



Sarasota Bay/Little Sarasota Bay Bottlenose Dolphin Abundance Estimates: 2015

**Prepared for National Marine Fisheries Service Northern Gulf of Mexico Bay, Sound,
and Estuary Bottlenose Dolphin Stock Blocks B20 and B35, Combined**

Prepared by:

Reny B. Tyson and Randall S. Wells

Chicago Zoological Society's Sarasota Dolphin Research Program

c/o Mote Marine Laboratory, 1600 Ken Thompson Parkway, Sarasota, FL 34236

rtyson@mote.org and rwells@mote.org

June 2016

Sarasota Bay/Little Sarasota Bay Bottlenose Dolphin Abundance Estimates: 2015
Prepared for National Marine Fisheries Service Northern Gulf of Mexico Bay, Sound, and Estuary
Bottlenose Dolphin Stock Blocks B20 and B35, Combined

Prepared by:

Reny B. Tyson and Randall S. Wells

Chicago Zoological Society's Sarasota Dolphin Research Program
c/o Mote Marine Laboratory, 1600 Ken Thompson Parkway, Sarasota, FL 34236
rtyson@mote.org and rwells@mote.org

Background

The common bottlenose dolphins (*Tursiops truncatus*) inhabiting the bay, sound, and estuary waters of the central west coast of Florida, near Sarasota, have been studied by the Sarasota Dolphin Research Program since 1970 (Irvine et al. 1981, Wells 2009, 2014). Multi-decadal, year-round residency has been well-documented for the Sarasota dolphins, with as many as five concurrent generations, including individuals up to 66 years of age (Wells et al. 1987, Wells 2014). Most of the resident dolphins are individually distinctive, from natural markings, tag scars, or from freeze-brands applied during health assessment studies (Wells 2009), facilitating abundance estimations from direct censuses (Wells 2009) or mark-recapture analyses (Irvine et al. 1981, Wells and Scott 1990). With the recent standardization of capture-mark-recapture approaches for bottlenose dolphin abundance estimation, we have developed a system for performing comparable analyses for Sarasota Bay dolphins, to be able to more easily and consistently provide abundance estimates for NMFS Stock Assessment Reports. A description of this approach, as well as the resulting abundance estimate, are presented below. It should be noted that this abundance estimate is specific to the geographic regions conforming to the NMFS stock that includes dolphins using Sarasota Bay and Little Sarasota Bay on a regular basis in 2015 (combined blocks B20 and B35). This estimate is not necessarily representative of estimates of numbers of animals comprising the Sarasota dolphin community, a unit that is described by social, behavioral, and genetic factors in addition to geography (Wells et al. 1987, Wells 2014).

Data Collection

Since 1992, standardized photographic-identification (photo-ID) capture-mark-recapture (CMR) surveys have been conducted each month in and around Sarasota Bay, Florida. The primary study area includes the waters identified by Waring et al. (2012) as Northern Gulf of Mexico Bay, Sound and Estuary Bottlenose Dolphin Stock Blocks 20 and 35 (Figure 1, Appendix). Surveys were conducted from 6-7 m, outboard-powered, center-console research vessels that traveled at the minimum speed allowable to maintain a plane during good sighting conditions (i.e., 10 to 14 knots; Beaufort Sea State ≤ 3) (Rosel et al. 2011). Three to five researchers were onboard each vessel including at least 1 photographer, 1 data recorder, and a boat driver. When a group of dolphins was sighted, the boat slowly approached the animals and recorded their GPS position, along with other environmental and biological data. A Nikon DSLR camera with 70 to 300 mm lens was used to take digital photographs of the dorsal fin and other distinguishing features (e.g., peduncle) of every dolphin in the group. If the group was too large, an attempt to obtain photographs of as many of the animals present, marked or unmarked, was made (Rosel et al. 2011).

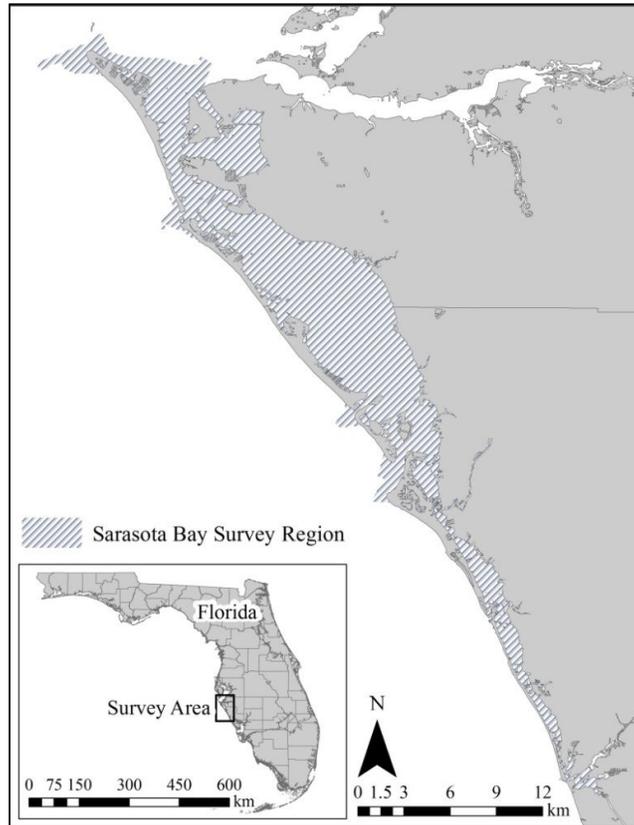


Figure 1. Sarasota survey study area showing regions included in abundance estimates (shaded).

Three or four times each year, efforts are made to survey the entire study area in one day by using three boats, and to repeat this two more times within as short a period of time as possible, depending largely on weather. These synoptic surveys are the equivalent of three or four primary periods each year, each containing three secondary periods (Rosel et al. 2011). In 2015 synoptic surveys were completed on March 2, 3, and 6; May 6, 7, and 8; August 5, 6, and 11; and November 3, 4, and 5.

Photo-ID processing and analyses followed methods outlined by Urian et al. (1999, 2013) and Rosel et al. (2011). Dorsal-fin images were cropped (ACDSee Pro 6.0™) and graded independently for photographic quality and overall distinctiveness of the fin. To minimize subjectivity and the possibility of making incorrect matches or missing matches altogether, poor-quality images (e.g., out of focus, not of suitable contrast, including only a partial fin, a fin that is not perpendicular, or a fin that is too distant) of poorly marked dolphins (i.e., low distinctiveness, not distinct) were not used in the analysis (Stevick et al. 2001, Friday et al. 2008, Rosel et al. 2011, Urian et al. 2013). To minimize false positive matches, as many distinctive features as possible were used to confirm matches. A second investigator verified every potential match of an individual dolphin from one encounter to another and double-checked the entire catalog for potential matches or mismatches that may have been overlooked. Images of newly identified distinctive dolphins were added to the catalog of individuals in the region and information regarding their sighting history (e.g., time, location, identification code) was stored.

Sighting histories of adults with average or very distinctive fins with a good to excellent photograph sampled within the ‘core’ Sarasota areas during the CMR surveys (N = 108) were isolated for use in the CMR analysis (Figure 2). Note: calves and neonates were excluded because they may exhibit heterogeneity in capture probabilities due to close associations with their mothers (N = 26) (Rosel et al. 2011).

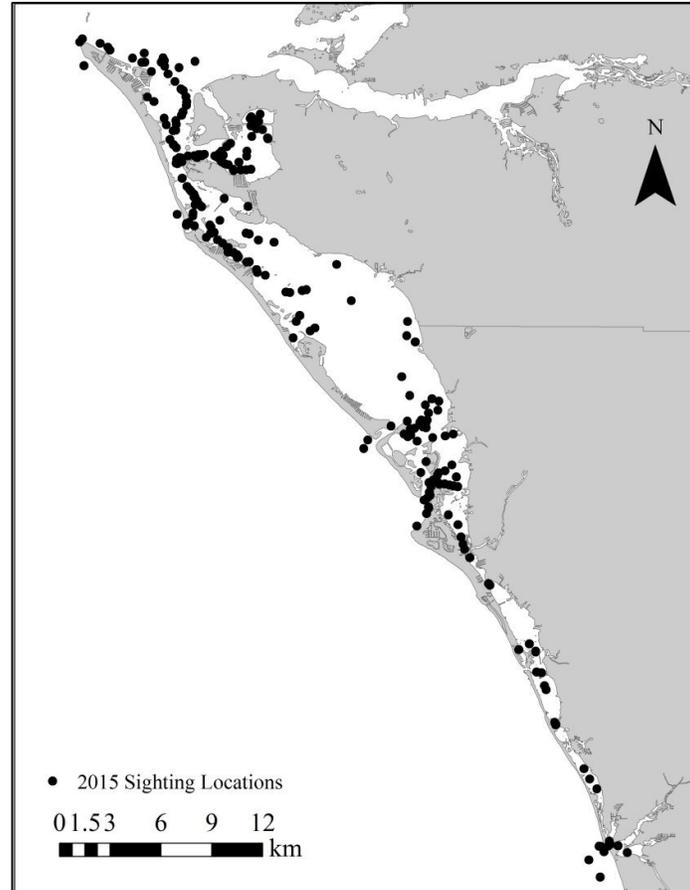


Figure 2: Sighting locations of dolphins used for the capture-mark-recapture analysis.

Abundance Estimates

Robust design CMR models assuming Markovian, random, and no emigration between sampling and constant or time-varying survival and recapture with or without heterogeneous capture probabilities (Pollock 1982, Kendall et al. 1997) were used to estimate the abundance of distinctive adult bottlenose dolphins using RMark (Table 1, Appendix; Laake 2013, R Core Team 2013). The model that assumed no emigration between sampling occasions, constant survival, and time-varying recapture probabilities had the lowest AICc value and the highest weight of all models examined (Table 1, Table 2, Figure 3), and therefore is assumed to be the most appropriate model for estimating dolphin abundance in Sarasota Bay, Florida, in 2015.

Table 1: Results of robust design CMR models run in RMark (Laake 2013, R Core Team 2013). Models included those assuming Markovian, random, and no emigration (no movement) with constant (.) or time-varying (t) survival (S), and constant, time-varying, heterogeneous (h), or time varying and heterogeneous (th) recapture (p) (Appendix).

Model	npar	AICc	DeltaAICc	Weight	Deviance
S(.)p(t) - No Movement	9	-248.53	0.00	0.79	126.62
S(t)p(t) - No Movement	11	-245.32	3.22	0.16	125.52
S(.)p(t) - Random	12	-242.04	6.50	0.03	126.62
S(.)p(th) - No Movement	16	-239.34	9.20	0.01	120.44
S(t)p(t) - Random	14	-238.75	9.79	0.01	125.50
S(.)p(t) - Markovian	14	-238.73	9.81	0.01	125.52
S(t)p(th) - No Movement	18	-235.89	12.65	0.00	119.34
S(.)p(th) - Random	18	-234.79	13.74	0.00	120.44
S(t)p(t) - Markovian	16	-234.27	14.26	0.00	125.50
S(.)p(.) - Random	9	-231.95	16.59	0.00	143.21
S(.)p(th) - Markovian	20	-231.30	17.24	0.00	119.31
S(t)p(th) - Random	20	-231.30	17.24	0.00	119.31
S(.)p(h) - Random	11	-230.69	17.84	0.00	140.15
S(.)p(.) - Markovian	11	-230.13	18.40	0.00	140.71
S(t)p(.) - Random	11	-230.05	18.48	0.00	140.79
S(.)p(h) - Markovian	13	-229.27	19.26	0.00	137.19
S(t)p(h) - Random	13	-229.27	19.26	0.00	137.19
S(t)p(.) - No Movement	8	-226.62	21.92	0.00	150.67
S(t)p(th) - Markovian	22	-226.59	21.95	0.00	119.34
S(t)p(.) - Markovian	13	-225.76	22.77	0.00	140.70
S(t)p(h) - No Movement	11	-225.57	22.97	0.00	145.27
S(t)p(h) - Markovian	15	-225.04	23.49	0.00	136.98
S(.)p(.) - No Movement	6	-216.74	31.80	0.00	164.78
S(.)p(h) - No Movement	9	-216.47	32.07	0.00	158.69

If we assume that the probability of capture is independent of whether or not an individual has long-lasting marks (Hammond 1990, Williams et al. 1993), we can expand our estimate to include calves and the non-distinctive population (Table 2, Figure 3). We achieved this by calculating the ratio of distinctive adults to total dolphins encountered during each survey day (Θ) from all photos that met or exceeded photo quality thresholds (Tyson et al. 2011). In this study, the variety of temporary skin markings (e.g., tooth rakes, discoloration) and fin shapes made it possible to distinguish non-distinctive dolphins within a particular sighting. Therefore, Θ was based on the actual number of distinctive adults versus non-distinctive adults and calves encountered during our study (Wilson et al. 1999). After summing the number of distinctive and total dolphins encountered the estimate was derived as:

$$N = \frac{\check{N}}{\Theta}$$

where N is the estimated total population size, \check{N} is the mark-recapture estimate of the distinctive adults, and Θ is the proportion of distinctive dolphins in the population (Williams

et al. 1993, Wilson et al. 1999). Standard errors of N were calculated using the delta method (Seber 1982, Williams et al. 2002):

$$SE(N) = \sqrt{N^2 \left(\frac{SE(\check{N})^2}{\check{N}^2} + \frac{1 - \theta}{n\theta} \right)}$$

where n is the total number of dolphins from which θ was estimated. Log-normal 95% confidence intervals (CI) were calculated with upper (CI_u) and lower (CI_l) bounds for each estimate following Burnham et al. (1987):

$$CI_u = \frac{N}{C} \text{ and } CI_l = N \times C$$

where $C = \exp \left(1.96 \sqrt{\ln \left(1 + \left(\frac{SE(N)}{N} \right)^2 \right)} \right)$

The coefficient of variation (CV) of N was calculated by dividing the SE of N by N (Pollock et al. 1990).

The estimated abundance of dolphins in Sarasota Bay during each primary period in 2015 is shown in Figure 3. The mean (median) \pm se estimated abundance over all primary periods is: **157.53 (144.46) \pm 43.05 (CV = 0.27)**.

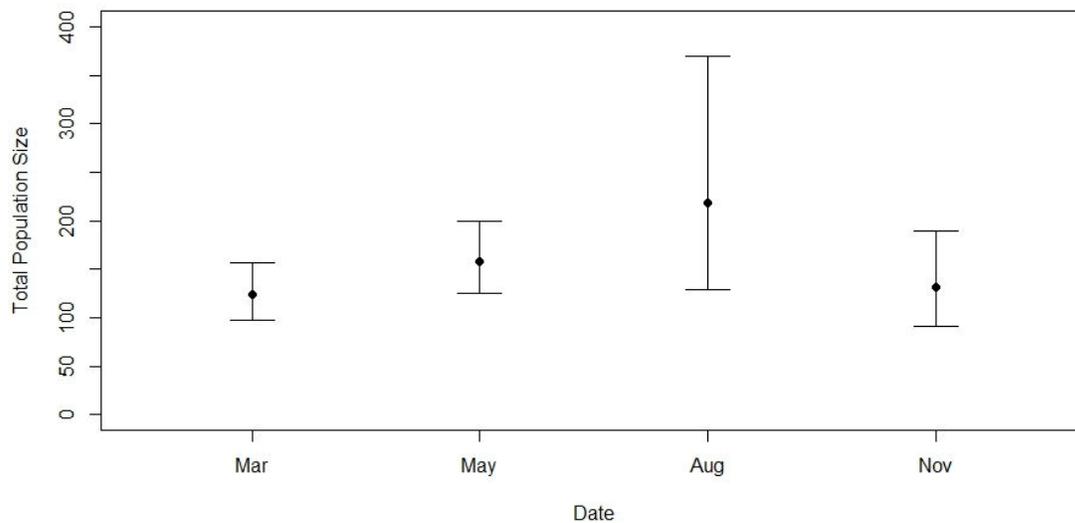


Figure 3: Estimated abundance of bottlenose dolphins in Sarasota Bay, Florida, for each primary survey period in 2015.

Table 2: Results of the $S(\cdot)p(t)$ – no emigration model for estimating abundance of bottlenose dolphins in Sarasota Bay, Florida, in 2015 (Table 1). \check{N} represents the abundance of distinctive adults, while N represents the abundance of all dolphins in Sarasota Bay. Θ represents the ratio of distinctive adults to total dolphins sampled. Estimates of each parameter can be found in the Appendix.

Month	Primary Sampling Occasion	\check{N}	Standard Error (\check{N})	Lower Confidence Limit (\check{N})	Upper Confidence Limit (\check{N})	Θ	N	Standard Error (N)	Lower Confidence Interval (N)	Upper Confidence Interval (N)	CV
March	1	93.79	10.57	79.52	123.13	0.76	123.04	15.20	96.67	156.61	0.12
May	2	116.83	12.70	98.13	149.46	0.74	157.79	18.99	124.73	199.60	0.12
August	3	139.94	35.58	89.67	234.81	0.64	218.15	59.81	128.70	369.77	0.27
November	4	97.94	17.13	74.13	144.30	0.75	131.13	24.50	91.21	188.53	0.19

Acknowledgements

We wish to thank Trent McDonald for reviewing earlier drafts of this document and providing helpful feedback regarding model comparisons.

Literature Cited

- Burnham, K. P., D. R. Anderson, G. C. White, C. Brownie and K. H. Pollock. 1987. Design and analysis methods for fish survival experiments based on release-recapture. Bethesda, Maryland, USA. 437pp.
- Friday, N. A., T. D. Smith, P. T. Stevick, J. Allen and T. Fernald. 2008. Balancing bias and precision in capture-recapture estimates of abundance. *Marine Mammal Science* 24:355-374.
- Hammond, P. S. 1990. Capturing whales on film: estimating cetacean populations using capture-recapture techniques. *Mammal Review* 20:17-22.
- Irvine, A. B., M. D. Scott, R. S. Wells and J. H. Kaufmann. 1981. Movements and activities of the Atlantic bottlenose dolphin, *Tursiops truncatus*, near Sarasota, Florida. *Fishery Bulletin U.S.* 79:671-688.
- Kendall, W. L., J. D. Nichols and J. E. Hines. 1997. Estimating temporary emigration using capture-recapture estimation of demographic parameters under the robust design. *Ecology* 78:563-578.
- Laake, J. L. 2013. RMark: An R Interface for Analysis of Capture-Recapture Data with MARK. AFSC Processed Rep 2013-01. Alaska Fisheries Science Center, NOAA, National Marine Fisheries Service, 7600 Sand Point Way NE, Seattle, WA 98115:25.
- Pollock, K. H. 1982. A capture-recapture design robust to unequal probability of capture. *Journal of Wildlife Management* 46:757-760.
- Pollock, K. H., J. D. Nichols, C. Brownie, J. E. Hines. 1990. Statistical inference for capture-recapture experiments. *Wildlife Monographs* 62: 1-135.
- R Core Team. 2013. R: a language and environment for statistical computing. R Foundation for Statistical Computing. Vienna, Austria.
- Rosel, P. E., K. D. Mullin, L. Garrison, L. Schwacke, J. Adams, B. Balmer, P. Conn, M. J. Conroy, T. Eguchi, A. Gorgone, A. Hohn, M. Mazzoil, C. Schwartz, C. Sinclair, T. Speakman, K. Urian, N. Vollmer, P. Wade, R. Wells and E. Zolman. 2011. Photo-identification Capture-Mark-Recapture Techniques for Estimating Abundance of Bay, Sound and Estuary Populations of Bottlenose Dolphins along the U.S. East Coast and Gulf of Mexico: A Workshop Report. NOAA Technical Memorandum NMFS-SEFSC-621. 30pp.
- Seber, G. A. F. 1982. The estimation of animal abundance, and related parameters. 1304 MacMillan, New York, USA. 654pp.
- Stevick, P. T., P. J. Palsboll, T. D. Smith, M. V. Bravington and P. S. Hammond. 2001. Errors in identification using natural markings: rates, sources, and effects on capture-recapture estimates of abundance. *Canadian Journal of Fisheries and Aquatic Science* 58:1861-1870.
- Tyson, R. B., S. M. Nowacek and D. P. Nowacek. 2011. Community structure and abundance of bottlenose dolphins *Tursiops truncatus* in coastal waters of the northeast Gulf of Mexico. *Marine Ecology Progress Series* 438:253-265.
- Urian, K. W., A. A. Hohn and L. J. Hansen. 1999. Status of the photo-identification catalog of coastal bottlenose dolphins of the western north Atlantic: report of a workshop of catalog contributors. NOAA Administrative Report NMFS-SEFSC-425, 22pp.
- Urian, K., A. Read, A. Gorgone, B. Balmer, R. Wells, P. Berggren, J. Durban, T. Eguchi, W. Rayment and P. Hammond. 2014. Recommendations for photo-identification methods

- used in capture-recapture models with cetaceans. *Marine Mammal Science*. DOI: 10.1111/mms.12141
- Waring, G. T., E. Josephson, K. Maze-Foley and P. E. Rosel (eds). 2012. U.S. Atlantic and Gulf of Mexico Marine Mammal Stock Assessments – 2012. Volume 1. National Marine Fisheries Service, Woods Hole, MA. <http://www.nefsc.noaa.gov/nefsc/publications/>.
- Wells, R. S. 2009. Learning from nature: Bottlenose dolphin care and husbandry. *Zoo Biology* 28:1-17.
- Wells, R. S. 2014. Social structure and life history of common bottlenose dolphins near Sarasota Bay, Florida: Insights from four decades and five generations. Pp. 149-172 In: J. Yamagiwa and L. Karczmarski (eds.), *Primates and Cetaceans: Field Research and Conservation of Complex Mammalian Societies*, Primatology Monographs, Tokyo, Japan: Springer. DOI 10.1007/978-4-431-54523-1_8.
- Wells, R. S., M. D. Scott and A. B. Irvine. 1987. The social structure of free-ranging bottlenose dolphins. Pp. 247-305 In: Genoways, H. (ed.), *Current Mammalogy*, Vol. 1. New York: Plenum Press.
- Wells, R. S. and M. D. Scott. 1990. Estimating bottlenose dolphin population parameters from individual identification and capture-release techniques. Pp. 407-415 In: P. S. Hammond, S. A. Mizroch and G. P. Donovan (eds.) *Individual Recognition of Cetaceans: Use of Photo-Identification and Other Techniques to Estimate Population Parameters*. Report of the International Whaling Comm., Special Issue 12, Cambridge, U.K. 440pp.
- Williams, J. A., S. M. Dawson and E. Slooten. 1993. The abundance and distribution of bottlenosed dolphins (*Tursiops truncatus*) in Doubtful Sound, New Zealand. *Canadian Journal of Zoology* 71:2080-2088.
- Williams, B. K., J. D. Nichols and M. J. Conroy. 2002. *Analysis and management of 1541 animal populations*. Academic Press, San Diego, California, USA.
- Wilson, B., P. S. Hammond and P. M. Thompson. 1999. Estimating size and assessing trends in coastal bottlenose dolphin population. *Ecological Applications* 9:288-300.

Appendix - SDRP Abundance Estimation

Reny Tyson, rtyson@mote.org

March 25, 2016

This document outlines the methods used to derive abundance estimates for SDRP in 2015 using the robust design capture-mark-recapture models within Mark using the RMark Package (Laake 2013).

Data Setup

For this analysis we will only include data collected from CMR Synoptic Surveys in "Core" Sarasota areas.

First we read in the sighting records of every individual.

```
sdrp <- read.csv(2015_SDRP_synoptics.csv',header=T,stringsAsFactors=F)
```

Next, we will exclude sightings of individuals if they were not within the 'Core' Sarasota Bay areas (waters identified by Waring et al. (2012) as Northern Gulf of Mexico Bay, Sound and Estuary Bottlenose Dolphin Stock Blocks 20 and 35).

```
# Define core Sarasota Bay areas
core.areas <- c('AMS', 'UPS', 'PSB', 'COR', 'LBP', 'ICW', 'SKF', 'BWS', 'WSB', 'BCS',
', 'NSB', 'ESS', 'ESB', 'SSB', 'LBS', 'OKC', 'NPS', 'RNG', 'BSP', 'PKI', 'RBC', 'LSB',
', 'BBB', 'VIC', 'VIN', 'BLK', 'BPB', 'BPN', 'KRB', 'LPN', 'LPS', 'NPN', 'SNP')
# Note: these are codes used by the SDRP to identify local areas in the gr
eater Sarasota Bay region.

# Identify if an animal is a core animal
sdrp$core <- rep(0, nrow(sdrp)) # Create an empty row filled with zeros
for (i in 1:nrow(sdrp)){
  for (j in 1:length(core.areas)){
    if(sdrp$Subarea[i] == core.areas[j]){
      sdrp$core[i] <- 1 # If the animal was seen in a core area, identify
it with a 1 in the core column
    }
  }
}

# Keep only the 'Core' SDRP animals
sdrp <- sdrp[sdrp$core == 1,]
```

We only want to include records of animals with good to excellent quality photographs (Q1 and Q2). SDRP follows methods outlined by Urian et al. (1999, 2014) to grade photographic quality:

- Partial - Fins that are fully visible (1); fins that are partially obscured (8)
- Contrast - Images of suitable contrast (1); images with excessive or minimal contrast (3)
- Angle - Fins are perpendicular in image (1); of a slight angle (2); or of oblique angles (8)
- Focus - Images of excellent focus (2); moderate focus (4); or poor focus (9)
- Distance - Subtle features of fin can be detected in image (1); very distant photo (5)

Individual scores were summed to obtain an overall quality score (QS). Scores for each category, apart from contrast, and the proportion of fin in the frame, were weighted in a way that inadequate quality in one category alone could not push the photograph over the poor-quality threshold:

Q1 (Excellent Quality) = $QS \leq 7$

Q2 (Good Quality) = $QS \leq 11$

Q3 (Poor) = $QS > 11$

```
quality <- sdrp[which(sdrp$Quality == 'Q1' | sdrp$Quality == 'Q2'),]
```

We also only want to include records of animals that have fins of average or high distinctiveness (D1 and D2).

```
QD <- quality[which(quality$Distinctiveness == 'D1' |
quality$Distinctiveness == 'D2'),]
```

We need to remove the calves because they can introduce heterogeneity in capture probabilities by being closely associated with their mothers (i.e., only keep adults).

```
QD.adults <- QD[which(QD$only.adult == 1),]
```

We can now create a sighting history index of all average to highly distinctive adults with good to excellent quality photographs.

```
sight.hist <- table(QD.adults$Code,QD.adults$date)
sight.hist[sight.hist > 1] <- 1 #if animal is seen several times on one da
y, correct so that it is only logged once per day (i.e., no re-sights).
```

Convert sighting histories into an .inp file for use in Mark/RMark

```
inp <- paste(sight.hist[,1],sight.hist[,2],sight.hist[,3],sight.hist[,4],s
ight.hist[,5],sight.hist[,6],sight.hist[,7],sight.hist[,8],sight.hist[,9],
sight.hist[,10],sight.hist[,11],sight.hist[,12]," 1;",sep="")
write.table(inp,paste("Sighting histories.inp"),row.names=F,col.names=F,qu
ote=F)
```

Capture-Mark-Recapture Analysis

We will now use Rmark to derive abundance estimates using the robust design CMR models. This package runs MARK in the background, which must be installed on your computer.

```
# Load appropriate libraries
library(RMark)
```

Read in the .inp file you created of sighting histories above:

```
dolphins = convert.inp("Sighting histories.inp", group.df = NULL, covariates = NULL, use.comments = FALSE)
```

Set up your data for the robust design models:

```
#set up for 12 occasions, 4 primary and secondary of 3 occasions each
time.intervals=c(0,0,1,0,0,1,0,0,1,0,0)
```

```
#Need to set one data set for typical robust models and one for robust with heterogeneity models
rd = process.data(data=dolphins, model = "Robust", time.intervals=time.intervals) #Robust design with Closed Population Estimation
rdhet = process.data(data=dolphins, model = "RDHet", time.intervals=time.intervals) #robust design with Heterogeneity Estimator
```

Set up models to run:

```
run.robust=function()
{
  ##-Define parameter models-----##

  # Survival:
  # Apparent survival is constant:
  S.constant = list(formula=~1)

  # or varies by time:
  S.time=list(formula=~time)

  # Recapture
  # Recapture is constant
  # p=c due to use of "share=TRUE"
  p.constant = list(formula=~1,share=TRUE) #Mo

  # Recapture varies by primary session but not among secondaries within primary
  p.time=list(formula=~session,share=TRUE) #Mt

  # Recapture is heterogeneous :
  pi.dot=list(formula=~1)
  p.mixture=list(formula=~mixture,share=TRUE) #Mh

  #or both:
  p.mixture.time = list(formula=~session:mixture,share=TRUE) #Mth

  # Time-varying temporary emigration can be
  # Markovian:
  GammaDoublePrime.markov=list(formula=~time)
  GammaPrime.time=list(formula=~time)

  # Random:
  GammaDoublePrime.random=list(formula=~time,share=TRUE)

  # Or not present:
  GammaDoublePrime.zeroTE=list(formula=~1, fixed=0, share=TRUE)

  ##-Set up Markovian Emigration Models-----##

  # Survival and recapture are constant - S(.)p(.)
  mod_markov_S.P. = mark(data=rd, design.parameters=
```

```

        list(GammaDoublePrime=list(time.bins=c(1,2,3,4)),
              GammaPrime=list(time.bins=c(2,3,4))),
        right=FALSE,
        model.parameters=list(S=S.constant,
                              p=p.constant,
                              GammaDoublePrime=GammaDoublePrim
e.markov,
                              GammaPrime=GammaPrime.time))

# Survival is constant, recapture varies by time - S(.)p(t)
mod_markov_S.Pt = mark(data=rd, design.parameters=
                      list(GammaDoublePrime=list(time.bins=c(1,2,3)),
                            GammaPrime=list(time.bins=c(2,3,4))),
                      right=FALSE,
                      model.parameters=list(S=S.constant,
                                              p=p.time,
                                              GammaDoublePrime=GammaDoublePrim
e.markov,
                                              GammaPrime=GammaPrime.time))

# Survival is constant, recapture is heterogeneous - S(.)p(h)
mod_markov_S.Ph = mark(data=rdhet, design.parameters=
                      list(GammaDoublePrime=list(time.bins=c(1,2,3)),
                            GammaPrime=list(time.bins=c(2,3,4))),
                      right=FALSE,
                      model.parameters=list(S=S.constant,
                                              p=p.mixture,
                                              pi=pi.dot,
                                              GammaDoublePrime=GammaDoublePrim
e.markov,
                                              GammaPrime=GammaPrime.time))

# Survival is constant, recapture is heterogeneous and varies by time - S
(.)p(th)
mod_markov_S.Pth = mark(data=rdhet, design.parameters=
                      list(GammaDoublePrime=list(time.bins=c(1,2,3,4)),
                            GammaPrime=list(time.bins=c(2,3,4))),
                      right=FALSE,
                      model.parameters=list(S=S.constant,
                                              p=p.mixture.time,
                                              pi=pi.dot,
                                              GammaDoublePrime=GammaDoublePrim
e.markov,
                                              GammaPrime=GammaPrime.time))

# Survival varies by time, recapture is constant - S(t)p(.)
mod_markov_StP. = mark(data=rd, design.parameters=
                      list(GammaDoublePrime=list(time.bins=c(1,2,3,4)),
                            GammaPrime=list(time.bins=c(2,3,4))),
                      right=FALSE,
                      model.parameters=list(S=S.time,
                                              p=p.constant,
                                              GammaDoublePrime=GammaDoublePrim

```

```

e.markov,
                                GammaPrime=GammaPrime.time))

# Survival varies by time, recapture varies by time - S(t)p(t)
mod_markov_StPt = mark(data=rd, design.parameters=
  list(GammaDoublePrime=list(time.bins=c(1,2,3,4)),
        GammaPrime=list(time.bins=c(2,3,4))),
  right=FALSE,
  model.parameters=list(S=S.time,
                        p=p.time,
                        GammaDoublePrime=GammaDoublePrim
e.markov,
                                GammaPrime=GammaPrime.time))

# Survival varies by time, recapture is heterogeneous - S(t)p(h)
mod_markov_StPh = mark(data=rdhet, design.parameters=
  list(GammaDoublePrime=list(time.bins=c(1,2,3,4)),
        GammaPrime=list(time.bins=c(2,3,4))),
  right=FALSE,
  model.parameters=list(S=S.time,
                        p=p.mixture,
                        pi=pi.dot,
                        GammaDoublePrime=GammaDoublePrim
e.markov,
                                GammaPrime=GammaPrime.time))

# Survival varies by time, recapture is heterogeneous and varies by time -
S(.)p(th)
mod_markov_StPth = mark(data=rdhet, design.parameters=
  list(GammaDoublePrime=list(time.bins=c(1,2,3,4)),
        GammaPrime=list(time.bins=c(2,3,4))),
  right=FALSE,
  model.parameters=list(S=S.time,
                        p=p.mixture.time,
                        pi=pi.dot,
                        GammaDoublePrime=GammaDoublePri
me.markov,
                                GammaPrime=GammaPrime.time))

##-Set up Random Emmigration Models-----##

# Survival and recapture are constant - S(.)p(.)
mod_random_S.P.= mark(data=rd, design.parameters=
  list(GammaDoublePrime=list(time.bins=c(1,2,3,4)),
        GammaPrime=list(time.bins=c(2,3,4))),
  right=FALSE,
  model.parameters=list(S=S.constant,
                        p=p.constant,
                        GammaDoublePrime=GammaDoublePrime
.random))

```

```

# Survival is constant, recapture varies by time - S(.)p(t)
mod_random_S.Pt = mark(data=rd, design.parameters=
  list(GammaDoublePrime=list(time.bins=c(1,2,3,4)),
    GammaPrime=list(time.bins=c(2,3,4))),
  right=FALSE,
  model.parameters=list(S=S.constant,
    p=p.time,
    GammaDoublePrime=GammaDoublePrim
e.random))

# Survival is constant, recapture is heterogeneous - S(.)p(h)
mod_random_S.Ph = mark(data=rdhet, design.parameters=
  list(GammaDoublePrime=list(time.bins=c(1,2,3,4)),
    GammaPrime=list(time.bins=c(2,3,4))),
  right=FALSE,
  model.parameters=list(S=S.constant,
    p=p.mixture,
    pi=pi.dot,
    GammaDoublePrime=GammaDoublePrim
e.random))

# Survival is constant, recapture is heterogeneous and varies by time - S
(.)p(th)
mod_random_S.Pth = mark(data=rdhet, design.parameters=
  list(GammaDoublePrime=list(time.bins=c(1,2,3,4)),
    GammaPrime=list(time.bins=c(2,3,4))),
  right=FALSE,
  model.parameters=list(S=S.constant,
    p=p.mixture.time,
    pi=pi.dot,
    GammaDoublePrime=GammaDoublePri
me.random))

# Survival varies by time, recapture is constant - S(t)p(.)
mod_random_StP.= mark(data=rd, design.parameters=
  list(GammaDoublePrime=list(time.bins=c(
1,2,3,4)),
    GammaPrime=list(time.bins=c(2,3,4)
)),
  right=FALSE,
  model.parameters=list(S=S.time,
    p=p.constant,
    GammaDoublePrime=Ga
mmaDoublePrime.random))

# Survival varies by time, recapture varies by time - S(t)p(t)
mod_random_StPt = mark(data=rd, design.parameters=
  list(GammaDoublePrime=list(time.bins=c(1,2,3,4)),
    GammaPrime=list(time.bins=c(2,3,4))),
  right=FALSE,
  model.parameters=list(S=S.time,
    p=p.time,
    GammaDoublePrime=GammaDoublePrim

```

```

e.random))

# Survival varies by time, recapture is heterogeneous - S(t)p(h)
mod_random_StPh = mark(data=rdhet, design.parameters=
  list(GammaDoublePrime=list(time.bins=c(1,2,3,4)),
    GammaPrime=list(time.bins=c(2,3,4))),
  right=FALSE,
  model.parameters=list(S=S.time,
    p=p.mixture,
    pi=pi.dot,
    GammaDoublePrime=GammaDoublePrim
e.random))

# Survival varies by time, recapture is heterogeneous and varies by time -
S(.)p(th)
mod_random_StPth = mark(data=rdhet, design.parameters=
  list(GammaDoublePrime=list(time.bins=c(1,2,3,4)),
    GammaPrime=list(time.bins=c(2,3,4))),
  right=FALSE,
  model.parameters=list(S=S.time,
    p=p.mixture.time,
    pi=pi.dot,
    GammaDoublePrime=GammaDoublePri
me.random))

##-Set up No Emigration Models-----##

# Survival and recapture are constant - S(.)p(.)
mod_ZeroTE_S.P.=mark(data=rd, model.parameters=list(S=S.constant,
  p=p.constant,
  GammaDoublePrime=Gam
maDoublePrime.zeroTE))

# Survival is constant, recapture varies by time - S(.)p(t)
mod_ZeroTE_S.Pt=mark(data=rd, model.parameters=list(S=S.constant,
  p=p.time,
  GammaDoublePrime=Gam
maDoublePrime.zeroTE))

# Survival is constant, recapture is heterogeneous - S(.)p(h)
mod_ZeroTE_S.Ph=mark(data=rdhet, model.parameters=list(S=S.constant,
  p=p.mixture,
  pi=pi.dot,
  GammaDoublePrime=
GammaDoublePrime.zeroTE))

# Survival is constant, recapture is heterogeneous and varies by time - S
(.)p(th)
mod_ZeroTE_S.Pth=mark(data=rdhet, model.parameters=list(S=S.constant,
  p=p.mixture.time,
  pi=pi.dot,
  GammaDoublePrime=
GammaDoublePrime.zeroTE))

```

```

# Survival varies by time, recapture is constant - S(t)p(.)
mod_ZeroTE_StP.=mark(data=rd, model.parameters=list(S=S.time,
                                                    p=p.constant,
                                                    GammaDoublePrime=Gam
maDoublePrime.zeroTE))

# Survival varies by time, recapture varies by time - S(t)p(t)
mod_ZeroTE_StPt=mark(data=rd, model.parameters=list(S=S.time,
                                                    p=p.time,
                                                    GammaDoublePrime=Gam
maDoublePrime.zeroTE))

# Survival varies by time, recapture is heterogeneous - S(t)p(h)
mod_ZeroTE_StPh=mark(data=rdhet, model.parameters=list(S=S.time,
                                                       p=p.mixture,
                                                       pi=pi.dot,
                                                       GammaDoublePrime=G
ammaDoublePrime.zeroTE))

# Survival varies by time, recapture is heterogeneous and varies by time
- S(.)p(th)
mod_ZeroTE_StPth=mark(data=rdhet, model.parameters=list(S=S.time,
                                                         p=p.mixture.time
,
                                                         pi=pi.dot,
                                                         GammaDoublePrime
=GammaDoublePrime.zeroTE))

# Return model table and list of models
return(collect.models())
}

```

Run the CMR models:

```
robust.results = run.robust()
```

Examine the model output:

```
options(width = 160)
```

```
robust.results
```

##	npar	AICc	DeltaAICc	weight	Deviance
## 19	9	-248.5346	0.000000	7.880921e-01	126.6232
## 23	11	-245.3188	3.215849	1.578571e-01	125.5242
## 11	12	-242.0384	6.496215	3.061553e-02	126.6232
## 20	16	-239.3357	9.198942	7.925964e-03	120.4364
## 15	14	-238.7482	9.786424	5.908566e-03	125.5018
## 3	14	-238.7258	9.808844	5.842701e-03	125.5242
## 24	18	-235.8889	12.645758	1.414443e-03	119.3374
## 12	18	-234.7899	13.744738	8.164789e-04	120.4364
## 7	16	-234.2703	14.264372	6.296626e-04	125.5018
## 9	9	-231.9487	16.585900	1.972398e-04	143.2091
## 4	20	-231.2961	17.238526	1.423241e-04	119.3150
## 16	20	-231.2961	17.238536	1.423234e-04	119.3150

```
## 10 11 -230.6931 17.841529 1.052781e-04 140.1499
## 1 11 -230.1342 18.400489 7.960888e-05 140.7089
## 13 11 -230.0528 18.481899 7.643347e-05 140.7903
## 2 13 -229.2725 19.262199 5.174204e-05 137.1916
## 14 13 -229.2725 19.262199 5.174204e-05 137.1916
## 21 8 -226.6185 21.916157 1.372600e-05 150.6732
## 8 22 -226.5875 21.947167 1.351482e-05 119.3374
## 5 13 -225.7615 22.773149 8.942325e-06 140.7026
## 22 11 -225.5696 22.965089 8.124025e-06 145.2735
## 6 15 -225.0402 23.494492 6.234661e-06 136.9793
## 17 6 -216.7366 31.798057 9.811075e-08 164.7763
## 18 9 -216.4665 32.068190 8.571523e-08 158.6914
```

```
names(robust.results)
```

```
## [1] "mod_markov_S.P." "mod_markov_S.Ph" "mod_markov_S.Pt"
## [4] "mod_markov_S.Pth" "mod_markov_StP." "mod_markov_StPh"
## [7] "mod_markov_StPt" "mod_markov_StPth" "mod_random_S.P."
## [10] "mod_random_S.Ph" "mod_random_S.Pt" "mod_random_S.Pth"
## [13] "mod_random_StP." "mod_random_StPh" "mod_random_StPt"
## [16] "mod_random_StPth" "mod_ZeroTE_S.P." "mod_ZeroTE_S.Ph"
## [19] "mod_ZeroTE_S.Pt" "mod_ZeroTE_S.Pth" "mod_ZeroTE_StP."
## [22] "mod_ZeroTE_StPh" "mod_ZeroTE_StPt" "mod_ZeroTE_StPth"
## [25] "model.table"
```

From these results it appears that the most appropriate model for the SDRP data is model #19 - S(.)p(t) No Movement. Let's examine this model:

```
# Best model with re-run
```

```
# Examine the Parameter Estimates
```

```
round(robust.results$mod_ZeroTE_S.Pt$results$real[,1:4],3)
```

```
##           estimate      se    lcl    ucl
## S g1 c1 a0 t1      0.872 0.053 0.727 0.945
## Gamma' g1 c1 a1 t2 0.500 0.000 0.500 0.500
## p g1 s1 t1        0.331 0.047 0.246 0.427
## p g1 s2 t1        0.277 0.032 0.219 0.344
## p g1 s3 t1        0.085 0.019 0.055 0.131
## p g1 s4 t1        0.205 0.037 0.142 0.287
## f0 g1 a0 s1 t0    27.794 10.574 13.521 57.134
## f0 g1 a0 s2 t0    43.835 12.698 25.129 76.463
## f0 g1 a0 s3 t0   106.944 35.578 56.673 201.810
## f0 g1 a0 s4 t0    48.935 17.134 25.128 95.300
## Gamma'' g1 c1 a0 t1 0.000 0.000 0.000 0.000
```

```
summary(robust.results$mod_ZeroTE_S.Pt)
```

```
## Output summary for Robust model
```

```
## Name : S(~1)Gamma' (~1)Gamma'()p(~session)c()f0(~session)
```

```
##
```

```
## Npar : 9
```

```
## -2lnL: -267.194
```

```
## AICc : -248.5346
```

```
##
```

```
## Beta
```

```
##           estimate      se    lcl    ucl
```

```

## S:(Intercept)      1.9165146  0.4773630  0.9808830  2.8521461
## GammaDoublePrime:(Intercept)  0.0000000  0.0000000  0.0000000  0.0000000
## p:(Intercept)     -0.7058660  0.2107485 -1.1189332 -0.2927988
## p:session2        -0.2532770  0.2646923 -0.7720739  0.2655200
## p:session3        -1.6651520  0.3214177 -2.2951307 -1.0351733
## p:session4        -0.6486825  0.3105198 -1.2573013 -0.0400637
## f0:(Intercept)    3.3248056  0.3804322  2.5791585  4.0704527
## f0:session2        0.4556196  0.4781690 -0.4815917  1.3928310
## f0:session3        1.3475029  0.5053747  0.3569686  2.3380373
## f0:session4        0.5656940  0.5170363 -0.4476971  1.5790852
##
##
## Real Parameter S
##
##      1      2      3
## 1 0.8717493 0.8717493 0.8717493
## 2      0.8717493 0.8717493
## 3      0.8717493
##
##
## Real Parameter GammaDoublePrime
##
##   1 2 3
## 1
## 2
## 3
##
##
## Real Parameter GammaPrime
##
##   2 3
## 1 0.5 0.5
## 2   0.5
##
##
## Real Parameter p
## Session:1
##      1      2      3
## 0.3305129 0.3305129 0.3305129
##
## Session:2
##      1      2      3
## 0.2770498 0.2770498 0.2770498
##
## Session:3
##      1      2      3
## 0.0854096 0.0854096 0.0854096
##
## Session:4
##      1      2      3
## 0.2051277 0.2051277 0.2051277
##
##
## Real Parameter c

```

```
## Session:1
##      2      3
## 0.3305129 0.3305129
##
## Session:2
##      2      3
## 0.2770498 0.2770498
##
## Session:3
##      2      3
## 0.0854096 0.0854096
##
## Session:4
##      2      3
## 0.2051277 0.2051277
##
##
## Real Parameter f0
## Session:1
##      0
## 27.79359
##
## Session:2
##      0
## 43.83468
##
## Session:3
##      0
## 106.9443
##
## Session:4
##      0
## 48.93533

#create object to hold derived estimates
best.mod <- robust.results$mod_ZeroTE_S.Pt$results$derived$`N Population Si
ze`
```

In order to expand these estimates to include calves and non-distinctive animals, we must calculate theta (the ratio of distinctive adults to total dolphins).

```
# Calculate the total number of adults that passed quality/distinctiveness
criteria.
```

```
x <- table(QD.adults$Code,QD.adults$date)
```

```
# We have a few animals that were seen more than once a day. Give them a
value of one (i.e., vs >= 2; no re-sights).
```

```
x[x > 1] <- 1
```

```
num.passed <- colSums(x) # Distinct adults sighted every survey date
```

```
# Calculate the total number of all individuals with good quality
photographs.
```

```
y <- table(quality$Code,quality$date)
```

```
y[y > 1] <- 1
```

```

num.total <- colSums(y) # Total animals sighted every survey date. This
includes non-distinct animals and calves

#Add the number of distinct adults and number of total animals seen for
each primary session (versus each boat day).
primarys <- c(1,1,1,2,2,2,3,3,3,4,4,4) #dummy for grouping primary
sessions
z <- as.data.frame(cbind(primarys,num.total,num.passed))
best.mod$n <- tapply(z$num.total,z$primarys,sum) #total number seen
best.mod$nd <- tapply(z$num.passed,z$primarys,sum) #number distinct adults
seen

```

Expand the estimates from the best model to non-distinctive animals using theta:

```

#Calculate Theta:
best.mod$0 <- best.mod$nd/best.mod$n # Gives a theta value for every
secondary session

```

```

best.mod$est.adj <- best.mod$estimate/best.mod$0

```

Calculate the SE of the adjusted population:

```

best.mod$SEN <- sqrt( (best.mod$est.adj^2) * (
((best.mod$se^2)/(best.mod$estimate^2)) + ((1 - best.mod$0)/(best.mod$n
* best.mod$0)) ) )

```

Calculate the lower and upper 95% CI bounds of the adjusted population:

```

C <- exp( 1.96 * sqrt(log(1 + (best.mod$SEN/best.mod$est.adj)^2) ) )
best.mod$lci <- best.mod$est.adj/C
best.mod$uci <- best.mod$est.adj*C

```

Calculate the CV of the adjusted population (dividing the SE of N by N):

```

best.mod$CV <- best.mod$SEN/best.mod$est.adj

```

Examine the model results:

```

best.mod
##      estimate      se      lcl      ucl      n nd      0 est.adj      S
EN      lci      uci      CV
## 1  93.79359 10.57358 79.52052 123.1342 122 93 0.7622951 123.0411 15.201
70  96.66747 156.6101 0.1235498
## 2 116.83468 12.69824 98.12949 149.4631 131 97 0.7404580 157.7870 18.992
36 124.73290 199.6005 0.1203671
## 3 139.94434 35.57811 89.67269 234.8096  53 34 0.6415094 218.1485 59.812
88 128.69994 369.7654 0.2741842
## 4  97.93533 17.13421 74.12763 144.3001  79 59 0.7468354 131.1337 24.497
79  91.21282 188.5268 0.1868153

```

References

Laake, J. L. 2013. RMark: An R Interface for Analysis of Capture-Recapture Data with MARK. AFSC Processed Rep 2013-01. Alaska Fisheries Science Center, NOAA, National Marine Fisheries Service, 7600 Sand Point Way NE, Seattle, WA 98115:25.

Urian, K. W., A. A. Hohn and L. J. Hansen. 1999. Status of the photo-identification catalog of coastal bottlenose dolphins of the western north Atlantic: report of a workshop of catalog contributors. NOAA Administrative Report NMFS-SEFSC-425, 22pp.

Urian, K., A. Read, A. Gorgone, B. Balmer, R. Wells, P. Berggren, J. Durban, T. Eguchi, W. Rayment and P. Hammond. 2014. Recommendations for photo-identification methods used in capture-recapture models with cetaceans. Marine Mammal Science. DOI: 10.1111/mms.12141.

Waring G.T., E. Josephson, K. Maze-Foley and P. E. Rosel (eds). 2012. U.S. Atlantic and Gulf of Mexico Marine Mammal Stock Assessments - 2012. Volume 1. National Marine Fisheries Service, Woods Hole, MA. <http://www.nefsc.noaa.gov/nefsc/publications/>.

Wells, R.S. 2009. Learning from nature: Bottlenose dolphin care and husbandry. Zoo Biology 28:1-17.