

Estimation of Demographic Parameters for New Zealand Sea Lions Breeding on the Auckland Islands

POP2010/01 Obj 3:
1997/98 – 2011/11

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Survival and Reproduction

- 2 key demographic processes
- Can be estimated from tag-resight data using mark-recapture methods
- Previous report highlighted importance of accounting for tag-loss
 - Artificially inflates mortality rates
- Sightability may be different for breeders/non-breeders, branded animals, number of flipper tags

Survival and Reproduction

- 4 components to model tag-resight data
 - Number of flipper tags each year
 - Survival from one year to next
 - Whether female breeds in a year
 - Number of sightings in a year

Survival and Reproduction

- Number of flipper tags in year t is multinomial random variable with 1 draw and category probabilities (T 's) that depends on number of tags in previous year (allows for non-independent tag loss)

		Number of tags in year t		
		0	1	2
Number of tags in year $t-1$	0	1	0	0
	1	$1 - T_{1,1}$	$T_{1,1}$	0
	2	$1 - T_{1,2} - T_{2,2}$	$T_{1,2}$	$T_{2,2}$

Survival and Reproduction

- Given female is alive, it's age and breeding status in year $t-1$, whether it is alive in year t is a Bernoulli random variable where probability of success (survival) is $S_{age,t-1,bred}$

Survival and Reproduction

- Given female is alive in year t , it's age and breeding status in year $t-1$, whether it breeds in year t is a Bernoulli random variable where probability of success (breeding) is $B_{age,t,bred}$

Survival and Reproduction

- 3 age-classes used for survival/reproduction: 0-3, 4-14, 15+
- OR, constant for 0-3, and logit-linear for age 4+
- Exploratory analysis investigating the use of splines also conducted
- Survival and breeding probabilities = 0 for “breeders” in 0-3 age class

Survival and Reproduction

$$y_{a,t,b} = \mu_{a,b} + \varepsilon_{t,b}, \quad \varepsilon_{t,b} : N(0, \sigma_b^2)$$

$$\theta_{a,t,b} = \frac{e^{y_{a,t,b}}}{1 + e^{y_{a,t,b}}}$$

- Annual variation depends upon previous breeding status

Survival and Reproduction

- Given female is alive, it's breeding status, presence of a brand, PIT tag and number of tags in year t , the number of times it's sighted during a field season is a zero-inflated binomial random variable with a daily resight probability $p_{t,bred,brand,tags}$
- 2 models; no zero-inflation or zero-inflation assumed time-constant, but different for each age/breeding class

Survival and Reproduction

- Branded animals have the same resight probability regardless of number of flipper tags.
- Animals with no flipper tags can only be resighted if they are chipped or branded.
- PIT tags have no effect on the resight probability if the unbranded animal has 1 or more flipper tags.
- There is a consistent odds ratio (δ) between resighting animals with 1 and 2 flipper tags.
- Resight probabilities are different for breeding and non-breeding animals.
- Resight probabilities vary annually.

Survival and Reproduction

- $p_{t,bred,brand}$ - applies to all females with brand
- $p_{t,bred,chip}$ - applies to unbranded females with no flipper tags
- $p_{t,bred,T1}$ - applies to unbranded females with one flipper tags
- $p_{t,bred,T2}$ - applies to unbranded females with two flipper tags

Survival and Reproduction

- Posterior distributions for parameters can be approximated with WinBUGS by defining a model in terms of the 4 random variables
- Some outcomes are actually latent (unknown) random variables, but their 'true' value can be imputed by MCMC
- Equivalent to a multi-state mark-recapture model

Survival and Reproduction

- 2 chains of at least 30,000 iterations
- Last 20,000 iterations retained for inference
- Prior distributions:
 - μ 's $\sim N(0, 3.78^2)$
 - σ 's $\sim U(0, 10)$
 - Other probabilities $\sim U(0, 1)$
 - $T_2 \sim \text{Dirichlet}(1, 1, 1)$
 - $\ln(\delta) \sim N(0, 10^2)$
- Chains demonstrated convergence and good mixing

Survival and Reproduction

- Model deviance can be calculated and compared for each model
- Same interpretation as for maximum-likelihood methods (e.g., GLM), but has a distribution not single value
- Comparison of distributions a reasonable approach to determine relative fit of the models

Survival and Reproduction

- Fit of model to the data can be determined using Bayesian p-values with deviance as test statistic
- For each iteration in MCMC procedure, a simulated data set is created using current parameter values, and the deviance value calculated
- Frequency of simulated deviance values $>$ observed deviance values provides a p-value for model fit

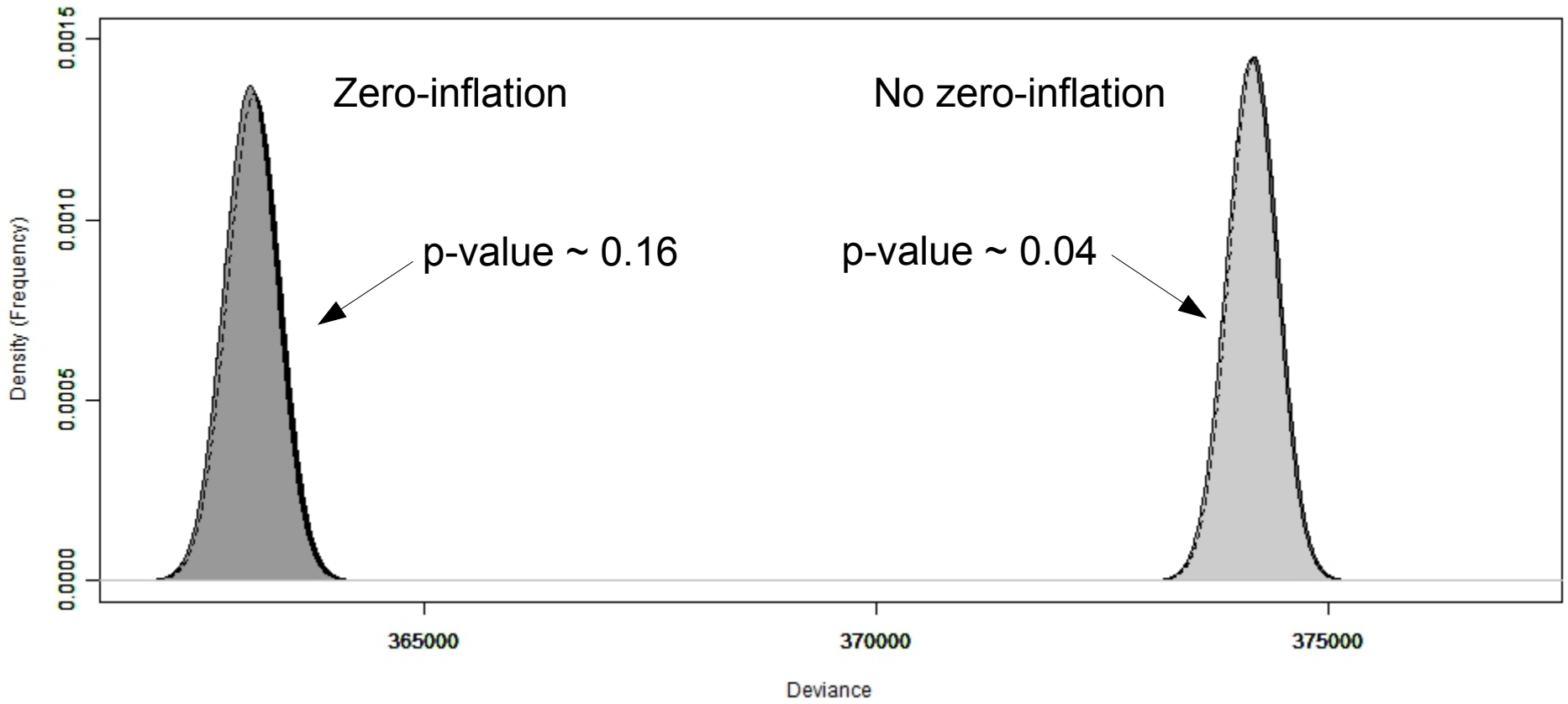
Survival and Reproduction: Data

- 1990-2006 tagging cohorts
- Resights from 1997/8-2010/11 in main field season at Enderby Island
- Stricter (status = 3) and liberal (status = 3 or 15) definitions of breeder used

Survival and Reproduction: Data

- Retagged females dealt with using the Lazarus approach
- Approximately 2300 tagged females included in analysis

Results (stricter defn.)



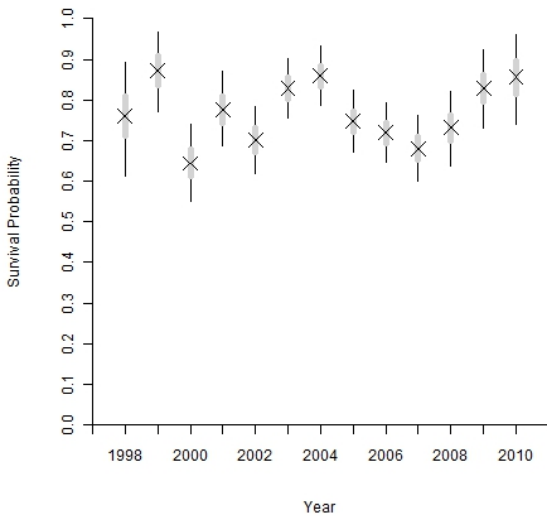
Results (strict defn.)

- Tag loss

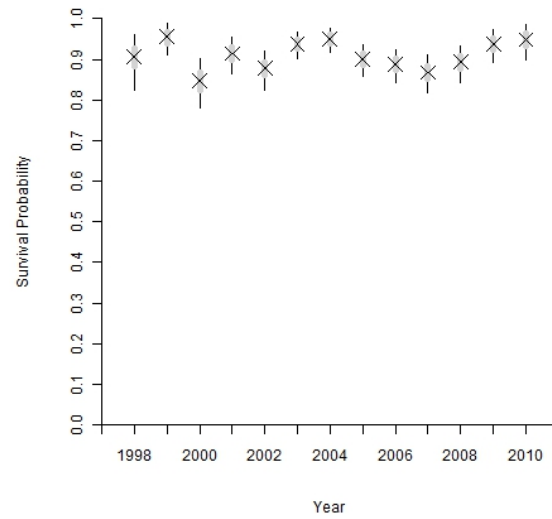
Tags at $t-1$	Tags at t	Probability
1	0	0.11 (0.10, 0.13)
	1	0.89 (0.87, 0.90)
2	0	0.04 (0.03, 0.05)
	1	0.14 (0.13, 0.16)
	2	0.82 (0.80, 0.83)

Non-breeder in $t-1$ survival

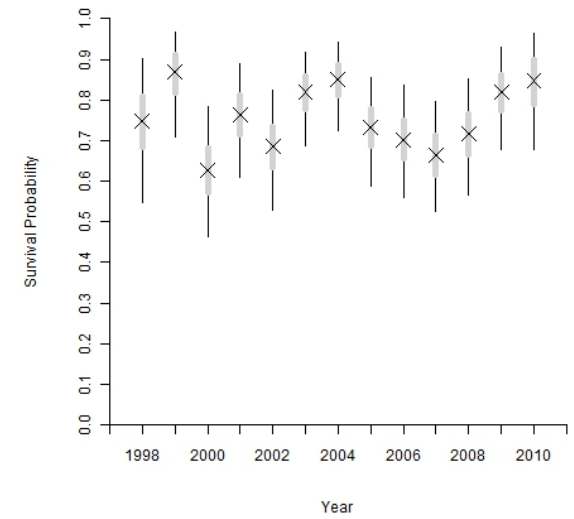
(Age Classes)



0-3



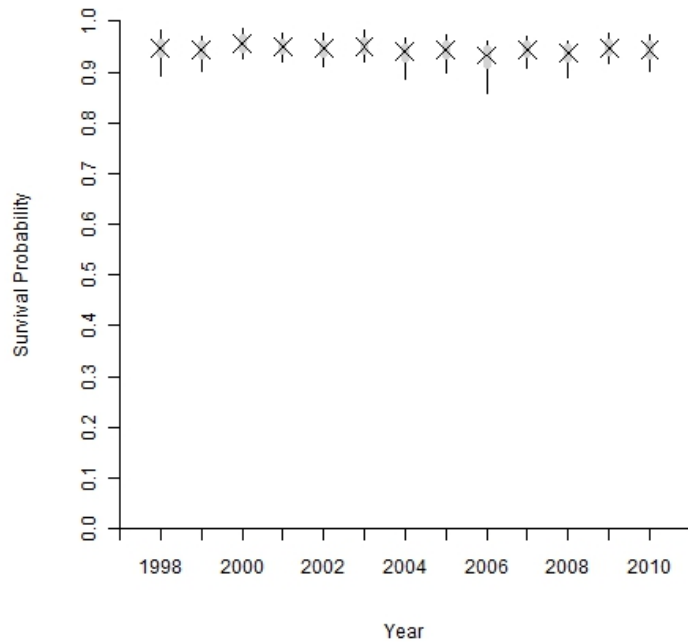
4-14



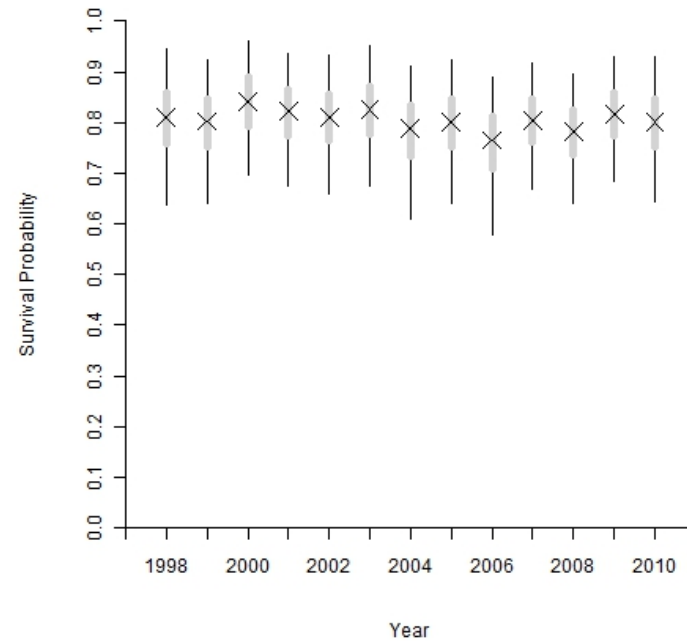
15+

Breeder in $t-1$ survival

(Age Classes)



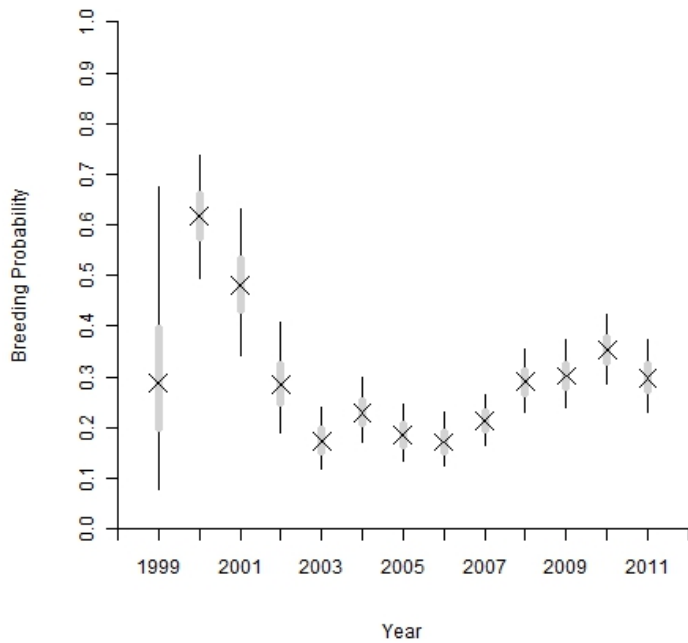
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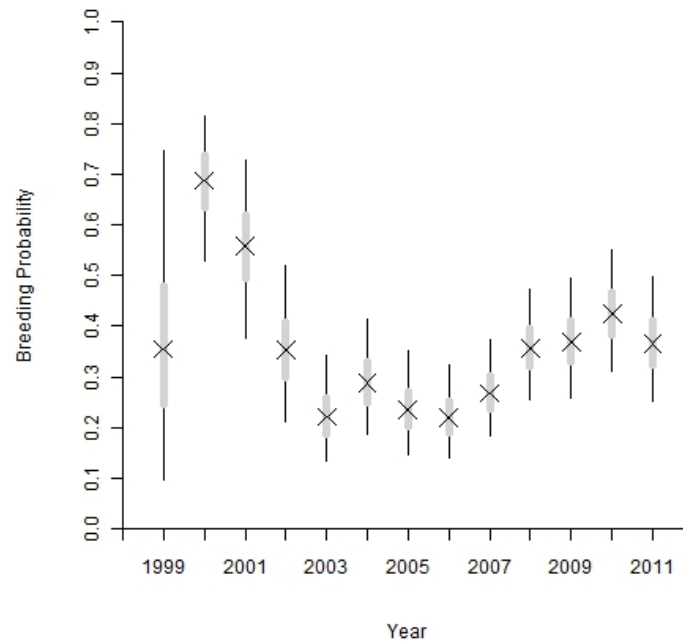
15+

Non-breeder in $t-1$ repro.

(Age Classes)



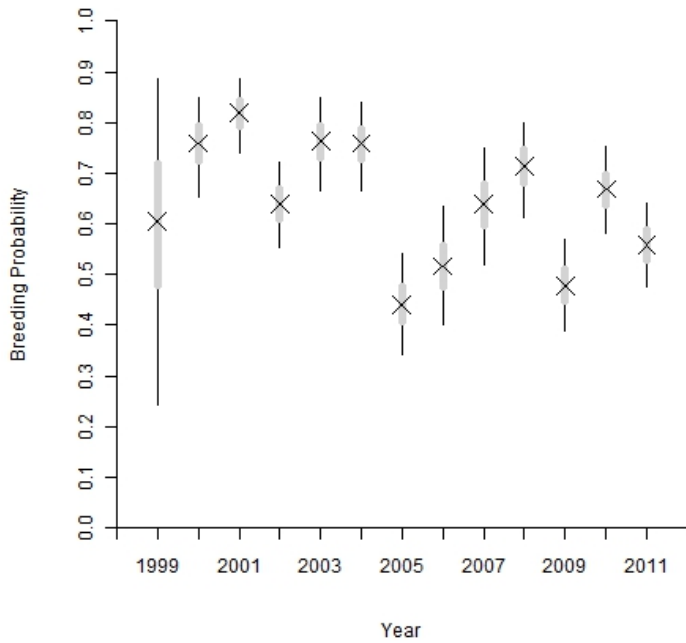
4-14



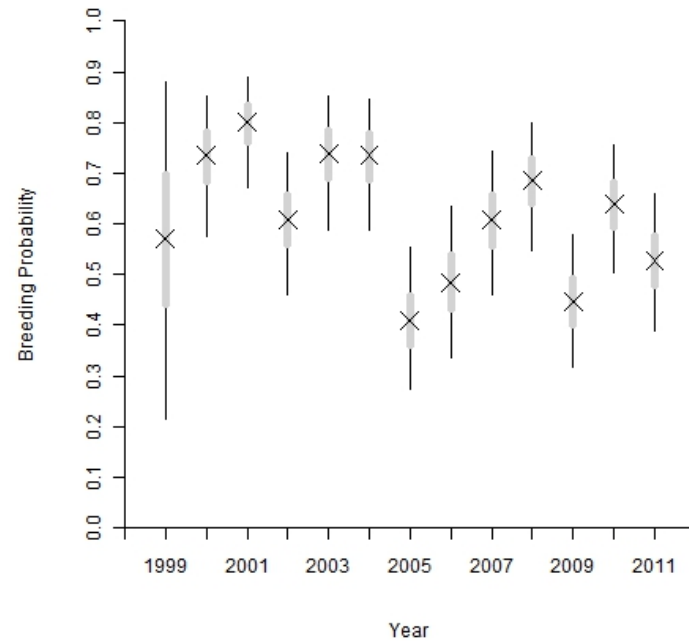
15+

Breeder in $t-1$ repro.

(Age Classes)



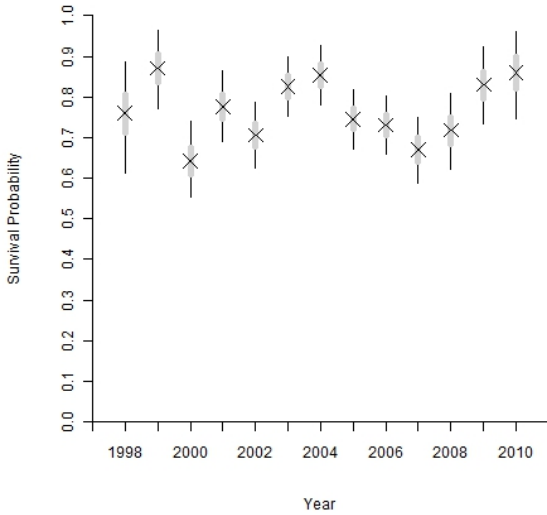
4-14



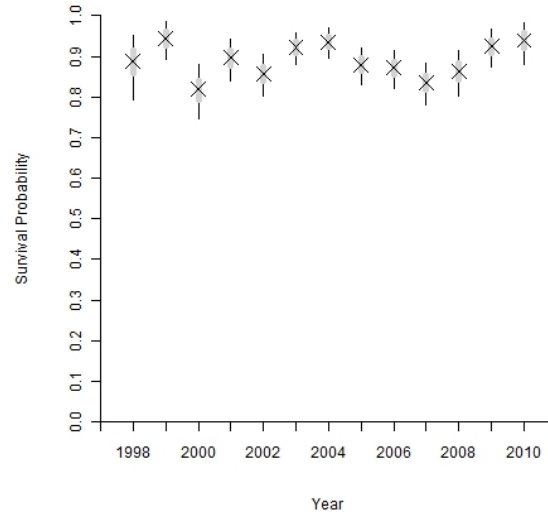
15+

Non-breeder in $t-1$ survival

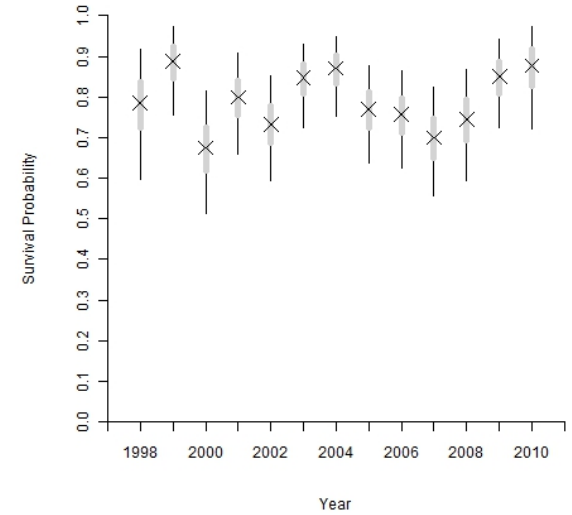
(Logit-linear)



0-3



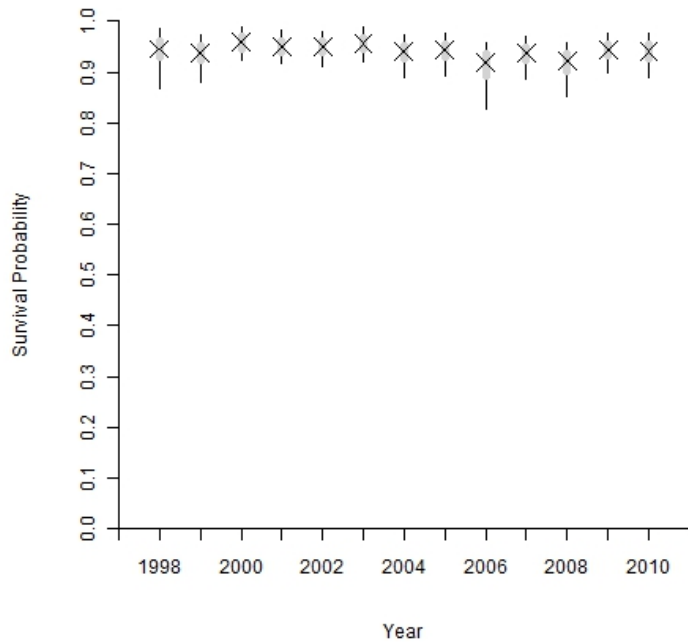
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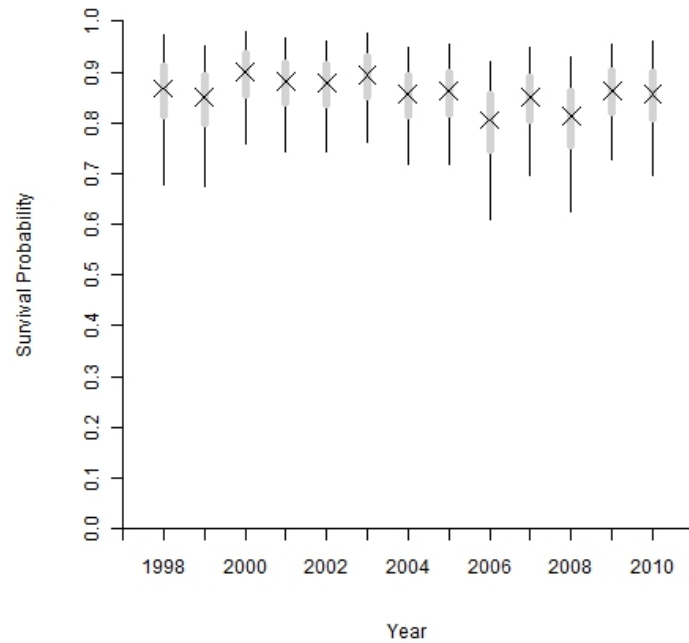
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Breeder in $t-1$ survival

(Logit-linear)



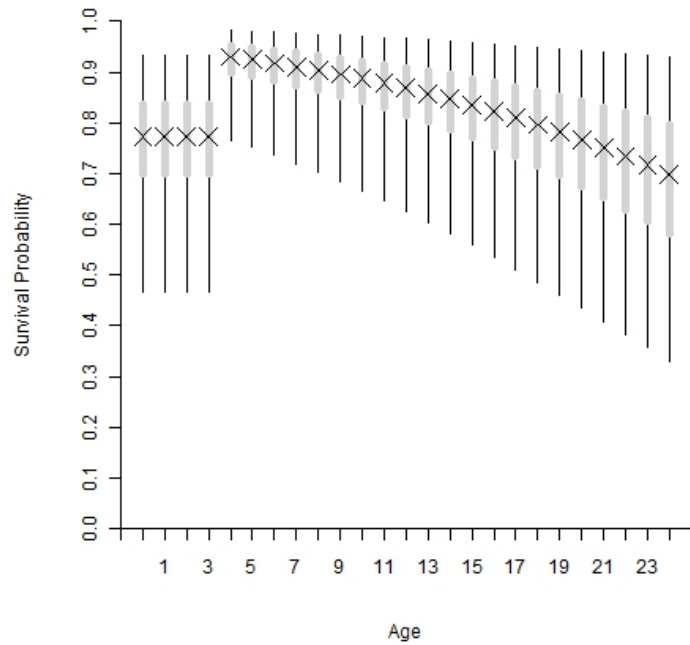
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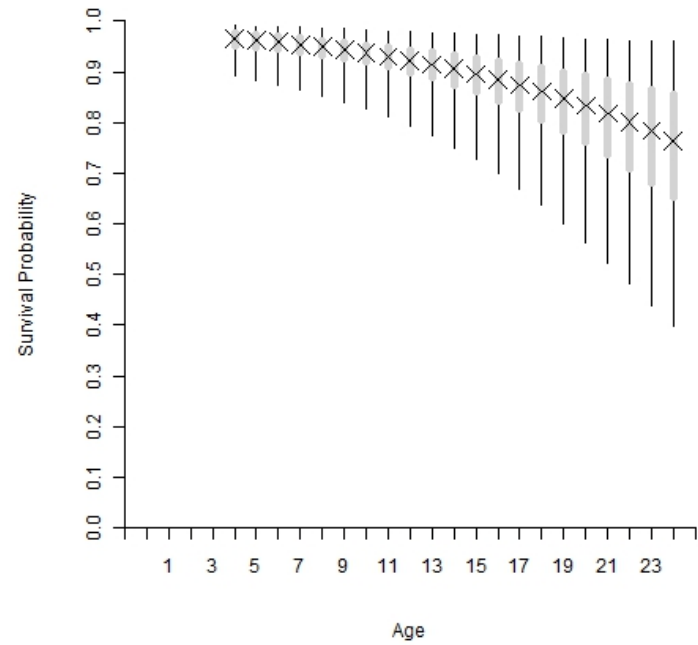
18

Survival vs Age

(Logit-linear)



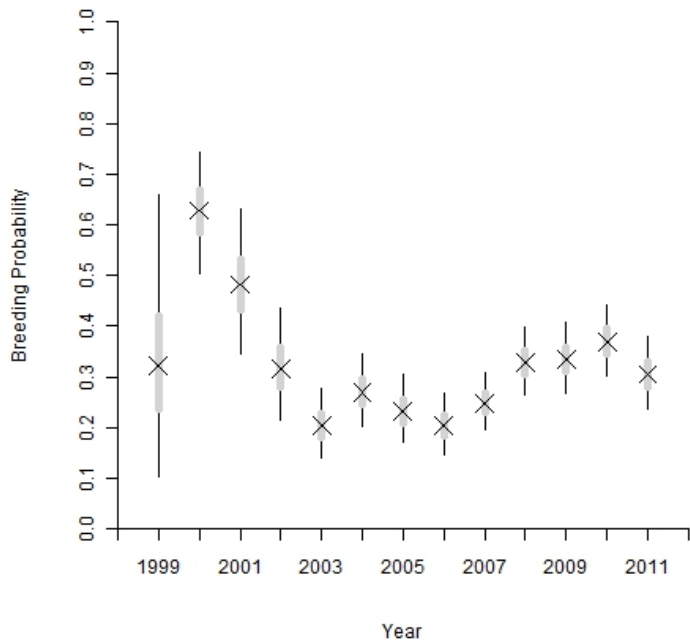
Non-breeder



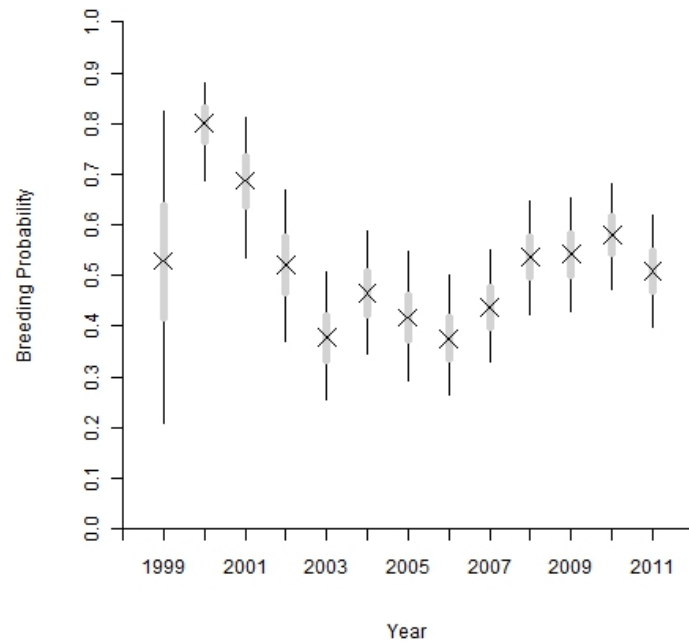
Breeder

Non-breeder in $t-1$ repro.

(Logit-linear)



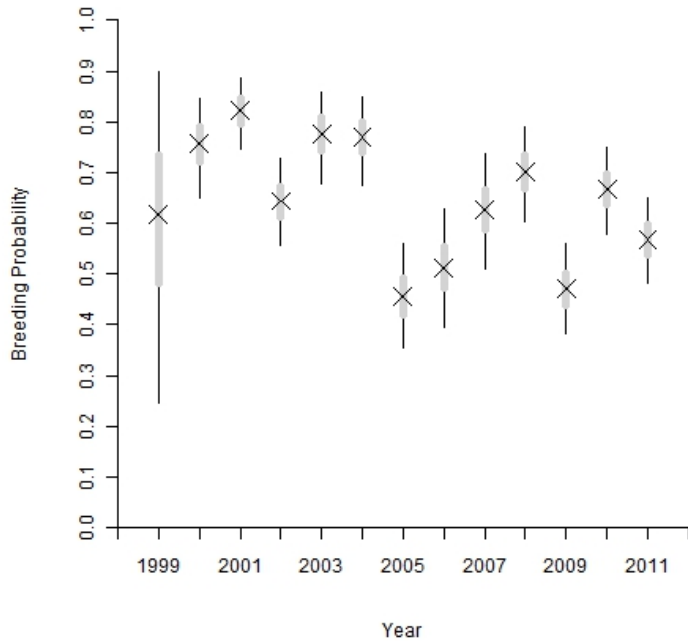
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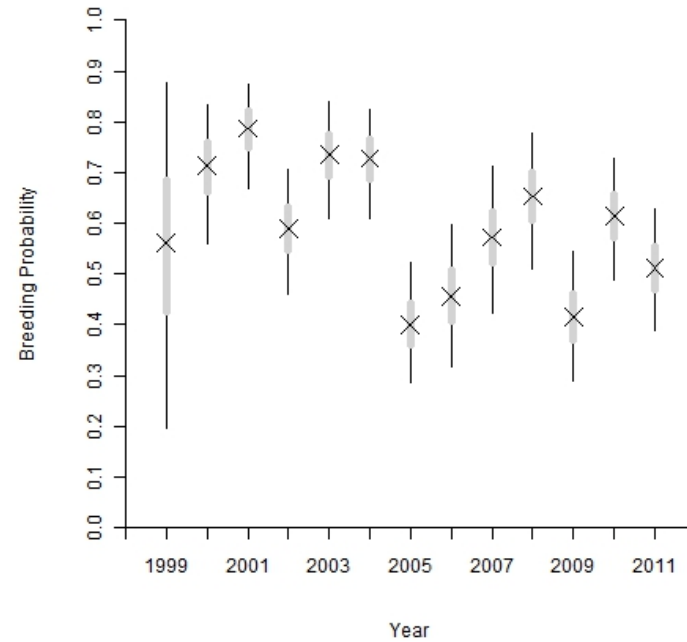
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Breeder in $t-1$ repro.

(Logit-linear)



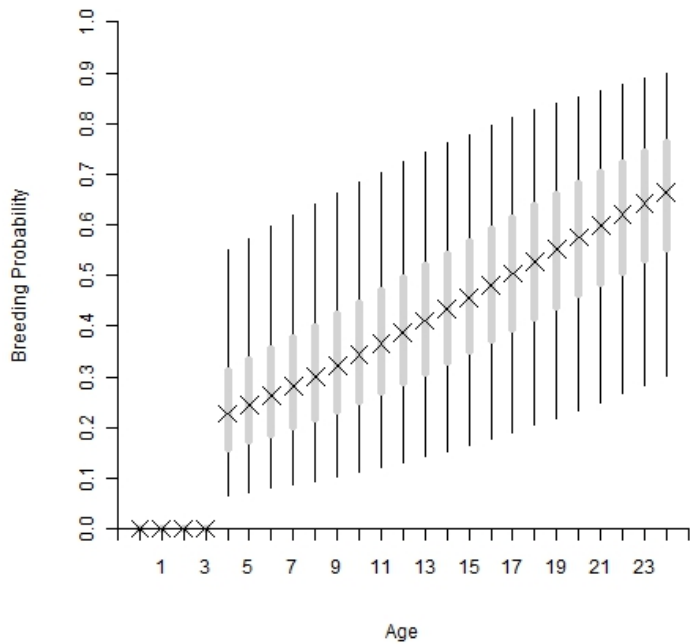
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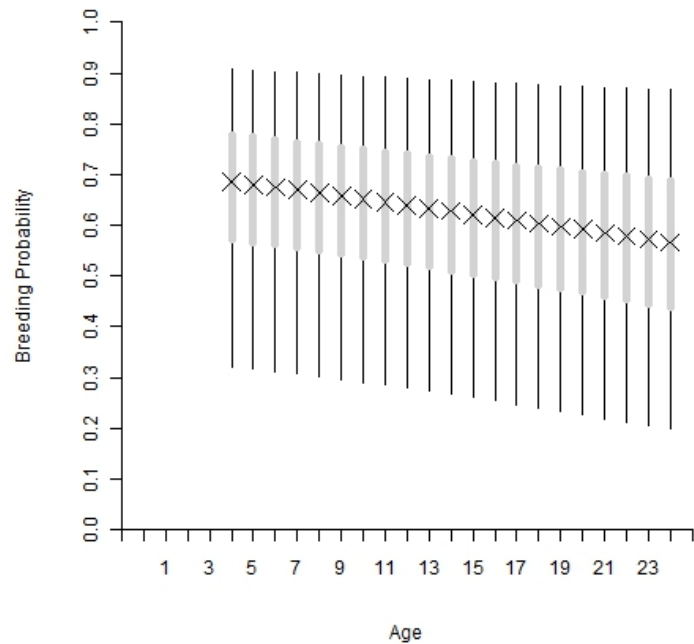
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Breeding vs Age

(Logit-linear)



Non-breeder



Breeder

Results – liberal definition

- Estimates from using the more liberal definition of breeder are very similar to above, although breeding probabilities tend to be slightly higher

Exploratory Analysis

- Exploratory analysis conducted to investigate semi-parametric relationships with age using splines
- 'Knots' are x-values where the nature of the relationship may change
- Y-value at each knot is defined by both relationships, hence creating a continuous 'curve'

Exploratory Analysis

- Linear and quadratic splines have been explored here, with knots at age 4, 8 and 12
- Survival probability for non-breeders aged 0-3 estimated as part of spline, or assumed as constant
- Breeding probability of non-breeders aged 0-3 assumed as constant

Exploratory Analysis

- Linear spline:

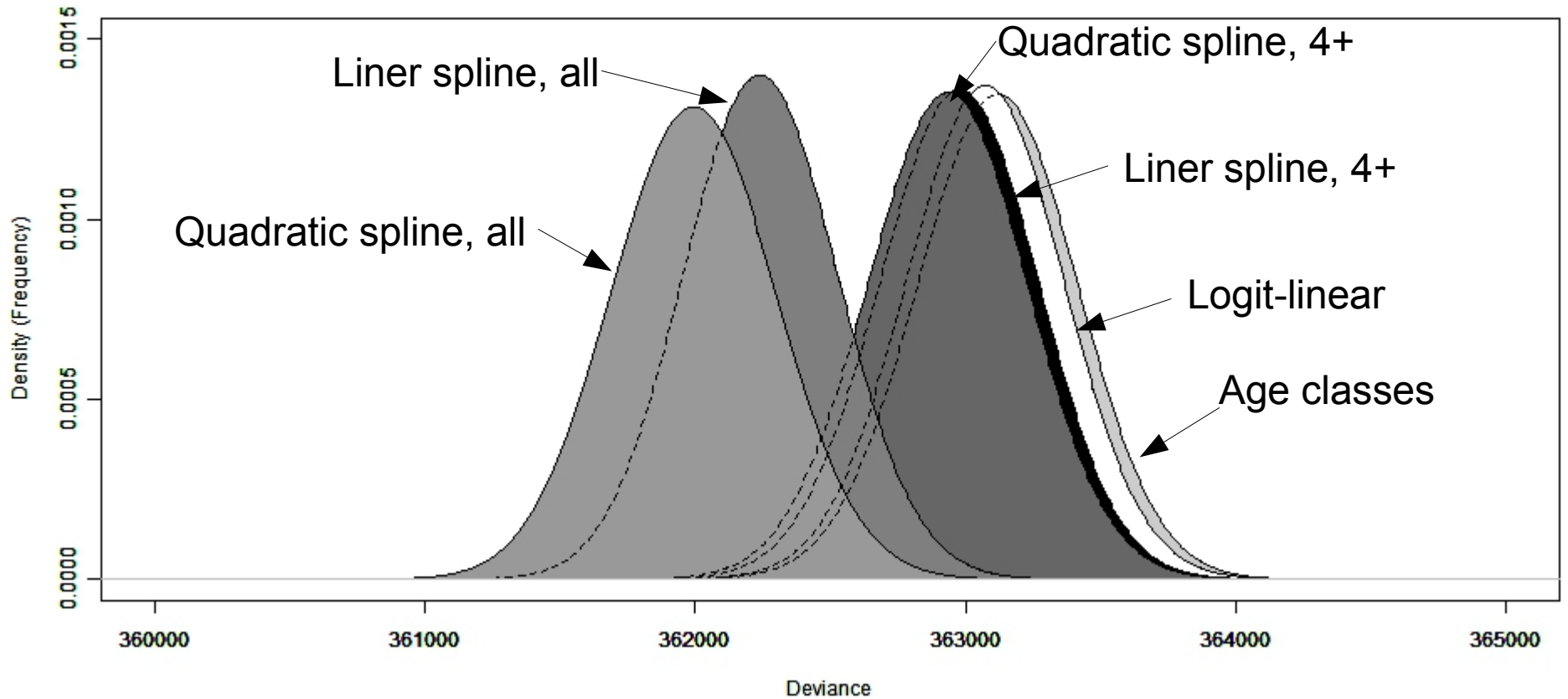
$$\text{logit}(\theta_{a,t,b}) = \alpha_{0,b} + \alpha_{1,b}(a-4) + \sum_{k=1}^K [\beta_{k,b}(a-\kappa_k) I(a \geq \kappa_k)] + \varepsilon_{t,b}$$

- Quadratic spline:

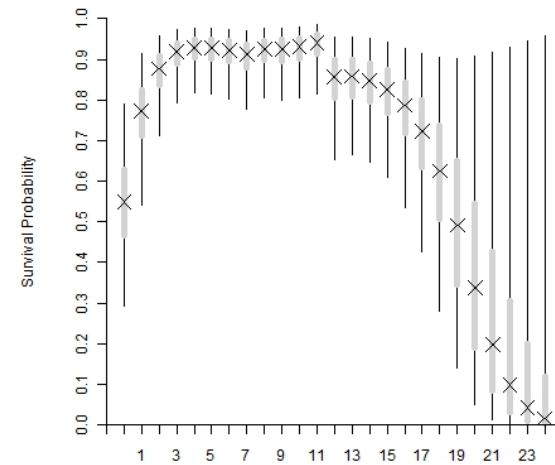
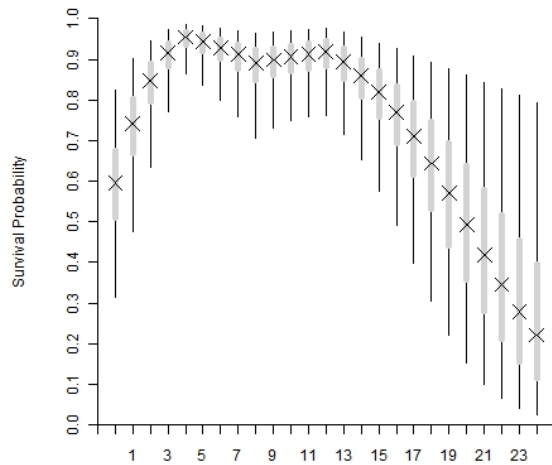
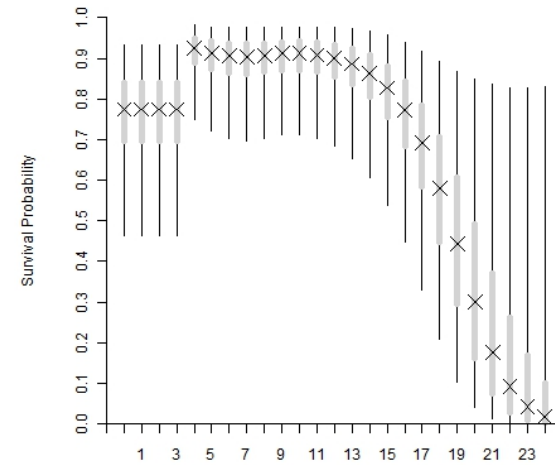
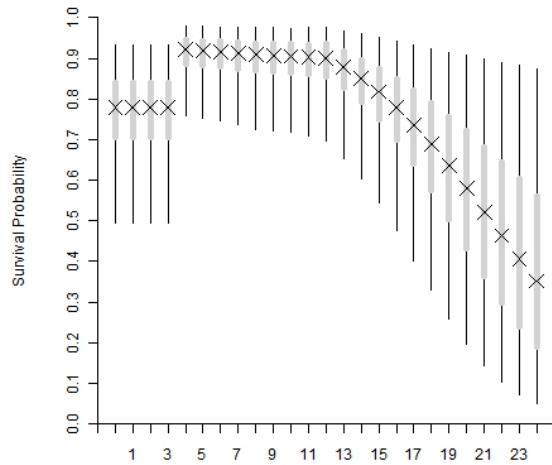
$$\text{logit}(\theta_{a,t,b}) = \alpha_{0,b} + \sum_{j=1}^2 \alpha_{j,b}(a-4)^j + \sum_{k=1}^K [\beta_{k,b}(a-\kappa_k)^2 I(a \geq \kappa_k)] + \varepsilon_{t,b}$$

- Fit using Bayesian methods where α 's and β 's are considered fixed and random effects respectively

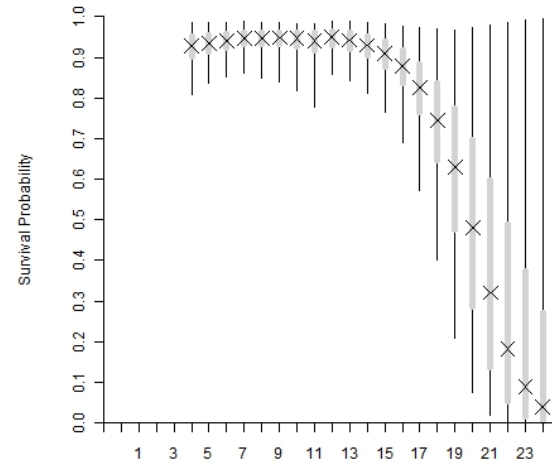
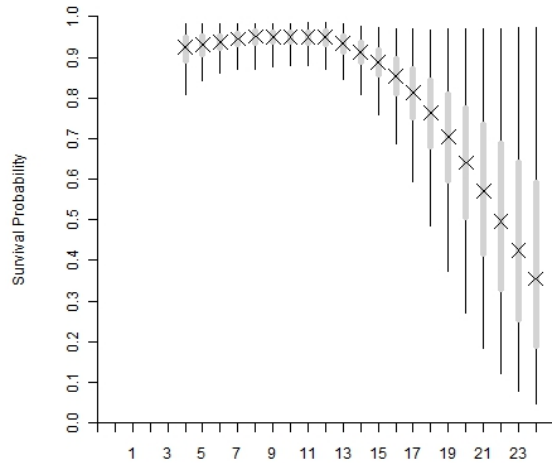
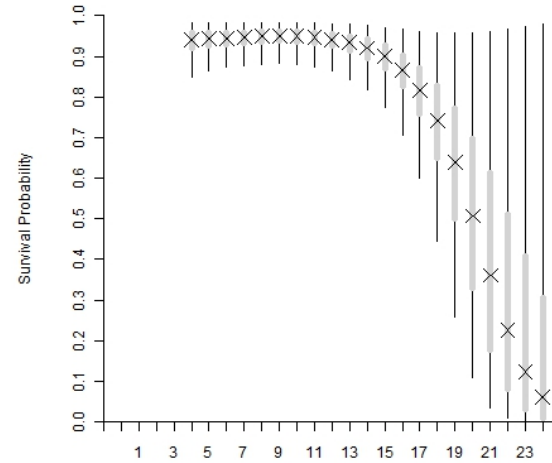
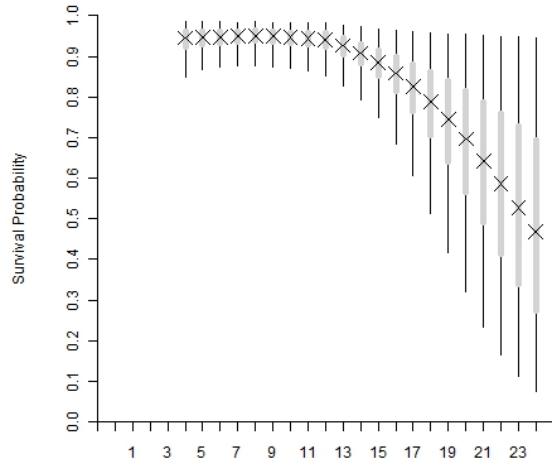
Exploratory Analysis



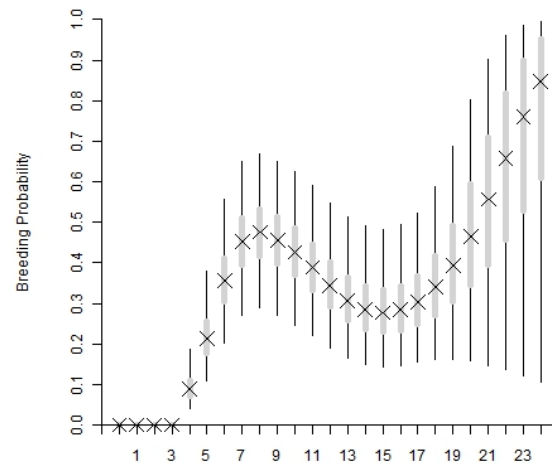
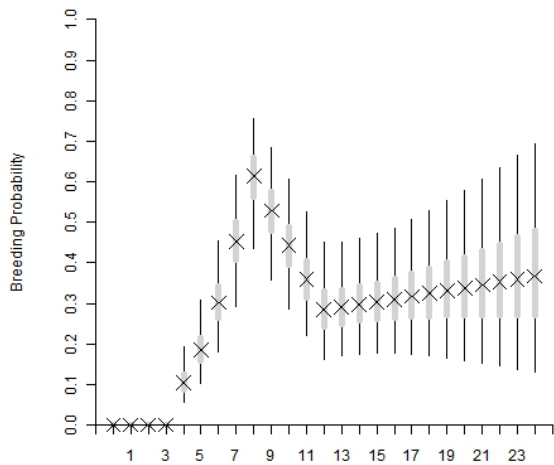
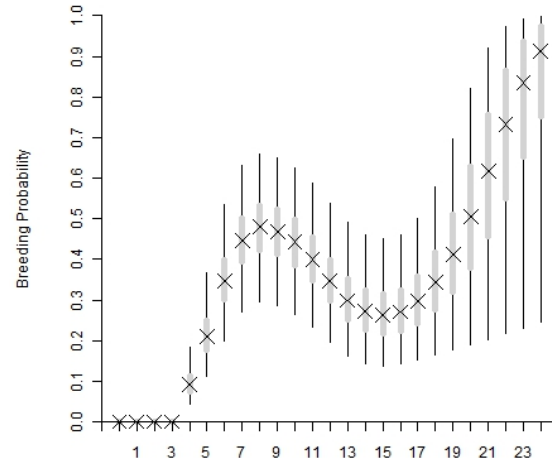
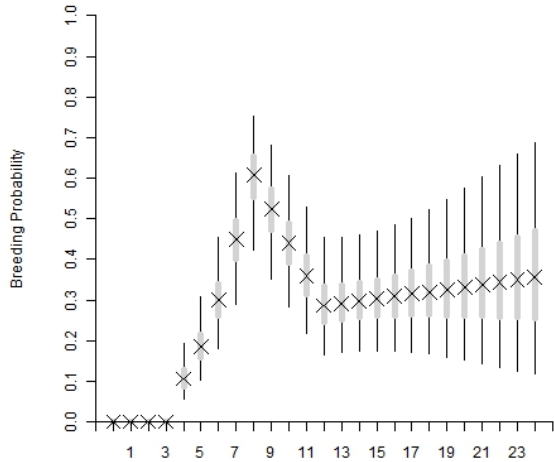
Non-breeder in $t-1$ survival



Breeder in $t-1$ survival



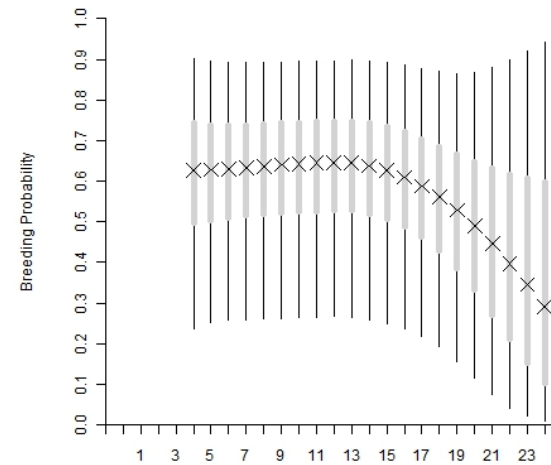
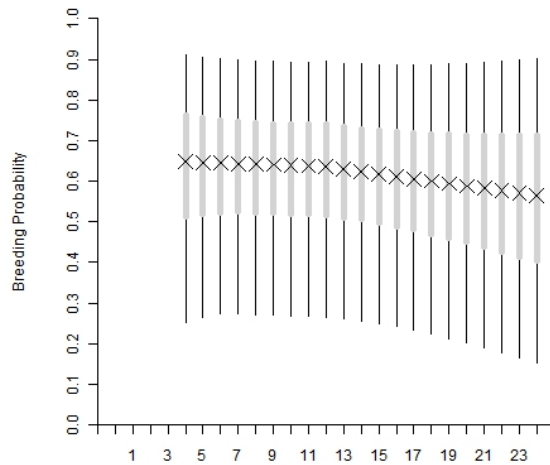
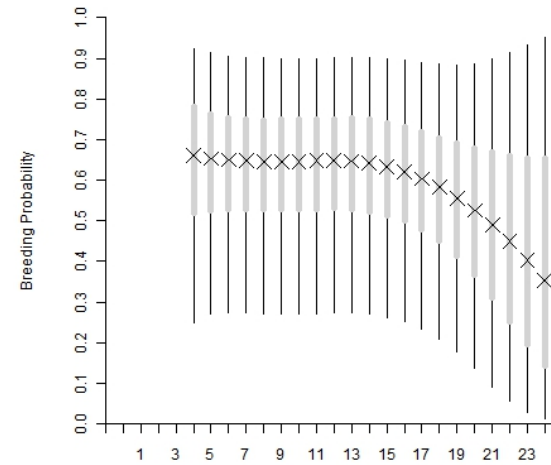
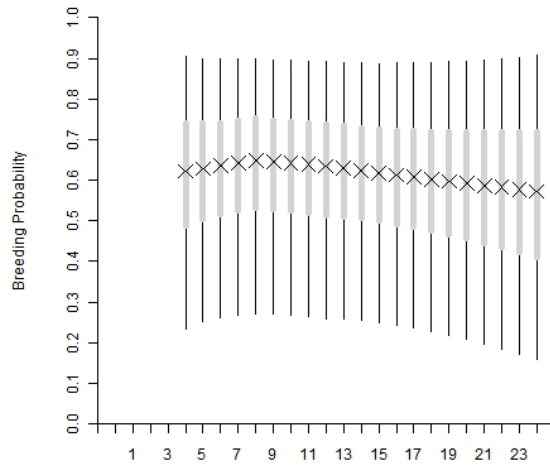
Non-breeder in $t-1$ repro.



Age

Age

Breeder in $t-1$ repro.



Age

Age

Conclusions

- Survival and reproductive rates are estimated to be similar to previous years
- Average rates for prime-age animals:
 - Non-breeder survival ≈ 0.90
 - Breeder survival ≈ 0.95
 - Non-breeder reproduction ≈ 0.30
 - Breeder reproduction ≈ 0.60

Conclusions

- Exploratory analysis suggests the use of splines looks promising, particularly for non-breeder reproduction
- Potential disadvantages include less control over defining biologically reasonable relationships and potential confounding of other factors with age relationship
- Still further issues to consider in a full analysis, e.g., number and position of knots