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

POP2007/01 Obj 3: 1997/98 – 2008/09

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#### Outline

Estimation of survival and reproduction probabilities

Estimation of "population" size

- 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

- 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

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

Number of tags in year t

Number of tags in year t-1

	0	1	2
0	1	0	0
1	1- π <sub>1,1</sub>	π <sub>1,1</sub>	0
2	$1-\pi_{1,2}-\pi_{2,2}$	π <sub>1,2</sub>	$\pi_{2,2}$

 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<sub>age,t-1,bred</sub>

 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<sub>age,t,bred</sub>

- 3 age-classes used for survival/reproduction: 0-3, 4-14, 15+
- Survival and breeding probabilities = 0 for "breeders" in 0-3 age class

 3 models considered with respect to nature of annual variation in demographic parameters

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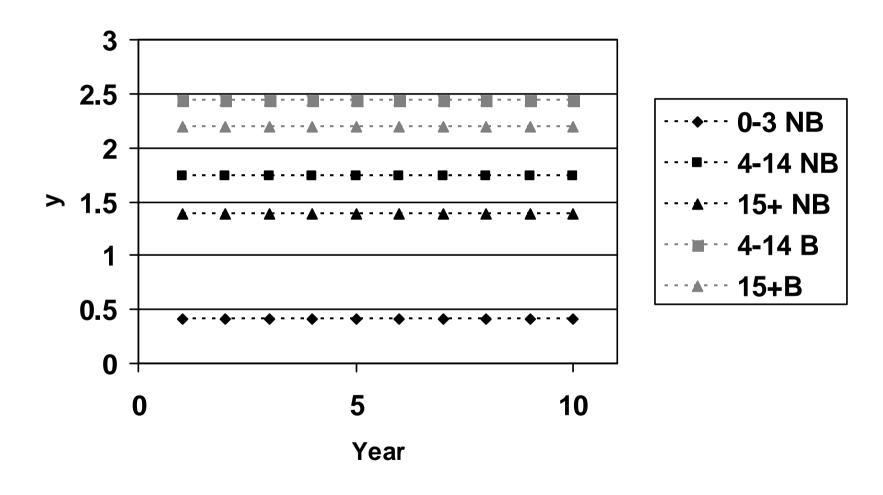
 3 models considered with respect to nature of annual variation in demographic parameters

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

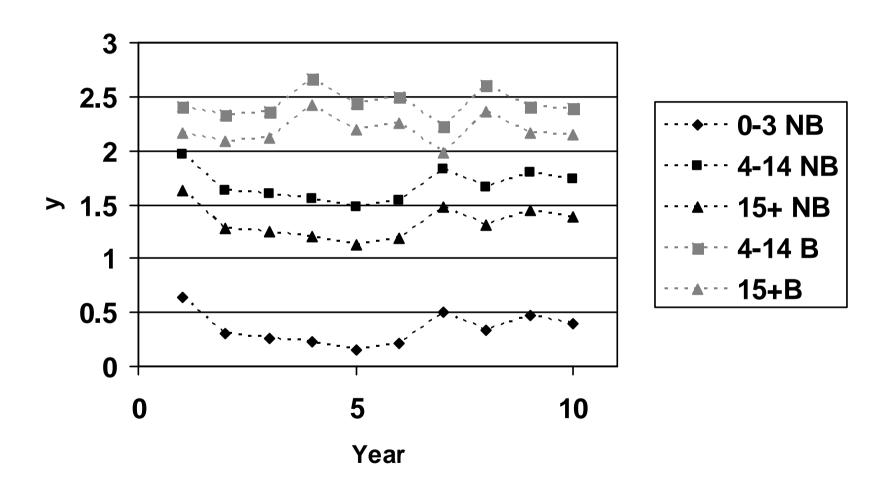
$$\theta_{a,t,b} = \frac{e^{y_{a,t,b}}}{1 + e^{y_{a,t,b}}}$$

- 1. No annual variation
- 2. Annual variation that depended upon previous breeding status
- Annual variation that depended upon age and breeding status

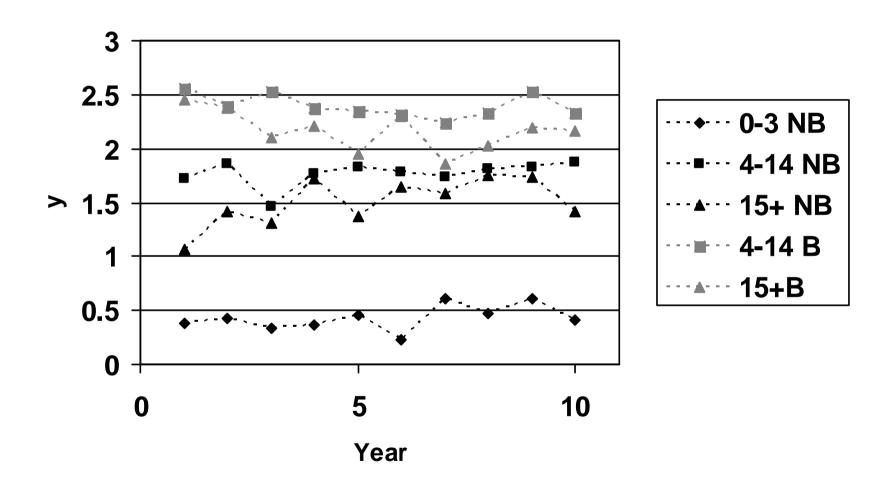
#### Model 1



# Model 2



# Model 3



 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 binomial random variable with a daily resight probability p<sub>t,bred,brand,tags</sub>

- 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 nonbreeding animals.
- Resight probabilities vary annually.

- $p_{t,bred,brand}$  applies to all females with brand
- p<sub>t,bred,chip</sub> 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

- 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

- 2 chains of 25,000 iterations
- First 5,000 iterations discarded as burn-in
- Prior distributions:
  - $\mu$ 's ~  $N(0,3.78^2)$
  - $\sigma$ 's ~ U(0,10)
  - Other probabilities ~ U(0,1)
  - π<sub>X.2</sub> ~ Dirichlet(1,1,1)
  - $ln(\delta) \sim N(0,10^2)$
- Chains demonstrated convergence and good mixing

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

- Fit of model to the data can be determined using Bayesian p-values with deviance as test statistic
- For each interaction 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

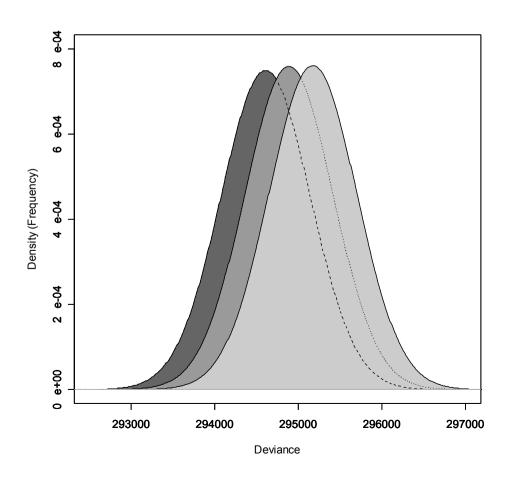
- 1990-2004 tagging cohorts
- Resights from 1997/8-2008/9 in main field season at Enderby Island
- 2 definitions considered for breeder according to assigned status in database
  - Confirmed breeders (status = 3)
  - Probable breeders (status = 3 or 15)

#### Survival and Reproduction: Data

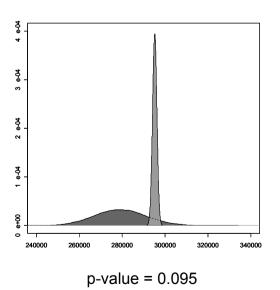
 Retagged females dealt with using the Lazarus approach

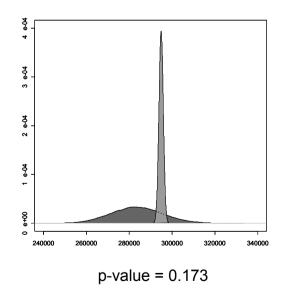
Approximately 1920 tagged females included in analysis

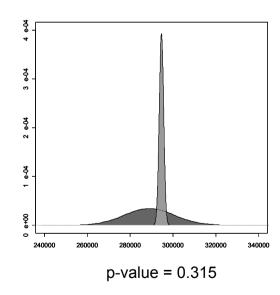
 Summary of posterior distribution for deviance values and Bayesian p-values



 Summary of posterior distribution for deviance values and Bayesian p-values



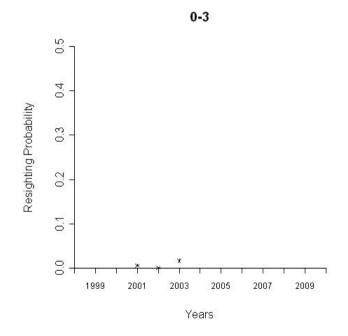


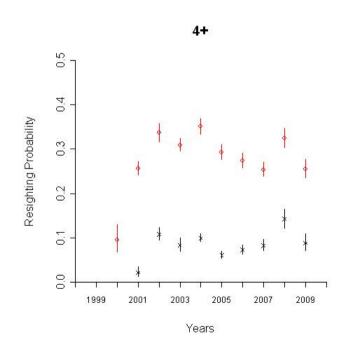


#### Tag loss

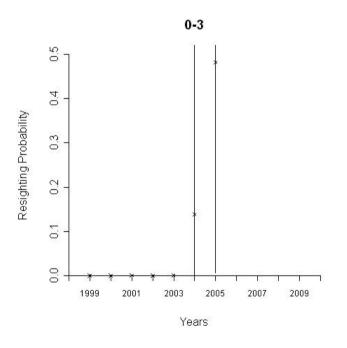
Tags at <i>t</i> -1	Tags at t	Probability
1	0	0.09 (0.08, 0.11)
	1	0.91 (0.89, 0.92)
2	0	0.07 (0.05, 0.09)
	1	0.15 (0.13, 0.17)
	2	0.78 (0.76, 0.80)

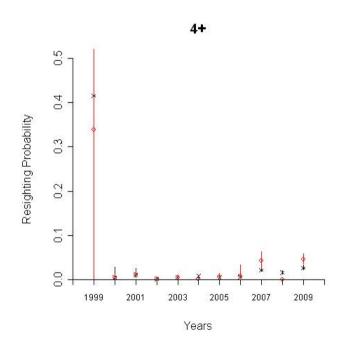
- Resight probabilities very similar from different models
- Branded animals



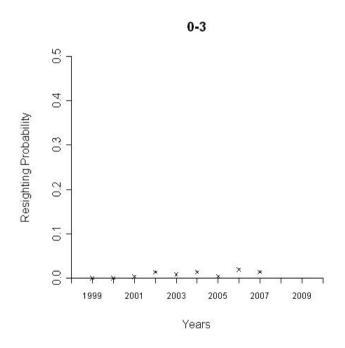


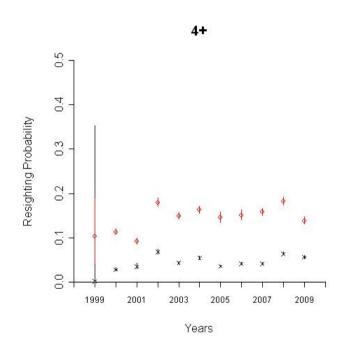
PIT-tagged only animals



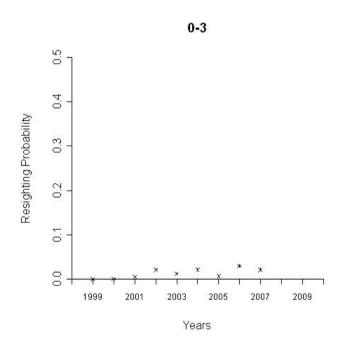


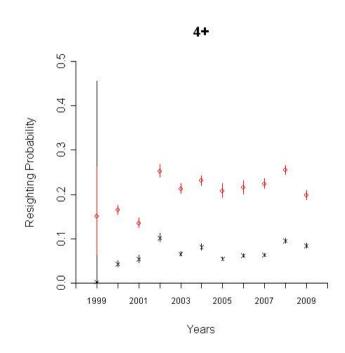
1 flipper tag



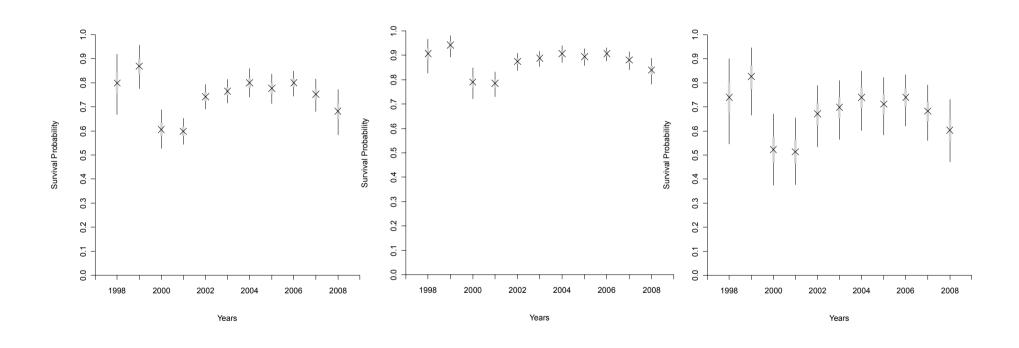


2 flipper tags

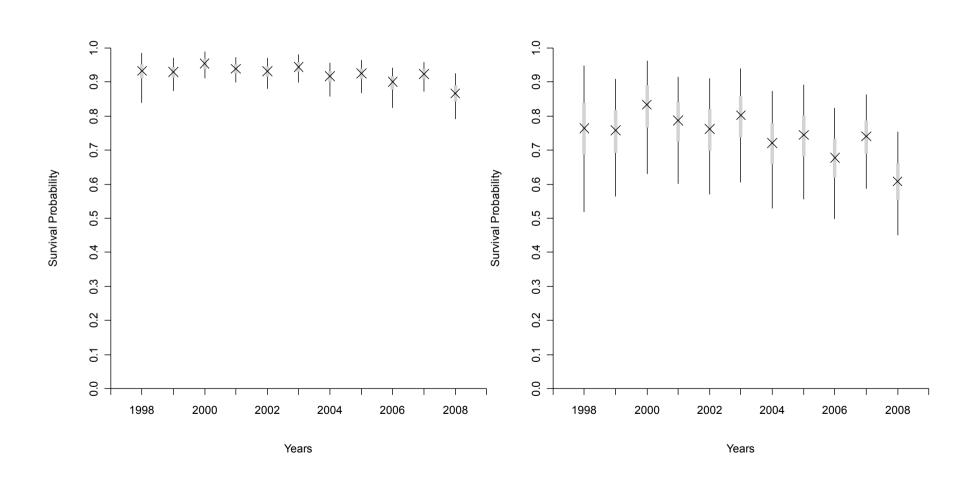




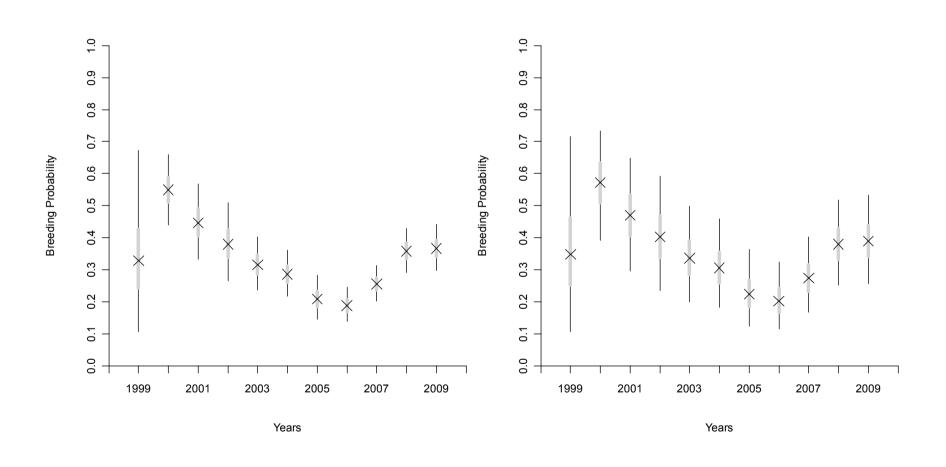
#### Non-breeder in t-1 survival



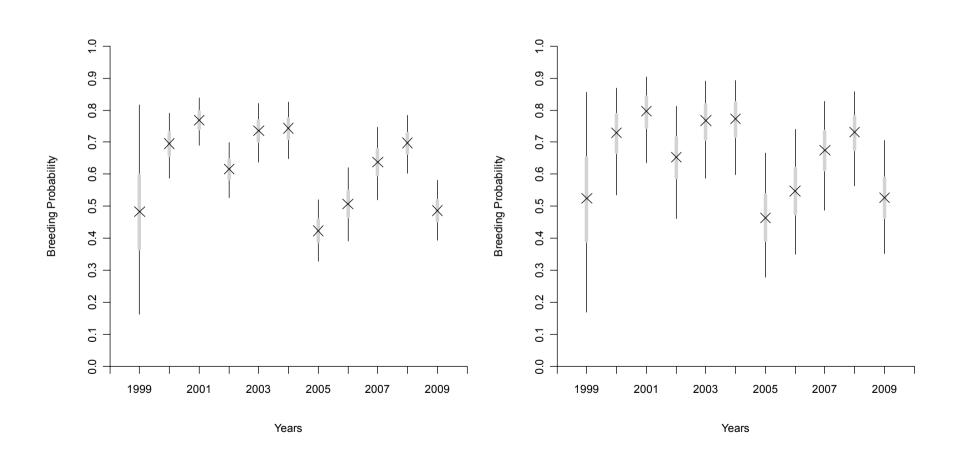
#### Breeder in t-1 survival



# Non-breeder in *t*-1 repro.



# Breeder in *t*-1 repro.



#### **Discussion Points**

Age and annual effects may be (partially) confounded

 Apparent dip in survival across all ageclasses of approx. 0.05 in 2008/09

 Direct estimation not possible given available data.

 Can predict number of survivors from each pupping cohort using estimated survival and reproduction rates.

- Given age and breeding status of a female in year t, in t+1 a female maybe:
  - Alive and breeding
  - Alive and not breeding
  - Dead

$$N_{cohort,t+1,bred \mid age,t,bred} \sim multinomial \left(N_{cohort,t,bred}, \psi_{age,t,bred}\right)$$

$$N_{cohort,t+1,bred} = \sum_{age,t,bred} N_{cohort,t+1,bred|age,t,bred}$$

 Previous applied to 1994/95 pupping cohorts onwards.

 Also older known-age females from early 1990's - different approach used for them

$$N_t^{4+,*} = \sum_{\substack{age,bred\\4\leq age\leq t}} N_{cohort,t,bred}$$

 Is number of females from 1997/98 pupping cohorts aged 4+ in year t

$$f_t = \frac{n_t^{4+,*}}{N_t^{4+,*}}$$

• Where  $n_t^{4+,*}$  is number observed in Sandy Bay

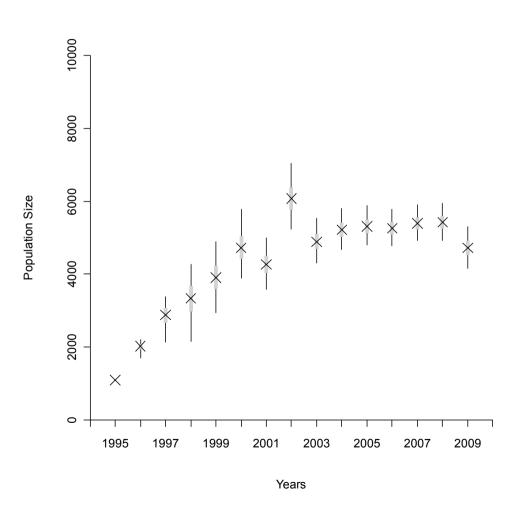
 Estimated number of early 1990's pups alive in Auckland Islands

$$N_t^{4+,\#} = \frac{n_t^{4+,\#}}{f_t}$$

• Where  $n_t^{4+,\#}$  is number of early 1990's pups observed in Sandy Bay

 Correction for older females only possible after 2001/02.

 By 2008/09 'population' consists of pupping cohorts 1989/1990-1992/92 and 1994/95-2008/09.



#### **Discussion Points**

- Population size estimates should be a key demographic parameter to fisheries/sea lion management
- Dynamic rates provide important information about how populations change, don't provide information on current state of population
- Current state of population likely to be a primary driver of management actions to achieve clearly defined management objectives