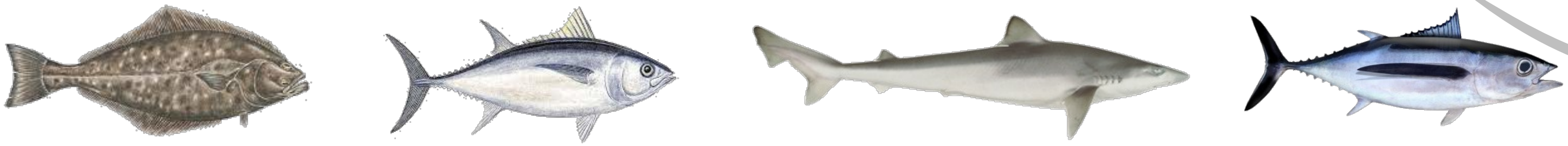
Close-Kin Mark-Recapture: overview for WCPFC

Mark Bravington, CSIRO: Sep 2021

O&A
www.csiro.au



Close-Kin Mark-Recapture-- overview

CKMR delivers:

absolute abundance

natural mortality (M)

and more

without relying on problematic data

eg CPUE

just with biopsies from small % of catch

One-time "ground-truth"...

and/or integrate with conventional data

in ongoing assessment & management

This first talk:

1. How it works
2. Examples brief
3. Requirements
4. Spatial issues brief
5. Comparison / summary

Can give more detail in subsequent talks

What is CKMR ?

Biopsies from juves & adults (dead is OK) over a few years

Some idea about age/sizes

Two "assumptions":

1. At birth, everything had 1 living mother and 1 living father

2. Reliably find ***Parent-Offspring-Pairs*** and ***Half-Sibling-Pairs*** with genetics

ie 2 animals with
same mum or dad

What is CKMR ?

Biopsies from juves & adults (dead is OK) over a few years

Some idea about age/sizes

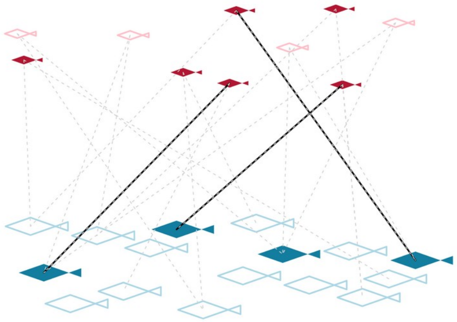
Parent-Offspring Pair

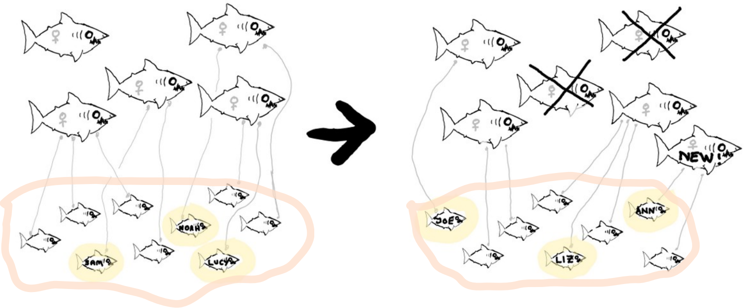
Each sampled juvenile*

marked its two parents at birth

cross-cohort Half-Sib Pair

Direct recapture (POPs) and **Indirect** (XHSPs)





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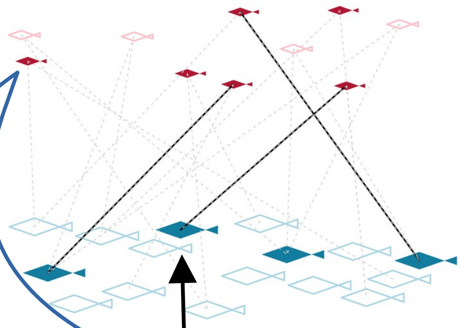
* Not necessarily very young

What is CKMR ?

Direct recapture (POPs)



Chance **that** ♀ is **my** Mum

$\approx 1/N_{\text{♀adult}}$

… but …

What is CKMR ?

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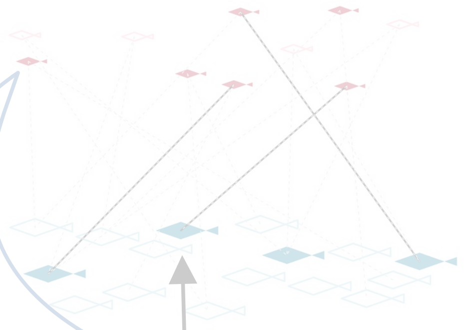

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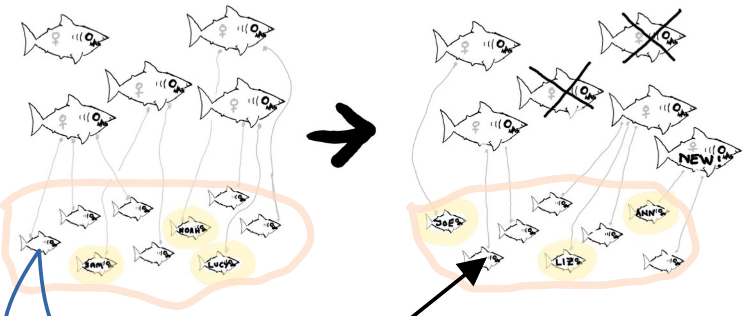

Chance **that** juve has same Mum as **me**

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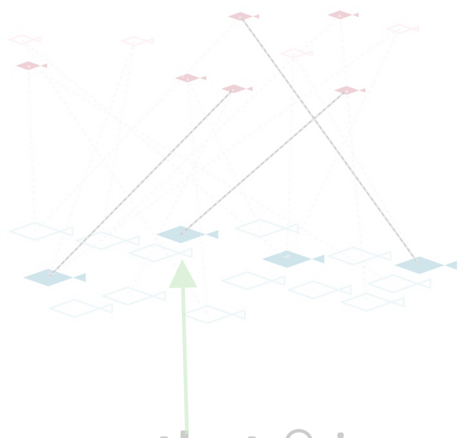
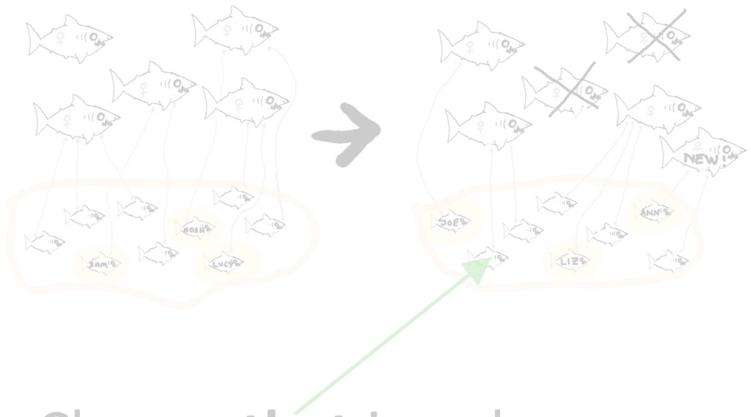




Chance **that** ♀ is **my** Mum

$\approx 1/N_{♀\mathrm{adult}}$

Chance **that** juve has same Mum as **me**

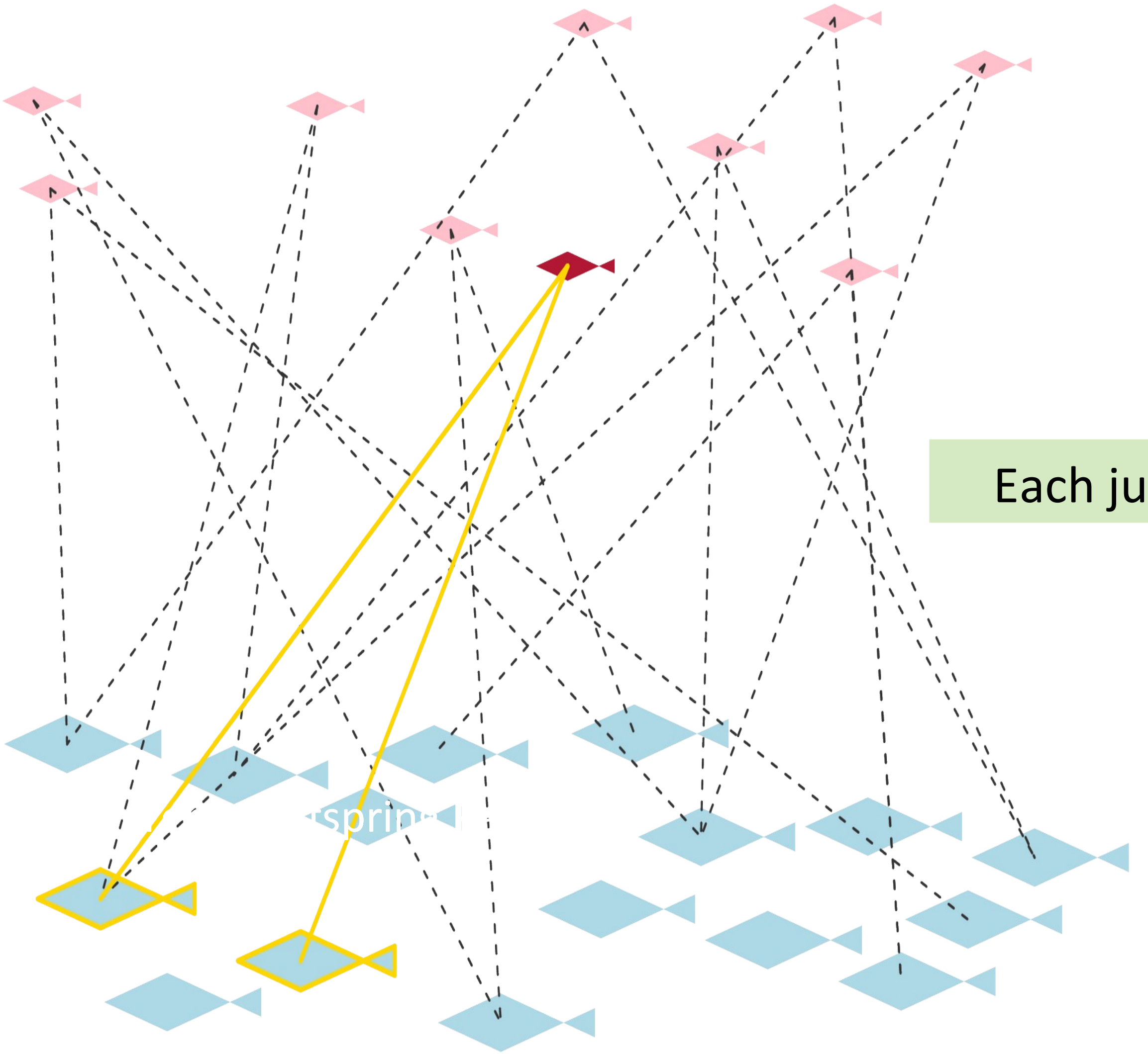
$\approx 1/N_{♀\mathrm{adult}}$

… but …

*mortality, time-gaps, growth / fecundity **also** affect prob*

so there is no simple formula for "estimated N"

CKMR cartoon for POPs

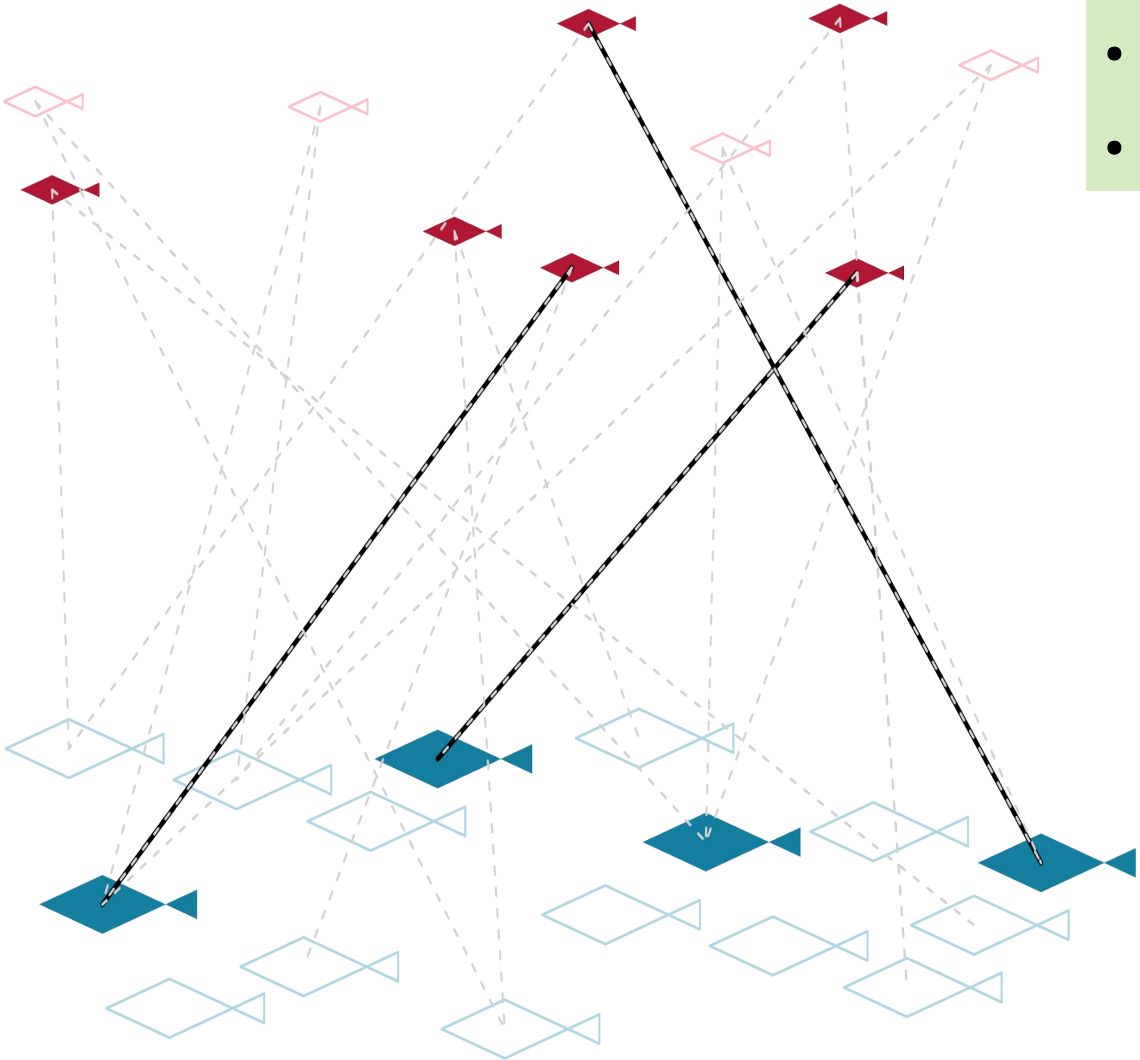


Each juvenile "marks" its two parents

CKMR cartoon for POPs

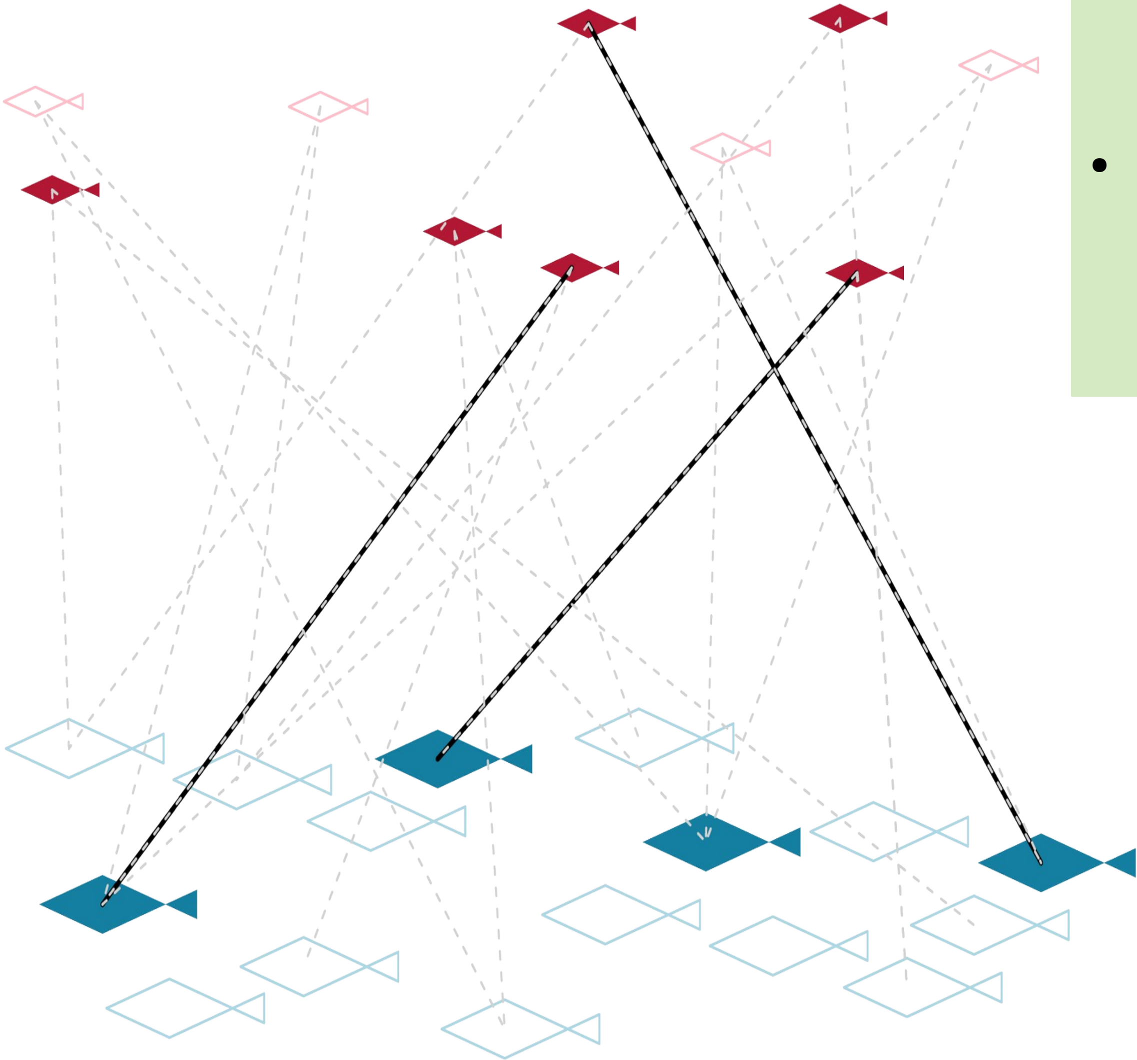
Sample adults and juves

- ... genotype them ...
- ... look for POPs ("marks")



POP: **P**arent - **O**ffspring **P**air

CKMR cartoon for POPs



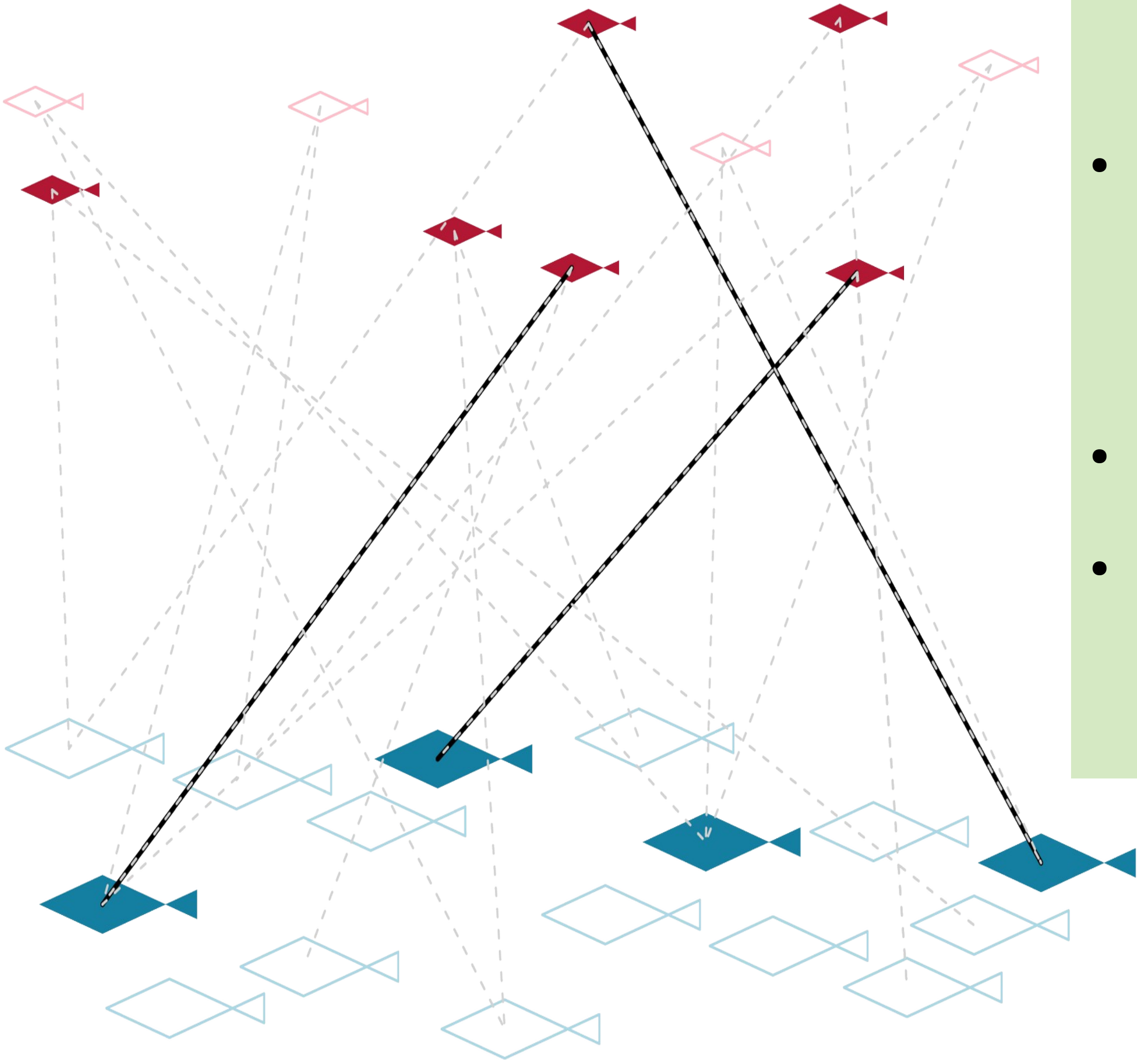
- Each adult-juve comparison:

  Prob[POP] =2/N_{adult}

- Sample 6 juves & 4 adults
  - 24 pairwise comparisons
  - 3 POPs found

POP: **P**arent - **O**ffspring **P**air

CKMR cartoon for POPs



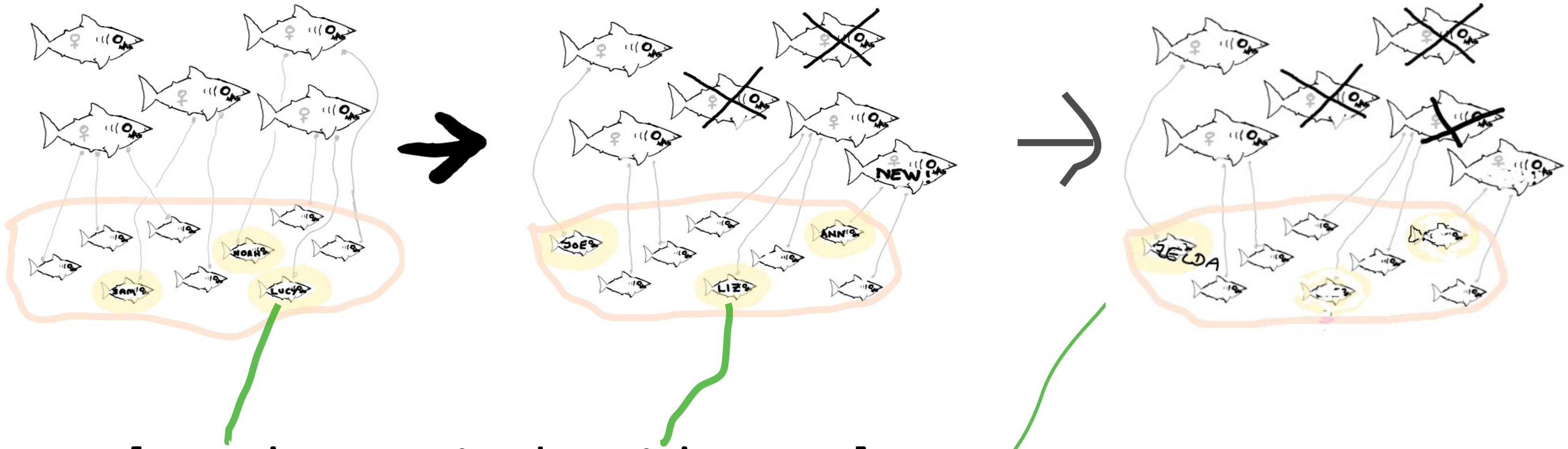
- Each adult-juve comparison:

  Prob[POP] =2/N_{adult}
- Sample 6 juves & 4 adults
  - 24 pairwise comparisons
  - 3 POPs found
- 24 * 2/N_{adult} gives 3
- Estimate of N_{adult} is 16

  ... which happens to be the right answer. Lucky !

POP: **P**arent - **O**ffspring **P**air

Mortality rate from XHSPs



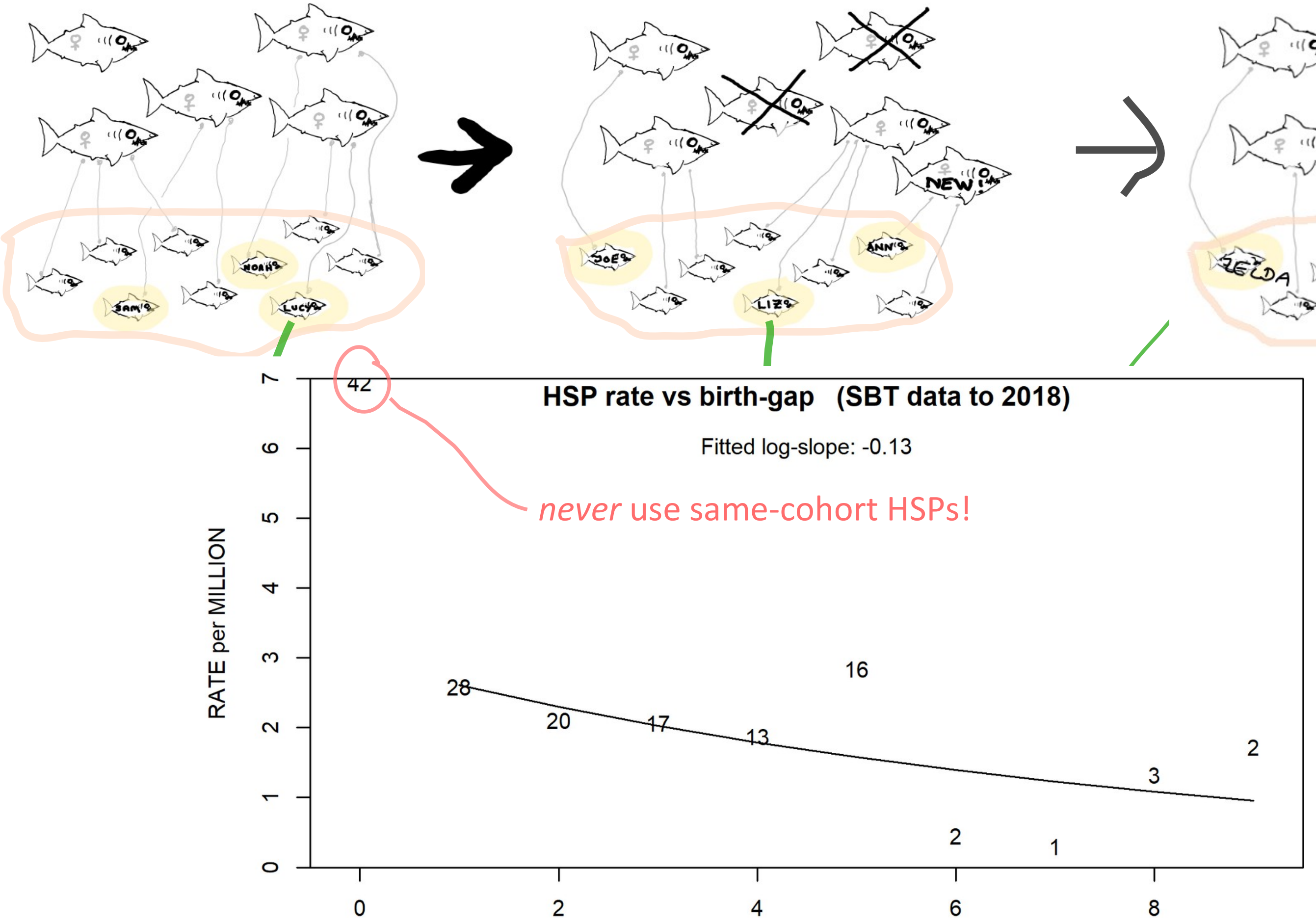
Pr[Lucy’s mum is also Liz’s mum]

>

Pr[Lucy's mum is also Zelda's mum]

XHSP: Cross-cohort Half-Sib Pair--- same mother or same father

Mortality rate from XHSPs



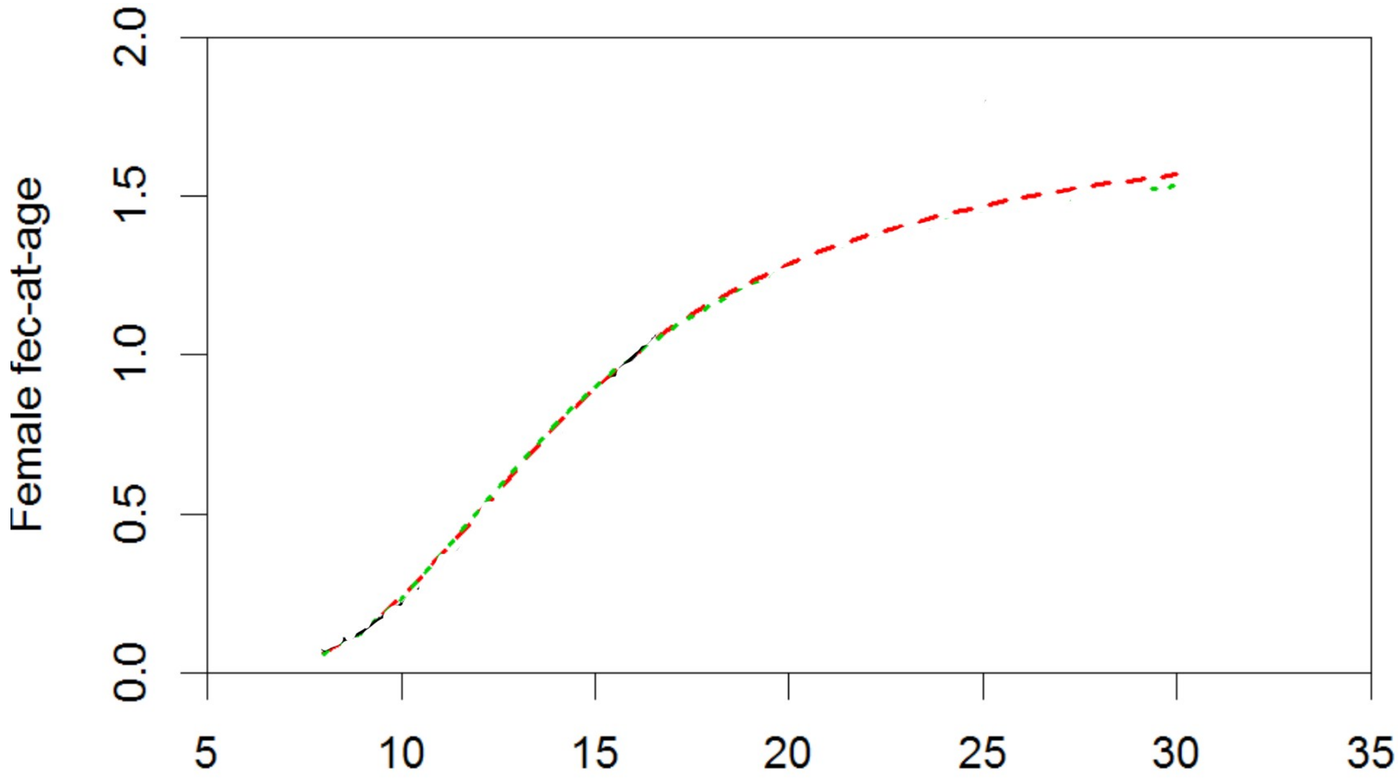
never use same-cohort HSPs!

This still needs *adjustment* before you have Z

Relative Fecundity from POPs

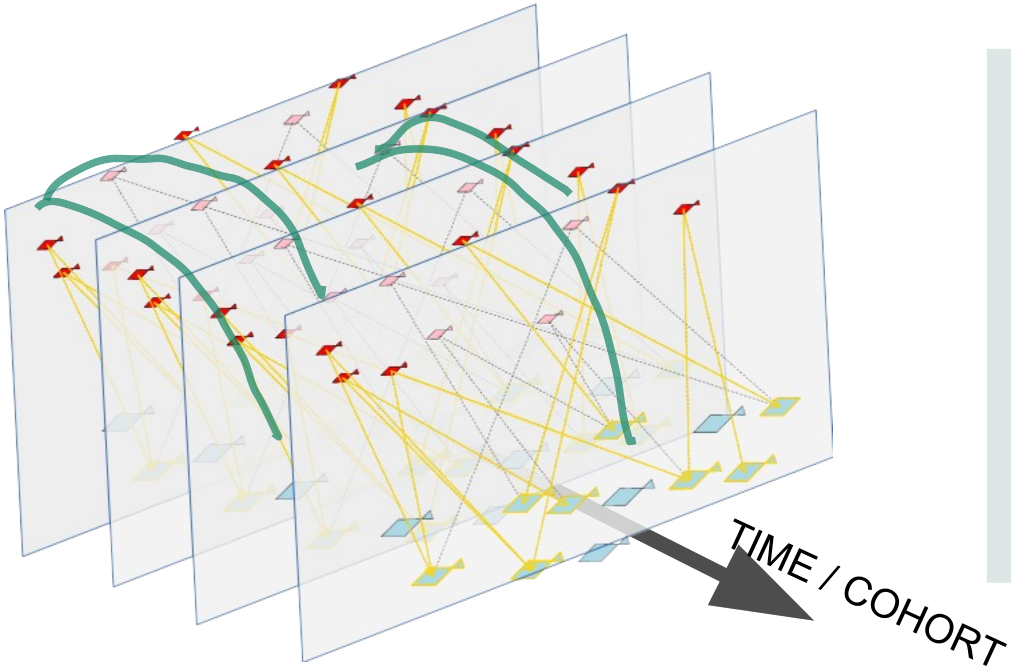
SBTuna: 2017 data, from fitted model

Curve for ♂ is similar



I really should do a better "empirical" graph for this !

Putting it all together



- Several cohorts / years / ages
- **Lots** of comparisons
- Different prob formulae
- More parameters than just “N”
- Need to fit pop dyn model

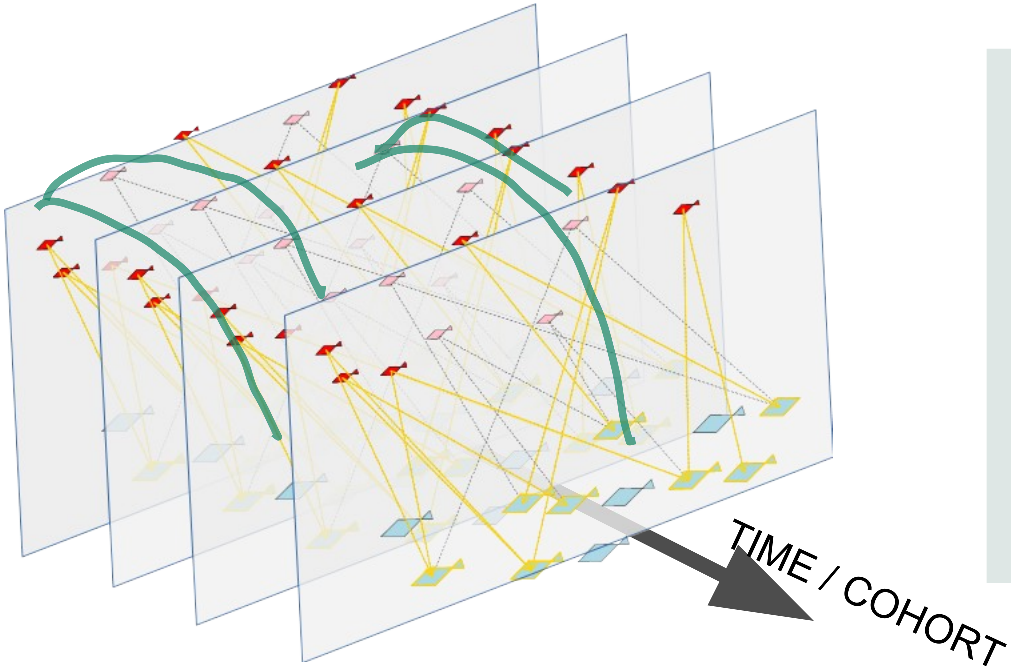
  as for normal stock assessment
- *not* just “one index per year”

POPs => N & rel fec-at-age/size

HSPs => Z

Z = F + M = Catch/N + M

Putting it all together



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POPs	=>	N	& rel fec-at-age/size
HSPs	=>	Z	
Z = F + M	=	Catch/N + M	

NB: you get *average* M across adults

NB: no (direct) info on *juvenile* M or N

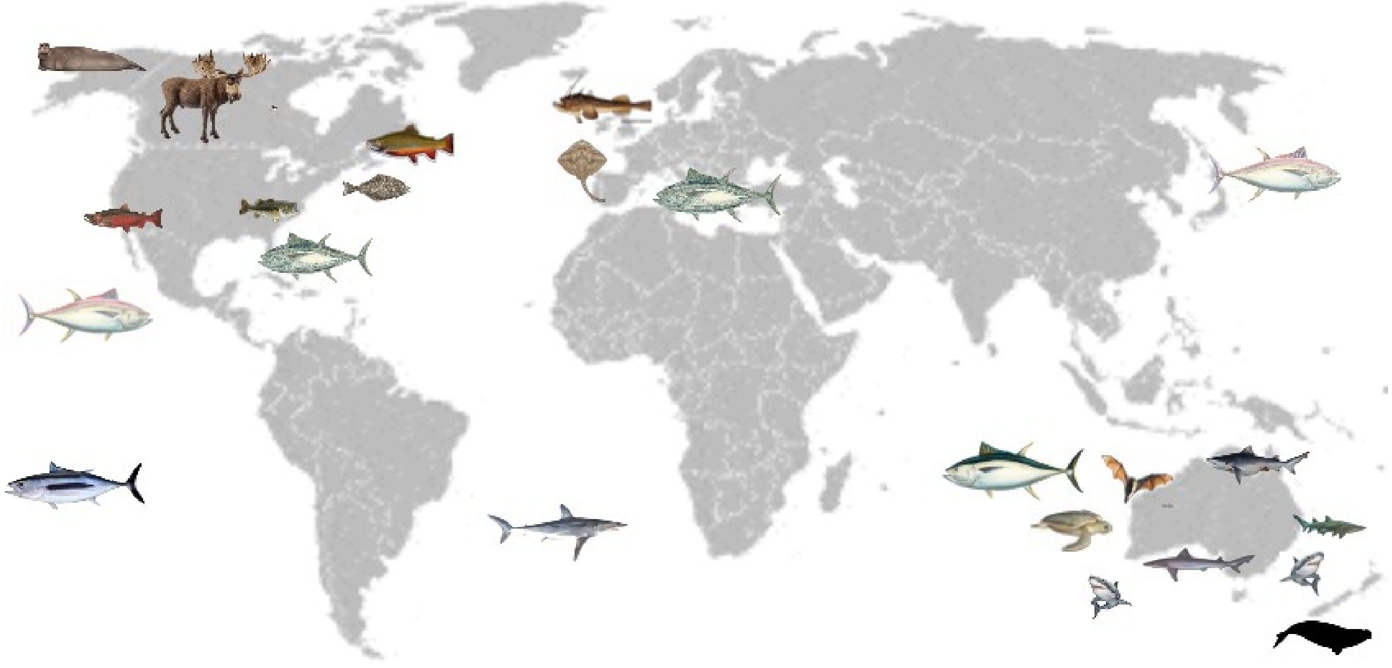
NB more complex in practice because of adult growth

CKMR Examples

Breed'n'die	Complete
Chinook Rawding@WDFW	2014

Commercial	"Complete"	WFC21 talk
SBTuna	2013 2017	Hillary
School Shark	2019	Thomson
Thornback Ray Trenkel@ IFREMER	2021	
WABTuna CSIRO+NOAA	2021	Walter

"Conservation"	"Complete"
White Shark * 2	2017
Glyphis glyphis * 2+	2018
G. garrickii	2018
Grey Nurse Shark	2018
Brook Trout Ruzzante@Dalhousie	2019



Publications...

so much to do, so little time

ARTICLE

Received 17 Nov 2015 | Accepted 8 Sep 2016 | Published 14 Nov 2016 DOI: 10.1038/ncomms13162 OPEN

Absolute abundance of southern bluefin tuna estimated by close-kin mark-recapture

Mark V. Bravington[1], Peter M. Grewe[1] & Campbell R. Davies[1]

OPEN Genetic relatedness reveals total population size of white sharks in eastern Australia and New Zealand

Received: 19 June 2017
Accepted: 10 January 2018

R. M. Hillary[1], M. V. Bravington[1], T. A. Patterson[1], P. Grewe[1], R. Bradford[1], P. Feutry[1], R. Gunasekera[1], V. Peddemors[2], J. Werry[3], M. P. Francis[4], C. A. J. Duffy[5] & B. D. Bruce[1]

Close-Kin Mark-Recapture

Mark V. Bravington, Hans J. Skaug and Eric C. Anderson

Methods in Ecology and Evolution BRITISH ECOLOGICAL SOCIETY

RESEARCH ARTICLE | Free Access

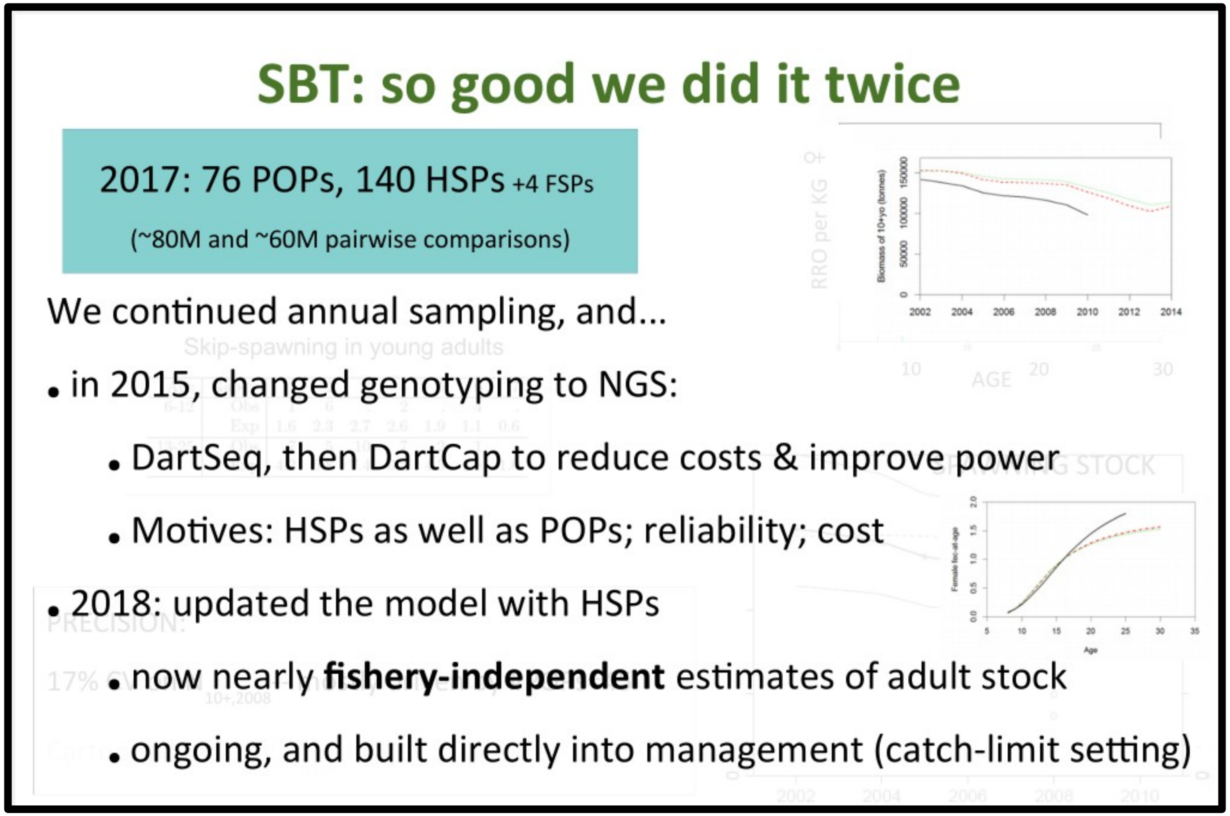
Validation of close-kin mark–recapture (CKMR) methods fo

estimating population abundance

Daniel E. Ruzzante, Gregory R. McCracken, Brage Førland, John MacMillan, Buhariwalla, Joanna Mills Flemming, Hans Skaug,

First published: 18 June 2019 | https://doi.org/10.1111/2041-210X.13243 |

SBT: more details in other talks...



SBT: so good we did it twice

2017: 76 POPs, 140 HSPs +4 FSPs

(~80M and ~60M pairwise comparisons)

We continued annual sampling, and...

- in 2015, changed genotyping to NGS:
  - DartSeq, then DartCap to reduce costs & improve power
  - Motives: HSPs as well as POPs; reliability; cost
- 2018: updated the model with HSPs
  - now nearly **fishery-independent** estimates of adult stock
  - ongoing, and built directly into management (catch-limit setting)

By 2021: nearing 30,000 samples, 100 POPs, 200 HSPs

CKMR requirements

At least 50 POPs/XHSPs to get a precise “N”... but not just “how many”

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At least 50 POPs/XHSPs to get a precise “N”... but not just “how many”

- *Adequate* numbers of juveniles[*], and of all sizes of adults
  - to get adequate POPs *and* XHSPs
  - Total sample size: “constant” * sqrt(N_{adult})
- *Adequate* number of juvenile cohorts
- *Adequate* spatial spread
- *Adequate* precision on age estimates
- careful **design** - what is “adequate”? - and execution

not actually constant!

---

[*] Not necessarily very young

CKMR design is...

"simulation" to work out cheapest sample size/composition/etc for *useful* precision

CKMR Design: Makos in the Atlantic

Can a new approach provide reliable estimates of shortfin mako shark abundance and productivity in the Atlantic Ocean?

Mark Bravington, CSIRO, Nov 2019

https://www.youtube.com/watch?v=q4lzzY4qRRc

Design is based on existing assessment (NAtl)...

... or, assuming current catches *just* sustainable (SAtl)

Summary:

details in https://doi.org/10.25919/qph0-cq22

Sampling XXXX juveniles (couple% of catch) across a handful of years should yield very useful **absolute abund** and **natural mortality** estimates...

... *if* assessment / assumptions are about right

Epigenetic age

Biggest CKMR headaches so far : poor age / length data

- CKMR needs *some* idea about age
- For young fish, length alone may be fine...
- ... but not for older fish

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- ... but not for older fish

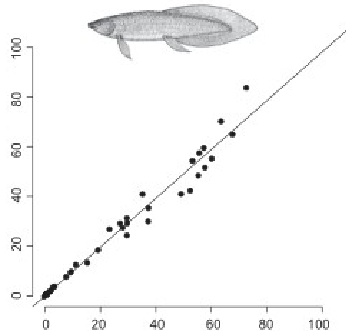
- 2020+: can estimate age **just from DNA in biopsies**

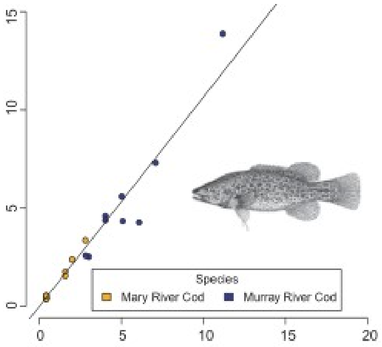
  - google Mayne lungfish age

- Easy setup; low unit cost: less than genotyping

- Needs calibrating per species precision varies; that's OK

- *so, large-scale otolith collection* ***not*** *needed for CKMR*





Genetics and kin-finding

- All thanks to massive progress in genotyping in last ~6 years
    - nothing to do with fish!

- With modern genetics (1000s of *high-quality* SNPs) it is no great problem to *reliably* find POPs and HSPs

- Routine, and inexpensive per sample at least if you do it *exactly the way we do at CSIRO, via DArT ...*
    - ie, high-read-depth ddRAD with “capture-probes/baits”

Spatial population structure

"Usually" it's *not very important* for CKMR

- at least in marine species
- mixing is *much* better than MR
- no need for synoptic coverage, a la CPUE

But it *can* matter... even when *not* heritable

- Spread your sampling
- Look for spatial pattern in the kin-pairs
- *Direct info* on *demographic* connectivity
- if you *do* find it, can *usually* fix up the model

Connectivity

Conventional population genetics will often *not* reveal demographically important substructure...

Thornback rays, Bay of Biscay Trenkel et al. 2020/1

Inshore / offshore: no difference in allele freqs

Connectivity

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Thornback rays, Bay of Biscay Trenkel et al. 2020/1

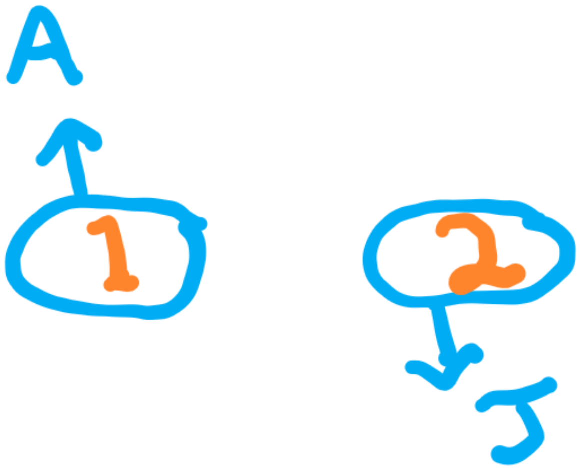
Inshore / offshore: no difference in allele freqs

POPs

In/In	In/Off	Off/Off
25	**0**	73

... but CKMR always will provided you sample widely and well enough

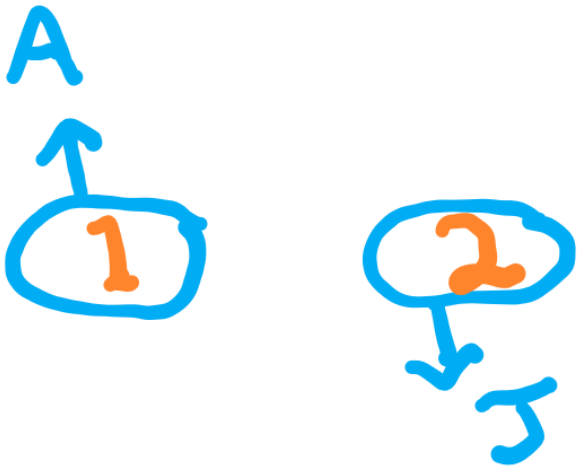
Hypothetical *bad* mixing: extreme case



no POPs: “abundance must be HUGE” ✗

at least the HSPs will *tell* you it’s wrong!

Hypothetical *bad* mixing: extreme case



no POPs: “abundance must be HUGE” ✗

at least the HSPs will *tell* you it’s wrong!

- So: spatial structure + poor sampling *can* be a problem
- Watch out when *all* sampling is linked to spawning grounds
- But: if *either* adult *or* juve samples are “well-mixed”:
  then you are basically OK
- Try to sample “everywhere” if poss but doesn’t need to be “evenly”

Spatial CKMR: degree-of-difficulty IMO...

SBTuna: easy

W ABTuna: pretty easy

PBTuna: do-able with *right* sampling

E ABTuna (Med): harder

(discrete spawning sites; most sampling is at those sites)

but do-able *with care*

Rabbits: probably not!

Abalone: forget it!

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SBTuna: easy
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"Tropical" tunas ? fine, if samples are spread ?

PBTuna: do-able with *right* sampling

E ABTuna (Med): harder
(discrete spawning sites; most sampling is at those sites)
but do-able *with care*

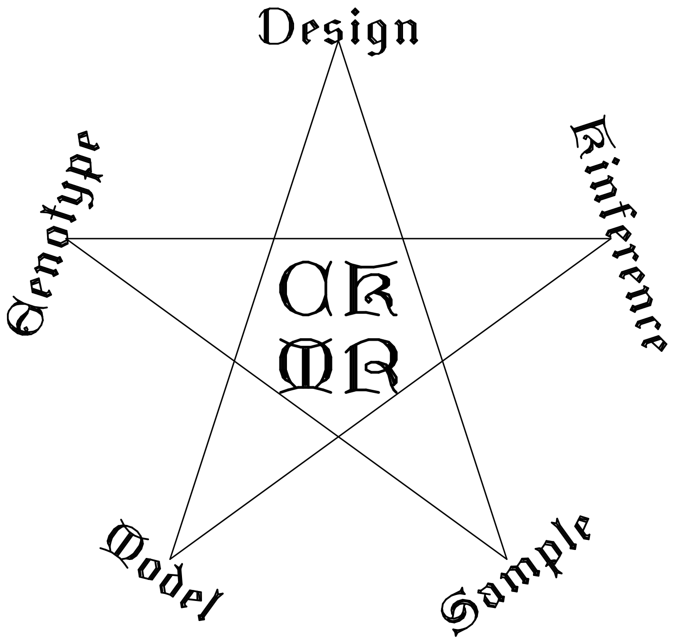
Rabbits: probably not!
Abalone: forget it!

CKMR: what could possibly go wrong..?

Most pitfalls are *logistics*

as long as sampling is

designed carefully



- CKMR needs a **team**
    - biology / sampling
    - genetics
    - modelling / stats

It **all** has to work for **any** of it to be useful...

CKMR Summary & comparisons

Absolute abundance and *M* from biopsy small % of catch over few years

- NB direct info only about adults, not juves

Integrate into assessment and/or as standalone ground-truth

No CPUE-linked assumptions & no relative/absolute drama

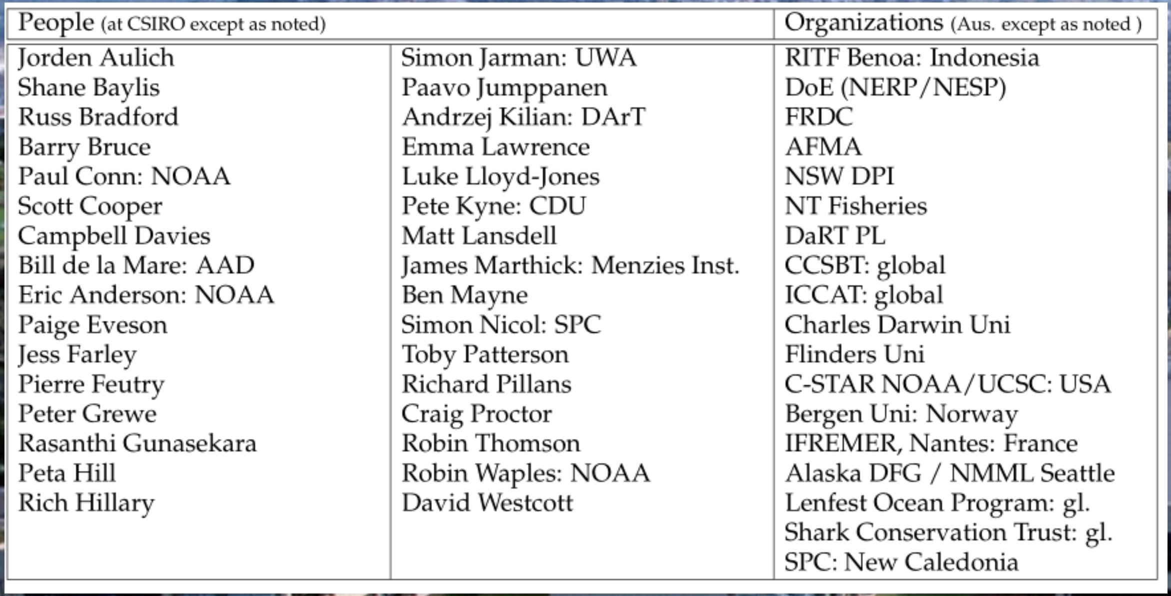
Unlike conventional MR, CKMR:

- no live relea$e
- no reporting rate issues
- better mixing
- directly addresses “connectivity/structure”

Widely applicable incl. tunas & many sharks

- “just” a matter of logistics ..?

Acknowledgements



People (at CSIRO except as noted)

- Jorden Aulich
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- Campbell Davies
- Bill de la Mare: AAD
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- Craig Proctor
- Robin Thomson
- Robin Waples: NOAA
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Organizations (Aus. except as noted)

- RITF Benoa: Indonesia
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- NT Fisheries
- DaRT PL
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- ICCAT: global
- Charles Darwin Uni
- Flinders Uni
- C-STAR NOAA/UCSC: USA
- Bergen Uni: Norway
- IFREMER, Nantes: France
- Alaska DFG / NMML Seattle
- Lenfest Ocean Program: gl.
- Shark Conservation Trust: gl.
- SPC: New Caledonia

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Rich Hillary
Campbell Davies

Pierre Feutry
Robin Thomson
Shane Baylis

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Tore Schweder- Oslo Uni, Norway

Andrzej Kilian- DArT, Canberra

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