

A brief introduction to Close-Kin Mark-Recapture

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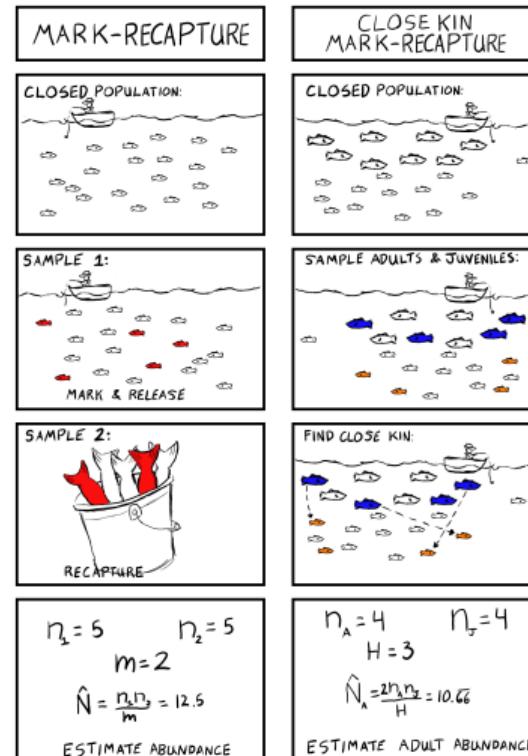
What is Close-Kin Mark-Recapture?

A simulation study for CKMR on Sable Island Grey Seals

A simple CKMR example

What is Close-Kin Mark-Recapture?

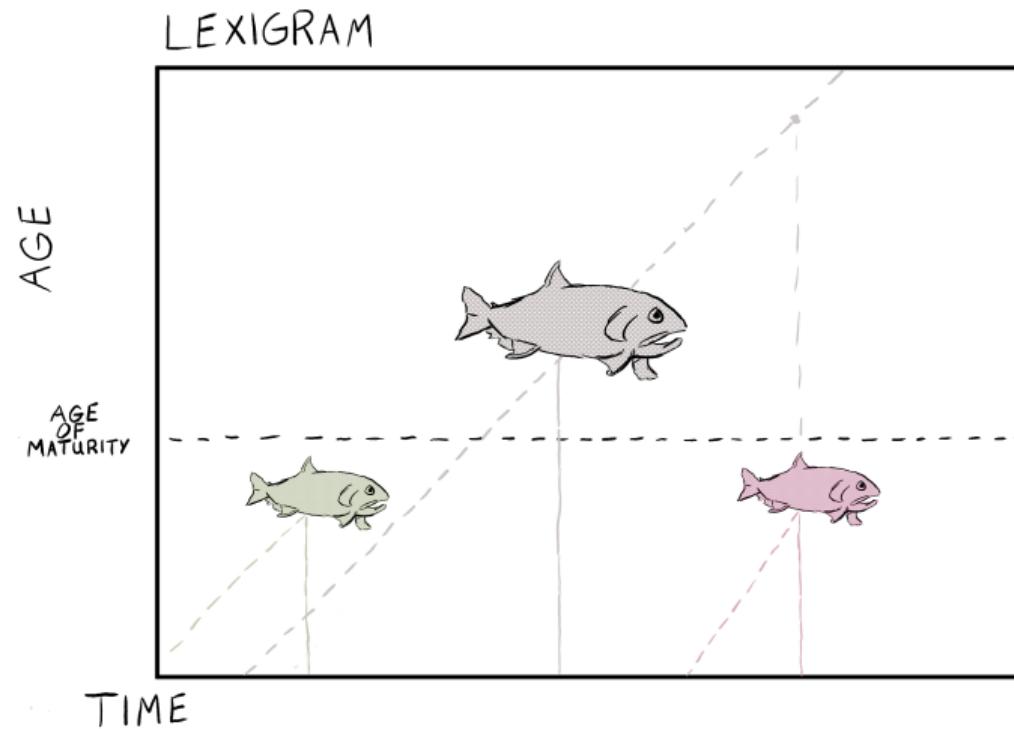
Cartoon Mark-Recapture and CKMR



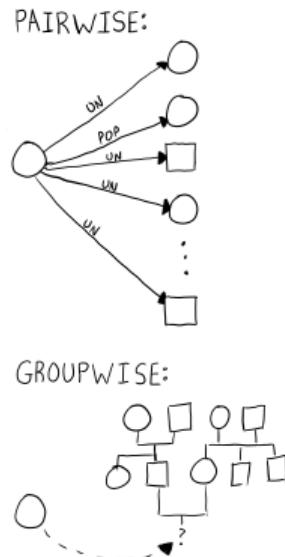
Kinship Probabilities

- Probabilities of two sampled individuals being close kin is what allows CKMR to estimate demographic parameters like abundance, survival and fecundity, etc.
- These probabilities can vary greatly from species to species and between sexes! Also relies on sampling, e.g., lethal vs. non-lethal

Kinship Probabilities



Kinship Detection



- Generally CKMR uses *pairwise* comparisons for kin detection between sampled individuals
- Pairwise only considers the relationships between a pair of individuals
- Groupwise considers all relationships simultaneously, trying to rebuild the pedigree
- Pairwise comparisons are less accurate but much quicker for the large number of samples required for CKMR

Kinship Detection

Relationship of A to B (\aleph)	κ_0	κ_1	κ_2
Unrelated	1	0	0
Offspring, parent	0	1	0
Full Sibling	$\frac{1}{4}$	$\frac{1}{2}$	$\frac{1}{4}$
Self, Identical twin	0	0	1
Niece, Nephew, Uncle	$\frac{1}{2}$	$\frac{1}{2}$	0
Grandparent, grandchild	$\frac{1}{2}$	$\frac{1}{2}$	0
Half-sib	$\frac{1}{2}$	$\frac{1}{2}$	0
First Cousin, Parent's Half-sib, Half-sib's Child	$\frac{3}{4}$	$\frac{1}{4}$	0
Double First Cousin	$\frac{9}{16}$	$\frac{6}{16}$	$\frac{1}{16}$
Half-sibs whose parents are sibs or PO	$\frac{3}{8}$	$\frac{1}{2}$	$\frac{1}{8}$
Half-sibs whose parents are half-sibs	$\frac{7}{16}$	$\frac{1}{2}$	$\frac{1}{16}$

Frequently Used Kinships

Parent-Offspring Pair:

- Inform us about adult abundance & fecundity
- With non-lethal sampling, POPs inform about adult survival as well

Half-Sibling Pair:

- Between-cohort HSPs inform about adult survival and abundance
- Within-cohort HSPs inform about the *variance* in number of offspring from adults in a year
- Within-cohort HSPs need to be handled differently as a result

Grandparent-Grandchild Pair:

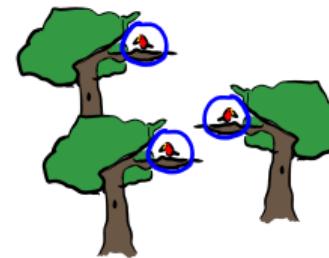
- GPGCPs also inform about adult survival and abundance

Sampling

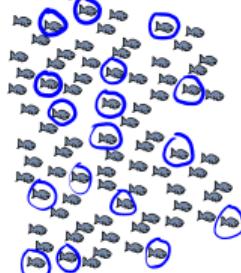
✗ NON-INDEPENDENT:



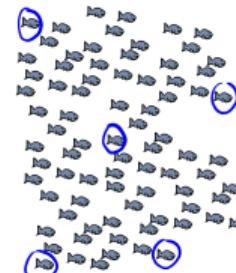
✓ INDEPENDENT:



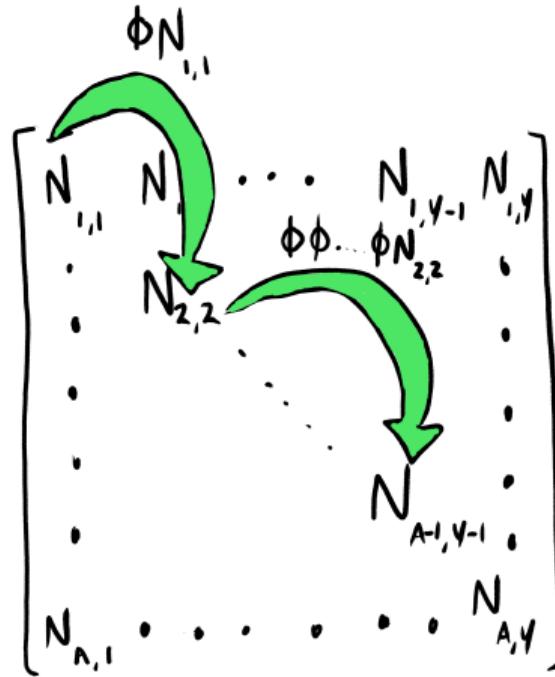
✗ DENSE:



✓ SPARSE:

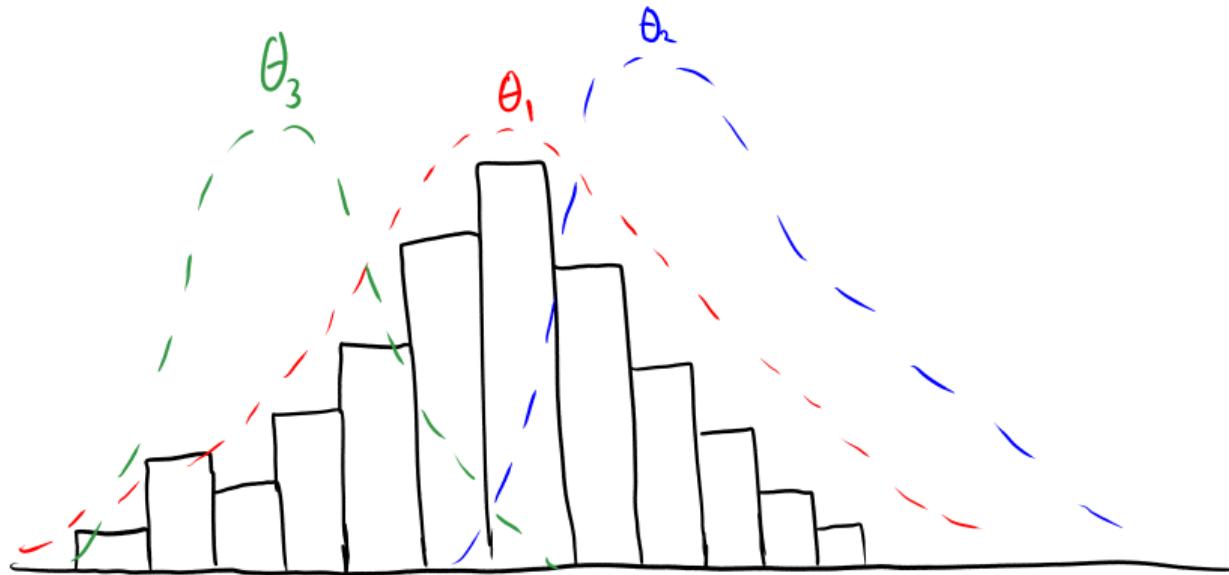


Population Dynamics Model



- Typically CKMR is performed with a population dynamics model
- Complexity depends on kinship probs.
- Fit using a Pseudo-Likelihood Approach

MAXIMUM LIKELIHOOD:



A simulation study for CKMR on Sable Island Grey Seals

Sable Island Grey Seal Colony



- Sable Island is a remote island ≈ 200 km off the coast of Nova Scotia
- Sable Island is home to the world's largest grey seal breeding colony
- Currently assessed using mark-recapture and aerial photography

Credit: Paul Gierzewski CC BY-SA 4.0

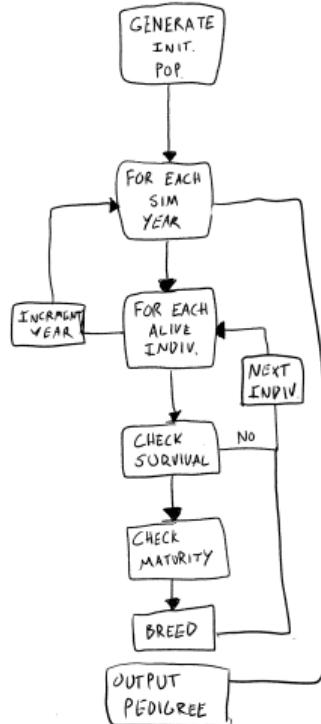
Overall Goal

- Assess how a *juvenile* only sampling scheme can estimate grey seal abundance
- Determine Potential Problems
- Test sampling schemes with similar structure to existing samples

Grey Seal Life History

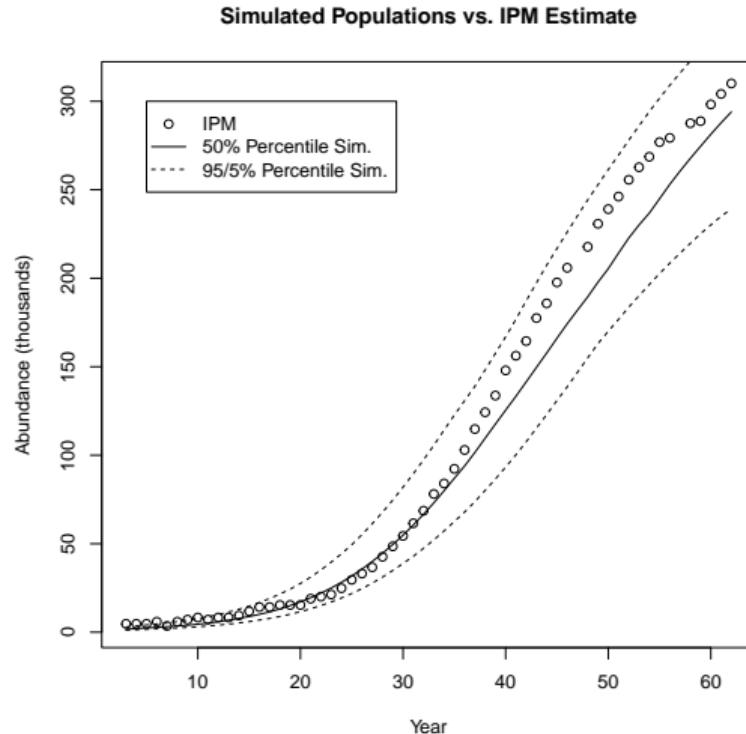
- Long Lived, 40+ years
- Females live longer than males
- Females can have 1 pup per year
- Females can mature at age 4
- Males can have multiple partners in a year, sized based
- Males mature later

Individual Based Simulation (IBM)



- IBMs track the births, deaths and offspring of all individuals
- Full knowledge of the pedigree
- Best way to evaluate CKMR

Individual Based Simulation



Sampling

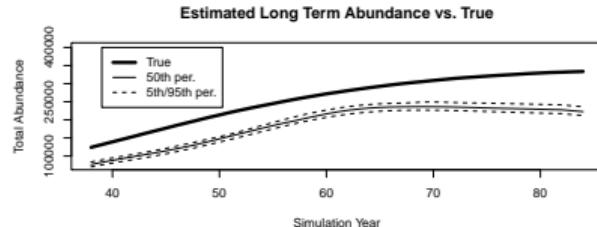
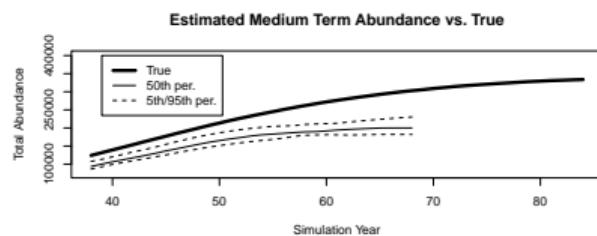
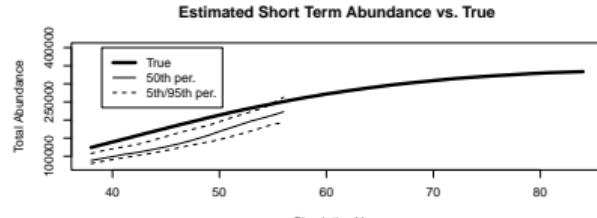
- Sampling Setup

	Short	Medium	Long
Years	38-42, 54-56	62-68	69-84
Annual Juveniles Sampled	500	700	700

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- The average number of kin pairs found in each of the three sampling schemes across the 1,000 samples taken.

Kin Pair	Short	Medium	Long
POP	19.21	62.62	180.49
HSP	334.70	837.96	2880.61
GPGC	5.08	61.07	248.27
Other	0.13	0.21	0.37

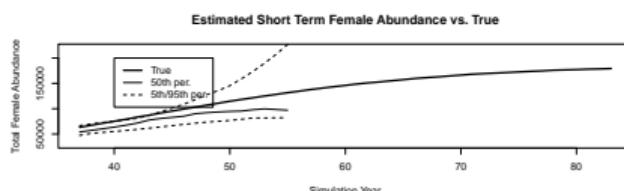
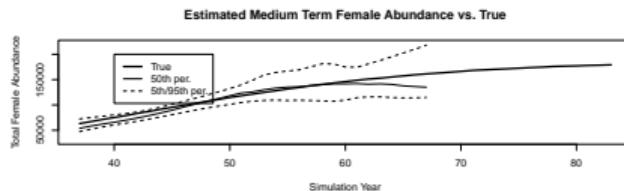
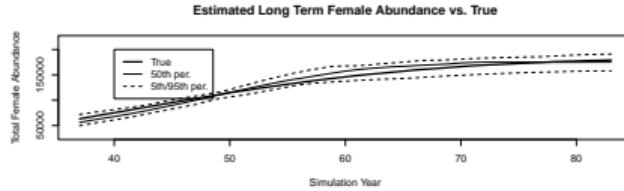
Two Sex CKMR Model



Summary

- Underestimates abundance
- Issues recovering male fecundity
- Issues with general trend

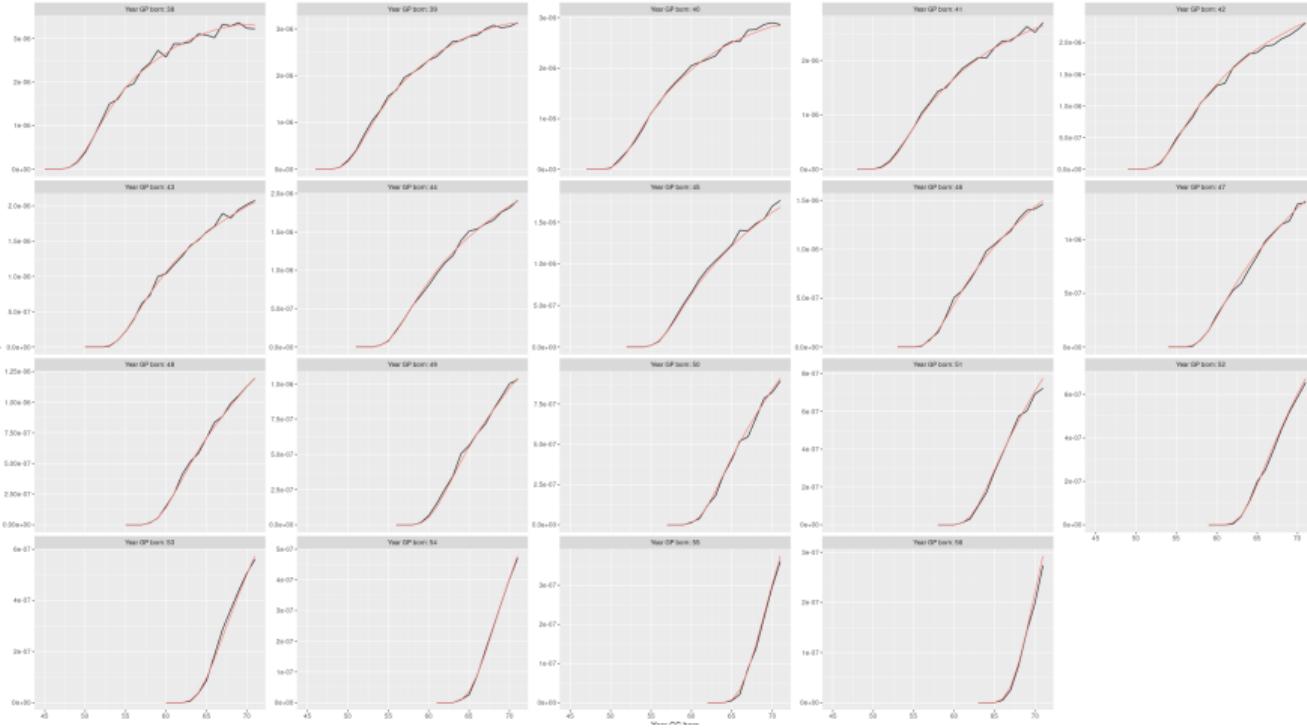
Removing Potential GPGC Pairs and Female Only Abundance



Summary

- Female Only
- All *potential* GPGC pairs removed
- Bias reduced

Checking GPGC pair probabilities



A simple CKMR example

Imaginaria creatura

Suppose we are interested in performing CKMR on the species *Imaginaria creatura* to determine the female adult abundance

Life History:

- It matures after one year
- Average Adult fecundity believed to be constant during it's lifetime
- Adult Survival is constant over their lifetime

Sampling:

- 10 year program
- Randomly sample 40 possible mothers and 40 juveniles *lethally*
- Only interested in POPs

Assumptions:

- We are assuming we can identify POPs exactly

- A simple individual based simulation was used to generate the data for this problem

`./sim.R`

"Finding" the Kin pairs

```
./makedata.R
```

The Data

B_j	No. of POPs	No. of comparisons
21	6	2440
22	2	2280
23	9	2440
24	5	2560
25	4	2240
26	4	2440
27	5	2480
28	5	2280
29	3	2160
30	1	1600

Parent Offspring Pair Probability

- Because we used lethal sampling only individuals sampled the same year or later than a juveniles birth year can be the mother
- Since average fecundity is the same for all adults we don't have to worry about some mothers being more likely than others
- Then the probability that individual i is j 's mother given a set of covariates (in this case just j 's birth date):

$$Pr(i \text{ is } j\text{'s mother} | B_j = y) = \frac{1}{N_{F,y}}$$

Population Dynamics

Parameters:

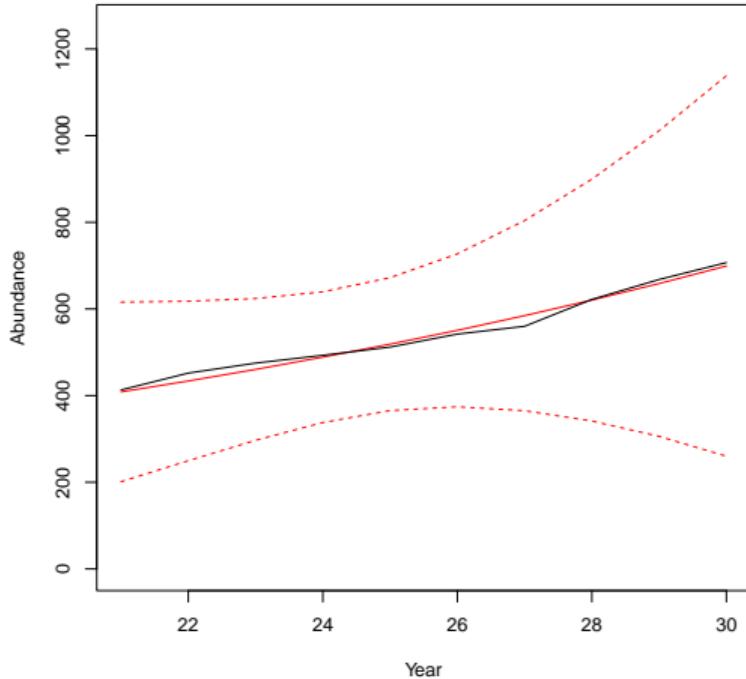
- $N_{F,1}$: The initial number of adult females in the population in the first year of the model
- r_g : The rate of growth in the number of adult females

$$N_{F,y} = \begin{cases} N_{F,1} & y = 1 \\ r_g N_{F,y-1} & y \neq 1 \end{cases}$$

- To implement the model we are using RTMB
- RTMB is the successor to TMB but allows us to implement the model in R rather than C++
- RTMB will give us the gradient (first derivative) to our model through Automatic Differentiation
- RTMB can also help us calculate the standard errors of quantities from the model using the delta method
- Can also help implement random effects via. the Laplace Approximation

```
./model.R
```

Results



Some suggested reading

Mark V. Bravington, Hans J. Skaug, and Eric C. Anderson. “Close-Kin Mark-Recapture”. *Statistical Science* 31.2 (May 2016), pp. 259–274. ISSN: 0883-4237. DOI: 10.1214/16-sts552. URL: <http://dx.doi.org/10.1214/16-ST552>

Sebastian Wacker et al. “Considering sampling bias in close-kin mark–recapture abundance estimates of Atlantic salmon”. *Ecology and Evolution* 11.9 (2021), pp. 3917–3932

Jonathan Babyn et al. “Estimating effective population size using close-kin mark–recapture”. *Methods in Ecology and Evolution* (2024)

Hal Caswell. *Matrix population models*. Vol. 1. Sinauer Sunderland, MA, USA, 2000