Survival and Abundance of Delmarva Fox Squirrels at Blackwater National Wildlife Refuge

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Introduction

The Delmarva fox squirrel (DFS*; Sciurus niger cinereus)* is a subspecies of the Eastern fox squirrel. The DFS once ranged from southeastern Pennsylvania (Poole, 1932) to the Southern part of the Delmarva Peninsula (Taylor, 1973). In 1967, the DFS was declared endangered, and in 1993 the DFS recovery team set up several sites to monitor DFS populations. We were contracted to assess adequacy of data collected at numerous sites (Fig 1) on and around the Blackwater National Wildlife Refuge to estimate survival and abundance of DFS.

Data Delivery and History

The USFWS sent numerous MS Excel files with capture histories for the Egypt, Jarrett, and Greenbrier capture sites. Extensive QA/QC revealed some data discrepancies that were addressed to the best of our ability and in communication with USFWS biologists. Some discrepancies were never resolved, and those individual records were removed from the data set. Specifically, in Jarrett, one recaptured individual of undetermined gender was not assigned a tag number of any kind. In Jarrett and Egypt, there was uncertainty in the identity of several recaptured individuals. This was due to the fact that no single identifier was consistently used in the database. If one tag was lost, but the other replaced, the individual was listed in the data base with two different tag combinations. In some cases, the remaining original ear tag would be lost, and replaced, which led to a third combination of tag numbers for one individual. In addition, there were two different ear tag types used before PIT tags were employed. The history of each individual was carefully studied, and the best effort was made to ensure that each one was properly represented in the data. In Egypt, there was one individual captured, that had irreconcilable uncertainty regarding its identity. From the data, it was impossible to determine if this capture represented a unique individual, or another individual in the data set -it was removed. Later years of the study used PIT tags, and these greatly aided in positive identification of all individuals in the study, including animals that had previously been tagged with ear tags.

Another collection of Excel files were sent from Dr. Carol Bocetti, (California University of Pennsylvania). These files contained additional study sites; Jarrett West (JARW), Kuehnle (KNLE), White Marsh (WHMA), the Treatment Sites owned by The Conservation Fund, (TCF1, TCF2, and TCF3). Egypt and Jarrett (Fig 1) are considered benchmark sites. Data collection was initiated in 1991 and 1992 respectively and is currently ongoing.

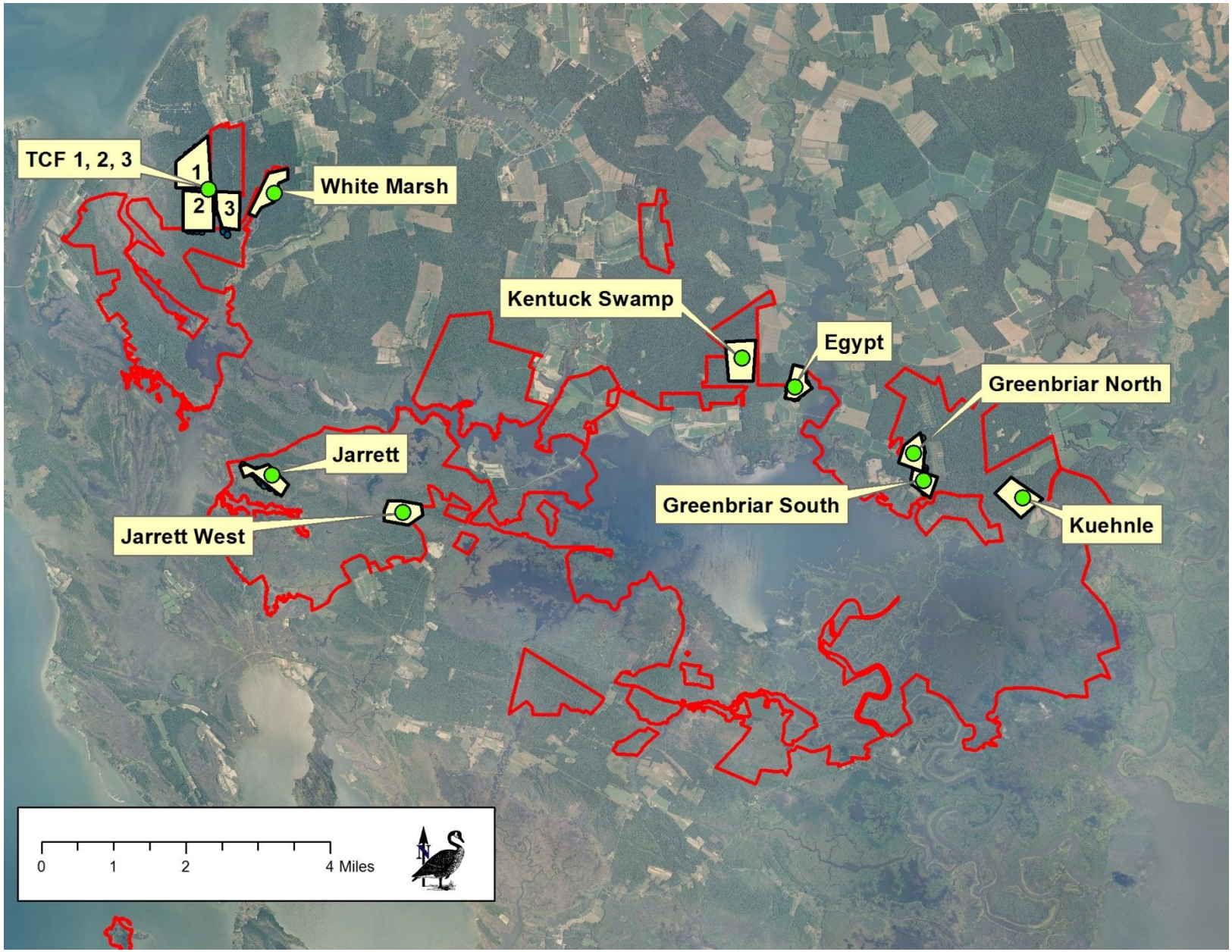

Figure 1. Eleven different study sites on or near the Blackwater National Wildlife Refuge are shown. Egypt and Jarrett are considered benchmark sites, and have the most years of data.

Data Summaries

Capture of the animals is done with cage traps baited with corn. Traps were checked frequently so as not to allow an animal to remain trapped and unattended for a prolonged period of time. Age (e.g., adult, sub-adult, juvenile) and gender, if determined, were recorded. Trapping was suspended during rain events to protect the health of the animal. Attempts were made to trap on consecutive days, however, weather and personnel constraints often required trap days to be moved. Jarrett West, Kuehnle, White Marsh, and the Treatment sites were all trapped spring and fall, with the treatment sites having a summer trapping session in 1997 and 1998 (Table 1). Egypt, Jarrett, Kentuck, (North and South) Greenbrier, (North and South) were all trapped during the spring (Table 2).

Table 1. Year, season, and site shown for Jarret West (JARW), Kuehnle (KNLE), White Marsh (WHMA), and the three treatment sites, (TCF1, TCF2, TCF3).

Year	Season	JARW	KNLE	WHMA	TCF1	TCF2	TCF3
1996	Spring				X	X	X
	Fall	X	X	X	X	X	X
1997	Spring	X	X	X	X	X	X
	Summer				X	X	X
	Fall	X	X	X	X	X	X
1998	Spring	X	X	X	X	X	X
	Summer				X	X	X
	Fall	X	X	X	X	X	X
1999	Spring	X	X	X	X	X	X
	Fall	X	X	X	X	X	X
2000	Spring	X	X	X	X	X	X
	Fall	X	X	X	X	X	X
2001	Spring	X	X	X	X	X	X
	Fall	X	X	X	X	X	X
2002	Spring	X	X	X	X	X	X
	Fall						

Spring and fall trapping sessions at Jarrett West, Kuehnle, White Marsh, and the Treatment sites typically lasted 5 days, while the summer sessions were variable. Trapping continued until enough squirrels were captured for the radio telemetry component of study.

Egypt data used for analysis spanned from 1991 to 2011. There were 227 individuals captured during those 21 years. There was an average of 29.38 individuals caught per year. Notable low years were 1995 (n=17) and 2008 (n=15). There were 47 different individuals captured in 1998. During the course of the study, 114 females were captured, and 113 males were captured. The years with the largest difference

Table 2. Trap date for the two benchmark sites, Egypt and Jarrett, and for Kentuck and Greenbrier Sites. Dates shown with a dash (-) indicate three or more consecutive days. Individual days are separated with a comma (,).

	Study Site					
Year	Egypt	Jarret	Kentuck North	Greenbrier North	Kentuck South	Greenbrier South
1991	Mar 29; Apr 1, 2					
1992	Apr 23, 24, 28	Apr 4, 8, 9				
1993	Apr 15, 19, 20	Apr 27 - 29				
1994	Apr 4, 5, 7	Apr 14 - 16				
1995	Mar 28; Apr 29, 31	Apr 27, 28; May 1				
1996	Mar 3; Apr 2 - 4	Apr 8, 10, 11				
1997	Apr 7 - 9	Apr 10, 11, 14				
1998	Apr 7, 8, 10	Mar 31; Apr 1, 2				
1999	Mar 23, 25, 26	Mar 30, 31; Apr 2				
2000	Apr 12 - 14	Mar 31; Apr 5, 6				
2001	Apr 18 - 20	Apr 9, 10, 12				
2002	Apr 16 -19	Apr 2 - 4	May 16, 17, 20	May 23, 30; Jun 3	May 16, 17, 20	May 28, 31; Jun 6
2003	Apr 14, 16, 22	Apr 23 - 25	Mar 17 - 19	Mar 18, 19, 24	Mar 17 - 19	Mar 18, 24 - 26
2004	Apr 15, 16, 19	Apr 7 - 9	Apr 28, 30; May 4	Apr 21 - 23	Apr 27, 29, 30	Apr 21 - 23
2005	Apr 11 - 13	Apr 19 - 21	Mar 21, 22, 24	Mar 29 - Apr 1, 7	Mar 21, 22, 24	Mar 29 - 31; Apr 7
2006	Apr 10 - 12	Apr 18 - 20		Mar 27 - 29		Mar 27 - 29
2007	Apr 18 - 20	Apr 2, 3, 5		Apr 10, 11, 13		Apr 10, 11, 13
2008	Mar 24 - 26	Mar 31, Apr 2 - 4		Apr 14, 15, 17		Apr 14, 15, 17
2009	Apr 8, 13, 16	Apr 7, 9, 10		May 6 - 8		Apr 17; May 23, 24
2010	Mar 18 - 22	Mar 31 - Apr 3, 5		Apr 6 - 8, 12		
2011	Mar 14 - 17, 22	Mar 14 - 18		Mar 25, 26, 28, 29, 31		

in captures between genders were 1995 (11 females, 6 males) and 2011 (24 females, 13 males). Of the 227 different individuals captured over the course of the study, 39 were originally captured as sub-adults, 188 as adults and 6 unknowns (all from 1992). The years with the highest percentage of sub-adults captured were 1991 (9 sub-adults of 33 total captured individuals), 2009 (4 of 25), 2010 (6 of 41) and 2011 (5 of 32).

Jarrett data used for analysis spanned from 1992 to 2011. There were 85 individuals captured during that time, with an average of 14.85 individuals per year. The year with the fewest individuals captured was 1994 (n=5), and the year with the most was 2010, (n=37). There were 44 individual males captured during that time, and 41 females. The only yearly 1:1 ratios were 2000, (four of each) and 2007 (ten of each). Some years were highly skewed. During the 2010 trapping season, 27 females were captured, and only 10 males were captured. In 1998, there were 12 males and 3 females captured, and in 1999 there were 15 males and 7 females. Few individuals caught were sub-adult, (14 females, 10 males) with the highest number of sub adults caught in 2010 (n=6).

A total of 65 individuals (25 Female, 40 Male) were caught 2002- 2012 at the Greenbrier North study area. There were 15 individuals caught in 2011 and 5 in 2012. The average number of individuals captured was 9.2. A total of 9 were sub-adults, (1 in 2003, 2004, and 2008, 2 in 2005, 2009, and 2011). There were several options for analysis. Initially, the Greenbrier – Kentuck area was analyzed as one study, and the Greenbrier North and South study as another. Ultimately, it was more beneficial to drop the Kentuck and Greenbrier South study sites and analyze the Greenbrier North study area as one continuous study (2002 – 2012). This last analysis is presented in this report.

The data from Kentuck North and South, and Greenbrier South was not analyzed, but the summaries are provided here. From 2002 to 2005, a total of 47 individuals were caught at the Kentuck North site, 39 adults and 8 sub-adults. There was a low of 13 captures in 2003 and a high of 29 in 2005. There was an average of 19.5 captures per year. There were 27 males and 20 females captured over the course of the study. From 2002 to 2005, there were 37 individuals captured in Kentuck South. Of these 34 were adult and 3 were sub-adult. There were 23 males and 14 females captured over the course of the study. There were 11 captures in 2003 and 2004 and 20 in 2005, with an average of 14 captures per year. From 2002 to 2009, there were 37 individuals captured in Greenbrier South. Of these 34 were adult and 3 were sub-adult (note identical to above). There were 21 males and 16 females. There was a low of only 3 captures in 2007, with a high of 14 in 2003. There was an average of 7.25 captures per year.

Carol Bocetti provided data from 6 sites. All of these spanned from 1996 to 2002. Over the course of the study, there were 64 individuals caught at Jarrett West (JARW). The fewest individuals captured was in 1996 when the trapping effort was limited (n = 5), and the highest was 27 in 1997 with an average of 18.6 per year. There were 28 males and 36 females captured, of which there were 11 sub-adults. At KNLE, there were 110 individuals captured over the course of the study. Yearly numbers of individuals ranged from 1 in 1996, to 41 in 2002 (mean = 28). There were 58 males and 52 females, of which there were 13 sub-adults. At the WHMA study site, 48 individuals were

captured over the course of the study; 25 males and 23 females, 9 of which were sub-adults. Yearly number of individuals varied from 3 in 1996 to 18 in 2002, (mean = 12.3). At the TCF1 study site, there were 61 individuals caught over the course of the study 32 males and 29 females, of which 10 were sub-adults, and 1 juvenile. Yearly number of individuals captured ranged from 9 in 1996 and 2000 to 30 in 1998 (mean = 15). At the TCF2 site, there were 47 individuals captured over the course of the study. Yearly numbers of individuals ranged from 7 in 1999 to 17 in 1998 (mean = 10.9). There were 27 males and 20 females, of which there were 7 sub-adults. At the TCF3 site, there were 58 individuals captured over the course of the study. The number of individuals yearly ranged from 7 in 2000 to 26 in 1998 (mean = 13). There were 30 males and 28 females, 10 of which were sub-adults and 2 of which were juveniles.

These sites were paired in order to determine effects of logging. Each of the treatment sites (TCF1, TCF2, and TCF3) were slated to be logged during the course of the study. For TCF1, spring 1996 – spring 1999 was considered pre-treatment. Fall 1999 to spring 2002 was considered post-treatment. For TCF2, pre-treatment was spring 1996 to summer 1998, with fall 1998 to spring 2002 considered post-treatment. For TCF3, spring 1996 to spring 1999 was pre-treatment, while fall 1999 to spring 2002 was post-treatment. In order to maintain continuity with the rest of the study areas, spring data was used to estimate survival rates, and to determine treatment effects.

Data Analysis

The robust design model (Pollock, 1982, Kendall, et al, 1995, Kendall et al, 1997) was used to analyze the data. Analyses treated daily recapture events within years as secondary occasions and different years of sampling as primary occasions. With the robust design the following parameters may be estimated: Survival (S_i), Gamma prime, (γ_i') and Gamma double prime (γ_i''), which represent the probability that an animal is available for capture at time *i*, capture probability (p_i), and recapture probability (c_i). Population size (N_i) is a derived parameter, (Huggins, 1991) and consequently did not change the number of parameters that are estimated in each model. In other words, the model is not trying to maximize across a parameter space in order to determine abundance estimate, but rather using algebraic equations. The standard error of abundance is dependent on the total number of animals captured, thus it will be the same for males and females in a given year.

For the sites that were trapped only in the spring, (Table 2), survival was estimated yearly. This also constituted time between primary occasions. For the sites that were trapped during spring, fall and sometimes, summer, (Table 1), S was initially estimated for multiple primary occasions during the year, and by year as a covariate. The estimation of S by primary occasion was not productive, and was dropped from the analysis. Finally, in order to maintain comparative survival estimates, only spring data was used for all sites.

While the trapping has been extensive for this project, some constraints were necessary to accommodate even simple robust models. Otherwise, parameter estimates and/or their associated variances will be impossible to obtain. The Gamma parameters (γ' and γ") were fixed to zero for all

years, in part through necessity and in part through justification from discussion with the biologist who noted little movement within the time frame of the trapping sessions. Data was processed, QA/QC'ed, and formatted in R (R Development Core Team 2009). The package RMark (Laake and Rexstad, 2013) was used to call Program MARK, (White and Burnham 1999) in which the actual analysis was done. Program MARK is an industry standard and has a proven engine for likelihood optimization. Example R code can be found in Appendix A.

Model selection was largely done using an information theoretic approach, (Burnham and Anderson 2002) however, models with lower AIC (or BIC) values were not necessarily chosen if coefficients or their associated standard errors could not be estimated. If either of these tended to zero or infinity, then the model was deemed inappropriate, and was not used. This is typical for models that do not have enough data to allow the optimization routine to converge.

Egypt

Analyses of the study area Egypt were performed using each day as a secondary occasion within a yearly primary occasion. A full suite of models were run using RMark (R and Program Mark). Of the 13 individuals captured in 2003, 12 were recaptured in 2004 (total recapture = 16) so survival (S) for 2003 was fixed at 1.0.

The top ranked model (AIC=1248.43) showed S and p varying by year (Table 3). This 62 parameter model had numerous convergence issues. In addition, estimates of the yearly survival rate had very large standard errors, (e.g., 0.22) leading to uninformative 95% confidence intervals (e.g., For 1997, 95% CI is 0.0001 to 1).

The next best model (ΔAIC =43.67) had S fixed across years and p varying by secondary occasion. Although this 28 parameter model produced much more stable population estimates, certain convergence issues persisted for time period 5. The estimate of S across all years was 0.62 (SE = 0.02, LCL = 0.59, UCL = 0.67).

Table 3. Model Selection table for the top models at Egypt study site including a model description, number of parameters (npar), Akaike Information Criteria adjusted for sample size (AICc), and the deviance.

Model	Number of Parameters	AICc	Delta AICc	Deviance
S(year)p(year)	62	1248.43	0.00	587.26
S(.)p(secondary occasion)	28	1292.10	43.67	710.54
S(time)p(year)	46	1298.79	50.36	676.29
S(sex+year) p(secondary occasion)	48	1303.18	54.75	675.97
S(pdsi) p(.)	25	1327.33	78.90	752.35
S(pdsi) p(pdsi)	26	1329.51	81.08	752.34

*For model description, Survival (S) and probability of capture (p) are denoted by letter. How the parameters are allowed to vary is denoted in parentheses. For instance, fixed across years is denoted as (.). If parameter is allowed to vary, then variation denoted within parentheses, (e.g, sex, secondary occasion, year, pdsi, etc).

The Palmer Drought Severity Index (PDSI) values for the fall and year were provided for the duration of the study, as were monthly average wind speed values and maximum temperature for 2003 – 2011. Although we hoped these covariates would explain variation in capture probability, reduce number of parameters, and increase precision, we found little support for models including covariates.

The lowest abundance estimate for females was 6.1 (SE = 1.5) for 2008, for males it was 6.9 (SE = 1.7) in 2007 (Table 4; Fig A1). The highest estimate for females was 25.9 (SE = 2.8) in 1998, and for males it was 23.5 (SE = 1.9) in 1999. All abundance estimates should be interpreted with caution. There is no definitive area associated with these estimates in order to obtain density.

Table 4. Abundance estimates, standard errors (SE), lower 95% confidence limit (LCL), and upper 95% confidence limit (UCL) for all males and females across all years at the Egypt study site.

	Females				Males			
Year	**N-hat**	**SE**	**LCL**	**UCL**	**N-hat**	**SE**	**LCL**	**UCL**
1991	16.8	2.7	13.2	24.3	15.8	2.7	12.2	23.3
1992	23.1	2.6	19.5	30.3	20.1	2.6	16.5	27.3
1993	24.9	2.8	21.1	32.5	22.9	2.8	19.1	30.5
1994	20.1	2.6	16.5	27.3	23.1	2.6	19.5	30.3
1995	12.1	1.7	10.1	17.6	8.1	1.7	6.1	13.6
1996	16.5	1.6	14.8	21.9	18.5	1.6	16.8	23.9
1997	12.7	2.1	10.0	18.9	16.7	2.1	14.0	22.9
1998	25.9	2.8	22.0	33.4	21.9	2.8	18.0	29.4
1999	22.5	1.9	20.3	28.4	23.5	1.9	21.3	29.4
2000	8.3	1.8	6.2	14.0	13.3	1.8	11.2	19.0
2001	18.2	2.2	15.3	24.7	14.2	2.2	11.3	20.7
2002	9.2	1.1	8.3	13.7	10.2	1.1	9.3	14.7
2003	8.9	1.7	7.0	14.4	9.9	1.7	8.0	15.4
2004	11.7	1.9	9.4	17.5	11.7	1.9	9.4	17.5
2005	14.5	2.1	11.9	20.6	13.5	2.1	10.9	19.6
2006	10.7	1.9	8.4	16.5	12.7	1.9	10.4	18.5
2007	12.9	1.7	11.0	18.5	6.9	1.7	5.0	12.5
2008	6.1	1.5	4.6	11.2	8.1	1.5	6.6	13.2
2009	8.3	1.8	6.2	14.0	13.3	1.8	11.2	19.0
2010	10.0	0.0	10.0	10.0	11.0	0.0	11.0	11.0
2011	16.0	0.0	16.0	16.0	9.0	0.0	9.0	9.0

Jarrett

The best model based on AIC value for Jarrett was with S constant across years, and p allowed to vary by secondary occasion (AIC = 599.14). The estimate for S in this model is 0.59 (SE = 0.04, LCL = 0.53, UCL = 0.67; Table 5).

Table 5. Model selection criteria for data study site including a model description, number of parameters (npar), Akaike Information Criteria adjusted for sample size (AICc), AICc weights, and the deviance.

Model	Number of Parameters	AICc	DeltaAICc	Weight	Deviance
S(.) p(secondary occasion)	27	599.14	0.00	0.23	296.63
S(fall.pdsi) p(.)	24	599.25	0.11	0.22	304.14
S(.) p(.)	23	600.17	1.03	0.14	307.48
S(pdsi) p(pdsi)	25	600.24	1.10	0.13	302.67
S(pdsi) p(secondary occasion)	28	600.25	1.10	0.13	295.22
S(pdsi) p(.)	24	601.28	2.13	0.08	306.16
S(fall.pdsi) p(fall.pdsi)	25	601.67	2.53	0.06	304.11
S(year) p(secondary occasion)	47	615.15	16.00	0.00	258.01

*For model description, Survival (S) and probability of capture (p) are denoted by letter. How the parameters are allowed to vary is denoted in parentheses. For instance, fixed across years is denoted as (.). If parameter is allowed to vary, then variation denoted within parentheses, (e.g, sex, secondary occasion, year, pdsi, etc).

Table 6. Abundance estimates, standard errors (SE), lower 95% confidence limit (LCL), and upper 95% confidence limit (UCL) for all males and females across all years at the Jarrett study site.

Year	N-hat	SE	LCL	UCL
1992	7.2	1.0	7.0	13.8
1993	6.1	0.9	6.0	12.2
1994	6.2	1.6	5.2	13.5
1995	12.8	1.3	12.1	19.6
1996	7.2	1.0	7.0	13.8
1997	10.6	1.2	10.0	17.3
1998	10.0	0.0	10.0	10.0
1999	13.9	1.4	13.1	20.8
2000	6.1	0.9	6.0	12.2
2001	9.4	1.1	9.0	16.2
2002	10.6	1.2	10.0	17.3
2003	8.3	1.1	8.0	15.0
2004	11.7	1.3	11.1	18.5
2005	9.4	1.1	9.0	16.2
2006	8.3	1.1	8.0	15.0
2007	10.6	1.2	10.0	17.3
2008	7.0	0.0	7.0	7.0
2009	6.1	0.9	6.0	12.2
2010	13.0	0.0	13.0	13.0
2011	8.0	0.0	8.0	8.0

Indistinguishable from the top model is a model where S is modeled using PDSI, (ΔAIC < 1). As with the Egypt study site, all estimates of S using PDSI have 95% CI's that contain 0.59, with a minimum of 0.48 (SE = 0.08) in 2002 and a maximum of 0.67 (SE = 0.06) in 1992. The beta parameter for PDSI was 0.28 (SE = 0.16).

For some years, abundance has very low standard errors because almost all individuals are captured at least once and therefore estimates of the number of individuals never captured are very small. The lowest abundance estimate is 6.1 (SE = 0.9) for three different years, (1993, 2000, and 2009; Table 6; Fig A2). The highest was 13.9 (SE = 1.4) in 1999 (Table 6)

Greenbrier North

The model with the lowest AIC score that did not have model convergence problems for the Greenbrier North study area was one that held S and p constant across years and secondary occasions (AIC = 721.56; Table 10). Survival (*S)* estimate for the study period is 0.62, (SE = 0.04, LC = 0.53, UCL = 0.70).

Table 7. Model Selection table for the top models at Greenbrier study site including a model description, number of parameters, Akaike Information Criteria adjusted for sample size (AICc), AICc weights, and the deviance.

Model	Number of Parameters	AICc	DeltaAICc	Weight	Deviance
S(.) p(.)	14	721.56	0.00	0.998	580.84
S(pdsi) p(.)	15	722.36	0.80	0.002	579.25
S(fall.pdsi) p(.)	15	723.83	1.46	0.000	580.72
S(pdsi) p(fall.pdsi)	16	724.76	0.93	0.000	579.22
S(pdsi) p(secondary session)	16	726.23	1.46	0.000	580.69
S(fall.pdsi) p(secondary session)	25	733.95	7.73	0.000	565.10

*For model description, Survival (S) and probability of capture (p) are denoted by letter. How the parameters are allowed to vary is denoted in parentheses. For instance, fixed across years is denoted as (.). If parameter is allowed to vary, then variation denoted within parentheses, (e.g, sex, secondary occasion, year, pdsi, etc).

Abundance estimates for Greenbrier North were made for males and females. Estimates for males ranged from a low in 2012 of 3.15 (SE = 1.30, LCL = 2.19, UCL = 8.81; Table 8) to a high of 18.79 (SE = 9.9, LCL = 12.0, UCL = 40.5; Table 8) in 2003. Estimates for females ranged from a low in 2012 of 3.15 (SE = 1.30, LCL = 2.19, UCL = 8.81) to a high of 14.79 (SE = 2.34, LCL = 11.94, UCL = 21.85; Table 8).

Table 8. Abundance estimates (N-hat) for Greenbrier North study site. Included are the standard errors (SE), lower 95% confidence limit (LCL), and the upper 95% confidence limit (UCL).

	Females				Males			
Year	N-hat	SE	Lower	Upper	N-hat	SE	Lower	Upper
2002	11.77	0.98	11.11	16.27	9.77	0.98	9.11	14.27
2003	14.79	2.34	11.94	21.85	18.79	2.34	15.94	25.85
2004	7.30	1.20	6.28	12.04	9.30	1.20	8.28	14.04
2005	9.32	1.57	7.70	14.74	18.32	1.57	16.70	23.74
2006	13.08	3.51	8.57	23.27	17.08	3.51	12.57	27.27
2007	6.66	2.97	3.49	16.63	7.66	2.97	4.49	17.63
2008	3.83	2.12	1.76	11.47	7.83	2.12	5.76	15.47
2009	6.47	1.30	5.33	11.53	5.47	1.30	4.33	10.53
2010	5.58	1.96	3.68	12.71	4.58	1.96	2.68	11.71
2011	6.17	1.59	4.60	11.84	7.17	1.59	5.60	12.84
2012	3.15	1.30	2.19	8.81	3.15	1.30	2.19	8.81

White Marsh (WHMA) and TCF1

The WHMA study site was used as a control and was paired with TCF1 to the treatment effects of logging. TCF1 was pre-treatment 1996 – 1999 (Spring) and post-treatment 1999 – 2002. In order to determine this, these sites were analyzed together. This was possible since trapping was done concurrently. In order to make comparable survival estimates to the other sites, analysis was done using only the spring data. S was allowed to vary between treatment and control sites (years) but p was held constant. Models that allowed S and p to vary across years and secondary occasions failed to converge properly. The top two models were virtually indistinguishable ($\Delta AIC < 1$). In the top model where S is held constant, the estimate for S is 0.52 (SE = 0.05, LCL = 0.42, UCL = 0.62). In the second model where S is allowed to vary by treatment, the estimate of S for control sites is 0.55 (SE = 0.06, LCL = 0.43, UCL = 0.67). For the treatment sites, the estimate for S is 0.42, (SE = 0.10, LCL = 0.24, UCL = 0.62). Note the overlapping 95% CI for survival. The slope for the treatment effect is negative, as indicated by the lower survival rate in the treatment sites. However, the evidence that the treatment significantly alters survival is weak, although the results suggest that further investigation is warranted.

Table 9. Model Selection table for the top models at White Marsh study site including a model description, number of parameters, Akaike Information Criteria adjusted for sample size (AICc), AICc weights, and the deviance.

Model	Number of Parameters	AICc	DeltaAICc	Weight	Deviance
S(.) p(.)	9	484.73	0.00	0.61	332.41
S(treat) p(.)	10	485.64	0.91	0.39	331.11

*For model description, Survival (S) and probability of capture (p) are denoted by letter. How the parameters are allowed to vary is denoted in parentheses. For instance, fixed across years is denoted as (.). If parameter is allowed to vary, then variation denoted within parentheses, (e.g, “treat” indicates survival varied by treatment).

Abundance estimates for White Marsh ranged from a low in 1996 of 3.0 (non SE obtainable) to a high of 26.1 (SE = 9.9, LCL = 12.0, UCL = 40.5; Table 10). Due to the low number of individuals, estimates for females and male had to be combined (Fig A7).

Table 10. Abundance estimates (N-hat) for White Marsh study site. Included are the standard errors (SE), lower 95% confidence limit (LCL), and the upper 95% confidence limit (UCL).

Year	N-hat	SE	LCL	UCL
1996	3.0	0.0	3.0	3.0
1997	11.9	3.1	10.2	28.1
1998	26.1	9.9	17.5	64.6
1999	12.0	0.0	12.0	12.0
2000	16.9	5.8	12.2	40.5
2001	17.0	0.0	17.0	17.0
2002	18.0	0.0	18.0	18.0

Abundance estimates for TCF1 vary from a low of 9.0 (SE is unobtainable) in 1996 to a high of 30.2 (SE = 1.1, LCL = 30.0, UCL = 37.6; Table 11) in 1998 (Fig A8). Due to the low number of individuals, females and males are combined.

Table 11. Abundance estimates (N-hat) for TCF1 study site. Included are the standard errors (SE), lower 95% confidence limit (LCL), and the upper 95% confidence limit (UCL).

Year	N-hat	SE	LCL	UCL
1996	9.1	0.9	9.0	15.0
1997	17.0	0.0	17.0	17.0
1998	30.4	1.1	30.0	36.9
1999	15.0	0.0	15.0	15.0
2000	9.1	0.9	9.0	15.0
2001	11.2	1.0	11.0	17.7
2002	18.4	2.8	15.4	27.7

Kuehnle (KNLE) and TCF2

The KNLE site was used as a control for the TCF2 site. TCF2 is considered pre-treatment from 1996 to 1998 (spring) and post-treatment from 1998 (fall) to 2002. Analysis was done in the same manner as the WHMA and TCF1 analysis. S was allowed to vary between treatment and control sites (years) but p was held constant. Models that allowed S and p to vary across years and secondary occasions failed to converge properly. The top two models were virtually indistinguishable ($\Delta AIC < 1$). In the

top model where S is held constant, the estimate for S is 0.57 (SE = 0.04, LCL = 0.50, UCL = 0.65; Table 12). In the second model where S is allowed to vary by treatment, the estimate of S for control sites is 0.60 (SE = 0.04, LCL = 0.51, UCL = 0.68). For the treatment sites, the estimate for S is 0.48, (SE = 0.09, LCL = 0.32, UCL = 0.64).

Table 12. Model Selection table for the top models at Kuehnle study site including a model description, number of parameters, Akaike Information Criteria adjusted for sample size (AICc), AICc weights, and the deviance.

Model	Number of Parameters	AICc	DeltaAICc	Weight	Deviance
S(.) p(.)	9	700.26	0.00	0.57	627.26
S(treat) p(.)	10	700.85	0.59	0.43	625.74

*For model description, Survival (S) and probability of capture (p) are denoted by letter. How the parameters are allowed to vary is denoted in parentheses. For instance, fixed across years is denoted as (.). If parameter is allowed to vary, then variation denoted within parentheses, (e.g, sex, secondary occasion, year, pdsi, etc).

Abundance estimates for females at the Kuehnle study site ranged from a low of 11.9 (SE = 1.1, LCL = 11.1, UCL = 17.1; Table 13) in 1999 to a high of 25.6 (SE = 2.5, LCL = 22.4, UCL = 32.8) in 2002. For males, the lowest estimate was in 1997; 12.8 (SE = 1.1, LCL = 12.1, UCL = 17.9). The highest estimate for males was in 2002; 26.6 (SE = 2.5, LCL = 23.4, UCL = 33.8; Table 13; Fig A6).

Table 13. Abundance estimates (N-hat) for Kuehnle study site. Included are the standard errors (SE), lower 95% confidence limit (LCL), and the upper 95% confidence limit (UCL).

	Females				Males			
Year	N-hat	SE	LCL	UCL	N-hat	SE	LCL	UCL
1997	14.8	1.1	14.1	19.9	12.8	1.1	12.1	17.9
1998	15.2	1.3	14.2	20.6	20.2	1.3	19.2	25.6
1999	11.9	1.1	11.1	17.1	17.9	1.1	17.1	23.1
2000	13.9	1.1	13.1	19.0	14.9	1.1	14.1	20.0
2001	20.5	1.2	20.0	27.5	20.5	1.2	20.0	27.5
2002	25.6	2.5	22.4	32.8	26.6	2.5	23.4	33.8

Abundance estimates for TCF2 ranged from a low of 8.0 (SE unobtainable) in 1996 to a high of 18.5 (SE = 2.3, LCL = 17.2, UCL = 30.0) in 1998 (Table 14; Fig A9). Estimates are for females and males combined. There were three years where standard errors were not obtainable; 1996, 1997 and 2001.

Table 14. Abundance estimates (N-hat) for TCF2 study site. Included are the standard errors (SE), lower 95% confidence limit (LCL), and the upper 95% confidence limit (UCL).

Years	N-hat	SE	LCL	UCL
1996	8.0	0.0	8.0	8.0
1997	12.0	0.0	12.0	12.0
1998	18.5	2.3	17.2	30.0
1999	15.0	7.5	8.7	45.0
2000	9.3	1.4	9.0	18.4
2001	13.0	0.0	13.0	13.0
2002	16.1	9.4	10.7	62.8

Jarrett West (JARW) and TCF3

The best model for the JARW and TCF3 study sites (AIC = 725.21) held S and p constant between sites and years (Table 15). The survival estimate is 0.63 (SE = 0.04, LCL = 0.54, UCL = 0.70).

Table 15. Model Selection table for the top models at Jarrett West study site including a model description, number of parameters, Akaike Information Criteria adjusted for sample size (AICc), AICc weights, and the deviance.

Model	Number of Parameters	AICc	DeltaAICc	Weight	Deviance
S(.) p(.)	9	725.21	0.00	0.73	661.61
S(treat) p(.)	10	727.23	2.02	0.26	661.50

*For model description, Survival (S) and probability of capture (p) are denoted by letter. How the parameters are allowed to vary is denoted in parentheses. For instance, fixed across years is denoted as (.). If parameter is allowed to vary, then variation denoted within parentheses, (e.g, sex, secondary occasion, year, pdsi, etc).

The survival estimates for the model where treatment is allowed to vary between control and treatment sites (years) are, (ΔAIC = 2.02) for JARW, 0.62 (SE = 0.04, LCL = 0.53, UCL = 0.70; Table 13) and for TCF3, 0.67 (SE = 0.04, LCL = 0.53, UCL = 0.70). In this particular case, the survival estimates are higher for the treatment site (years).

Table 16. Abundance estimates (N-hat) for Jarret West study site. Included are the standard errors (SE), lower 95% confidence limit (LCL), and the upper 95% confidence limit (UCL).

Year	N-hat	SE	LCL	UCL
1996	5.0	0.0	5.0	5.0
1997	31.3	4.2	27.9	48.5
1998	27.9	3.0	25.6	40.3
1999	20.0	0.0	20.0	20.0
2000	13.0	0.0	13.0	13.0
2001	23.0	0.0	23.0	23.0
2002	17.0	0.0	17.0	17.0

The low number of individuals at Jarrett West required abundance estimates for females and males be combined. The estimates ranged from a low of 5.0 (No SE obtainable) in 1996 to 31.3, (SE = 4.2, LCL = 27.9, UCL = 48.5) in 1997 (Table 16; Fig A5).

Abundance estimates for TCF3 (females and males combined), ranged from a low of 8.0 (SE unobtainable) in 1996 to a high of 29.6 (SE = 3.4, LCL = 26.8, UCL = 43.4) in 1998 (Table 17) (Fig A10).

Table 17. Abundance estimates (N-hat) for TCF3 study site. Included are the standard errors (SE), lower 95% confidence limit (LCL), and the upper 95% confidence limit (UCL).

Year	N-hat	SE	LCL	UCL
1996	8.0	0.0	8.0	8.0
1997	15.7	2.0	15.0	27.9
1998	29.6	3.4	26.8	43.4
1999	11.5	2.9	10.1	26.9
2000	7.6	1.9	7.0	19.6
2001	13.1	1.2	13.0	21.3
2002	12.1	1.2	12.0	19.9

Summary

Ideally, all statistical models would be as close to the real biological system as possible. It is known that real survival probabilities (as well as capture probabilities) vary by year, gender, age and other factors. In constructing these models, every attempt was made to include the most basic variations relating to year and gender, however, the amount of data available made this impossible, or at least rendered the estimates unreliable. A conservative approach was used. Often times, estimates of S or p would be provided by a model run, but standard errors would be nonsensical (i.e. would tend to zero or infinity). In these cases, it was decided that more parameters were being estimated than the data reliably allowed, and that it would be better to estimate fewer parameters, but do so more reliably. This leads to a known bias, since as previously stated; these estimates undoubtedly do not tend to the real values of each year, gender and age combination. However, since the standard errors are reduced, it also increases precision. This is a constant trade off when constructing biological models of any kind.

The average of each study's estimate of survival is 0.59 (SD = 0.096; Table 18). It is important to note this estimate encompasses different years for different sites (Table 18). For all study sites, this can be thought of as survival from spring to spring.

Table 18. Survival estimates, associated standard errors, lower and upper confidence limits, and years for each study site.

Site	S	SE	LCL	UCL	Years of Study
Egypt	0.62	0.02	0.59	0.67	1991 - 2011
Jarrett	0.59	0.04	0.53	0.67	1992 - 2011
Greenbrier	0.62	0.04	0.53	0.70	2002 - 2012
JARW - TCF3	0.63	0.04	0.54	0.70	1996 - 2002
KNLE - TCF2	0.57	0.04	0.50	0.65	1996 - 2002
WHMA - TCF1	0.52	0.05	0.42	0.62	1996 - 2002

These estimates are consistent with previous studies that indicated survival is between 0.56 to 0.76 at Blackwater NWR (Paglione, 1996) and from 0.24 to 0.57 at Chincoteague NWR (Pednault-Willet, 2002). Tag loss was not considered here, as double tags were used early in study, and pit tags were later. There was one individual in the data set that indicated both tags were lost at once, and this individual was removed from the analysis. These are estimates of apparent survival and permanent emigration could also affect estimates, but there is limited information to indicate dispersal from study sites or to separate mortality from permanent emigration.

Year-specific survival estimates were obtained for each study area the resulting standard errors led to very large 95% confidence intervals, thus rendering the estimates of little value. There are analytical techniques that can be used to reduce these standard errors, but great care should be taken to distinguish increased precision from actual gain of knowledge. If the number of extraneous variables is reduced, (i.e., hold p constant across all capture events) then the standard errors on survival will be reduced, however, after consultation with the biologist (fox squirrels do respond differently after consecutive days of trapping) and inspecting the data, it is my belief that removing this variable from the model would lead to false sense of confidence regarding the survival probabilities. The attempt is to present the best possible estimates without overstating our confidence. In other words, estimates of uncertainty should reflect the uncertainty we really have, not what an “improved” model can lead us to believe.

Age and gender were investigated as possible covariates to improve precision and increase our knowledge regarding gender-and age-specific survival. In most cases, data were not adequate to support these sources of variation in the top ranked models. However, examination of estimates from lower ranked models that included these effects indicates little variation caused by sex or age.

Previous studies have found that the Palmer Drought Severity Index suggests unfavorable trends for the fox squirrel populations (Hildebrand et al, 2007). PDSI was incorporated into the model selection process, but it did not improve model rank. There was some improvement in parameter precision, but estimates of survival were simply pulled towards the mean, and ultimately, model inference is not improved. This is not to suggest that current findings contradict previous studies. To the contrary, model performance using PDSI suggests that it is relevant, however, given the data, it

simply does not improve model performance. This climate variable, as well as others, should be collected for future analysis as the study continues.

In general, abundance estimates from any traditional mark-recapture experiment must be interpreted with caution (Chandler and Royle, 2011). Estimates of abundance (N) are routinely produced, as they were in the analysis for this study. However, area effectively sampled is usually unknown, and thus density is also unknown (Wilson and Anderson, 1985). Ad hoc estimators assigning some arbitrary value to a home range area can be used, but these invariably fail to account for changes in behavior and movement that could be interpreted as changes in abundance. For instance, if food availability is high, there could be less movement on the part of animals. If predators or competitors change their behavior, or are introduced to an area, movement of the animals in question can be greatly affected. Changes in behavior can be caused by crop selection, garbage storage, disturbance, hiking trails, noise, light and any number of other anthropogenic causes. All of these can lead to apparent changes in abundance, when in fact there are no changes, or worse, when there are real trends in the opposite direction. In order to address these problems, spatially explicit capture-recapture models (SECR) were developed (Borchers and Efford 2008) and we suggest that these models, along with changes in the sampling design, would likely be useful if density is of interest.

Recommendations if survival over time remains the monitoring goal and trapping continues to be used. (Note: We recognize that in the future, occupancy modeling using cameras might also be used to monitor somewhat different objectives, e.g. population persistence and the dynamics of DFS occurrence across the refuge).

1) For most of the study areas, the recapture rate is unusually high. Reduce the density of traps by half or one third and increase the area trapped by 2 or 3 times. This should increase the area of inference, but should not reduce the information obtained. This should increase the scope of inference and provide a sample of individuals that will lead to a more biologically meaningful interpretation if abundance were changing. For example, a change from 50 to 25 individuals is a stronger inference than a change from 10 to 5 individuals.
2) When running consecutive trapping sessions (e.g., fall trapping) in areas that are close together, space trap days throughout those areas as evenly as possible (weather permitting). For example, one day at TCF1, then the next day at TCF2, then the next day at TCF3. Then go back to TCF1. Ideally, trapping will be stretched out as little as possible, but it is understood that there are limitations in traps and personnel. If, for example, JARW could be trapped on the same day at TCF1, KNLE on the same day as TCF2, etc, then there is more flexibility to combine analyses. This will allow future analyses to (hopefully) combine capture and recapture probabilities, allowing for more power to estimate survival.
3) Overall trapping effort (man hours) should not be reduced at this stage if possible. However, after one year of incorporating the above recommendations, this should be revisited. It might be possible to reduce the overall trapping effort by reducing the number of trapping

days. The data will have to be inspected to determine if the number of recaptures stays high enough with the lower density of traps (No. 1 above), and to determine if the increase in efficiency from running concurrent trapping (No. 2 above) helps sufficiently.

4) Along these lines, in depth analysis of both cage trap data and reader data (should this be attempted) is recommended after one year. Preliminary analysis of the reader data should occur after the initial testing period (e.g., spring).
5) Data archiving should be done with one data base (e.g, MS Access, MySQL), conducive to inclusion of every applicable Delmarva Fox Squirrel. This could be done in cooperation with the Region V IT personnel.
6) Historical data QA/QC. I have flagged (and fixed) several historical entries for Jarrett and Egypt. I think these should be noted in the archives. However, I feel each change should be inspected by at least one refuge biologist. All files available on request.

Note: During discussions with biologist, it was stated that density estimates would be useful. We recommend a pilot study investigating the usefulness of spatially-explicit capture-recapture methods (see below).

Recommendations if interested in estimating density using spatially explicit capture-recapture (SECR)

Intuitively, it is clear that animals far from traps are less likely to get caught than animals close to traps. Animals sufficiently far from any trap will have a near zero (or zero) probability of being captured. A variety of detectors can be and have been used in various studies; cameras (Royle et al, 2009a, b), hair snares with DNA analysis (Efford et al 2009a), cages (Efford et al 2005) and vocalizations (Efford et al, 2009b). The fundamental requirement of these devices is that their location is known and there is a means of identifying individuals at each detector. While not strictly required, it is best if the study divides time into discrete intervals, (e.g., individual days, seasonal trapping periods). Certain MR studies that have been done before SECR models were developed to adhere to the basic requirements of SECR analysis, thus allowing for past studies to be analyzed using SECR methods.

For the simplest approach, if trap density is sufficient enough that individuals are caught in many locations, but not caught in every location, than certain inferences regarding the home range of that individual can be made. A centroid can be assigned to an animal's movements, it need not have any biological significance, the centroid is merely is a way of associating an animal with a single location. Capture probability is then modeled as a function of distance between the centroid and the traps.

Traps may be of the type that hold an animal for the duration of an occasion and rendered inactive for the remainder of the occasion. This would be the case for a cage trap used when analyzing DFS

data using each day as an occasion. A trap that can continue trapping other animals for the duration of an occasion (i.e. mist net in avian studies) could also be used. Devices that record the presence of an individual without any physical trapping are referred to as proximity detectors. They do not hold the animal in any way. A common example of this type of detector is a camera. Tags readable from a photo, or more commonly natural markings on the animal, are used to identify individuals.

In the simplest of approaches, the traps themselves are used to map the home range of animals as they move through the study area. However, the devices used to trap animals for the mark-recapture component of the study (i.e. cage traps for DFS) do not necessarily have to be the same devices used to relocate known individuals. An example of this can be a PIT Tag reader associated with a PVC pipe through which fox squirrels will go. Unlike the traps, these readers can be and should be moved frequently. If they are picking up readings daily, then they should be moved daily. The intent is to use the readers as a surrogate for telemetry data, and obviously the more points where these readers can pick up PIT tags, the better.

Ideally, every animal tagged will be detected enough times that a home range can be defined. The exact spacing is not important, but like the traps, knowing the exact location of the reader is important. This should be recorded as a lat-long with as many significant digits as reasonable, given the accuracy of the GPS used. If an alternative grid system exists that can yield comparable or better x – y coordinates, then that is acceptable. Density of readers should be limited by the number of PIT tag readers available. The more reader locations used the better. Also, there is no reason that use of the readers should be limited to the trapping days. They should be deployed before and after as well as during each seasonal trapping session. The idea is simply to get a season specific estimate of home range. This probably does not change much the weeks before and the weeks after trapping, but it probably does change from season to season.

Recommendations for a pilot study of spatially – explicit capture – recapture (if attempting to use the SERC approach to measure density)

For the purpose of these recommendations, home range refers to the temporally relevant range of the animal during the trapping season, not a yearly home range. The recommendations below are intended to initiate a SECR study should one be desired. As stated within the recommendations, changes can be and probably should be made as the pilot study is being conducted. It is understood that this may be too labor intensive for the refuge to perform. As noted below, effort can be reduced if home ranges are not estimated for every animal. Consultation with the authors is encouraged to reach an obtainable study design that can enhance future DFS studies.

1) Recollection suggests that Blackwater NWR has 3 to 4 PIT tag readers. The following recommendations were written with that in mind.
2) Record daily weather variables, (highs, lows, precipitation, etc).

3) Pick one study site. For this pilot study, it need not be randomly chosen from all sites. We are less interested in inference and more interested in logistics at this point. It is recommended a site that affords biological technicians the easiest access is selected for this initial pilot study.
4) Two or three weeks before a trapping period begins, deploy pvc pipe attractants with PIT tag readers and data recorders. Final determination of the time span before trapping should be biologically driven. You want to capture the behavior that will be displayed during trapping. Therefore, food availability, temperatures, predator presence, etc should be roughly the same as the trap period.
5) Spacing of the detectors will depend on the suspected home range of the animals. Larson (1991) estimated the home range on Assateague Island to be 4.1 hectares. Assuming a square home range, then individuals would roam in an area about 200m x 200m. In this case, detectors every 100 m would probably delineate a home range sufficiently. Likewise, assuming a circular home range, an individual might roam an area with a radius of about 113 m. Again, 100 m spacing should work. Spacing should be adjusted based on what is known about home ranges of DFS at the particular site.
6) A 100 x 100 m grid laid out over a square 25 hectare site would yield 25, 100 x 100 m plots. If a detector is placed at the corner of each block, thus each block is sampled one day. Since only the corners are the sample points, the entire site would be sampled over the course of 15 days. This is an ideal situation, and still it is labor intensive.
7) Data loggers should be checked daily. If they are logging animals' presence on a daily occurrence, then they should be moved daily. Repeated detections of the same animal at the same site are less valuable then a new detection at a new site. The goal is to delineate a home range.
8) With that in mind, keep accurate records of **where** and **when** traps are set, even if they DO NOT capture an animal. Ideally, enough detections for each marked animal in the study site will be collected so that each individual's home range can be delineated. However, it is better to have fewer home ranges delineated completely, then to have all partially delineated. There isn't an exact process to establish what is "good enough". This will be somewhat arbitrary, and will have to be determined by inspecting the data as the study progresses. Hopefully, this pilot study will yield a good rule of thumb for the number of captures needed to inform future DFS SECR studies. The relevant metric here is that an appropriate centroid needs to be established. It is possible that 3 "perfect" detections could yield an accurate centroid, but it is not likely. More likely, 6 to 10 captures will be needed. Visually inspecting the data should give an idea if the full home range is being captured.
9) Trapping should be carried out according to recommendations in this report. Records of where animals are caught should also be kept, as these can inform the home range analysis.
10) Though not mandatory, analysis can be done in R using the SECR package (Efford, 2011) freely available with documentation at the R website.

11) Perform an analysis after ONE trapping session, (i.e. 5 days of trapping and the needed number of days deploying the detectors). This should be done in order to determine if;
    a. the process is sound
    b. enhanced results merit the increase in effort
    c. if any changes should be implemented

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Appendix A

Graphs of Abundance by Year and Gender

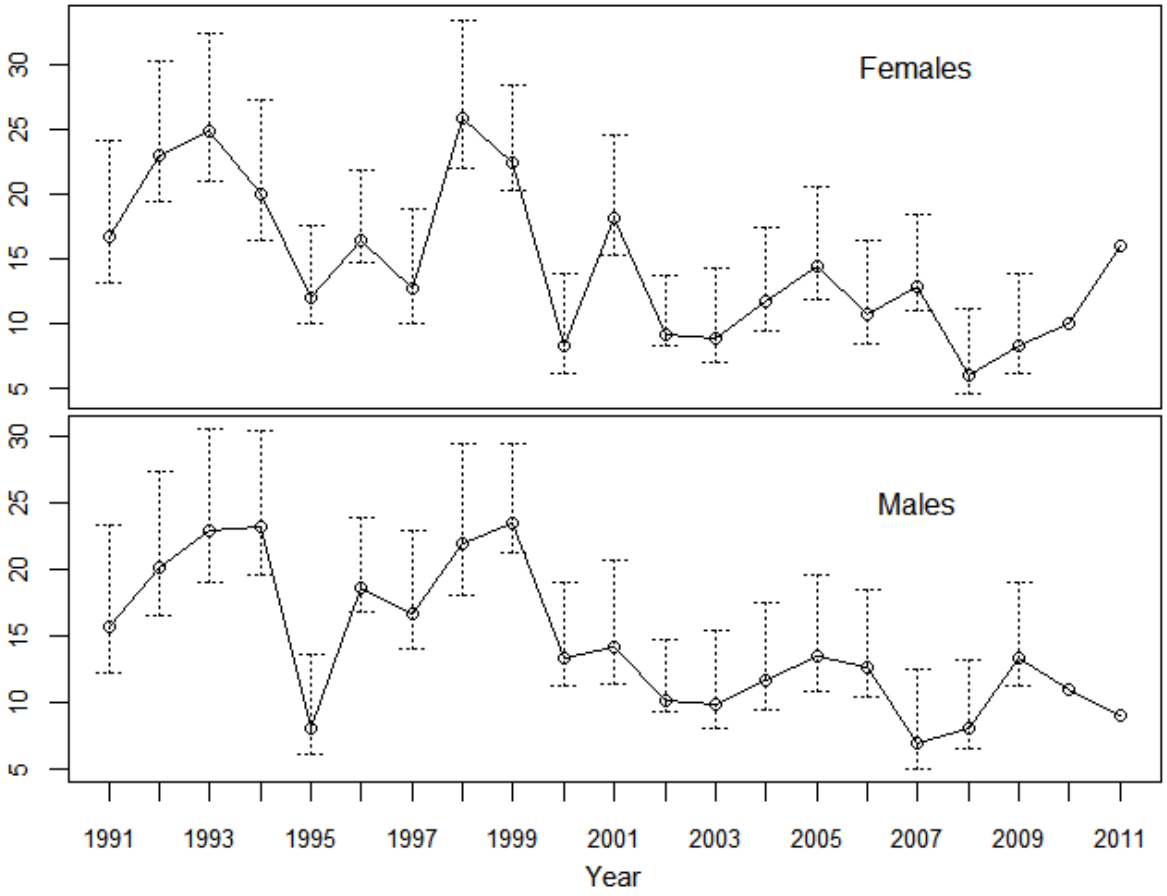

Figure A1) Abundance for Egypt. The point estimates without error bars are estimates where standard errors were not estimates, or approached zero.

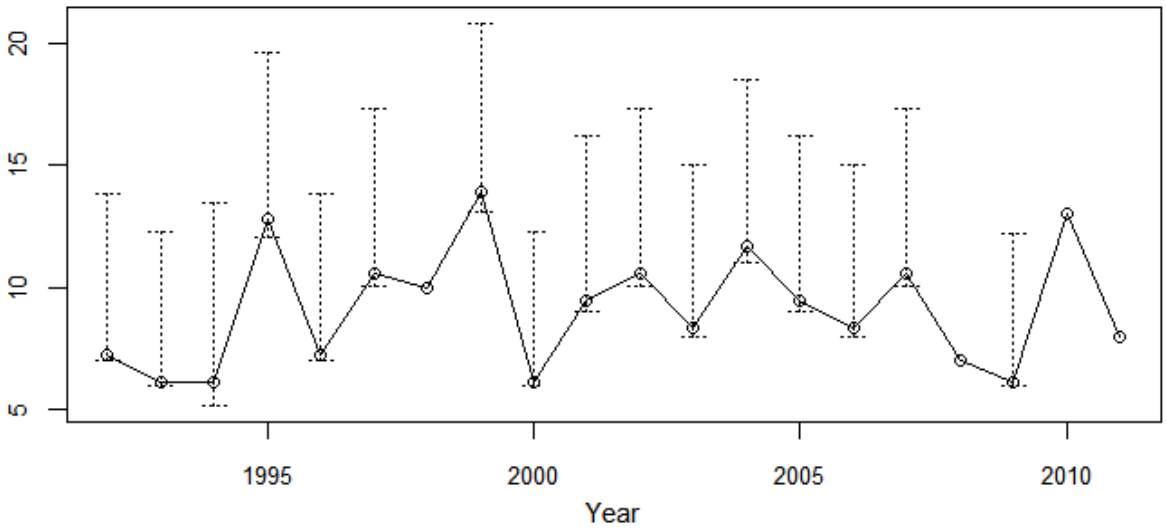

Figure A2) Abundance for Jarrett. The point estimates without error bars are estimates where standard errors were not estimates, or approached zero. Genders are combined for Jarrett.

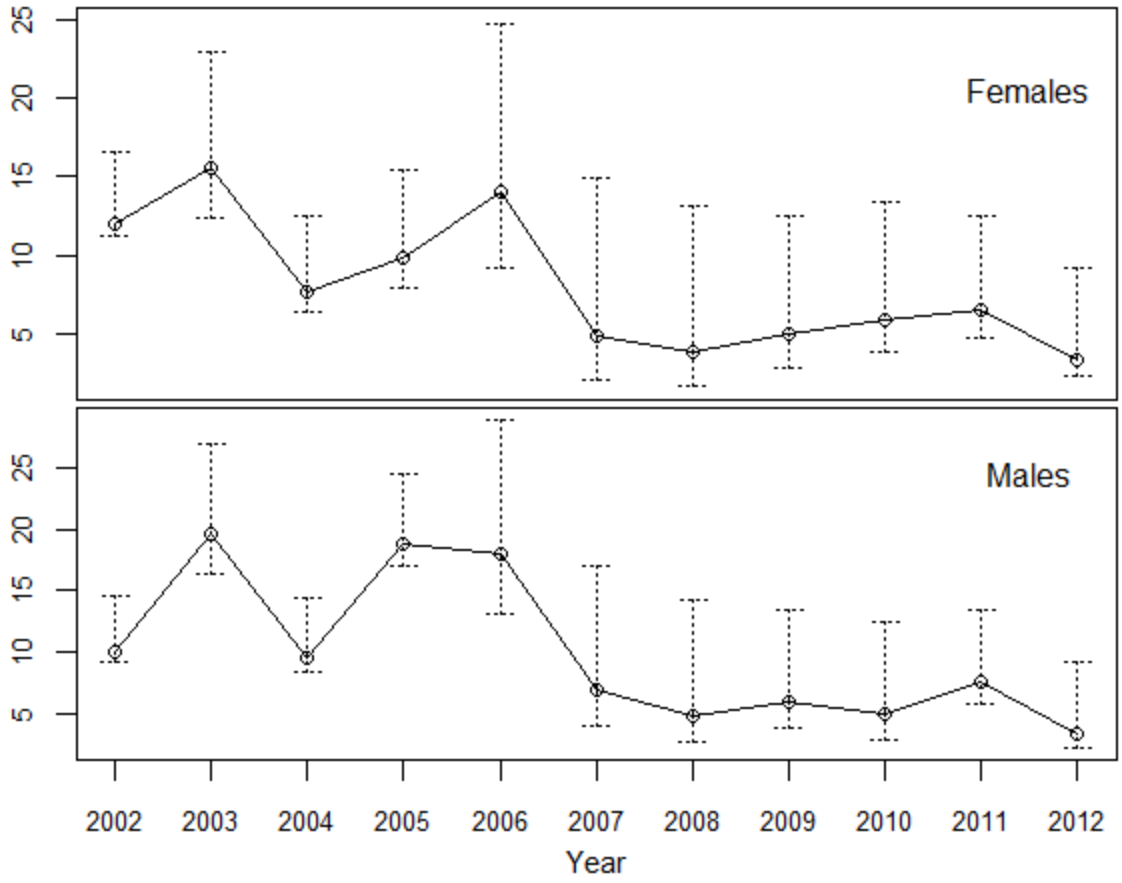

Figure A3), Abundance estimates for the Greenbrier Study site. Females shown on the top graph and males are shown on the bottom graph.

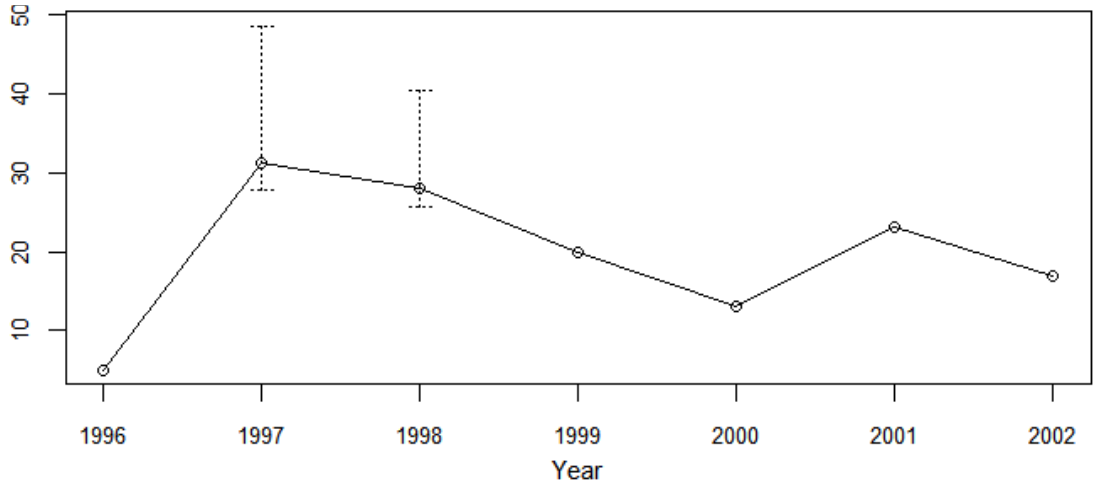

Figure A5) Abundance estimates for the Jarrett West study site. Both genders were combined for this analysis and separate estimates of abundance were not possible. Note the high number of years with no error bars since standard errors were not obtainable for those years.

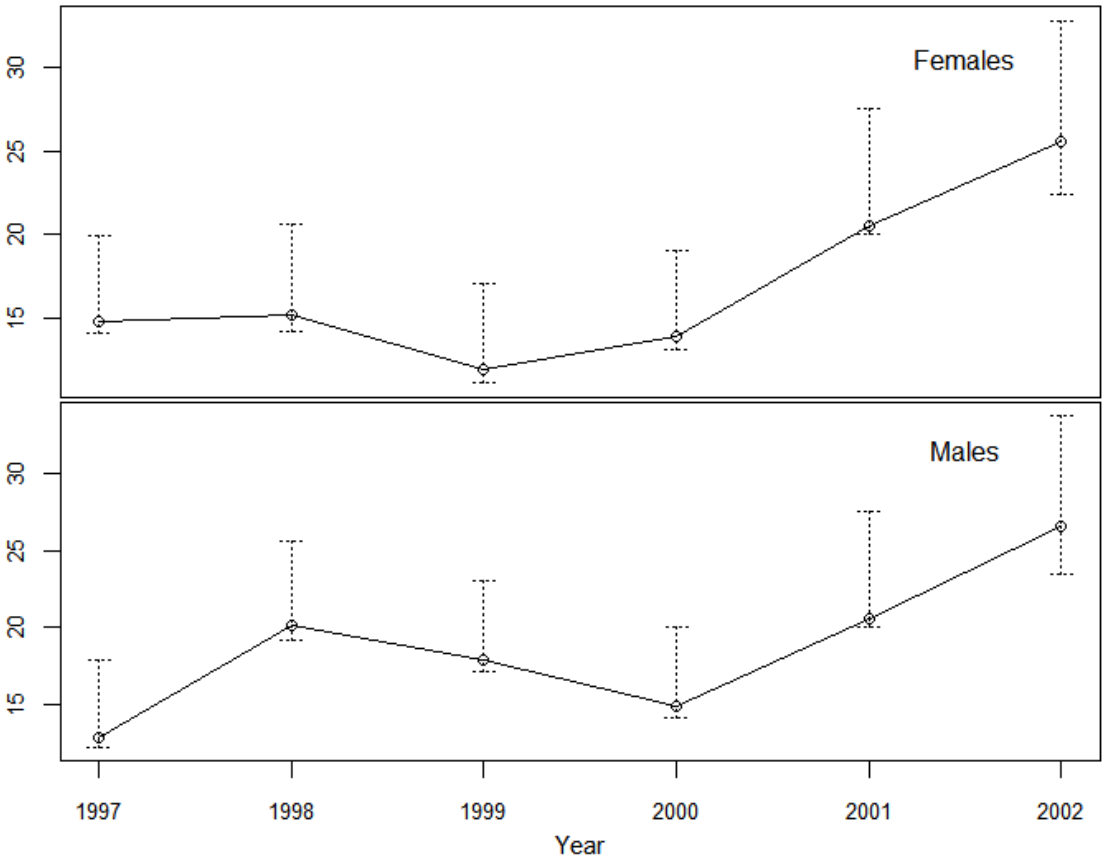

Figure A6) Abundance estimates for the Kuehnle study site. Females shown on the top graph and males are shown on the bottom graph. Estimates were not obtainable for the first year of the study.

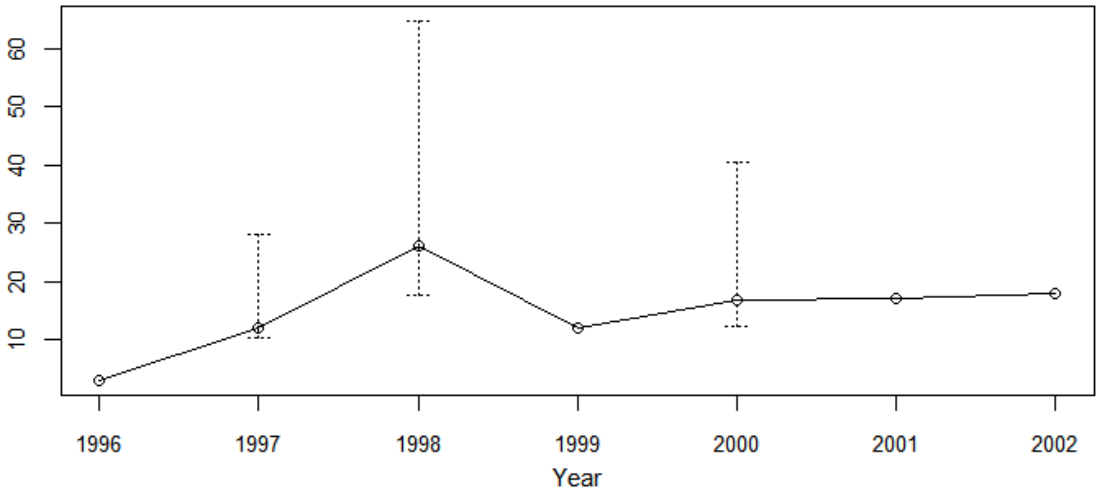

Figure A7) Abundance estimates for the White Marsh study site. Both genders were combined for this analysis and separate estimates of abundance were not possible. Note the high number of years with no error bars since standard errors were not obtainable for those years.

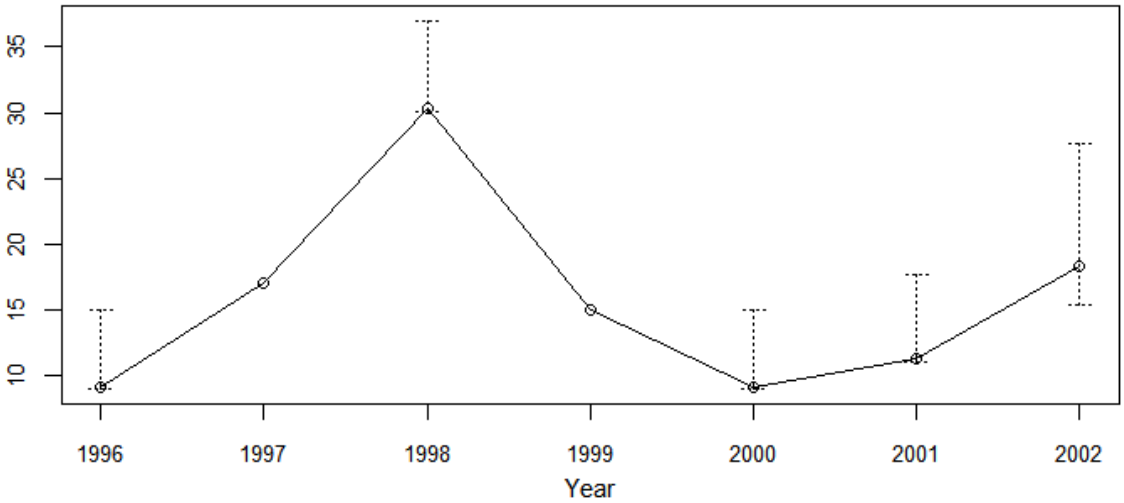

Figure A8) Abundance estimates for the TCF1 study site. Both genders were combined for this analysis and separate estimates of abundance were not possible. Standard errors were not obtainable for the two years without error bars.

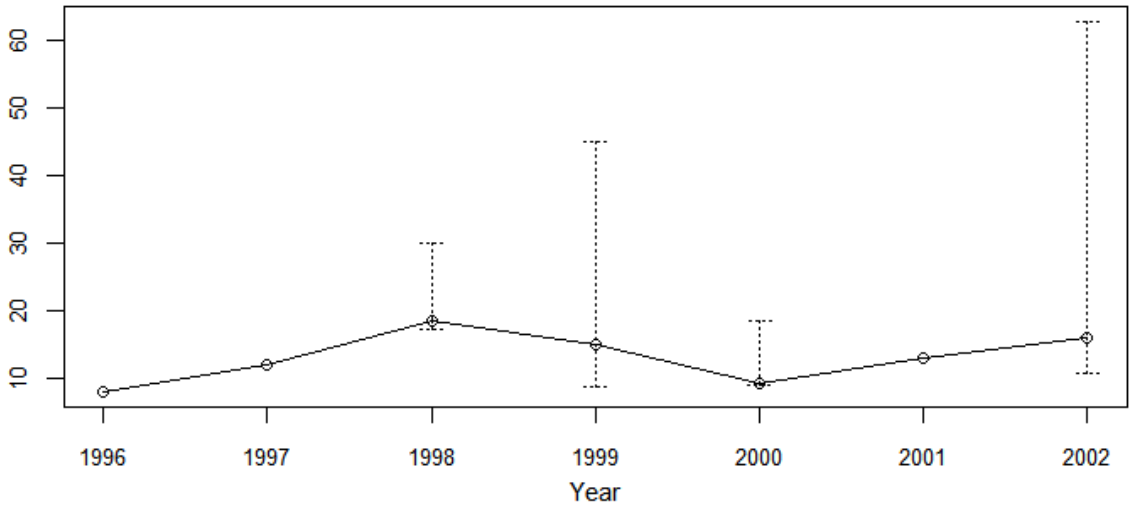

Figure A9) Abundance estimates for the TCF2 study site. Both genders were combined for this analysis and separate estimates of abundance were not possible. Standard errors were not obtainable for the three years without error bars.

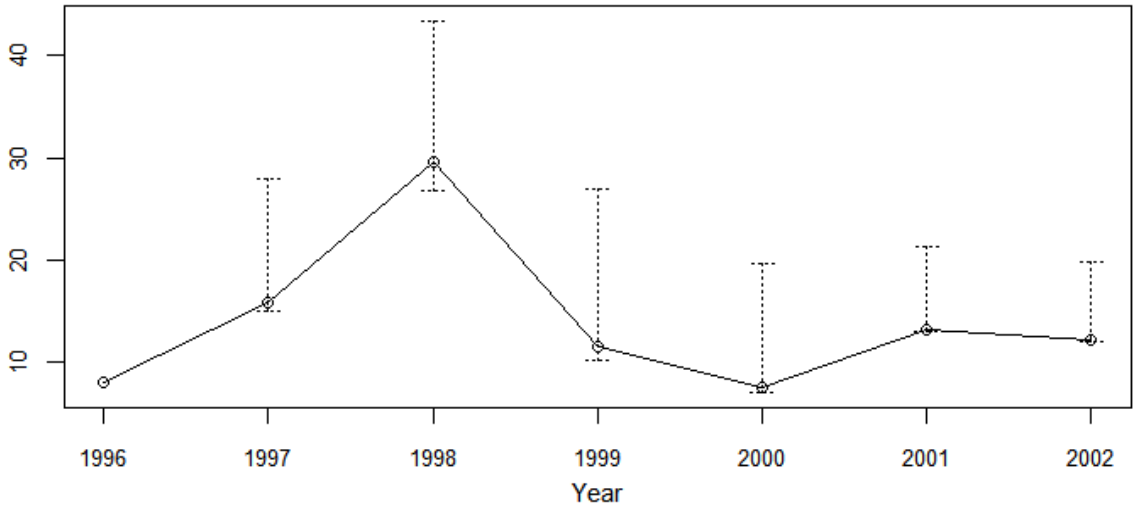

Figure A10) Abundance estimates for the TCF3 study site. Both genders were combined for this analysis and separate estimates of abundance were not possible. Standard errors were not obtainable for 1996.

Appendix A

Example R Code for RMark / MARK analysis

```
library(RODBC)
library(RMark)

chan <- odbcConnectExcel("D:\\PostDoc\\Delmarva Fox
Squirrel\\Data\\DFS_EGYPT_ 1991-2011-input.xls")                    #
DFS_EGYPT_1991-2011.xlsx
Egypt_imp <- sqlFetch(chan,"91-11 data", as.is = c(1:27))
#Egypt_imp <- sqlFetch(chan,"91-11 data")
close(chan)
head(Egypt_imp, 1)
egypt.1 <- Egypt_imp
egypt <- egypt.1[order(egypt.1$Date), ]


individs <- data.frame()
individs[1,1] <- egypt$key[1]
for (i in 2:nrow(egypt)) {
    newrow <- nrow(individs) + 1
    if(is.na(match(egypt$key[i], individs[ ,1]))) {
          individs[newrow, 1] <- egypt$key[i]
                                                  }
                           }

 dates <- data.frame()
 dates[1,1] <- egypt$Date[1]
 for (i in 2:nrow(egypt)) {
    newrow <- nrow(dates) + 1
    if(is.na(match(egypt$Date[i], dates[ ,1]))) {
          dates[newrow, 1] <- egypt$Date[i]
                                                  }
                           }


capt.hist <- data.frame(individs, matrix(0, nrow(individs),
nrow(dates)))
for (i in 1:nrow(egypt)) {
    col.num <- match(egypt$Date[i], dates[,1]) + 1 # cause first
column is key names
    row.num <- match(egypt$key[i], individs[,1])
    capt.hist[row.num, col.num] <- 1
                           }

dates.2 <- as.data.frame(as.POSIXct(strptime(dates[ ,1], '%Y-%m-%d
%H:%M:%S')))
colnames(dates.2) <- "date"
Date.test <- as.character(dates.2[ ,1])
e.capt.hist <- capt.hist        # for egypt_robust.r code
egypt.capt.hist <- capt.hist
names(egypt.capt.hist)[1:70] <- c("Individs", Date.test[1:69])
```

```
egypt.ch <- e.capt.hist

# Really want to make this work,... but won't
#egypt.ch$ch <- with(egypt.ch, paste(get(names(egypt.ch)[2:70]),
sep=''))


egypt.ch$ch <- with(egypt.ch, paste(X1, X2, X3, X4, X5, X6, X7, X8,
X9,
                                    X10, X11, X12, X13, X14, X15,
X16, X17, X18, X19,
                                    X20, X21, X22, X23, X24, X25,
X26, X27, X28, X29,
                                    X30, X31, X32, X33, X34, X35,
X36, X37, X38, X39,
                                    X40, X41, X42, X43, X44, X45,
X46, X47, X48, X49,
                                    X50, X51, X52, X53, X54, X55,
X56, X57, X58, X59,
                                    X60, X61, X62, X63, X64, X65,
X66, X67, X68, X69, sep = ''))

Egypt <- egypt.ch[ , c(1, 71)]

#  robust<-Egypt
#run.robust=function(x) {
#robust <- x # change for running in function
#
# data from Robust.dbf with MARK
# 5 primary sessions with secondary sessions of length 2,2,4,5,2
#
#1991 - Mar 29
#       Apr 2
#1992   Mar 23, 24, 28
#1993   Mar 15, 19, 20
#1994   Mar  4,  5,  7
#1995   Mar 28, 29, 31          #14
#1996   Mar  3,                  #15  *
#       Apr  2,  3,  4
#1997   Apr  7,  8,  9          #21
#1998   Mar  7,  8, 10          #24
#1999   Mar 23, 25, 26
#       Apr  1                  #28    *
#2000   Apr 12, 13, 14
#2001   Apr 18, 19, 20
#2002   Apr 16, 17, 18, 19      #38    *
#2003   Apr 14, 16, 22
#2004   Apr 15, 16, 19
#2005   Apr 11, 12, 13
#2006   Apr 10, 11, 12
```

```
#2007   Apr 17, 18, 19
#2008   Mar 24, 25, 26
#2009   Apr  8, 13, 16
#2010   Mar 18, 19, 20, 21, 22  #64  *
#2011   Mar 14, 15, 16, 17, 22  #69   *

time.intervals=c(0, 1,                                          #1991
                 0, 0, 1,
                 0, 0, 1,
                 0, 0, 1,
                 0, 0, 1,
                 0, 0, 0, 1,                                     #1996
                 0, 0, 1,
                 0, 0, 1,
                 0, 0, 0, 1,
                 0, 0, 1,                                        #2000
                 0, 0, 1,
                 0, 0, 0, 1,
                 0, 0, 1,
                 0, 0, 1,
                 0, 0, 1,
                 0, 0, 1,
                 0, 0, 1,
                 0, 0, 1,
                 0, 0, 1,
                 0, 0, 0, 0, 1,                                   #2010
                 0, 0, 0, 0)

egypt.proc <- process.data(Egypt, model="Robust", begin.time=1991,
time.intervals = time.intervals)

####################################
### Make covariates              ###
####################################
egypt.ddl <- make.design.data(egypt.proc)

## Create a data frame of pdsi vals ##
## anuual (pdsi) and fall (f.pdsi)  ##

yrs  <- seq(from = 1991, to = 2011, by =1)
pdsi <- c(3.92, 5.25, 4.25, 4.17, 4.33, 4.17, 3.42, 3.67, 4.67,
4.42, 3.75, 4.83,
          4.83, 1.58, 3.50, 4.17, 3.00, 5.00, 4.33, 2.42, 3.83)
f.pdsi <- c(5, 4, 4.5, 4, 5, 4, 4, 4.5, 4.5, 3, 4, 7, 1, 3, 4, 3.5,
5.5, 4.5, 4, 3.5, 4)
PDSI <- data.frame(yrs, pdsi, f.pdsi)

#egypt.ddl=add.design.data(egypt.proc, dipper.ddl, parmameter="p"
## merge pdsi df with S and p data ##
```

```
nam <- names(egypt.ddl$p)
temp <- merge(egypt.ddl$p, PDSI, by.x='session', by.y='yrs', sort=F)
egypt.ddl$p <- temp[c(nam, 'pdsi', 'f.pdsi')]

nam <- names(egypt.ddl$S)
temp <- merge(egypt.ddl$S, PDSI, by.x='time', by.y='yrs', sort=F)
egypt.ddl$S <- temp[c(nam, 'pdsi', 'f.pdsi')]

### End coavariate addition ###

## Define the model choices ##

S.dot=list(formula=~1)
S.time=list(formula=~time, fixed=list(time=2003, value=1))
S.time2=list(formula=~time, fixed=list(time=c(2003, 2011), value=1))
S.time3=list(formula=~session, fixed=list(time=c(2003, 2011),
value=1))
S.pdsi=list(formula=~pdsi)
S.pdsi2=list(formula=~pdsi, fixed=list(time=2003, value=1))
S.f.pdsi=list(formula=~f.pdsi)

p.dot=list(formula=~1)
p.time=list(formula=~time)
p.session=list(formula=~session)
p.pdsi=list(formula=~1+pdsi)
p.f.pdsi=list(formula=~f.pdsi)
p.time.session=list(formula=~-1+session:time,share=TRUE)

GP.dot=list(formula=~1)
GP.fix=list(fixed = 0)

GDP.dot=list(formula=~1)
GDP.fix=list(fixed = 0)


### Run the models ###

model.1    <- mark(data = egypt.proc, model.parameters = list(S =
S.time,
                                                              p =
p.time,

GammaPrime = GP.dot,

GammaDoublePrime = GDP.dot))

model.2    <- mark(data = egypt.proc, model.parameters = list(S =
S.time,
                                                              p =
p.time,
```

```
GammaPrime = GP.fix,

GammaDoublePrime = GDP.fix),
                   model.name = 'S(~time)gdp(fix)gp(fix)p(~time)'
)

model.3    <- mark(data = egypt.proc, model.parameters = list(S =
S.time,
                                                              p =
p.dot,

GammaPrime = GP.fix,

GammaDoublePrime = GDP.fix),
                   model.name = 'S(~time)gdp(fix)gp(fix)p(~1)'
)

model.4    <- mark(data = egypt.proc, model.parameters = list(S =
S.dot,
                                                              p =
p.time,

GammaPrime = GP.fix,

GammaDoublePrime = GDP.fix),
                   model.name = 'S(~1)gdp(fix)gp(fix)p(~time)'
)

model.5    <- mark(data = egypt.proc, model.parameters = list(S =
S.dot,
                                                              p =
p.dot,

GammaPrime = GP.fix,

GammaDoublePrime = GDP.fix),
                   model.name = 'S(~1)gdp(fix)gp(fix)p(~1)'
)       # parameter est check

model.6    <- mark(data = egypt.proc, model.parameters = list(S =
S.time2,
                                                              p =
p.time,

GammaPrime = GP.fix,

GammaDoublePrime = GDP.fix),
              model.name = 'S(~time2)gdp(fix)gp(fix)p(~time)'
)          # parameter est check
```

```
model.7    <- mark(data = egypt.proc, model.parameters = list(S =
S.time2,
                                                              p =
p.dot,

GammaPrime = GP.fix,

GammaDoublePrime = GDP.fix),
             model.name = 'S(~time2)gdp(fix)gp(fix)p(~1)'
)           # parameter est check

model.8    <- mark(data = egypt.proc, egypt.ddl, model.parameters =
list(S = S.time2,
                                                              p =
p.pdsi,

GammaPrime = GP.fix,

GammaDoublePrime = GDP.fix),
             model.name = 'S(~time2)gdp(fix)gp(fix)p(~pdsi)'
)           #

model.9   <- mark(data = egypt.proc, egypt.ddl, model.parameters =
list(S = S.pdsi,
                                                              p =
p.dot,

GammaPrime = GP.fix,

GammaDoublePrime = GDP.fix),
             model.name = 'S(~pdsi)gdp(fix)gp(fix)p(~1)'
)           #

model.10   <- mark(data = egypt.proc, egypt.ddl, model.parameters =
list(S = S.pdsi,
                                                              p =
p.pdsi,

GammaPrime = GP.fix,

GammaDoublePrime = GDP.fix),
             model.name = 'S(~pdsi)gdp(fix)gp(fix)p(~pdsi)'
)           #

model.11    <- mark(data = egypt.proc, egypt.ddl, model.parameters =
list(S = S.time2,
                                                              p =
p.f.pdsi,
```

```
GammaPrime = GP.fix,

GammaDoublePrime = GDP.fix),
             model.name = 'S(~time2)gdp(fix)gp(fix)p(~f.pdsi)'
)           #

model.12   <- mark(data = egypt.proc, egypt.ddl, model.parameters =
list(S = S.f.pdsi,
                                                                   p =
p.dot,

GammaPrime = GP.fix,

GammaDoublePrime = GDP.fix),
             model.name = 'S(~f.pdsi)gdp(fix)gp(fix)p(~1)'
)           #

model.13   <- mark(data = egypt.proc, egypt.ddl, model.parameters =
list(S = S.f.pdsi,
                                                                   p =
p.f.pdsi,

GammaPrime = GP.fix,

GammaDoublePrime = GDP.fix),
             model.name = 'S(~f.pdsi)gdp(fix)gp(fix)p(~f.pdsi)'
)           #

model.14   <- mark(data = egypt.proc, egypt.ddl, model.parameters =
list(S = S.pdsi2,
                                                                   p =
p.dot,

GammaPrime = GP.fix,

GammaDoublePrime = GDP.fix),
             model.name = 'S(~pdsi2)gdp(fix)gp(fix)p(~1)'
)           #

model.15   <- mark(data = egypt.proc, egypt.ddl, model.parameters =
list(S = S.pdsi2,
                                                                   p =
p.pdsi,

GammaPrime = GP.fix,

GammaDoublePrime = GDP.fix),
             model.name = 'S(~pdsi2)gdp(fix)gp(fix)p(~pdsi)'
)           #
```

```
model.16    <- mark(data = egypt.proc, model.parameters = list(S =
S.time2,
                                                                   p =
p.session,

GammaPrime = GP.fix,

GammaDoublePrime = GDP.fix),
              model.name = 'S(~time2)gdp(fix)gp(fix)p(~session)'
)          # parameter est check

model.17    <- mark(data = egypt.proc, model.parameters = list(S =
S.time,
                                                                   p =
p.session,

GammaPrime = GP.fix,

GammaDoublePrime = GDP.fix),
              model.name = 'S(~time)gdp(fix)gp(fix)p(~session)'
)

collect.models()
```