixmod$lambda)
(SDSIZES <- mixmod$sigma)
(MEANSIZES <- mixmod$mu)

plot(mixmod,which=2)
lines(density(y), lty=2, lwd=2)

###############################################################################
# Bayesian Analysis of the Normal Mixture Model (No fixed Year Effects)
###############################################################################
sink("size.txt")
cat("
   model {

   # Priors for mean size of each class
   mu[1] ~ dnorm(25,1.0E-4)
   mu[2] <- mu[1]+theta1
   theta1 ~ dnorm(0,1.0E-4)I(0,)
   mu[3] <- mu[2]+theta2
   theta2 ~ dnorm(0,1.0E-4)I(0,)

   # Assign priors to standard deviation for each of the size classes
   for (i in 1:3){
   tau[i] ~ dgamma(0.01,0.01)
   sigma[i] <- pow(tau[i],-0.5)
   }

   # Assign priors to the probabilities for membership in each size class (must sum to 1)
   prob[1:3] ~ ddirich(alpha[])
```

```r
  # Likelihood
  for(i in 1:nind){
  class[i] ~ dcat(prob[]) # choose which distribution to try
  y[i] ~ dnorm(mu[class[i]],tau[class[i]])  # Body size (y) of individual i is normally distributed
  }                                 # with a mean and sd dependent on the estimated class
  }
  ",fill = TRUE)
sink()

# Bundle data
win.data <- list(y=y,nind=length(y),alpha=c(1,1,1))

# Initial values
inits <- function(){list(mu=c(runif(1,15,40),NA,NA),
                theta1=runif(1,10,20),
                theta2=runif(1,10,20),
                tau=runif(3,0.03,0.1),
                class=sample(x=c(1,2,3),size=length(y),replace=T))}

# Parameters monitored
params <- c("mu","sigma","prob")

# MCMC settings
ni <- 10000
nt <- 10
nb <- 5000
nc <- 3

# Call JAGS from R (~ 1 min)
system.time(OUT <- jags(win.data, inits, params, "size.txt", n.chains = nc, n.thin = nt, n.iter = ni, n.burnin = nb))

# Or use WinBUGS
# library(R2WinBUGS)
# system.time(OUT <- bugs(win.data, inits, params, "size.txt", n.chains = nc, n.thin = nt, n.iter = ni, n.burnin = nb,
debug=TRUE))

# Summarize posteriors
print(OUT, dig = 4)
OUT.MUs <- OUT$BUGSoutput$mean$mu
OUT.SDs <- OUT$BUGSoutput$mean$sigma
OUT.PROBs <- OUT$BUGSoutput$mean$prob

# Table comparing truth and model estimates
Table <- data.frame(rbind(c(meansizes,sdsizes,c(prob1,prob2,prob3)),c(OUT.MUs,OUT.SDs,OUT.PROBs)))
row.names(Table) <- c("True","Estimated")
names(Table) <- c("mu[1]","mu[2]","mu[3]","sd[1]","sd[2]","sd[3]","prob[1]","prob[2]","prob[3]")
print(Table)
```

```
##################################################################################################
# Bayesian Analysis of Normal Mixture Model with Fixed Year Effects on mu, sigma, prob
##################################################################################################
model {

# Priors for mean size of each class (differing by year)
for (t in 1:6){
  mu[1,t] ~ dnorm(25,1.0E-6)
  mu[2,t] <- mu[1,t]+theta1[t]
  theta1[t] ~ dnorm(0,1.0E-6)I(0,)
  mu[3,t] <- mu[2,t]+theta2[t]
  theta2[t] ~ dnorm(0,1.0E-6)I(0,)

# Assign priors to standard deviation for each of the size classes (differing by year)
  for (c in 1:3){
    tau[c,t] ~ dgamma(0.0001,0.0001)
    sigma[c,t] <- pow(tau[c,t],-0.5)
  } # close c-loop (class)

# Assign priors to the probabilities for membership in each size class
  prob[1:3,t] ~ ddirich(alpha[,t])
}   # close t-loop (year)

# Likelihood
for(i in 1:nind){
  class[i] ~ dcat(prob[,year[i]])
  y[i] ~ dnorm(mu[class[i],year[i]],tau[class[i],year[i]])
} # close i-loop

# Derived Quantities - Percent change in mean adult body size between years
muC[1]<-(mu.mean[3,2]-mu.mean[3,1])/mu.mean[3,1]
muC[2]<-(mu.mean[3,3]-mu.mean[3,1])/mu.mean[3,1]
muC[3]<-(mu.mean[3,4]-mu.mean[3,1])/mu.mean[3,1]
muC[4]<-(mu.mean[3,5]-mu.mean[3,1])/mu.mean[3,1]
muC[5]<-(mu.mean[3,6]-mu.mean[3,1])/mu.mean[3,1]
muC[6]<-(mu.mean[3,3]-mu.mean[3,2])/mu.mean[3,2]
muC[7]<-(mu.mean[3,4]-mu.mean[3,2])/mu.mean[3,2]
muC[8]<-(mu.mean[3,5]-mu.mean[3,2])/mu.mean[3,2]
muC[9]<-(mu.mean[3,6]-mu.mean[3,2])/mu.mean[3,2]
muC[10]<-(mu.mean[3,4]-mu.mean[3,3])/mu.mean[3,3]
muC[11]<-(mu.mean[3,5]-mu.mean[3,3])/mu.mean[3,3]
muC[12]<-(mu.mean[3,6]-mu.mean[3,3])/mu.mean[3,3]
muC[13]<-(mu.mean[3,5]-mu.mean[3,4])/mu.mean[3,4]
muC[14]<-(mu.mean[3,6]-mu.mean[3,4])/mu.mean[3,4]
muC[15]<-(mu.mean[3,6]-mu.mean[3,5])/mu.mean[3,5]
muC[16]<-(abs(muC[1])+abs(muC[6])+abs(muC[10])+abs(muC[13])+abs(muC[15]))/5  # Difference among sequential years

} # end model
```

```
###############################################################################
# Bayesian growth curve analysis (Modified from Eaton & Link, 2011)
###############################################################################

# Model inputs
#############
# f = vector (length = # of individuals) indicating the survey of first capture for each individual
# l = vector (length = # of individuals) indicating the date of the last survey at each study plot
# Plot = vector (length = # of individuals) indicating plot numbers for each individual
# Winter = matrix (# Plots x # Surveys) providing a 0/1 indicator of whether the recapture interval spanned the winter period
# Rain = matrix (# Plots x # Surveys) giving mean daily rainfall at each plot between the current and previous survey
# Temp = matrix (# Plots x # Surveys) giving mean daily temperature at each plot between the current and previous survey

 model {

   # Prior Specification (Growth Model)
   lambda ~ dunif(0.001,20)
   a ~ dunif(40,100)
   tau.eps ~ dunif(0.001,10)
   sd.eps <- 1/sqrt(tau.eps)

   for (par in 1:4){
    beta[par] ~ dunif(-5,5)
   }

   # Likelihood
   for (i in 1:NInd){                    # Loop through individuals
    for (t in f[i]:f[i]){                # First survey
      y[i,t] ~ dnorm(H[i,t],tau.eps)     # Measured size is the expected size +/- measurement error
      H[i,t] ~ dgamma(P[i,t],lambda)     # True size at first capture is gamma distributed with shape=Pit, rate=lambda
      P[i,t] <- lambda*H.m[i,t]          # Shape of gamma distribution is a product of lambda and the expected size at first capture
      H.m[i,t] ~ dunif(10,80)            # Prior: Expected size at first capture
    }

    for (t in (f[i]+1):l[i]){                      # Loop through surveys (1st capture to last survey date at each plot)
      y[i,t] ~ dnorm(H[i,t],tau.eps)
      H[i,t] <- H[i,t-1]+increment[i,t]            # True size = previous size plus a random gamma increment
      increment[i,t] ~ dgamma(P[i,t],lambda)
      P[i,t] <- lambda*abs(H.m[i,t]-H.m[i,t-1])
      H.m[i,t] <- H.m[i,t-1]+(a-H.m[i,t-1])*(1-exp(-k[i,t]*Interval[Plot[i],t]/1000))  # Expected size at time t
      log(k[i,t]) <- beta[1] + beta[2]*Winter[Plot[i],t] + beta[3]*Rain[Plot[i],t] + beta[4]*Temp[Plot[i],t]
    } #t
   } #i
  } #model
```

```
###############################################################
# Fit CJS Model to Recapture Data
###############################################################

# Model Inputs
#############
# f = vector (length = # of individuals) indicating the survey of first capture for each individual
# l = vector (length = # of individuals) indicating the date of the last survey at each study plot
# Plot = vector (length = # of individuals) indicating plot numbers for each individual
# DryDays = matrix (# Plots x # Surveys) giving days since the last soaking rain at the time of survey
# H = matrix (# Individuals x # Surveys) giving body size (mm SVL) at last capture for each individual

model {

    # Prior Specification
    for (par in 1:4){
    beta.p[par] ~ dunif(-10,10)
    }

    phi ~ dunif(0,1)

    # Likelihood
    for (i in 1:NInd){            # Loop through individuals
    for (t in f[i]:f[i]){
    z[i,t] <- 1              # All individuals alive on first capture
    }

    for (t in (f[i]+1):l[i]){      # Loop through surveys (1st to last at each plot)
    # Observation Component
    Y[i,t] ~ dbern(muy[i,t])
    muy[i,t] <- z[i,t]*p[i,t]
    logit(p[i,t]) <- beta.p[1] + beta.p[2]*DryDays[Plot[i],t] + beta.p[3]*H[i,t]
    + beta.p[4]*H[i,t]*DryDays[Plot[i],t]

    #State Component
    z[i,t] ~ dbern(muz[i,t])
    muz[i,t] <- pow(phi,(Interval[Plot[i],t]/30)) * z[i,t-1]

    } #t
    } #i
} #model
```

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