Towards CKMR software

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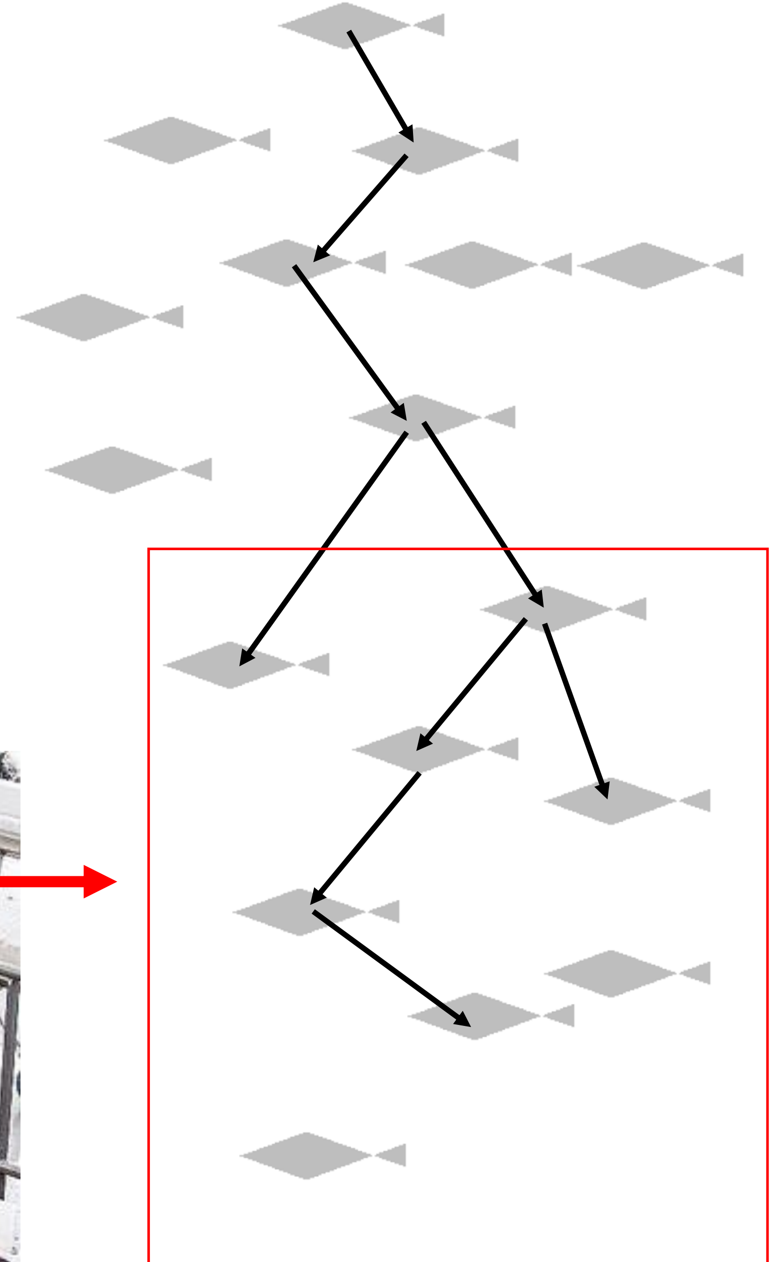
CAPAM 2019, Wellington

Hypothesis:

In the future you will know the pedigree of your fish catch

... but 50 kin pairs is enough



Acknowledgement

- CKMR method developement in fisheries has been driven by CSIRO in Hobart, and particular by Mark Bravington

Outline

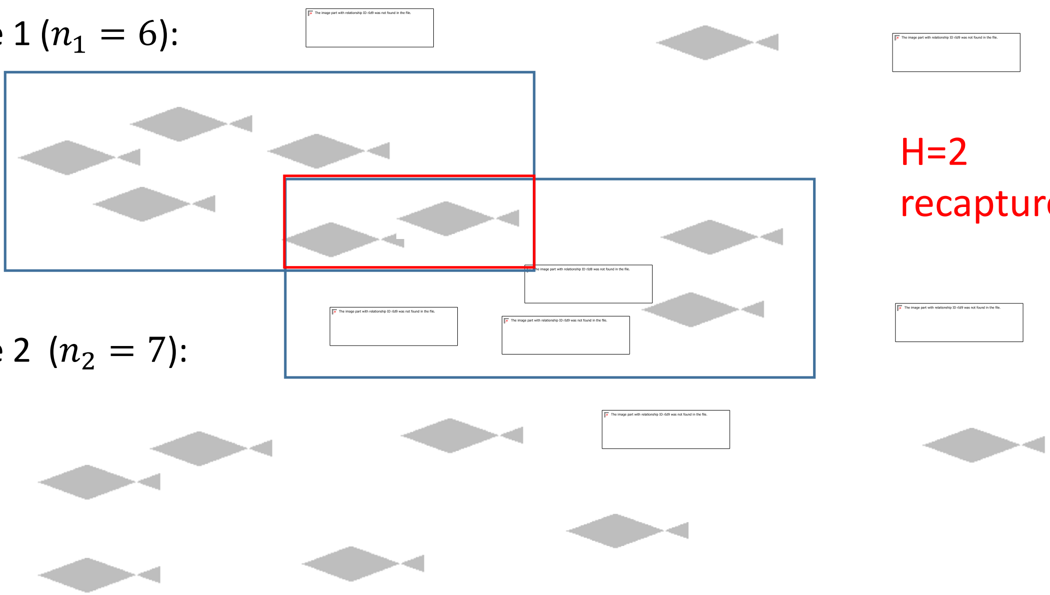
- Close-kin Mark-Recapture (CKMR)
  - What is it?
  - How does it relate to standard Mark-Recapture
- Towards CKMR software
  - What are the “good” software abstractions?

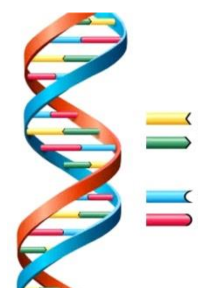
Mark-Recapture (MR)

- Estimate abundance, mortality, fecundity in **animal** populations
- Requires <u>at least two </u>sampling occasions

Sample 1 ($n_1 = 6$):

Sample 2 ($n_2 = 7$):





Lincoln-Petersen estimator: $\widehat{N} = \frac{n_1 n_2}{H} = \frac{6 \cdot 7}{2} = 21$

Close-Kin Mark-Recapture (CKMR)

Genetically determined parent-offspring pair

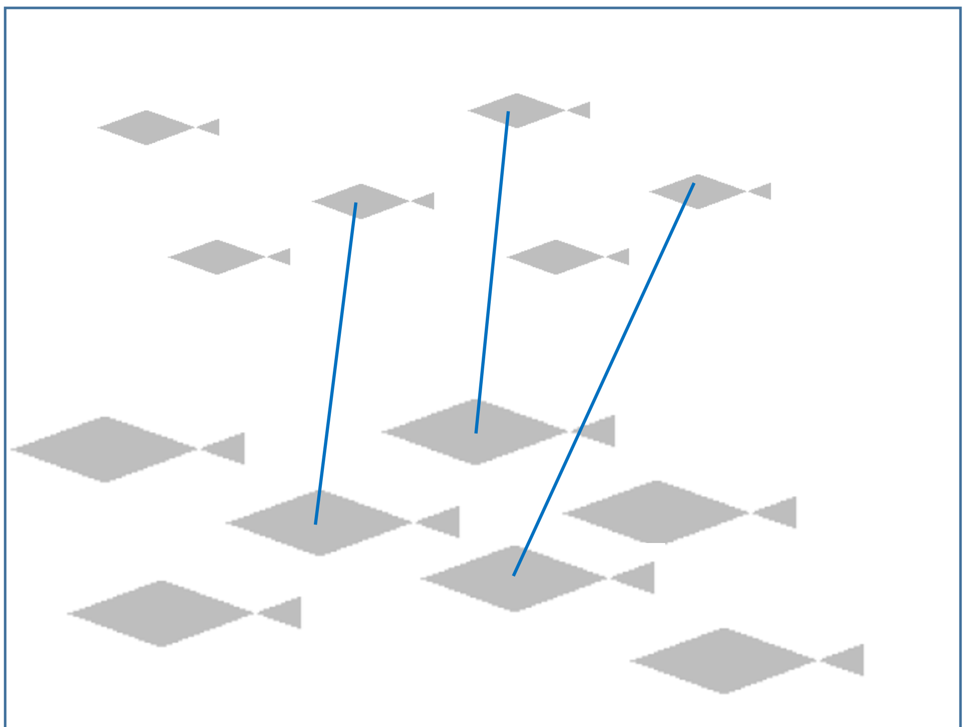
- Bravington et al, (2016 Stat. Science)
- Toy example with juveniles and adults
- Only <u>single</u> sample needed

2 parents

Juveniles ($n_J = 6$)
(immature animal)

Adults ($n_A = 7$)

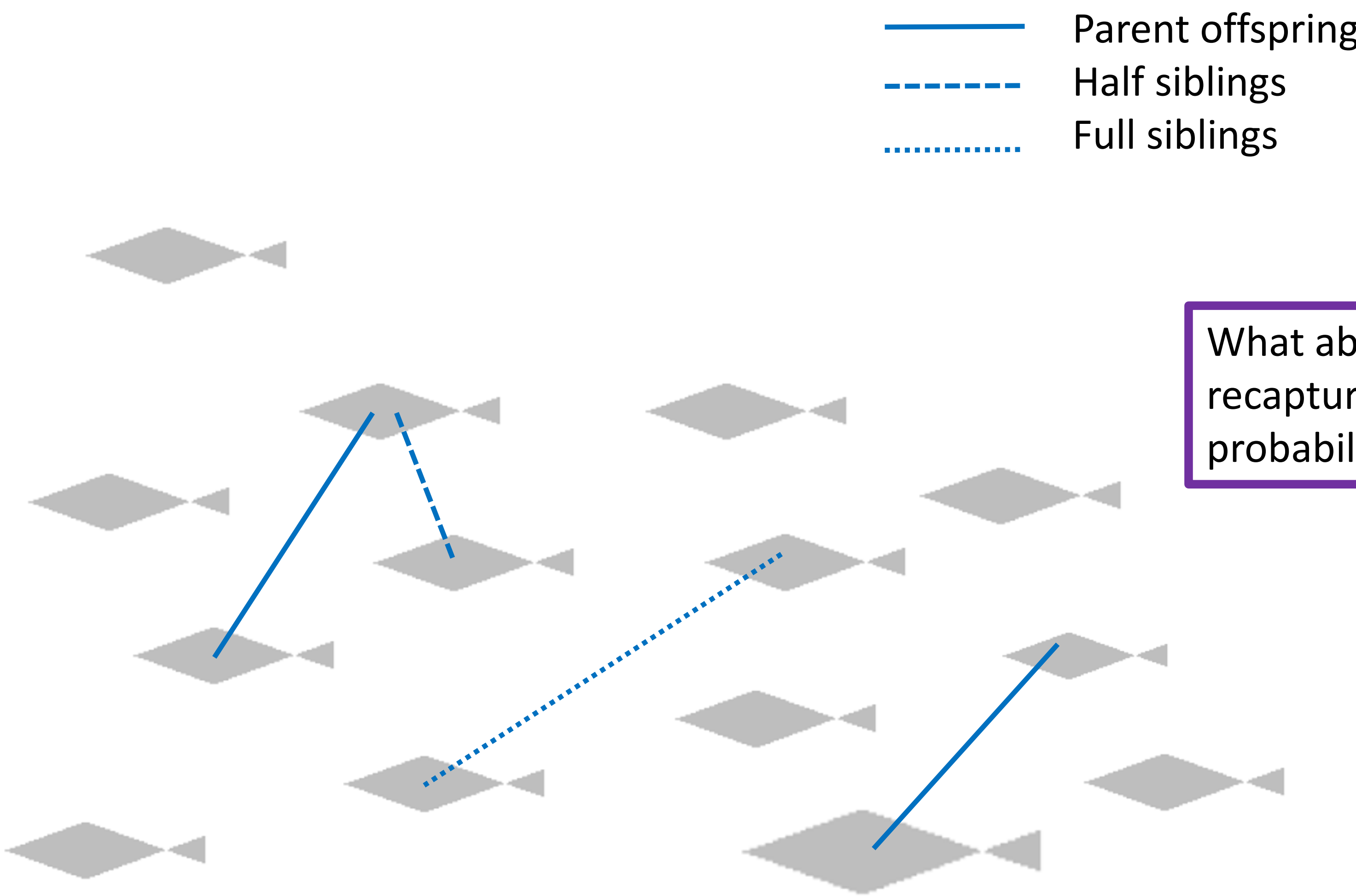
H = 3 parent-offspring pairs



CKMR estimator:

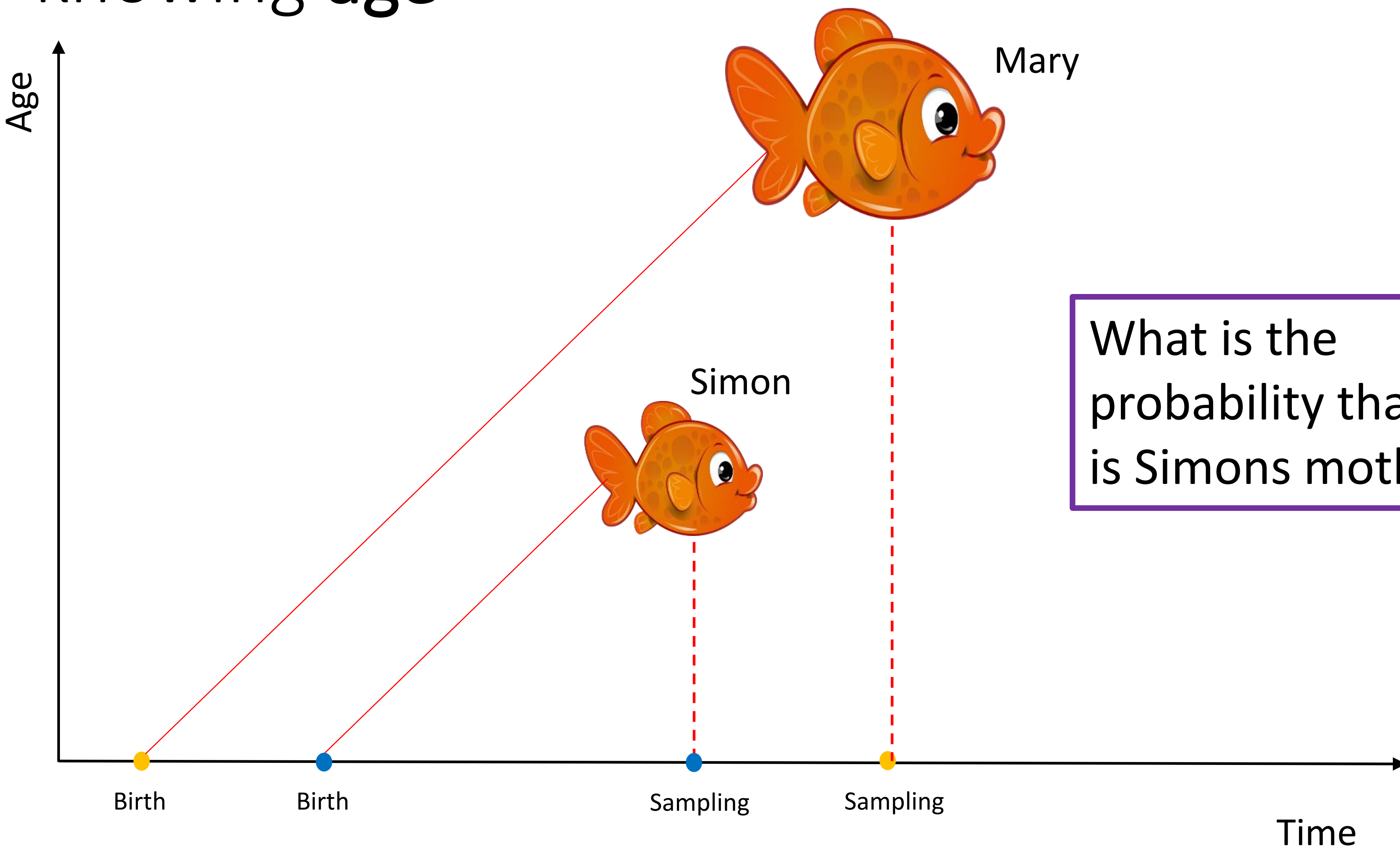
$$\widehat{N}_A = \frac{2 n_J n_A}{H} = \frac{2 \cdot 6 \cdot 7}{3} = 28$$

Different types of recaptures (kinship)



What about recapture probabilities?

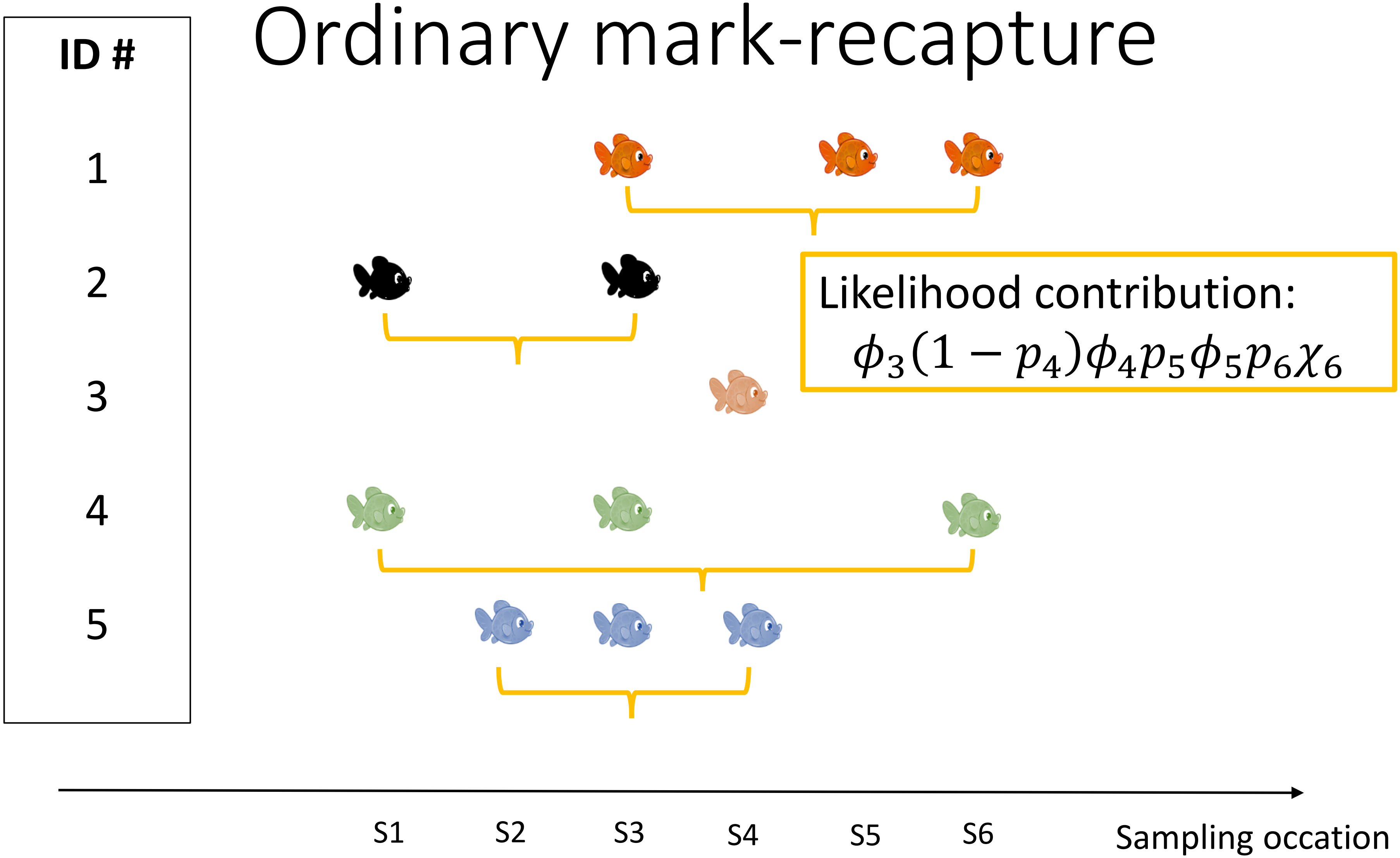
Recapture probabilities: the importance of knowing **age**



What is the probability that Mary is Simons mother?

We will now move towards likelihood construction for CKMR data

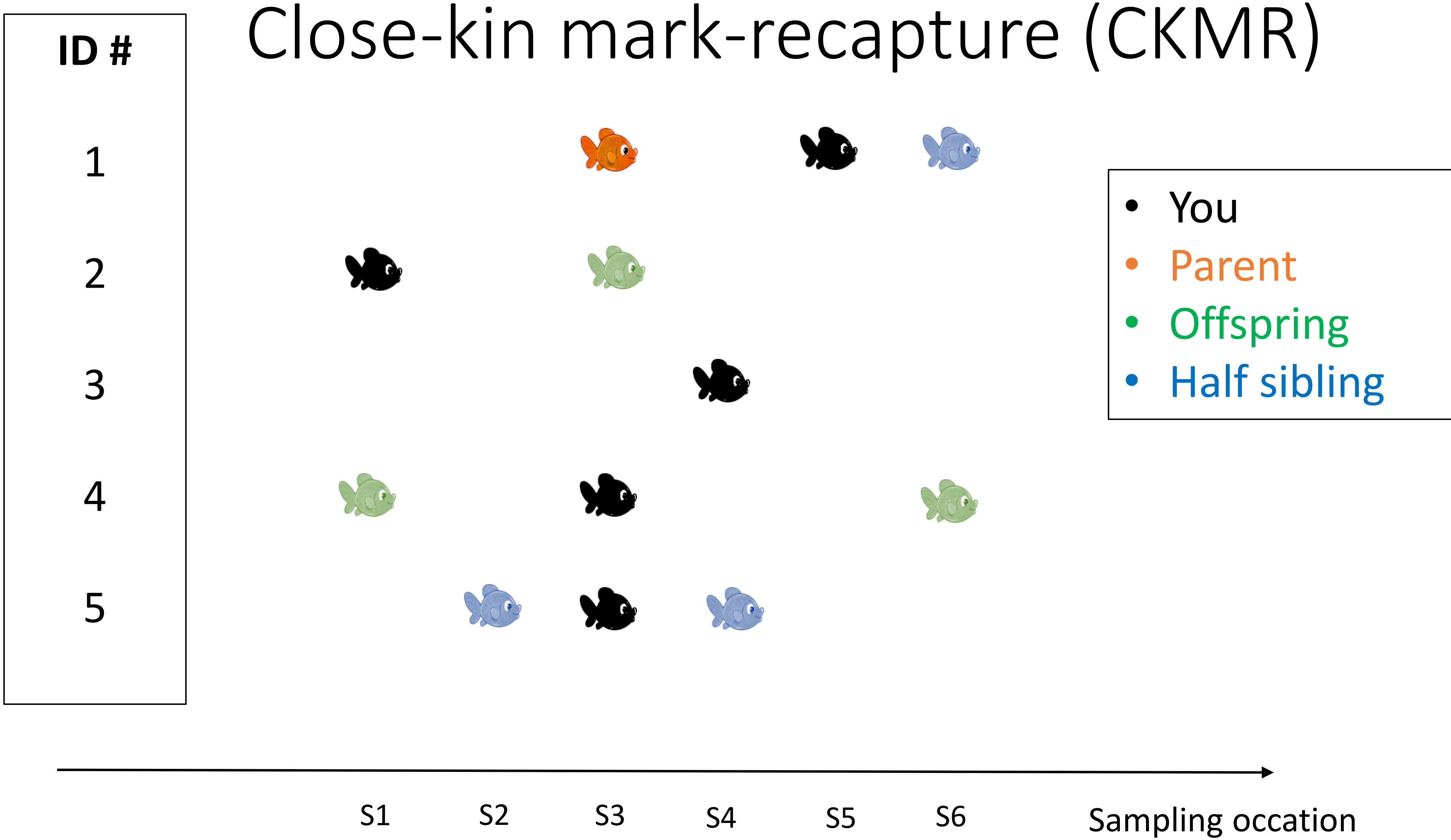
Ordinary mark-recapture



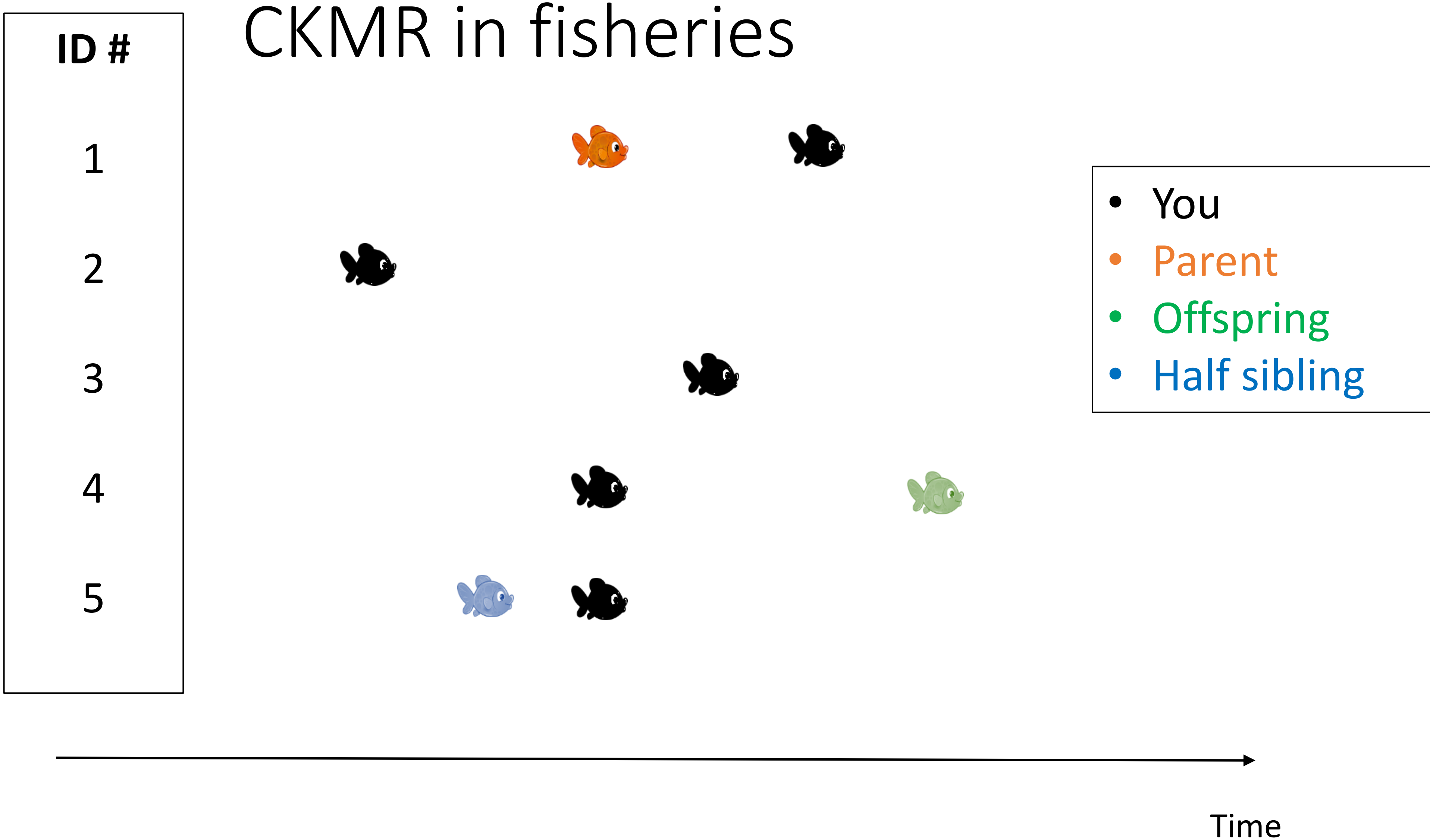
Likelihood contribution:

$$\phi_3(1-p_4)\phi_4 p_5 \phi_5 p_6 \chi_6$$

Close-kin mark-recapture (CKMR)

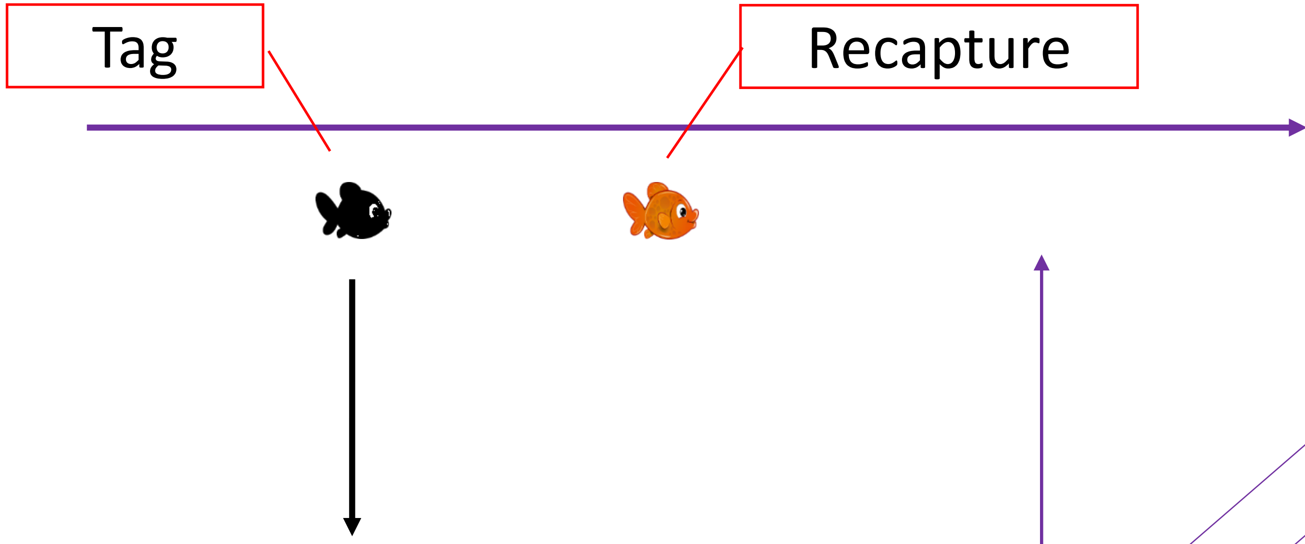


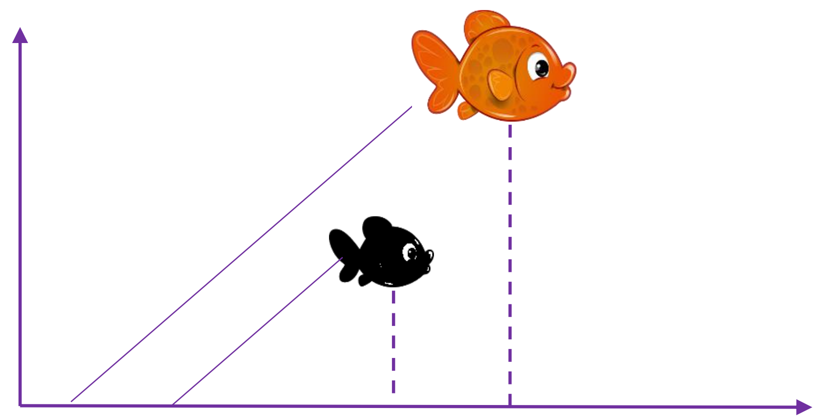
CKMR in fisheries



Expected number of parents alive

- You
- Parent





Age

$$\begin{bmatrix} .1 & .2 & .3 & .3 & .2 & .1 \\ .2 & .3 & .3 & .3 & .2 & .2 \\ .3 & .3 & .2 & .1 & .2 & .1 \\ .3 & .2 & .1 & .1 & 0 & 0 \\ .2 & .1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix}$$

Time

Likelihood contribution
(observed versus expected numbers)

- You
- Parent

Expected number of parents sampled in this cell:

$$p \cdot n = \frac{0.2}{84321} \cdot 8$$

Sample sizes:

$$\begin{bmatrix} 12 & 2 & 4 & 1 & 2 & 4 \\ 2 & 12 & 2 & 6 & 7 & 9 \\ 4 & 2 & 8 & 3 & 9 & 2 \\ 3 & 4 & 2 & 4 & 2 & 2 \\ 7 & 4 & 14 & 6 & 8 & 3 \\ 4 & 20 & 14 & 4 & 2 & 6 \end{bmatrix}$$

Expected #parents alive:

Age

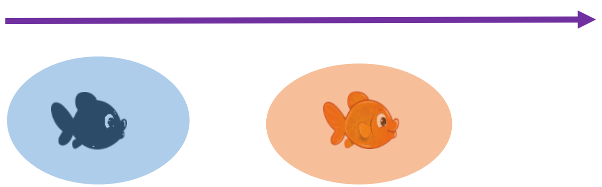
$$\begin{bmatrix} .1 & .2 & .3 & .3 & .2 & .1 \\ .2 & .3 & .3 & .3 & .2 & .2 \\ .3 & .3 & .2 & .1 & .2 & .1 \\ .3 & .2 & .1 & .1 & 0 & 0 \\ .2 & .1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix}$$

Time

Population numbers:

$$\begin{bmatrix} & & \vdots & & \\ \cdots & \cdots & 84321 & \cdots & \cdots \\ & & \vdots & & \end{bmatrix}$$

Software abstraction



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Pseudo code
ckmr_pop P(T=10,A=15,…){…}
ckmr_tag T1(P,t=1,a=1)
double E = T1.E(t=4,a=4)
Likelihood(E,…) contribu.
```

Age

$$\begin{bmatrix} .1 & .2 & .3 & .3 & .2 & .1 \\ .2 & .3 & .3 & .3 & .2 & .2 \\ .3 & .3 & .2 & .1 & .2 & .1 \\ .3 & .2 & .1 & .1 & 0 & 0 \\ .2 & .1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix}$$

Time

Population numbers:

$$\begin{bmatrix} & & \vdots & & \\ & & \vdots & & \\ \cdots & \cdots & 84321 & \cdots & \cdots \\ & & \vdots & & \\ & & \vdots & & \end{bmatrix}$$

Discussion

- Expected number of siblings (E) may be hard to calculate
  - Requires detailed knowledge of life history of species in question
- Is it possible with general software?
  - Fisheries & non-fisheries