Technical Details for Survey and Data Analysis Methods

Reproductive Outcome and Survival of Common Bottlenose Dolphins Sampled in Barataria Bay, Louisiana, USA Following the Deepwater Horizon Oil Spill

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Methods

Satellite-linked and VHF Tagging

Seven dolphins were given a single tag in order to reduce handling time due to very poor health condition, unstable behavior during processing (e.g. abnormal heart rate and/or abnormal respirations), and/or later term pregnancy (2\textsuperscript{nd} trimester or later). Two dolphins were outfitted with a single tag due to the small size of their dorsal fin. Two additional dolphins were not tagged at all: one because its dorsal fin was severely damaged from previous human interaction (entanglement and boat-strike), while the other was released prior to complete processing due to increasingly unstable behavior. Attachment of VHF and/or satellite-linked transmitters followed methods as described by Balmer et al. [1]. The satellite-linked tags were set to transmit during two four-hour ‘windows’ each day (02:00-05:59 and 08:00-11:59 local), based on ARGOS satellite pass prediction values, looking for satellites with >20\textdegree{} elevation for at least three minutes. Based on programmed transmission times and anticipated battery life, the tags were expected to transmit up to 240 tracking days.

The Argos DCS uses multiple, polar-orbiting satellites to receive data from Argos tags and transmits these data to ground-based processing centers [2]. Tag locations were calculated using the Doppler Effect on transmission frequency and a location processing algorithm (Kalman
filtering) to provide higher numbers of accurate locations. Data were categorized into location classes (LCs) based upon estimated error: LC3, <250m; LC2, 250m-500m; LC1, 500m-1500m; LC0, >1500m. Only the highest LCs (LC3 and LC2) were used for plotting tagged animal locations.

**Vessel-based surveys**

*Photographic-identification surveys for mark-recapture analysis*

In June 2010, intensive photo-ID surveys for mark-recapture analysis were initiated in Barataria Bay. Mark-recapture photo-ID surveys have been used extensively to estimate abundance and determine survivorship of small cetaceans within a given region [3-5]. The mark-recapture photo-ID surveys in Barataria Bay were based on a robust design [6], and each primary session included three traversals of a defined survey route [4] (Figure 1). In all, ten primary sessions were conducted from June 2010 through April 2014, six of which followed the 2011 health evaluations.

*Radio-tracking and freeze brand monitoring surveys*

Surveys were initiated in September 2011 specifically to re-sight dolphins sampled during the preceding health evaluations. The objective of these surveys was to maximize the chance of encountering one or more of the 32 sampled dolphins by focusing survey effort in areas utilized by the sampled animals. *Ad hoc* survey routes were determined daily based on weather, sighting conditions, recent satellite-linked transmitter locations, and sightings of freeze-branded individuals from prior photo-ID surveys.

Surveys, each covering three days, were conducted at three, five, and ten weeks post capture-release. Two, 4-element mast-mounted Yagi antennas [Advanced Telemetry Systems (ATS),
Isanti, MN, USA] attached to ATS R2000 scientific receivers were used to scan all tagged animal frequencies at 60-second intervals. Once a tag signal was received, observers on the tracking vessel would attempt to visually locate the tagged animal, obtain photos of it along with any associated dolphins, and record a GPS position. The goal within each three-day tracking interval was to visually locate and obtain photos of all tagged dolphins.

Additional monitoring surveys were conducted following the expected transmission life of the VHF tags, with the primary objective to monitor tag migration and loss [1]. Animals were identified by the freeze brands applied during the health evaluations. These survey sessions, each lasting 3-5 days, were conducted in February, March, April, and May 2012.

Reproductive outcome surveys

Surveys specifically designed to document reproductive outcomes, utilizing photo-ID survey methods as described above and in greater detail by Melancon et al. [7], were conducted over one-week periods in June, July, and August 2012. The objective of these surveys was first to locate pregnant females from the August 2011 health evaluations (determined via ultrasound), and second to document the presence or absence of an accompanying neonate as they were expected to give birth in spring 2012. Survey routes were designed to provide coverage of areas encompassing previous sightings and recent satellite-linked locations of the targeted females. Additional surveys were conducted in April 2014, May 2014, May 2015 and July 2015.
R code to estimate CJS models

Data Preparation:

The following code sets up data for later MCMC sampling, and is common to all models. Here, H32 is the 32 X 20 matrix of capture histories (Table 1). I is a vector of interval lengths between occasions, computed as fractions of a year (I = [1 1 1 3 1 1 1 1 1 1 8 2 5 5 1 1 1 1 0 1 2] / 12). survHealth and survMRecap are matrices of indicators for Health Evaluation and Photo-ID survey types. (survHealth[1,] = [0 0 0 0 0 0 0 0 0 0 1 0 0 0 1 0 0 0], survMRecap[1,] = [0 0 1 1 0 1 0 0 0 1 0 1 1 0 0 0 0 0]).

F.fix.censors <- function(H){
  # Replace occasions after '2' in capture history with NA's.
  for( i in 1:nrow(H)){
    if( sum(H[i,]==2, na.rm=T) > 0){
      col.with.2 <- (1:ncol(H))[H[i,]==2]
      H[i,(col.with.2+1):ncol(H)] <- NA
      H[i,col.with.2] <- 1
    }
  }
  H
}

ch <- F.fix.censors(H32)

# Vector of first encounters
get.first <- function(x) min(which(x!=0))
f <- apply(ch,1,get.first)

# Toss individuals first seen at last occasion (no information for CJS)
ch <- ch[f!=ncol(ch),]
f <- f[f!=ncol(ch)]

sHealth <- survHealth[1,]
sMRecap <- survMRecap[1,]
ints <- I
ns <- ncol(ch)
nan <- nrow(ch)

Utility function to execute MCMC chains and compute DIC:

The following function is a copy of the coda.samples function contained in rjags, with the addition of DIC computation and modification to return a list object.

coda.samples.dic <- function (model, variable.names = NULL, n.iter, thin = 1, ...)

```
{
  load.module('dic') # necessary for pD and deviance monitor

  start <- model$iter() + thin
  varnames = c(variable.names, c('deviance', 'pD'))
  out <- jags.samples(model, varnames, n.iter, thin,
                      type = "trace", ...)
  deviance <- out$deviance
  pD <- out$pD
  out$deviance <- NULL
  out$pD <- NULL
  nch <- model$nchain()
  ans <- vector("list", nch)
  for (ch in 1:nch) {
    ans.ch <- vector("list", length(out))
    vnames.ch <- NULL
    for (i in seq(along = out)) {
      varname <- names(out)[[i]]
      d <- dim(out[[i]])
      if (length(d) < 3) {
        stop("Invalid dimensions for sampled output")
      }
      vardim <- d[1:(length(d) - 2)]
      nvar <- prod(vardim)
      niter <- d[length(d) - 1]
      nchain <- d[length(d)]
      values <- as.vector(out[[i]])
      var.i <- matrix(NA, nrow = niter, ncol = nvar)
      for (j in 1:nvar) {
        var.i[, j] <- values[j + (0:(niter - 1)) * nvar +
                            (ch - 1) * niter * nvar]
      }
      vnames.ch <- c(vnames.ch, rjags:::coda.names(varname, vardim))
      ans.ch[[i]] <- var.i
    }
    ans.ch <- do.call("cbind", ans.ch)
    colnames(ans.ch) <- vnames.ch
    ans[[ch]] <- mcmc(ans.ch, start = start, thin = thin)
  }
  dic <- mean(as.vector(deviance)) + .5 * var(as.vector(deviance))
  return(list(samples=mcmc.list(ans), dic=dic))
}
```

**JAGS code and execution:**

The following is JAGS code used to fit the \{constant,constant\} model.

```r
require(rjags)
modelString = "
model {
  # Survival: Constant
  # Capture: Constant
```

5
# Priors:
mean.phi ~ dunif( 0, 1 )
mean.p ~ dunif(0,1)

# Constraints:
for( i in 1:nan ){
    for( j in f[i]:(ns-1)){
        phi[i,j] <- mean.phi^ints[j]
        p[i,j] <- mean.p
    }
}

# Likelihood:
for( i in 1:nan ){
    # Latent state at first encounter
    z[i,f[i]] <- 1
    for ( j in (f[i]+1):ns ) {
        # State process
        phi.eff[i,j] <- z[i,j-1]*phi[i,j-1]
        z[i,j] ~ dbern(phi.eff[i,j])

        # Observation process
        p.eff[i,j] <- z[i,j] * p[i,j-1]
        ch[i,j] ~ dbern( p.eff[i,j] )
    }
}

# Write the modelString to a file, using R commands:
.temp = file("model.txt","w")
writeLines(modelString,con=.temp)
close(.temp)

#----------------------------------------------------------------------------
dataList = list(
    ch = ch ,
    f = f,
    ints = ints,
    ns = ns,
    nan = nan
)
#----------------------------------------------------------------------------
# Initial values
z = matrix(NA, nan, ns)
for(i in 1:nan) {
    indx = which(ch[i] == 1)
    if( max(indx) > f[i]){
        z[i,(f[i]+1):max(indx)] = 1
    }
}
initsList = list(z = z, mean.phi=0.85, mean.p=.5)
#----------------------------------------------------------------------------
# Run chains.
parameters = c( "mean.phi", "mean.p" )
adaptSteps = 2000
burnInSteps = 15000
nChains = 3
numSavedSteps = 2000
thinSteps = 1
nIter = ceiling((numSavedSteps * thinSteps) / nChains)

source("coda.samples.dic.r")  # routine to compute dic, returns mcmc.object
jagsModel = jags.model( "model.txt" , data=dataList , inits=initsList ,
                      n.chains=nChains , n.adapt=adaptSteps )
cat( "Burning in the MCMC chain...\n" )
update( jagsModel , n.iter=burnInSteps )
cat("Sampling final MCMC chain...\n")
samples = coda.samples.dic( jagsModel , variable.names=parameters ,
                          n.iter=nIter , thin=thinSteps )

Other models:

Following are JAGS model statements for the remaining 5 models. Remaining code for data, initial values, and model executions is nearly identical to the above with minor modification.

model {
  # Survival: Random Walk
  # Capture: Constant

  # Priors:
  PHI[1] ~ dunif(0, 1)
  mean.p ~ dunif(0,1)
  sigma.phi ~ dunif(0,10)

  # Constraints:
  mu.phi[1] <- log(PHI[1]/(1-PHI[1]))
  for(j in 2:(ns-1)){
    mu.phi[j] <- mu.phi[j-1] + epsilon[j]
    logit(PHI[j]) <- mu.phi[j]
  }
  tau <- pow(sigma.phi,-2)

  for( i in 1:nan ){
    for( j in f[i]:(ns-1)){
      phi[i,j] <- PHI[j]^ints[j]
      p[i,j] <- mean.p
    }
  }
  for(j in 2:(ns-1)){
    epsilon[j] ~ dnorm(0,tau)
  }

  # Likelihood:
  for( i in 1:nan ){
    # Latent state at first encounter
    z[i,f[i]] <- 1
    for( j in (f[i]+1):ns ){
      # State process
      phi.eff[i,j] <- z[i,j-1]*phi[i,j-1]
      z[i,j] ~ dbern(phi.eff[i,j])
    }
  }
}
# Observation process
p.eff[i,j] <- z[i,j] * p[i,j-1]
ch[i,j] ~ dbern( p.eff[i,j] )
}
}

# Survival: Constant
# Capture: Random Walk

# Priors:
P[1] ~ dunif( 0, 1 )
mean.phi ~ dunif(0,1)
sigma.p ~ dunif(0,10)

# Constraints:
mu.p[1] <- log(P[1]/ (1-P[1]))
for(j in 2:(ns-1)){
  mu.p[j] <- mu.p[j-1] + epsilon[j]
  logit(P[j]) <- mu.p[j]
}
tau <- pow(sigma.p,-2)

for( i in 1:nan ){
  for( j in f[i]: (ns-1)) {
    phi[i,j] <- mean.phi^ints[j]
    p[i,j] <- P[j]
  }
}

for(j in 2:(ns-1)){
  epsilon[j] ~ dnorm(0,tau)
}

# Likelihood:
for( i in 1:nan ){
  # Latent state at first encounter
  z[i,f[i]] <- 1
  for( j in (f[i]+1):ns ){
    # State process
    phi.eff[i,j] <- z[i,j-1]*phi[i,j-1]
    z[i,j] ~ dbern( phi.eff[i,j] )

    # Observation process
    p.eff[i,j] <- z[i,j] * p[i,j-1]
    ch[i,j] ~ dbern( p.eff[i,j] )
  }
}

# Survival: Random Walk
# Capture: Random Walk

# Priors:
\[
P[1] \sim \text{unif}(0, 1)
\]
\[
PHI[1] \sim \text{unif}(0, 1)
\]
\[
sigma \cdot phi \sim \text{unif}(0, 10)
\]
\[
sigma \cdot p \sim \text{unif}(0, 10)
\]

# Constraints:
\[
mu \cdot phi[1] \leftarrow \log(PHI[1] / (1-PHI[1]))
\]
\[
mu \cdot p[1] \leftarrow \log(P[1] / (1-P[1]))
\]

for (j in 2:(ns-1)) {
    mu.phi[j] <- mu.phi[j-1] + epsilon.phi[j]
    logit(PHI[j]) <- mu.phi[j]
    mu.p[j] <- mu.p[j-1] + epsilon.p[j]
    logit(P[j]) <- mu.p[j]
}

\[
tau \cdot phi \leftarrow \text{pow}(sigma \cdot phi, -2)
\]
\[
tau \cdot p \leftarrow \text{pow}(sigma \cdot p, -2)
\]

for (j in 2:(ns-1)) {
    epsilon.phi[j] ~ \text{dnorm}(0, tau.phi)
    epsilon.p[j] ~ \text{dnorm}(0, tau.p)
}

for (i in 1:nan) {
    for (j in f[i]: (ns-1)) {
        phi[i, j] <- PHI[j]^ints[j]
        p[i, j] <- P[j]  # Actually, capture prob at occasion j+1
    }
}

# Likelihood:
for (i in 1:nan) {
    # Latent state at first encounter
    z[i, f[i]] <- 1
    for (j in (f[i]+1):ns) {
        # State process
        phi.eff[i, j] <- z[i, j-1]*phi[i, j-1]
        z[i, j] ~ \text{dbern}(phi.eff[i, j])

        # Observation process
        p.eff[i, j] <- z[i, j] * p[i, j-1]  # p[i, j-1] = P(capture at occasion j)
        ch[i, j] ~ \text{dbern}( p.eff[i, j] )
    }
}

------------------------------------------------------------
model {

    # Survival: Random Effects
    # Capture: Survey type

    # Priors:
    \mu \cdot \text{mean} \cdot phi \sim \text{dnorm}(2, 3.5)
    \sigma \sim \text{unif}(0, 10)
    for (i in 1:3) {

beta[i] ~ dnorm(0,10)

# Constraints:
tau <- pow(sigma,-2)
for(j in 1:(ns-1)){
    mu.phi[j] ~ dnorm( mu.mean.phi, tau )
    logit(PHI[j]) <- mu.phi[j]
}

for(j in 1:(ns-1)){
    mu.p[j] <- beta[1] + beta[2]*sHealth[j] + beta[3]*sMRecap[j]
}

for( i in 1:nan ){
    for( j in f[i]:ns ) {
        phi.eff[i,j] <- z[i,j]*phi[i,j]
        phi[i,j] <- PHI[j]^ints[j]
        logit(p[i,j]) <- mu.p[j]
    }
}

# Likelihood:
for( i in 1:nan ){
    # Latent state at first encounter
    z[i,f[i]] <- 1
    for ( j in (f[i]+1):ns ) {
        # State process
        phi.eff[i,j] <- z[i,j-1]*phi[i,j-1]
        z[i,j] ~ dbern(phi.eff[i,j])

        # Observation process
        p.eff[i,j] <- z[i,j] * p[i,j-1]
        ch[i,j] ~ dbern( p.eff[i,j] )
    }
}

model {

    # Survival: Constant
    # Capture: Survey type

    # Priors:
    mu.mean.phi ~ dnorm( 2, 3.5 )
    for(i in 1:3){
        beta[i] ~ dnorm(0,10)
    }

    # Constraints:
    for(j in 1:(ns-1)){
        logit(PHI[j]) <- mu.mean.phi
    }

    for(j in 1:(ns-1)){
        mu.p[j] <- beta[1] + beta[2]*sHealth[j] + beta[3]*sMRecap[j]
    }
}
for( i in 1:nan ){
    for( j in f[i]:(ns-1)){
        phi[i,j] <- PHI[j]^ints[j]
        logit(p[i,j]) <- mu.p[j]
    }
}

# Likelihood:
for( i in 1:nan ){
    # Latent state at first encounter
    z[i,f[i]] <- 1
    for ( j in (f[i]+1):ns ) {
        # State process
        phi.eff[i,j] <- z[i,j-1]*phi[i,j-1]
        z[i,j] ~ dbern(phi.eff[i,j])

        # Observation process
        p.eff[i,j] <- z[i,j] * p[i,j-1]
        ch[i,j] ~ dbern( p.eff[i,j] )
    }
}
}
Figure S1. Timing and types of surveys used in the survival and reproductive outcome analysis. Numbers above each symbol represent the number of surveys conducted in each month.
Table S1. Summary information for individual dolphins monitored following the 2011 health evaluations in Barataria Bay, LA. Criteria for overall prognosis, lung disease, and hematological and serum biochemical panels were defined in Schwacke et al. [8]. A “1” indicates the individual was classified as out-of-range for the given panel, “0” indicates the individual was within normal range. *Indicates the serum aldosterone was below assay detection limit (5.5 pg/mL).

| FB | Sex | Age (Years) | Pregnant | Length (cm) | Weight (kg) | Overall Prognosis | Poor Body Condition | Lung Disease | Inflammation Panel | Hypoglycemia | Iron Panel | Hepatobiliary Panel | Anemia | Aldosterone (pg/mL) | Cortisol (µg/dL) |
|----|-----|------------|----------|-------------|-------------|-------------------|--------------------|-------------|---------------------|-------------|-----------|---------------------|--------|----------------------|-----------------|
| Y05 | F   | 16         | 0        | 251         | 154         | grave            | severe             | grave       | 1                   | 1           | 1         | 1                   | 1      | 5.5*                | 2.6             |
| Y12 | M   | 16         |          | 261         | 149         | grave            | severe             | 1           | 1                   | 0           | 1         | 1                   | 1      | 23.9                | 2.35            |
| Y29 | F   | 0          | 217      |             |             |                  |                    |             | 0                   | 0           | 0         | 0                   | 0      | 5.5*                | 2.69            |
| Y35 | F   | 1          | 224      |             |             | good             | normal             | 0           | 0                   | 0           | 0         | 0                   | 0      | 5.5*                | 0.92            |
| Y11 | F   | 19.5       | 0        | 253         | 173         | guarded          | severe             | 0           | 0                   | 1           | 0         | 0                   | 0      | 13.49               | 2.23            |
| Y37 | F   | 1          | 225      |             |             | fair             | mild               | 1           | 0                   | 0           | 0         | 0                   | 0      | 5.5*                | 0.2             |
| Y01 | F   | 42         | 1        | 243         | 143         | good             | normal             | 1           | 0                   | 0           | 0         | 0                   | 0      | 5.5*                | 1.59            |
| Y02 | M   | 17         |          | 263         | 201         | guarded          | 0                  | mild        | 1                   | 0           | 0         | 0                   | 0      | 5.5*                | 0.34            |
| Y10 | M   | 258        | 1        | 258         | 191         | poor             | severe             | 0           | 1                   | 1           | 0         | 0                   | 0      | 5.5*                | 0.59            |
| Y23 | F   | 4          | 0        | 187         | 82          | good             | mild               | 0           | 0                   | 0           | 0         | 0                   | 0      | 5.5*                | 0.24            |
| Y18 | M   | 271        | 253      |             |             | fair             | 0                  | mild        | 0                   | 1           | 0         | 0                   | 0      | 5.5*                | 0.93            |
| Y25 | F   | 1          | 239      |             |             |                  |                    |             | 0                   | 0           | 0         | 0                   | 0      | 13.22               | 0.27            |
| Y06 | M   | 4          |          | 210         | 114         | fair             | 0                  | normal      | 0                   | 0           | 0         | 0                   | 0      | 5.5*                | 1.55            |
| Y13 | F   | 17         | 1        | 230         | 143         | good             | normal             | 0           | 0                   | 1           | 0         | 0                   | 0      | 117.46              | 2.74            |
| Y27 | F   | 1          | 239      | 183         |             | good             | 0                  | mild        | 0                   | 0           | 0         | 0                   | 0      | 48.72               | 1.86            |
| Y00 | M   | 8          |          | 232         | 130         | good             | 1                  | mild        | 0                   | 0           | 0         | 0                   | 0      | 27.13               | 0.82            |
| Y04 | M   | 21         |          | 255         | 182         | fair             | 0                  | mild        | 0                   | 0           | 0         | 0                   | 0      | 67.07               | 2.43            |
| Y14 | M   | 5.75       |          | 216         | 120         | fair             | 0                  | normal      | 1                   | 0           | 0         | 0                   | 0      | 189.11              | 3               |
| Y16 | M   | 21         |          | 273         | 169         | guarded          | 1                  | mild        | 1                   | 1           | 0         | 1                   | 0      | 5.5*                | 0.83            |
| Y03 | F   | 6.5        | 0        | 221         | 119         | guarded          | 0                  | moderate    | 1                   | 0           | 0         | 0                   | 0      | 91.16               | 2.19            |
| Y07 | F   | 5          | 0        | 199         | 105         | guarded          | 0                  | normal      | 1                   | 0           | 0         | 0                   | 1      | 133.03              | 3.56            |
| Y08 | M   | 13         |          | 274         | 202         | 1                 | 0                  | 0           | 0                   | 0           | 0         | 0                   | 0      | 5.5*                | 0.4             |
| Y09 | F   | 22         | 0        | 241         | 148         | fair             | 0                  | moderate    | 0                   | 0           | 1         | 0                   | 0      | 37.99               | 0.89            |
| Y15 | F   | 3.75       | 0        | 198         | 88          | guarded          | 0                  | normal      | 0                   | 0           | 0         | 1                   | 0      | 181.18              | 5.38            |
| Y17 | F   | 5          | 0        | 209         | 92          | guarded          | 0                  | mild        | 1                   | 0           | 0         | 0                   | 0      | 5.5*                | 1.96            |
| Y19 | F   | 6          | 0        | 227         | 117         | good             | 0                  | normal      | 0                   | 0           | 0         | 0                   | 0      | 132.09              | 2.84            |
| Y20 | M   | 21         |          | 267         | 240         | fair             | 0                  | mild        | 0                   | 0           | 0         | 0                   | 0      | 5.5*                | 0.45            |
| Y21 | F   | 16         | 1        | 234         | 158         | poor             | severe             | 0           | 1                   | 0           | 0         | 0                   | 0      | 25.69               | 1.22            |
| Y22 | M   | 12         |          | 234         | 150         | fair             | 0                  | normal      | 1                   | 1           | 1         | 1                   | 0      | 38.93               | 1.37            |
| Y31 | F   | 1          | 239      | 175         |             | poor             | 0                  | moderate    | 1                   | 1           | 1         | 1                   | 0      | 5.5*                | 1.78            |
| Y33 | F   | 1          | 228      | 156         |             | guarded          | 0                  | moderate    | 0                   | 0           | 0         | 0                   | 1      | 5.5*                | 0.62            |
| Y39 | F   | 1          | 242      |             |             | guarded          | moderate          | 1           | 0                   | 1           | 0         | 0                   | 0      | 5.5*                | 0.34            |
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