Close Kin Mark Recapture – can we integrate it into stock assessment packages?
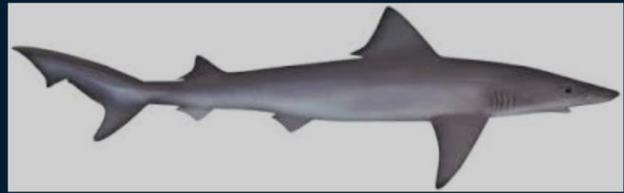
Robin Thomson, Mark Bravington, Rich Hillary
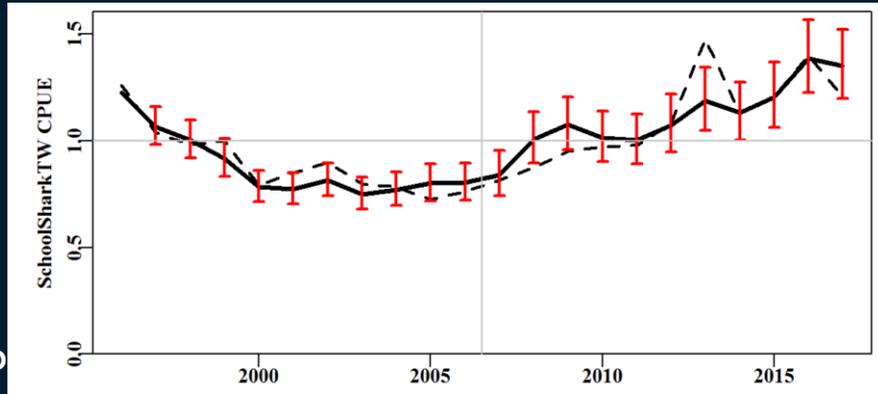
CAPAM Next Generation Stock Assessment Methods workshop
November 2019, Wellington, NZ

Introduction

- SESSF
- School shark – targeted fishery closed
- Choke species for gummy shark

- Index of abundance??

- Dedicated survey….or CKMR

What is CKMR?

- It's a *MARK-RECAPTURE* method able to estimate:
  - Absolute abundance time series (of breeding animals)
  - Natural mortality (and total mortality), for adults
 - (relative) Fecundity-at-age
  - Mean age of adult population
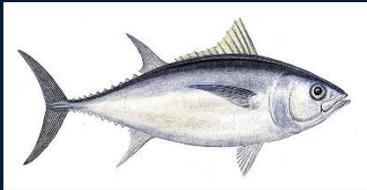
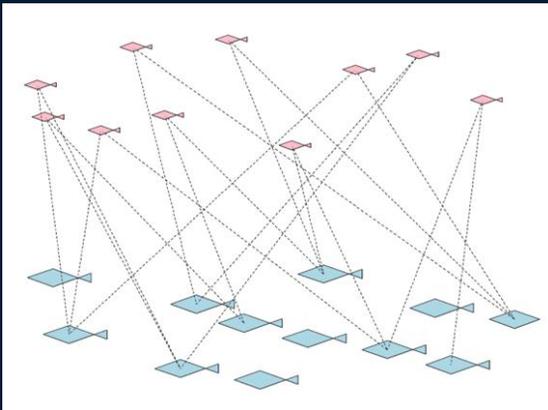| What	with	gives	and
POPs		*ideal* "SSB"	rel.fec@A
close HSPs	POPs	$\bar{A}_{adult}$	N_{ya}
far HSPs	POPs, HSPs	$\bar{z}_{adult}$	
C@A or @L	HSPs	sel@A	m_{adult}

What data does CKMR need?

- All it needs is
  - A bunch of tissue samples with meta-data -> genotypes

    fit-for-purpose

    (age), length, date, (location, ….)

  - Total catch-at-age (or length) data *(but you don't have to)*
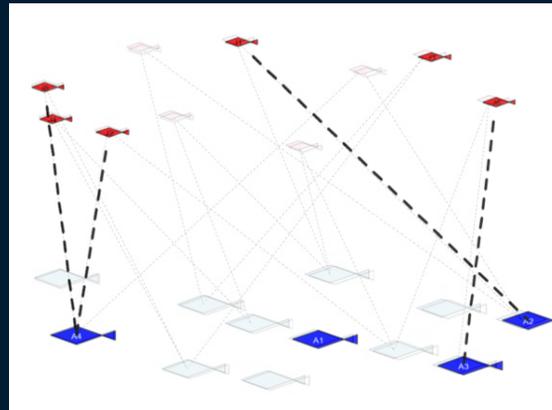
- NOT CPUE or survey indices
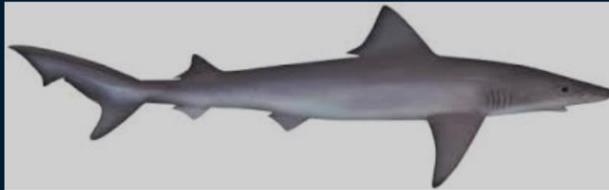
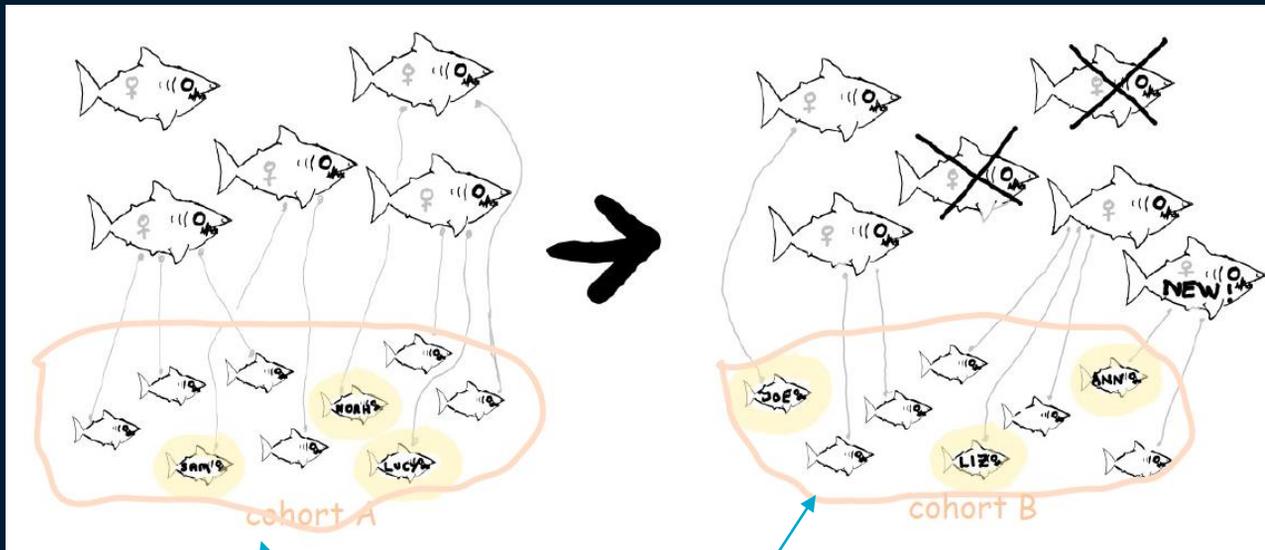# How does CKMR work? POPs

Population

Sample, and POPs

"Assumption": Every fish has just one mother (and one father)

Model: Pr [this pair is a POP] = 2/N

Data: Number of POPs observed and comparisons done

More complicated in practice (*but see Ruzzante et al brook trout, MEE*)

Model: Pr [i_A has the same mother as j_B] = her survival / N_B

More complicated in practice

Classic population dynamics model
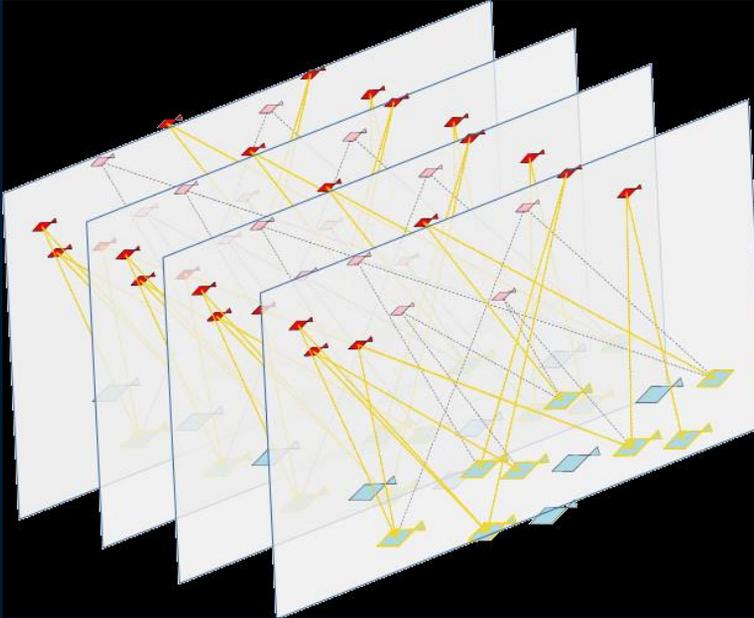
- Age & sex structured population model to calculate the prob's
- Each prob'y depends on age/length, sex, birth year of the samples
- Fecundity at age (length) & sex
- Log-likelihood – CKMR is LOTS of Bernoulli trials
  - can use CPUE, surveys … e.g. SBT

CKMR code: POPs

- POP probability loops
  - s_1: Loop over parent's sex
    - y_1: Loop over sampling years (for 'parent')
      - a_1: Loop over ages (age-at-maturity to plus-1 for 'parent')

    - y_2: Loop over sampling years (for 'offspring')
      - a_2: Loop over ages (age-at-maturity to plus-1 for 'offspring')
        - b_2: $y_2 - a_2$

      - $\Pr[\, s_1, y_1, a_1, y_2, a_2 \,] = \text{fec}(\, s_1, a_{1\_in\_b2}) \,/\, \Sigma_{a'} \,[\, N_{s1, a', b2} \,\text{fec}(s_1, a')\,]$

CKMR code: POPs

- POP probability loops
  - s_1: Loop over parent's sex
    - y_1: Loop over sampling years (for 'parent')
      - a_1: Loop over ages (age-at-maturity to plus-1 for 'parent')

      - b_2: Loop over birth years (for 'offspring'), $y_2 - a_2$

        - $\Pr[\, s_1, y_1, a_1, y_2, a_2 \,] = \mathrm{fec}(\, s_1, a_{1\_in\_b2}) \,/\, \Sigma_{a'} [\, N_{s1,\, a',\, b2}\ \mathrm{fec}(s_1, a') \,]$

- *Might* be complications e.g.
  - might know length, not age, for (some) samples
  - fecundity might be length &/ age dependant
  - lethal/non-lethal eg GNS
  - length error or ageing error
  - populations / stock structure
  - other dimensions?
  - *plus group*

- HSPs
  - s_p: Loop over unseen parent's sex
    - b_1: Loop over birth year of first animal
      - b_2: Loop over birth year of second animal

      - $P(s_p, b_1, b_2) = \Sigma_{a'} N_{sp,a',b1} *$ survival(s_p, a', b_1, b_2) * {fec $(s_p, a\_b_1) / \Sigma_{a''} [N_{a'',b1}]$} * {fec $(s_p, a\_b_2) / \Sigma_{a''} [N_{a'',b2}]$}

  - Again, dims could blow out
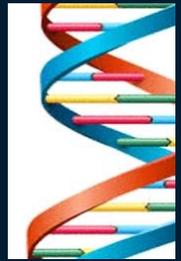   - sex of sibs (for length)
    - length error, location, ?

CKMR steps

1. Design
2. Sampling
3. Genetics / kin finding the right kind!
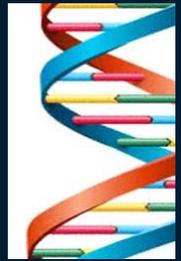4. Close kin model

1. Design

- How many samples will we need?
  - -> cost of project
  - -> followed by full CKMR project

- Uses the same probability calculations
  - (probably ignoring complications)

- No estimation of abundance / parameters necessary
  - these are assumed, use existing assessment if possible

- Code should be able to run in 'design mode'

CKMR 'module'

- What are the essential elements of a CKMR model?
  - known for *typical* teleost & *typical* shark
  - But only 5-ish species have completed CKMR studies at CSIRO (2 published)
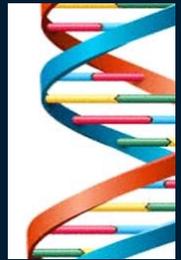 - How many will be bespoke?
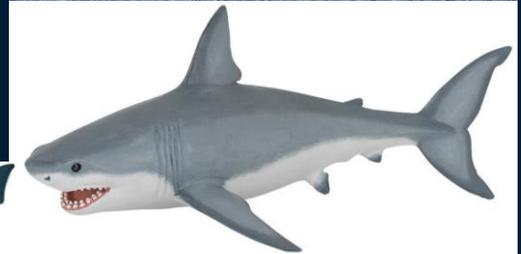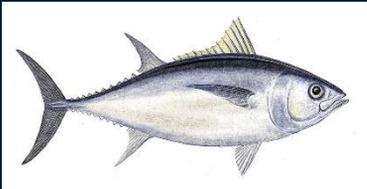
CKMR 'module'

- LOTS of dimensions!
- Can we remove some? e.g. length
  - A big / fecund 10yo was a big / fecund 5yo -> systematic
  - Does this matter?

- Can we deal with spatial structure?
  - Yes for Mediterranean ABT
  - Seems OK for Paul Conn's bearded seal dispersion simulation

- How bespoke are these models?

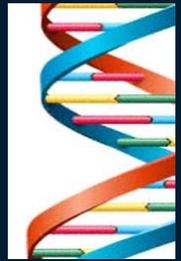# Summary

- CKMR is magic!
  - Gives absolute abundance, M, …
  - No issues with tag loss, tag reporting…
  - Forgiving sampling design (need not sample everywhere)

- CKMR for next gen stock assessment model
  - Fits into existing statistical stock assessment paradigm
  - Additional Likelihood component
  - Still working out the 'generic CKMR model'
  - Design mode

- Generic 'stand-alone' CKMR model for SESSF (under development)

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┌─────────────────┐      ┌─────────────────┐      ┌─────────────────────┐
│ CKMR data       │      │                 │      │ N-at-age & covariance│
│ Catch-at-length │ ───► │  CKMR model     │ ───► │ Survival, etc       │
│ Age-at-length   │      │                 │      └─────────────────────┘
└─────────────────┘      └─────────────────┘      ┌─────────────────────┐
                                         ╲         │ Likelihood component │
                                          ╲───►    │ for assessment      │
                                                   └─────────────────────┘
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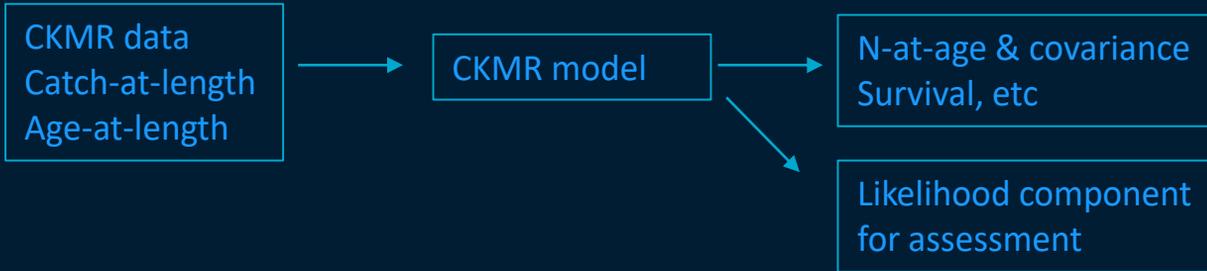
- Experiment with what's possible

Thank you