



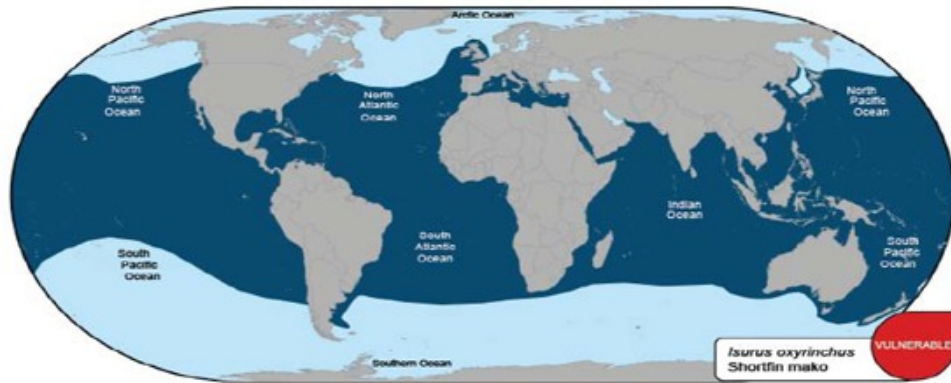
Can a new approach provide reliable estimates of shortfin mako shark abundance and productivity in the Atlantic Ocean?

O&A
www.csiro.au

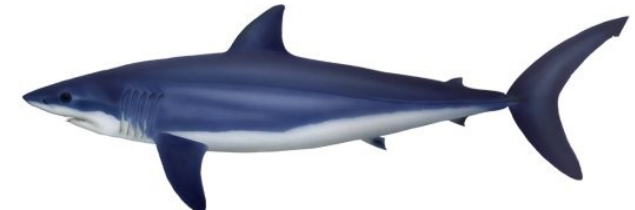
Mark Bravington, CSIRO, Nov 2019



Background: shortfin mako sharks



Map: IUCN



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Background:

makos, Atlantic, assessment, etc

Close-Kin Mark-Recapture:

principles, examples

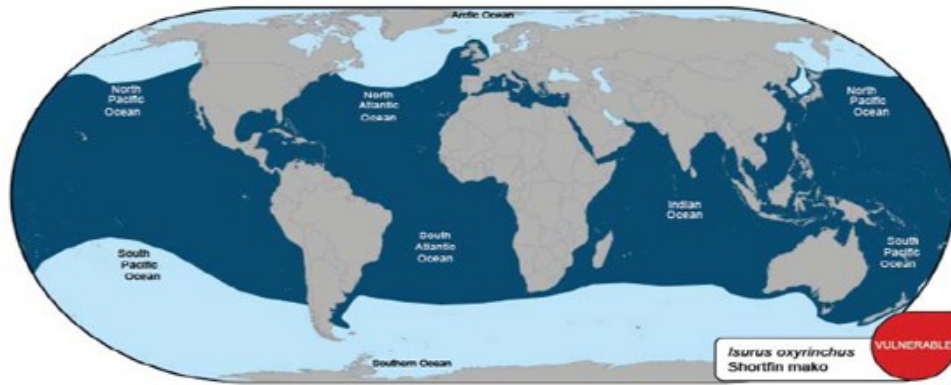
Mako CKMR design:

general, North Atl, South Atl

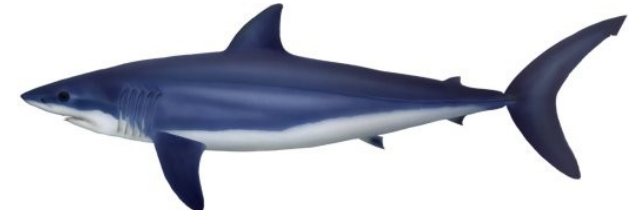
Summary:

could this really work ?!

Background: shortfin mako sharks



Map: IUCN



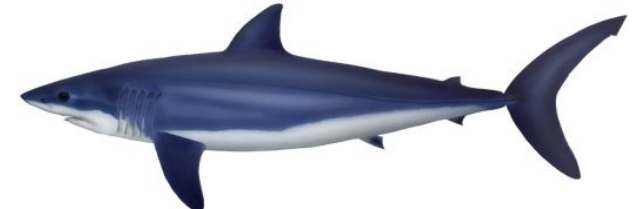
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DISCLAIMER...

Background: shortfin mako sharks



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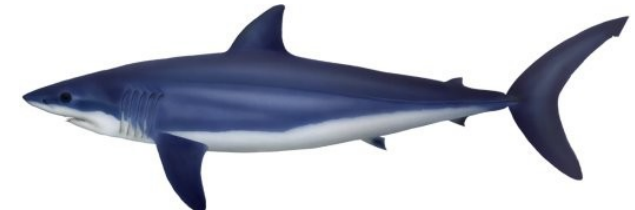
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- Worldwide, but separate populations
 - N vs S Atl; S Atl mostly vs Indian
- Widely caught on pelagic longlines
 - high market value for flesh
 - fins
 - bycatch or target?

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- Worldwide, but separate populations
 - N vs S Atl; S Atl mostly vs Indian
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Max size:

♀: ~ 3.5m

♂: ~ 2.5 m

Maturity:

♀: ~ 20 yo

♂: ~ 10 yo

Litter size:

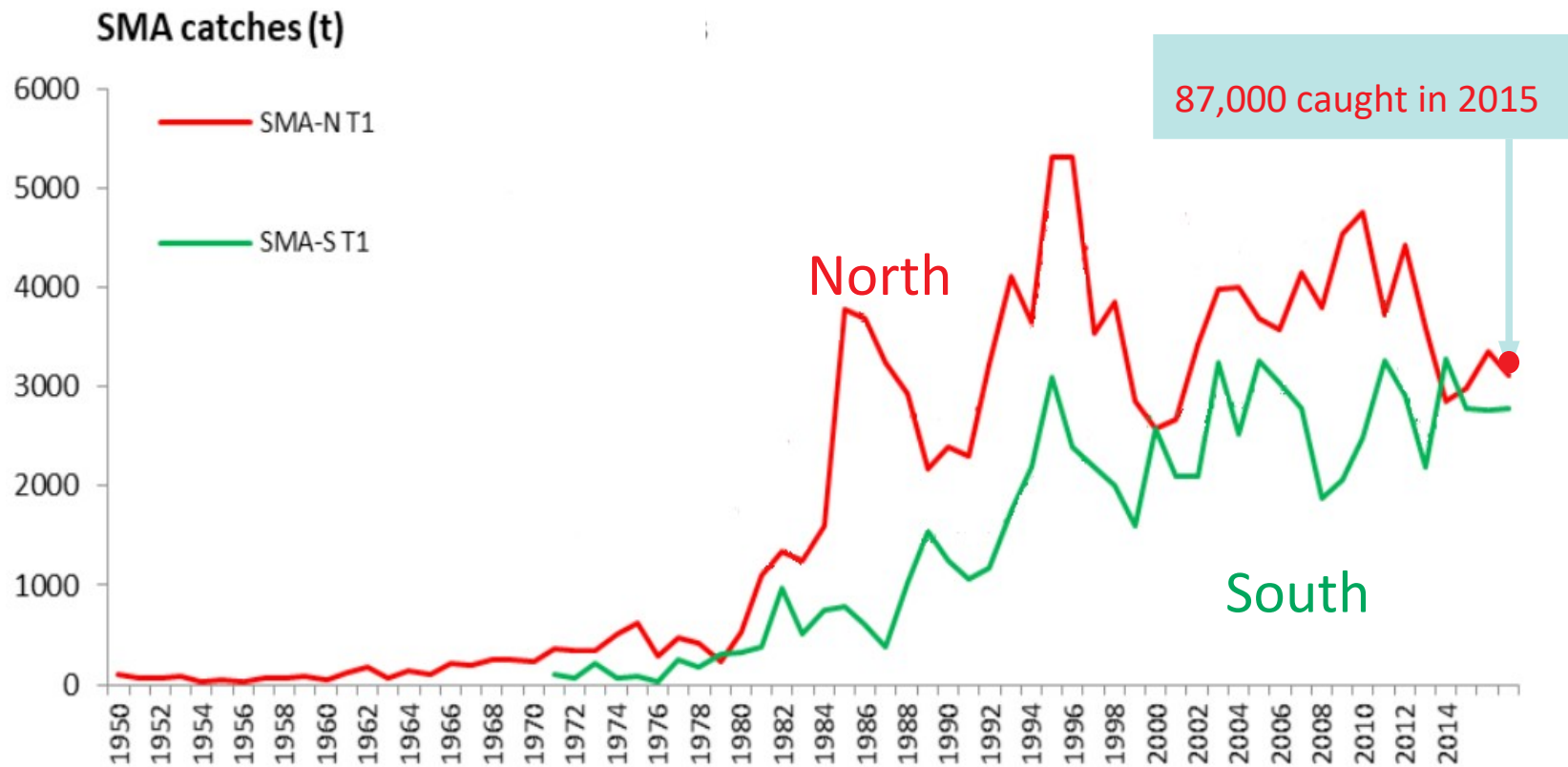
~ 10--20

some link to ♀ size

Breeding cycle:

3 years (?)

Fisheries and stock status: Atlantic



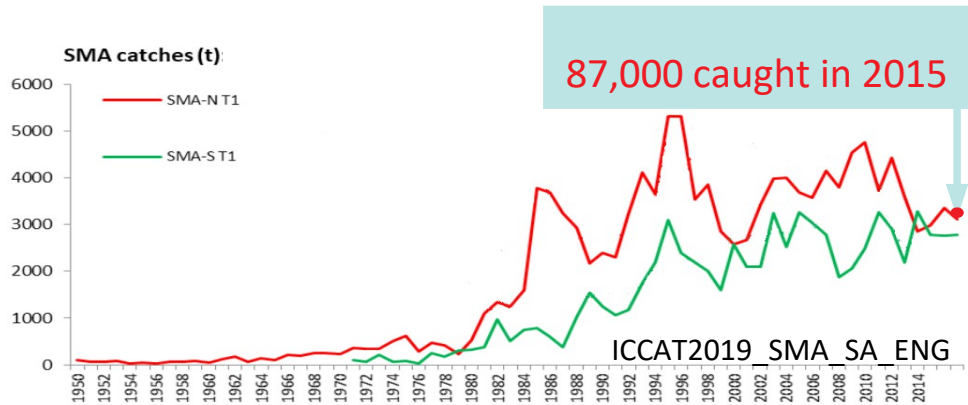
Mostly immatures 2-10yo;

3% young adult ♂;

hardly any adult ♀

See ICCAT2019_SMA_SA for full details

Fisheries and stock status: North Atlantic



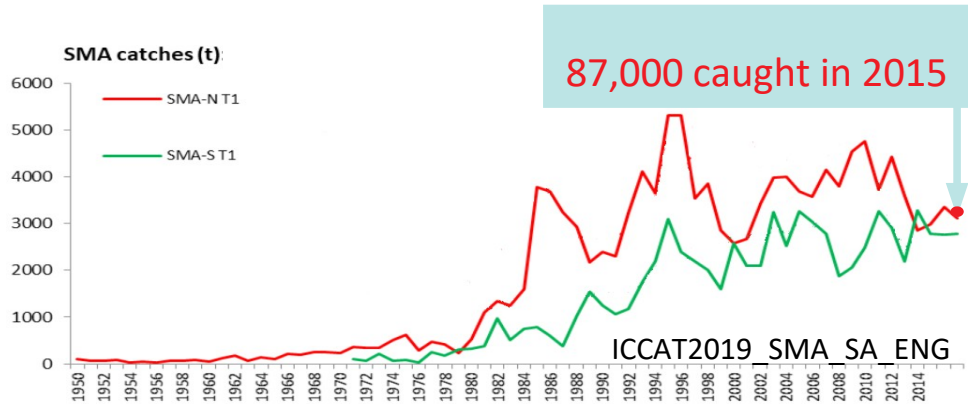
2008, 2012: attempts at full assessment

... data revisions ...

2017: defensible age-based CPUE-driven assessment

See ICCAT2019_SMA_SA for full details

Fisheries and stock status: North Atlantic



Assessment results

(m assumed 0.08)

Est. adult abund 2015:

♀: 140,000 mostly 30yo+

♂: 270,000

$F_{2015} \approx 400\% * F_{MSY}$

$SPRR_{2015} \approx 21\%$

Overfished ie B

Overfishing ie F

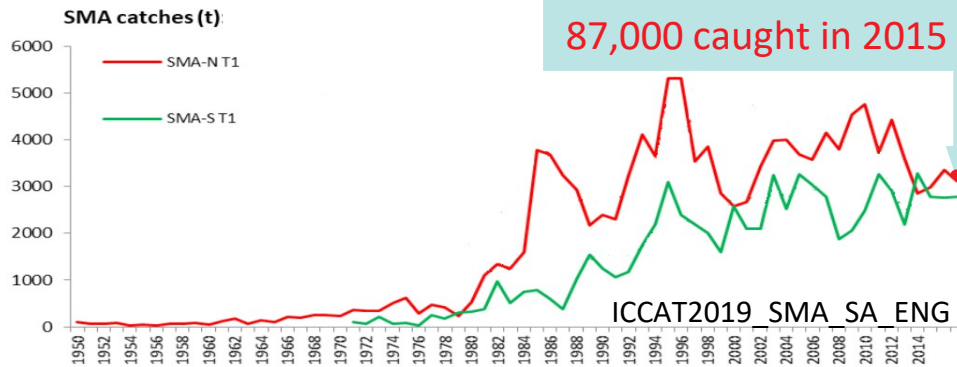
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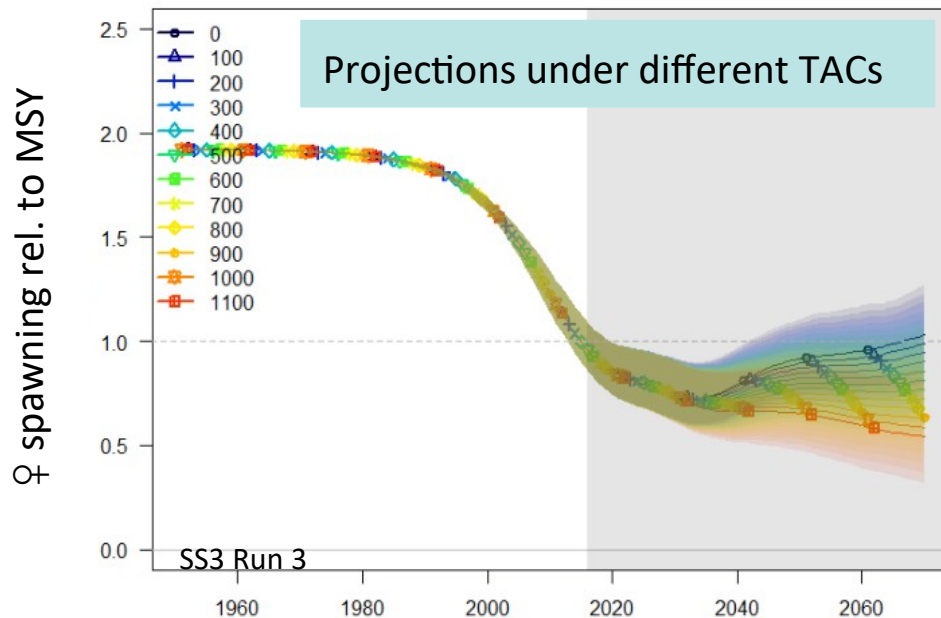
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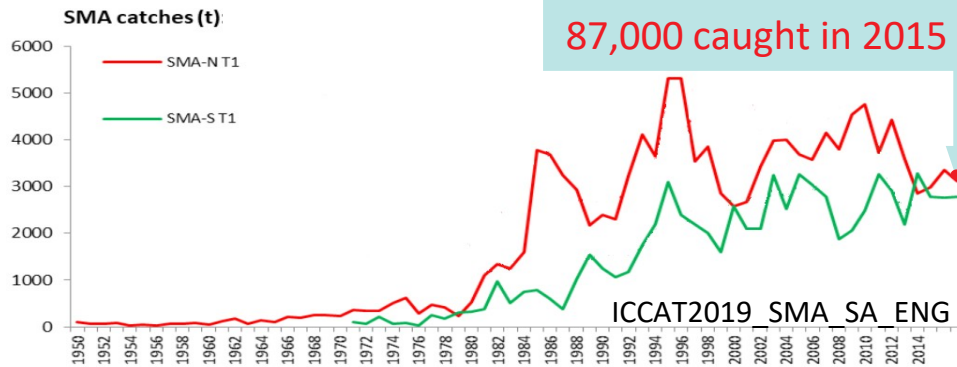
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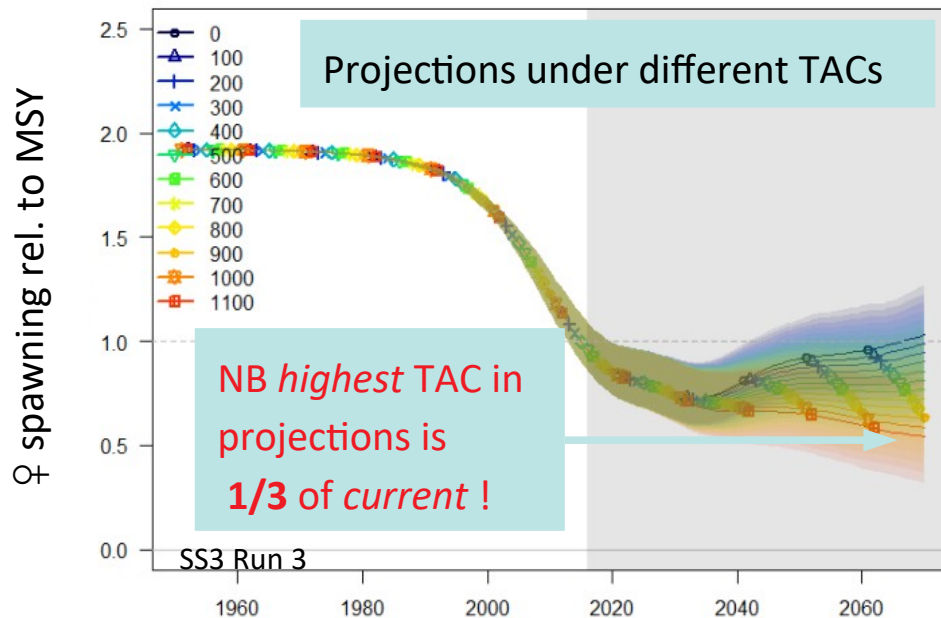
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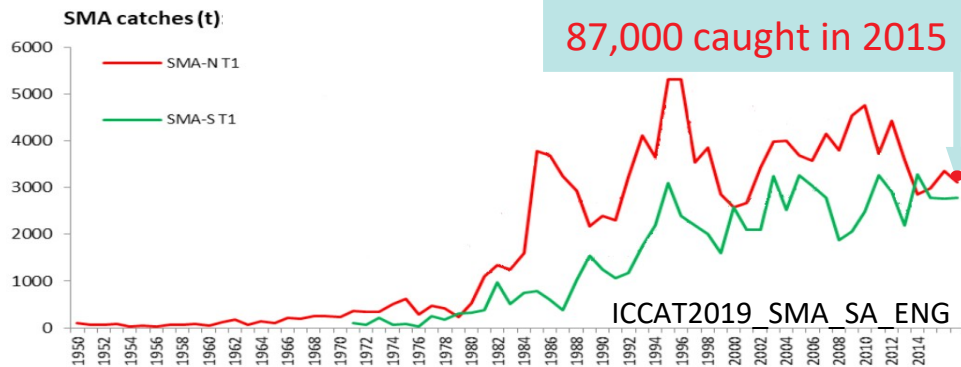
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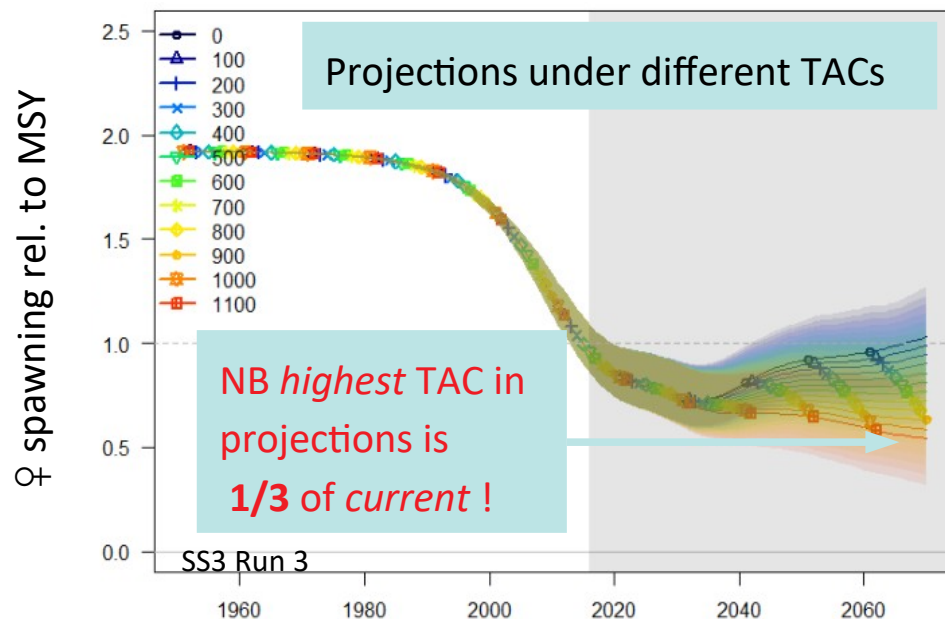
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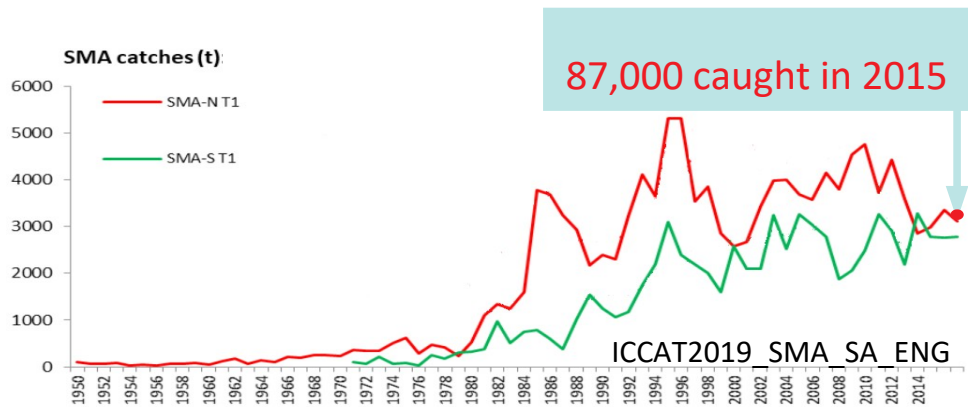
Overfishing ie F



- Stock will decline til 2035 *regardless*
- At 500t TAC: (NB current catch ~3000t)
Pr[rebuild by 2070] $\approx 50\%$
- Current (2018) management i.e. live-release insufficient to rebuild

See ICCAT2019_SMA_SA for full details

Fisheries and stock status: South Atlantic



Catches still going up...

... and so is CPUE !

No useful assessment is possible

Assessment results



Overfished ???

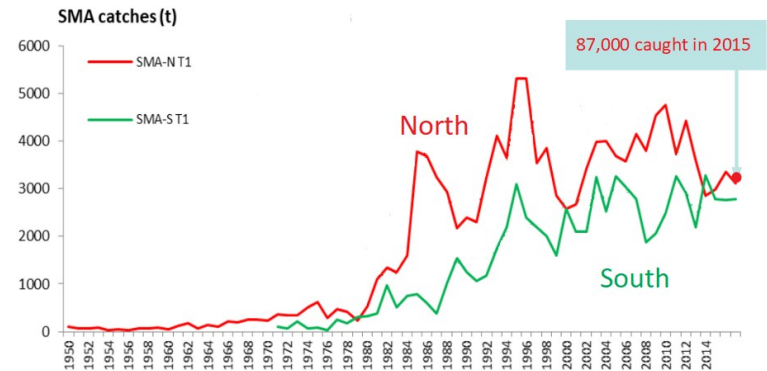
Overfishing ???

See ICCAT2019_SMA_SA for full details

Fisheries and stock status: recommendations

North Atlantic:

- 2017: No-retention, or 500t TAC: *rejected*
live-release: *adopted* "notwithstanding..."
- 2019: No-retention: *proposed*
- Data: record discards and live-releases



South Atlantic:

- 2017: 2000t TAC: *rejected*
- 2019: *proposed* again

CITES Apx II listing: 2019

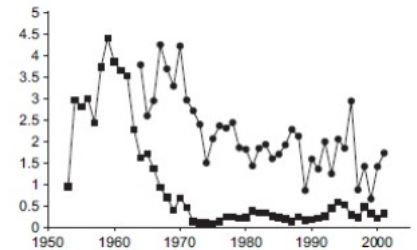
See ICCAT 2019_SMA_SA, 2017_SCRS, 2017_Comm for details

CPUE: Catch Per Unit Effort: a few polite comments...

The ICCAT 2017 mako assessment is a big accomplishment!

But..it is still CPUE-reliant

- *Lots* of things affect CPUE, not just abundance
 - Holes in coverage ?
 - Changes in distribution boats and/or fish ?
 - Changes in fishing / targeting practice ?
- It's free
- You certainly get what you pay for
- Even when OK--- it's still just a *relative* index



from Maunder et al 2006 ICES JoMS

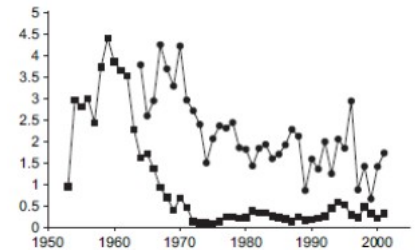


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from Maunder et al 2006 ICES JoMS



If there was anything better, you'd surely prefer to use that...

CPUE for makos: and what's more...

- Catch and CPUE is all *immature*
- So, no direct tracking of *adults*
- By the time CPUE falls via low recruitment, *adults* **well in trouble**

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Effect of future management measures?

- Targeting incentive: affects " q " ie $CPUE \div abundance$
- Releases and survival: what is "catch" ?

How will you tell if measures are working?

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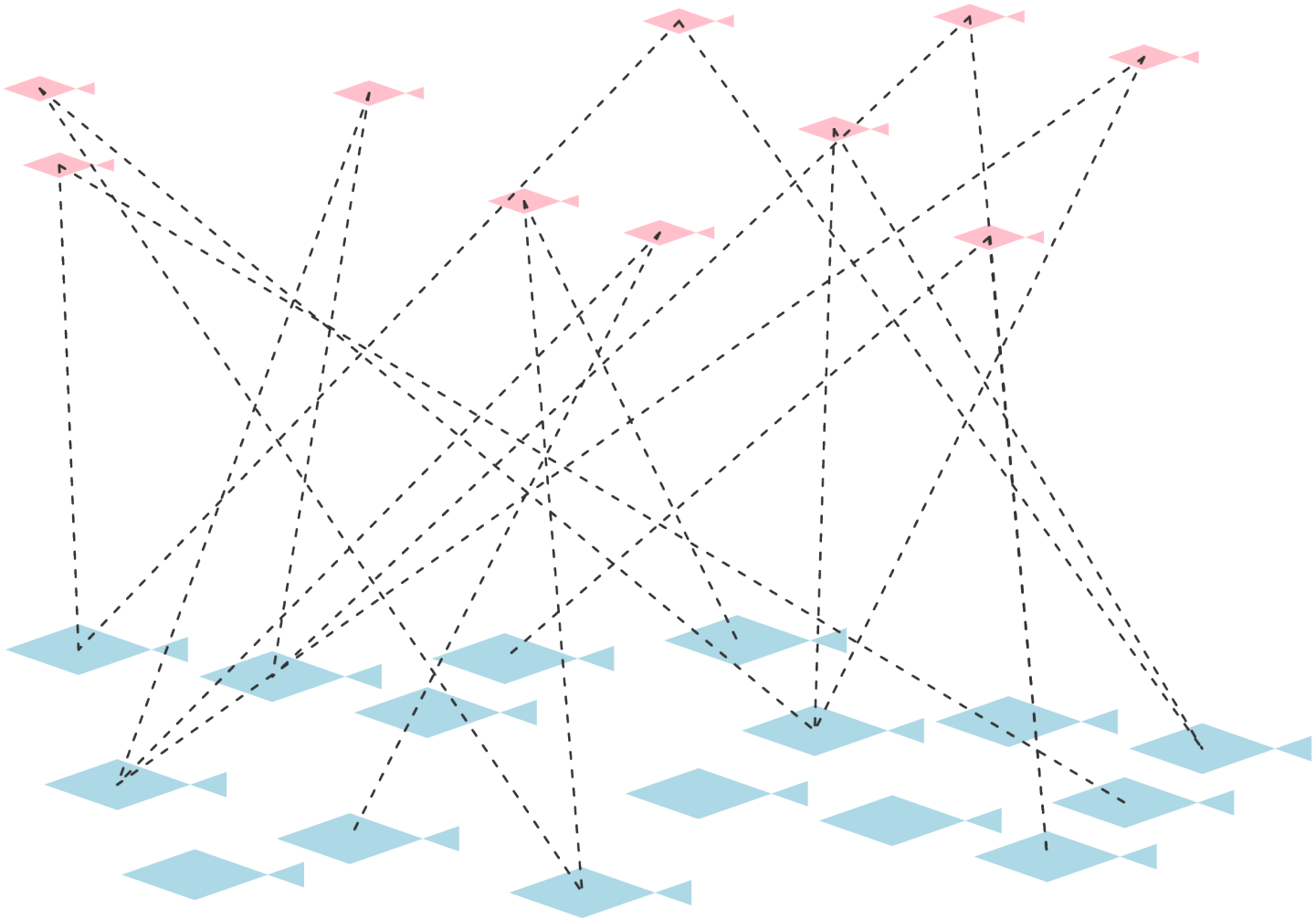
- Holes in coverage ?
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What else could you do? Tagging (mark-recapture)

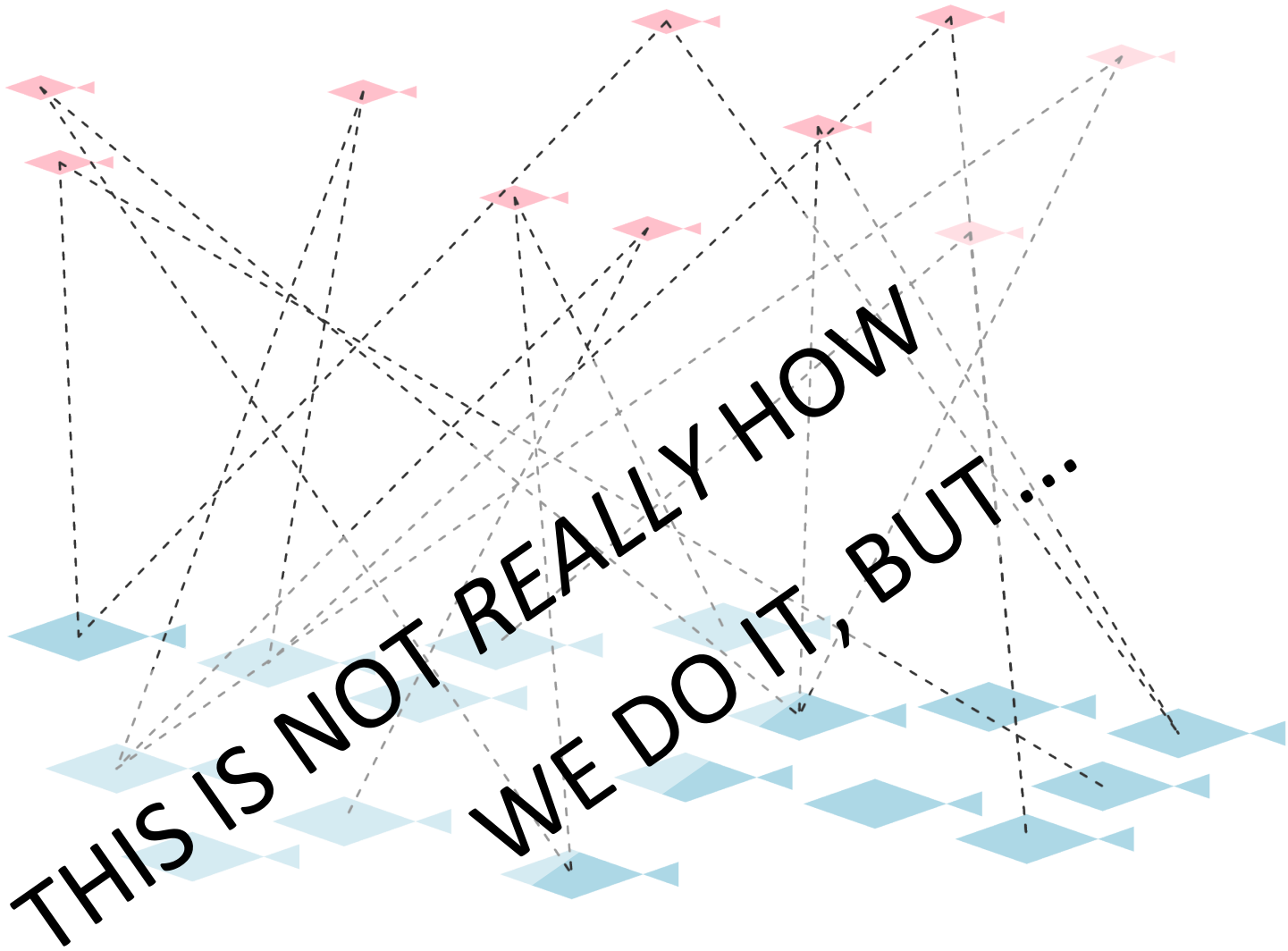
But...

- Logistics e.g. live-release; sample sizes
- Mixing
- Reporting rate
- Only applies to "fishable" ages
- Dead animals are useless

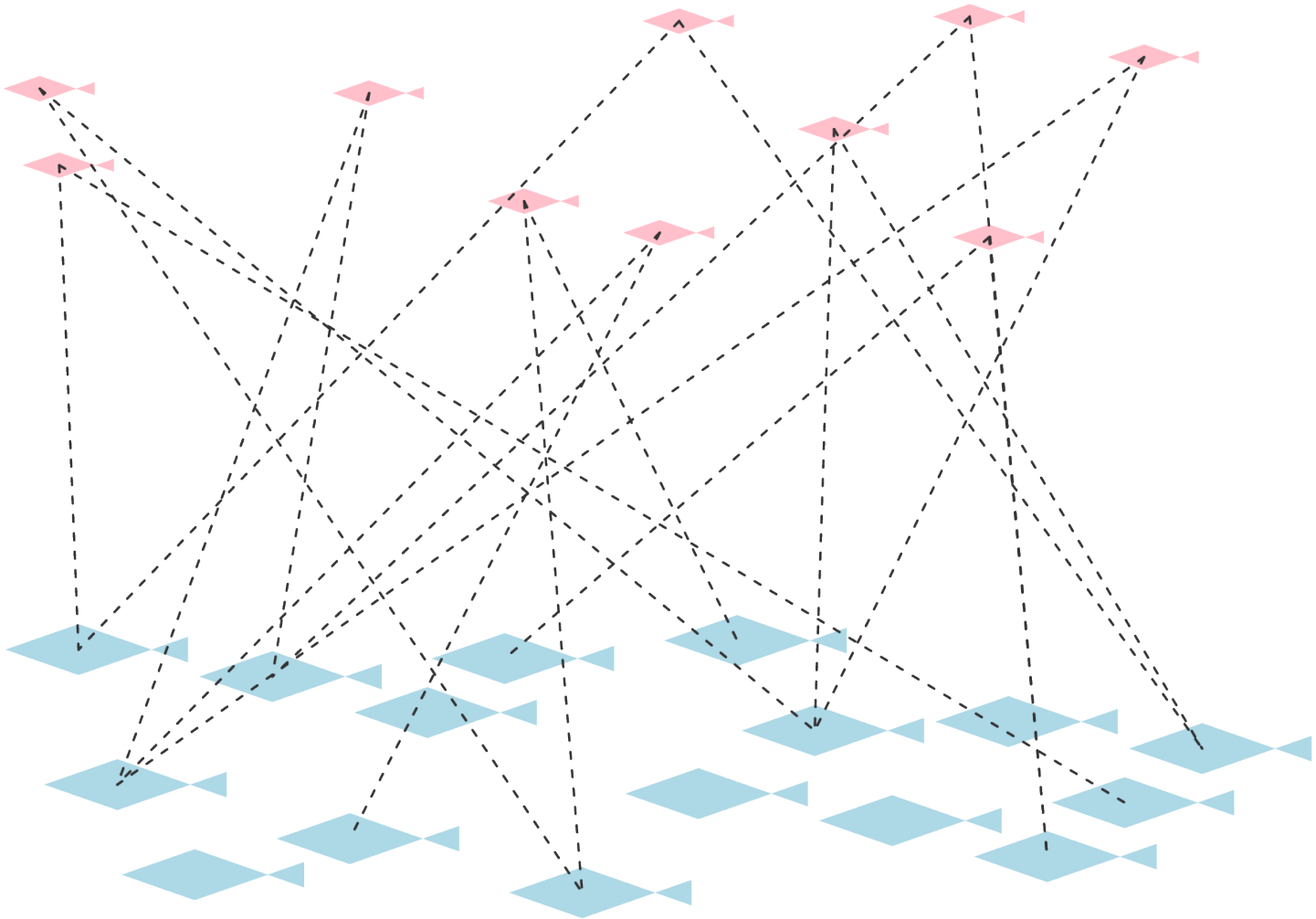
CKMR principles: POP *cartoon*



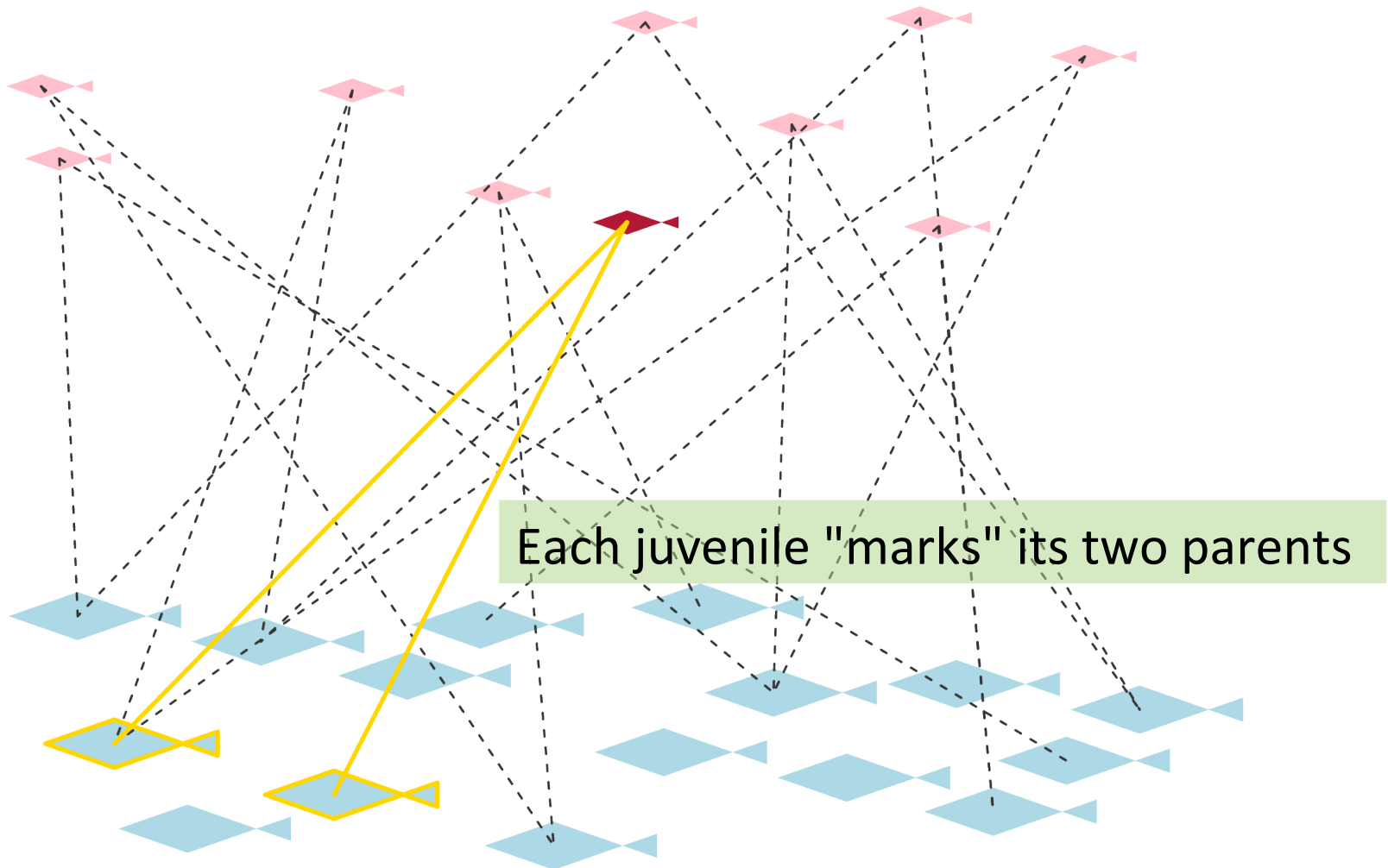
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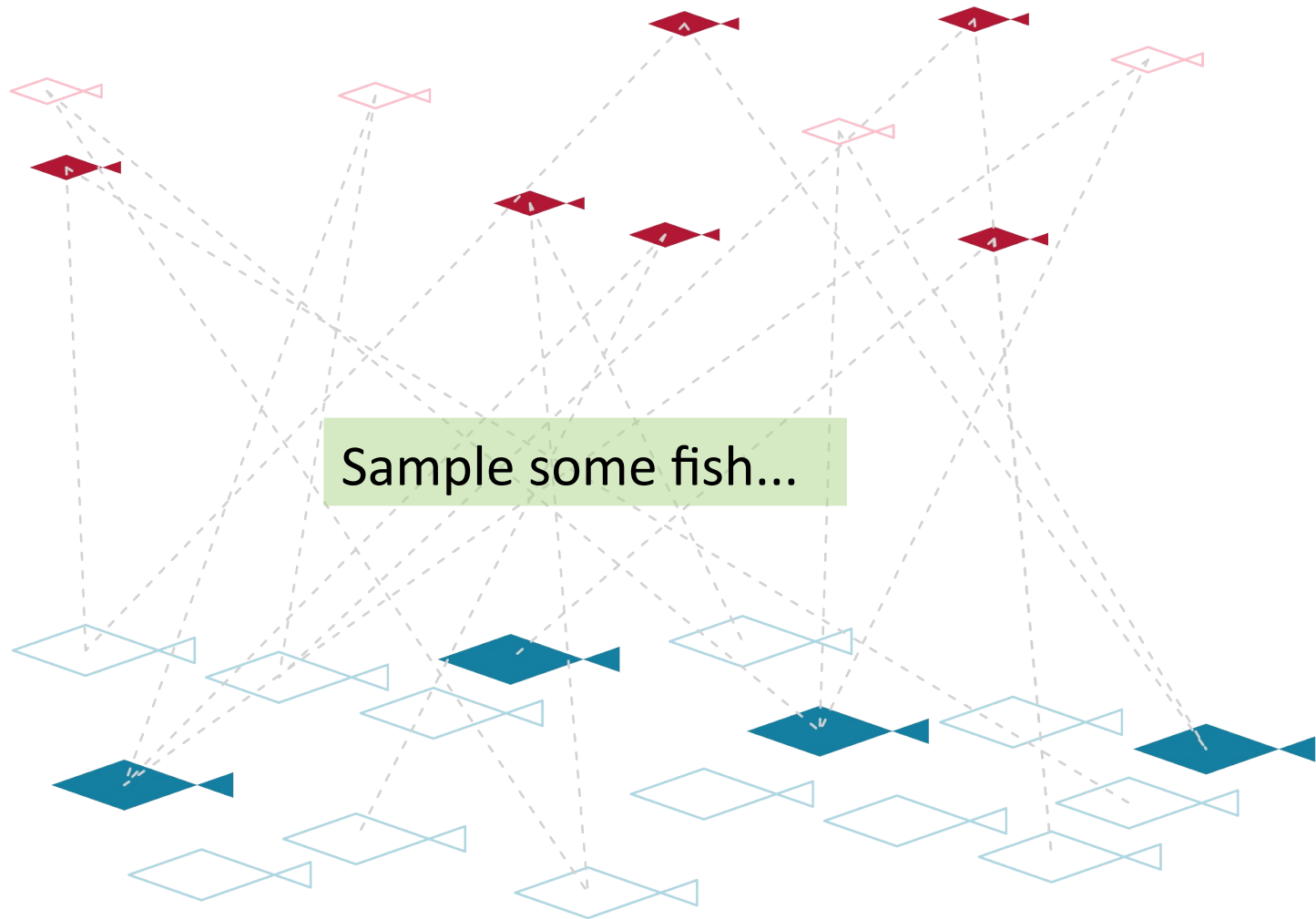
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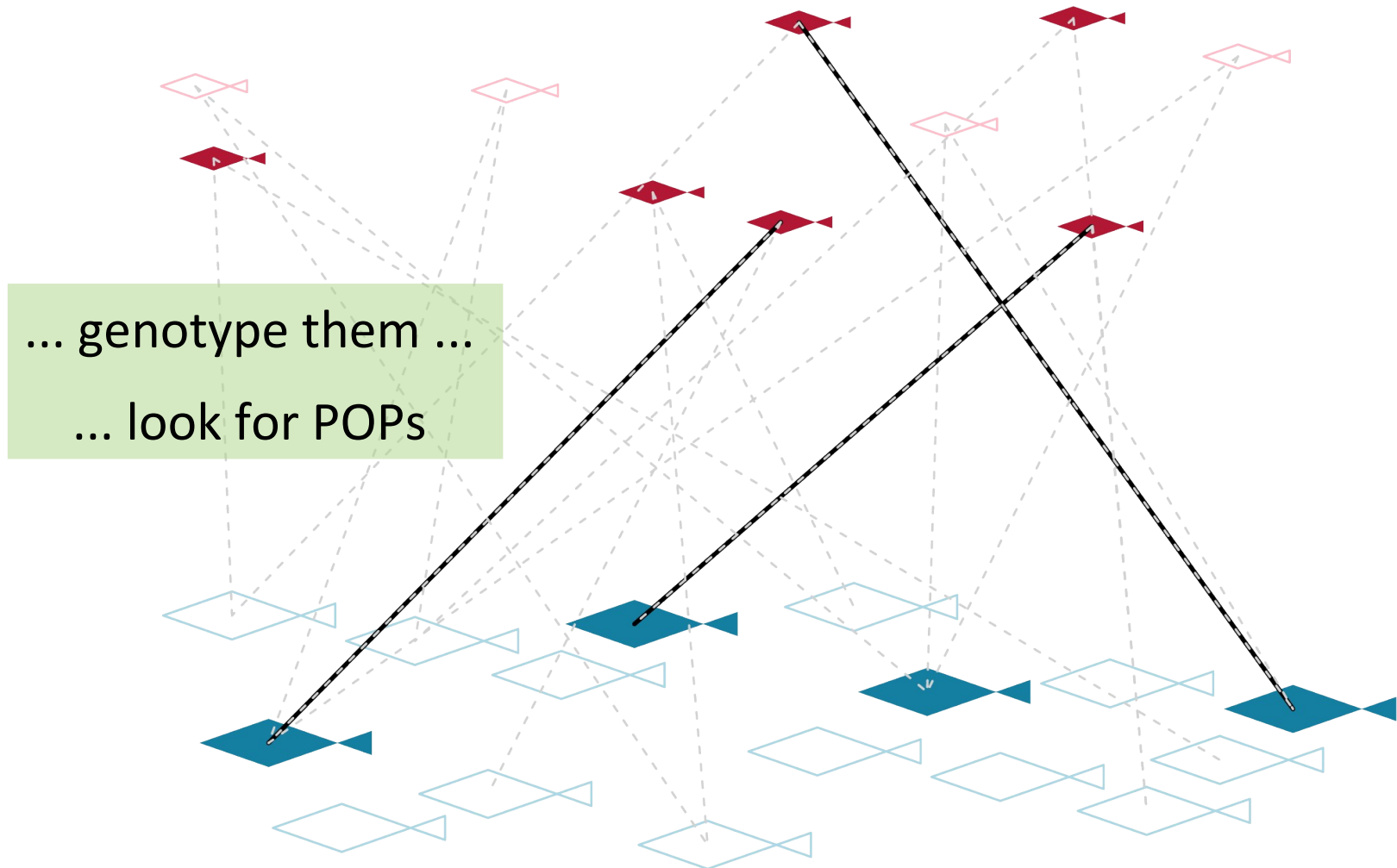
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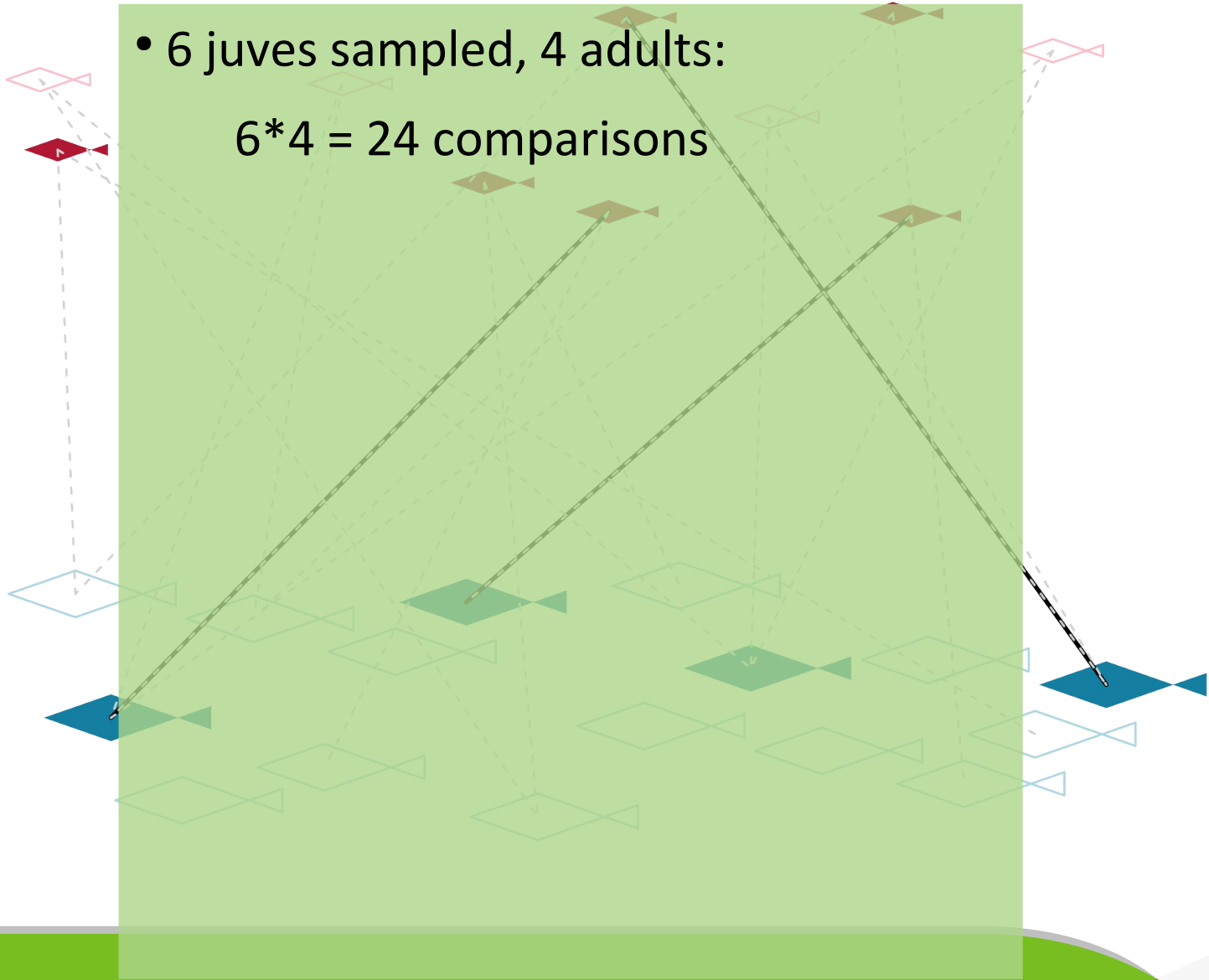
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- 6 juves sampled, 4 adults:

$$6 * 4 = 24 \text{ comparisons}$$



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- True value of N_{adult} is ... 16 !

CKMR principles: POP cartoon

- 6 juves sampled, 4 adults:

$$6 * 4 = 24 \text{ comparisons}$$

- Each comp: $\Pr[\text{POP}] = 2 / N_{\text{adult}}$

DON'T apply this cartoon idea literally! It will

- Expected POPs = $24 * 2 / N_{\text{adult}}$

give you the **wrong answer** for most

- Observed POPs = 3

real cases. And that will be **your** fault.

- Estimate: $N_{\text{adult}} = 48 / 3 = 16$

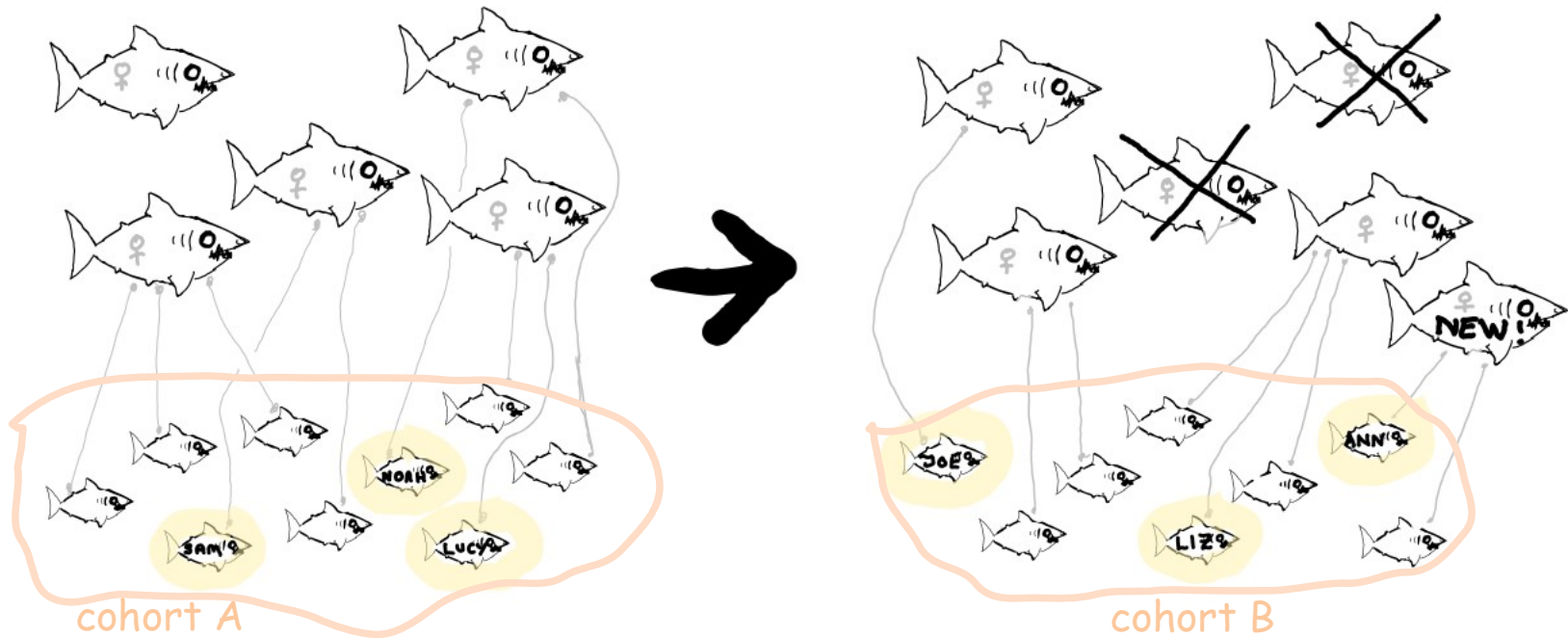
BUT, it can be *modified* to work right.

- True value of N_{adult} is ... 16 !

YAY !

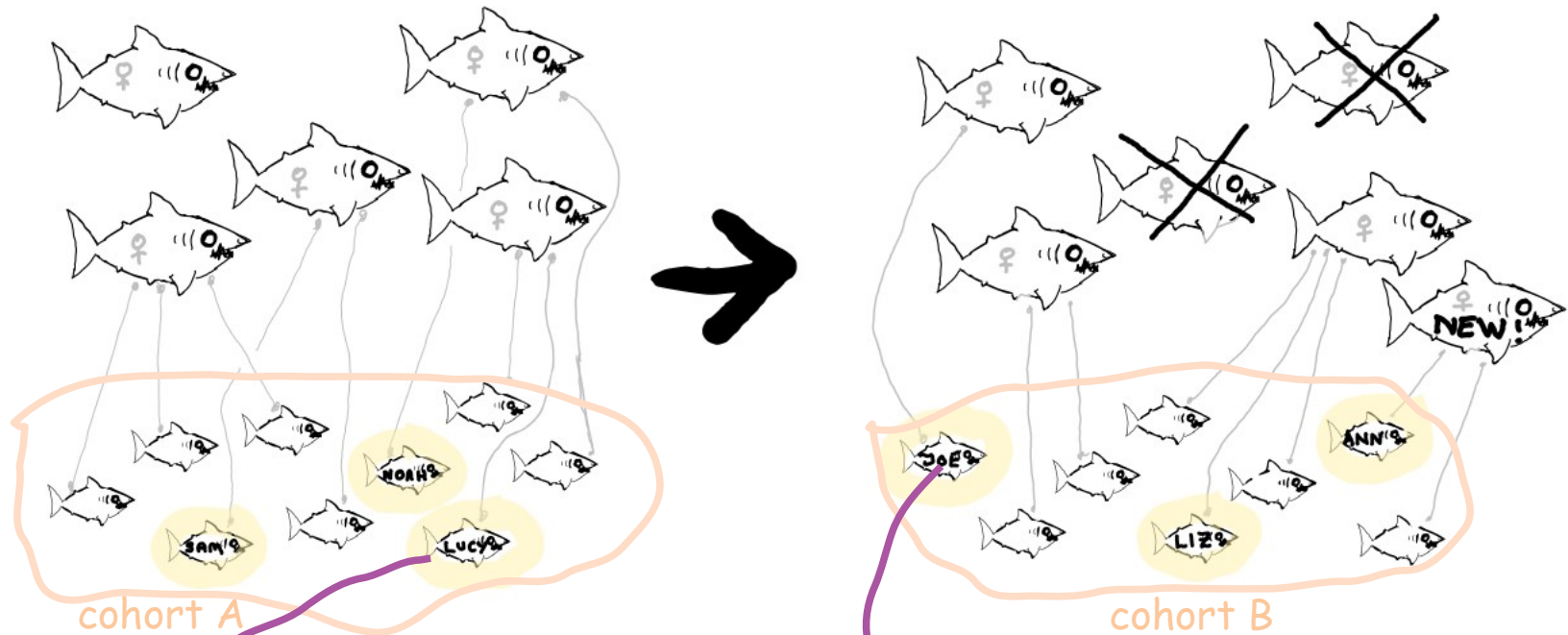
HSP*-based CKMR

[*] HSP = Half-Sib(ing) Pair,
i.e. Half-Brother/Sister
i.e. **either** same mother, **or** same father



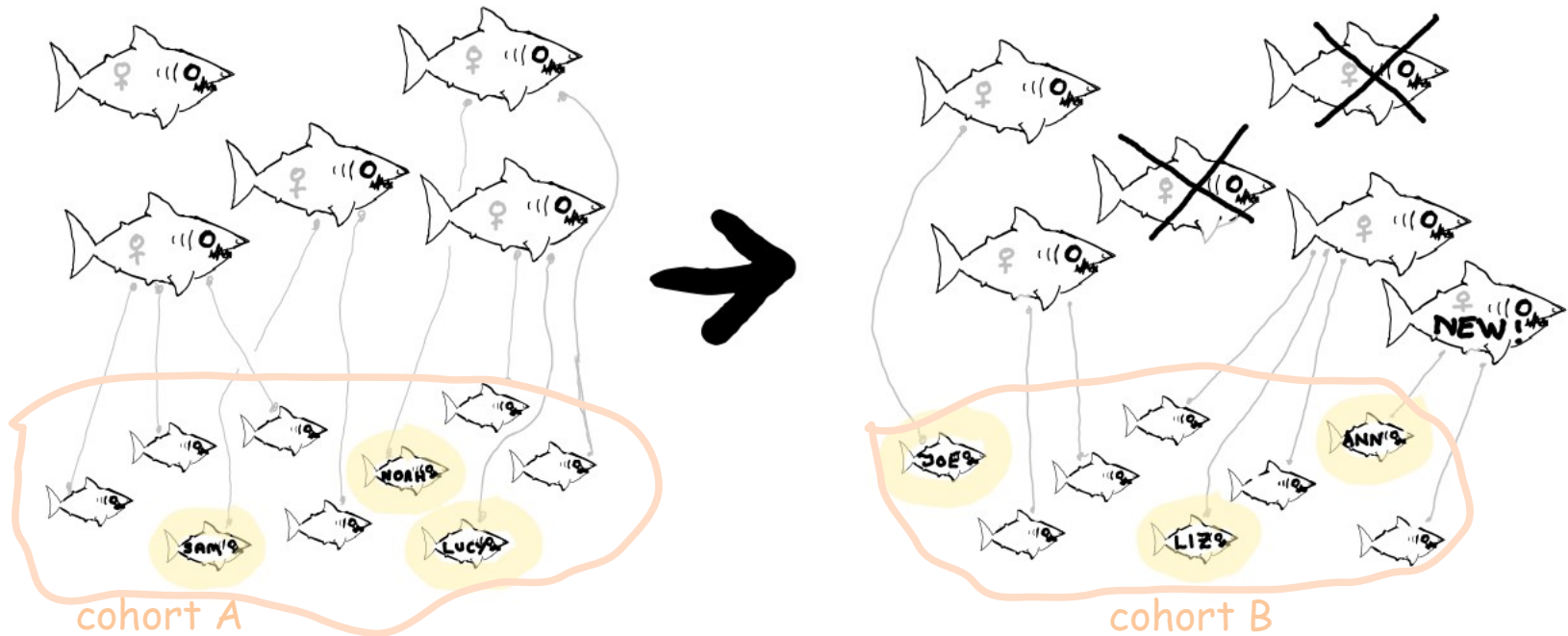
Sample *only* from the juveniles !

HSP*-based CKMR



$\Pr[\text{Lucy from cohort A is maternal HSP to Joe from B}]$
 $= \Pr[\text{Lucy's mother survived}] \div (\text{number of } \text{♀} \text{ adults at Joe's birth})$

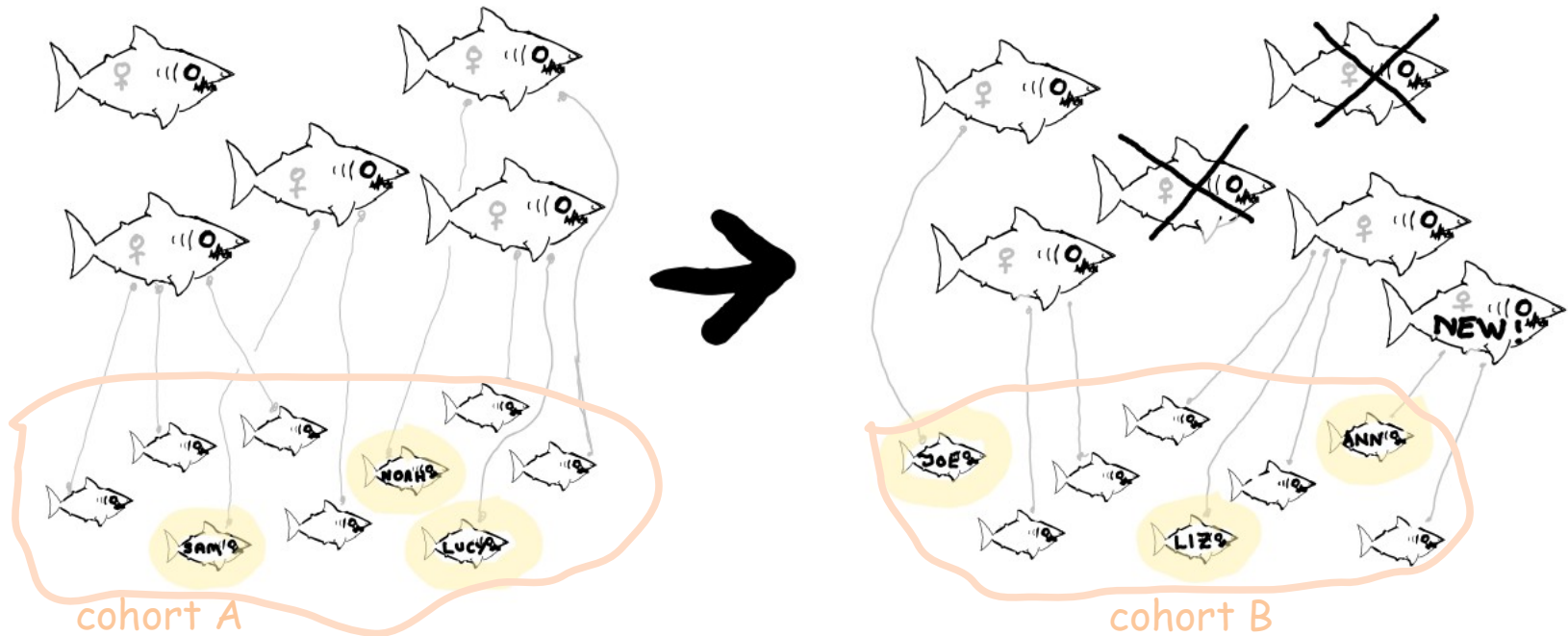
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- Can estimate adult *mortality rate* as well as *absolute abundance*
- Need several cohorts

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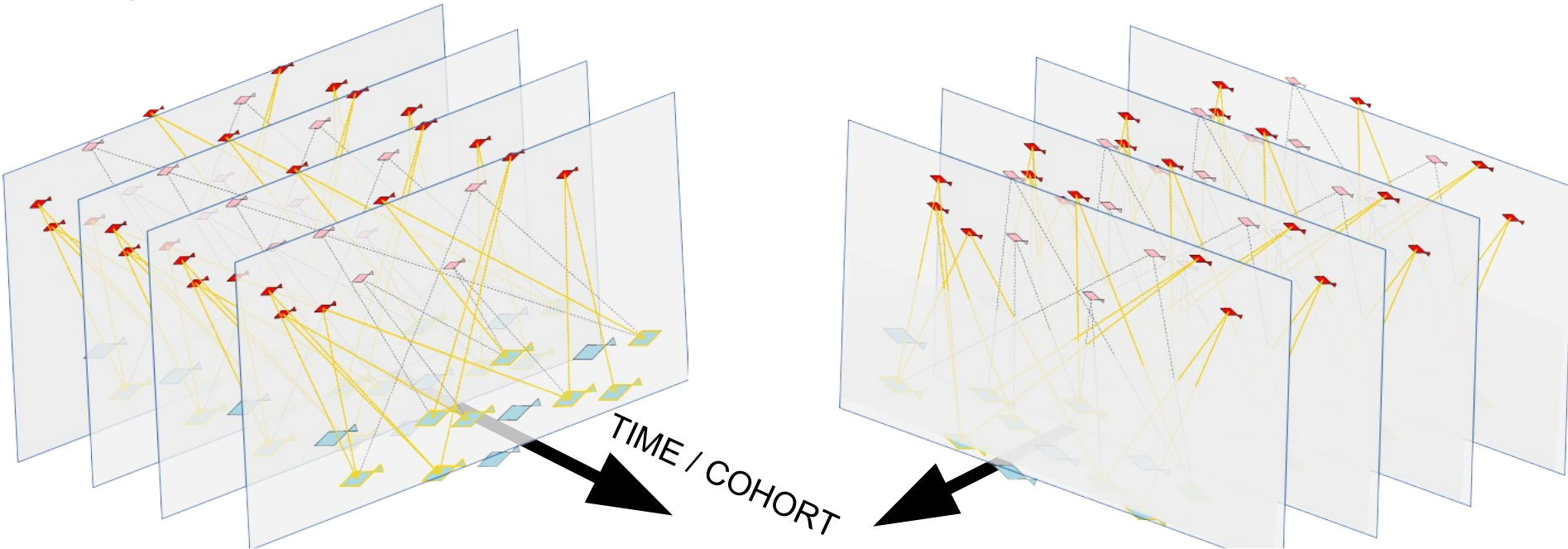
This is a cartoon ! Reality is more complicated...

- Breaks down *within* a cohort; effect of body size / growth

CKMR in practice

Lots of different (juvenile) cohorts; **time series**

Tags: **direct** (POPs) or **indirect** (HSPs)



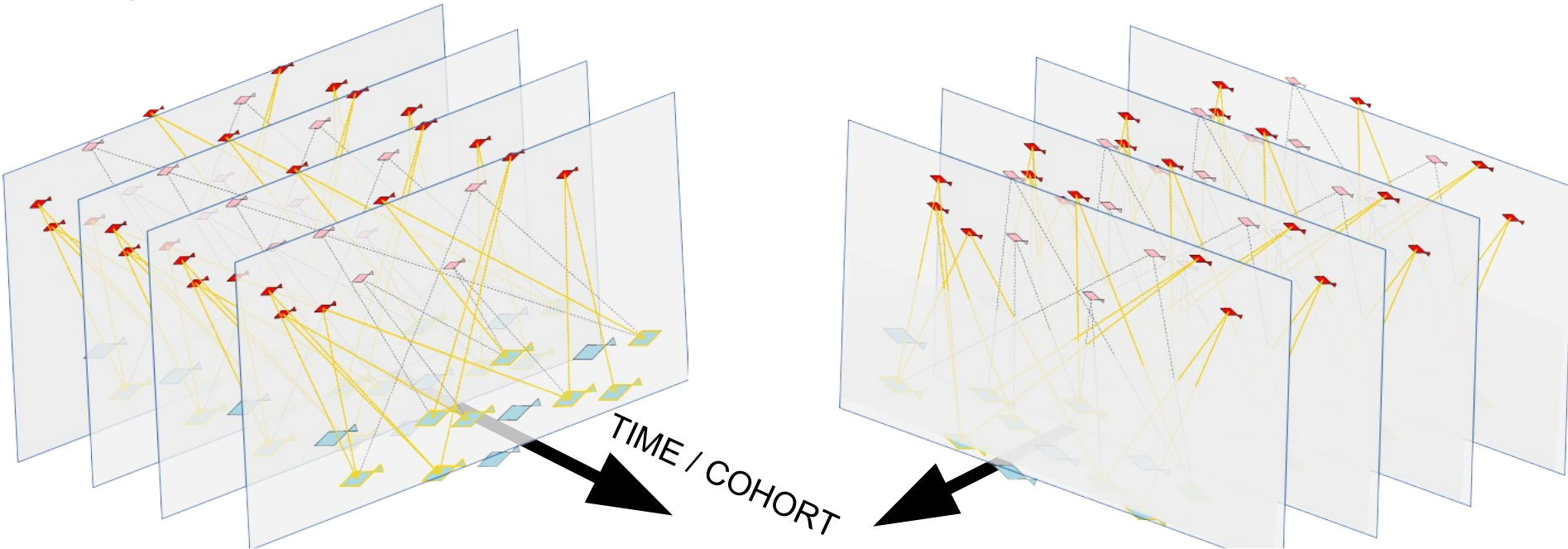
Use all samples together, in one single model

Compare each sample to every^[*] other sample: lots of pairs

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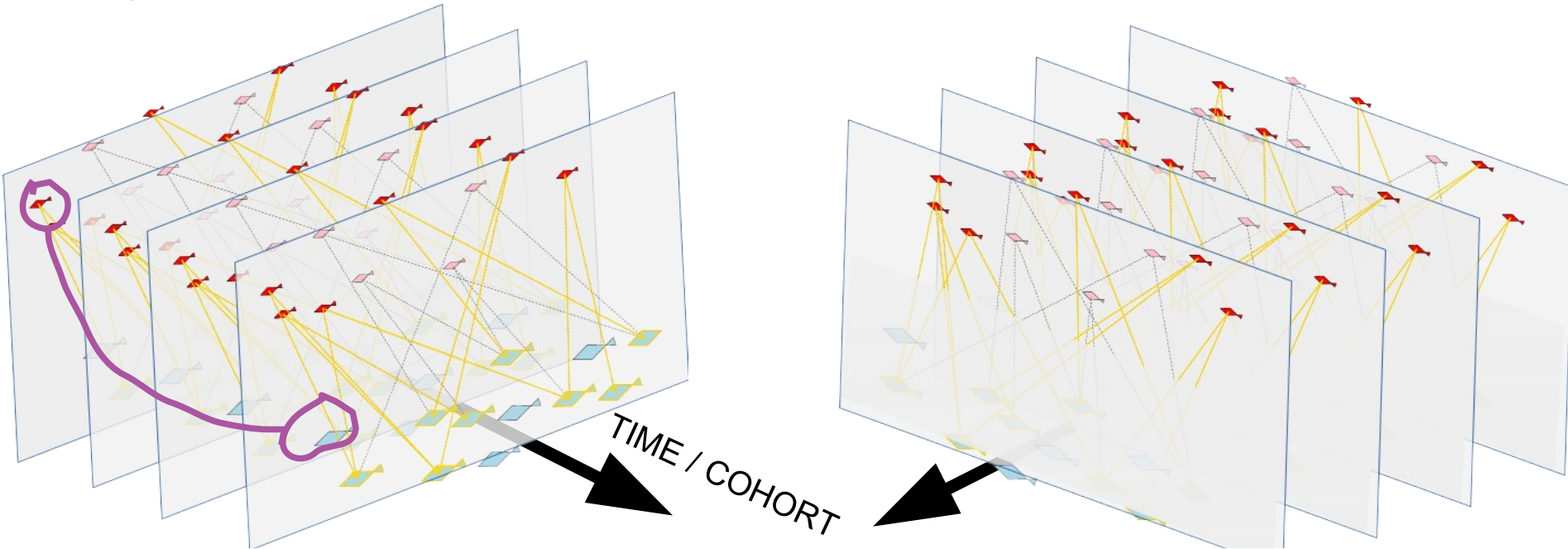
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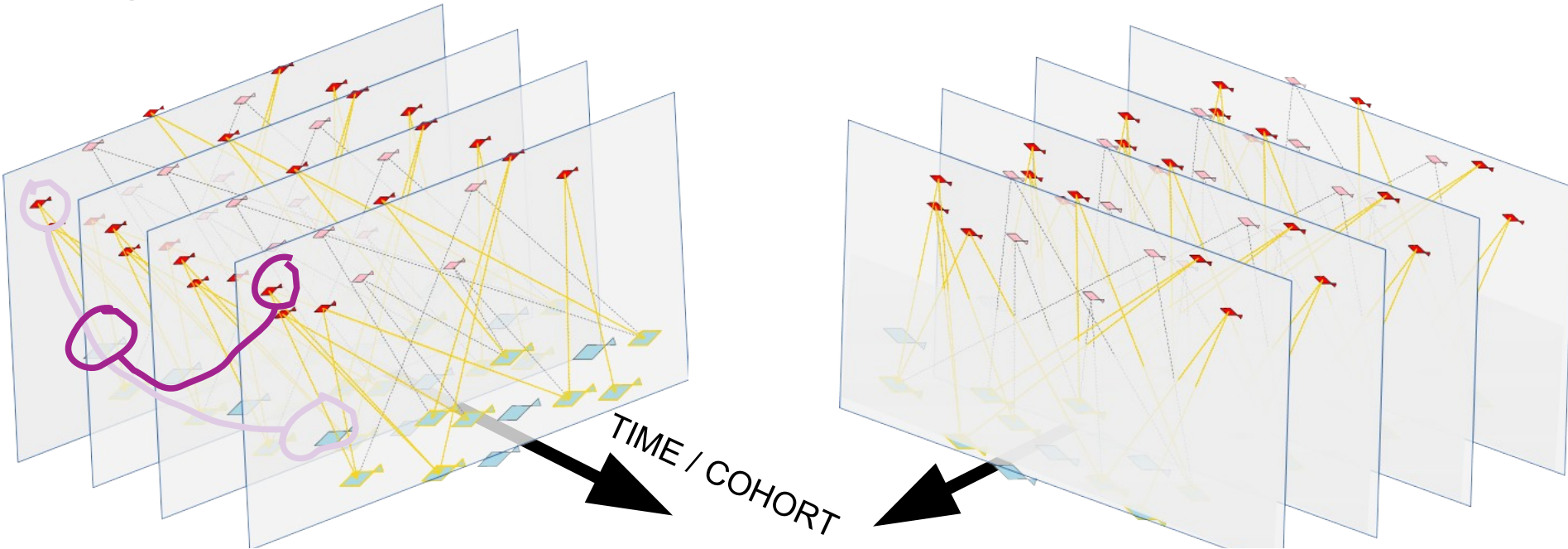
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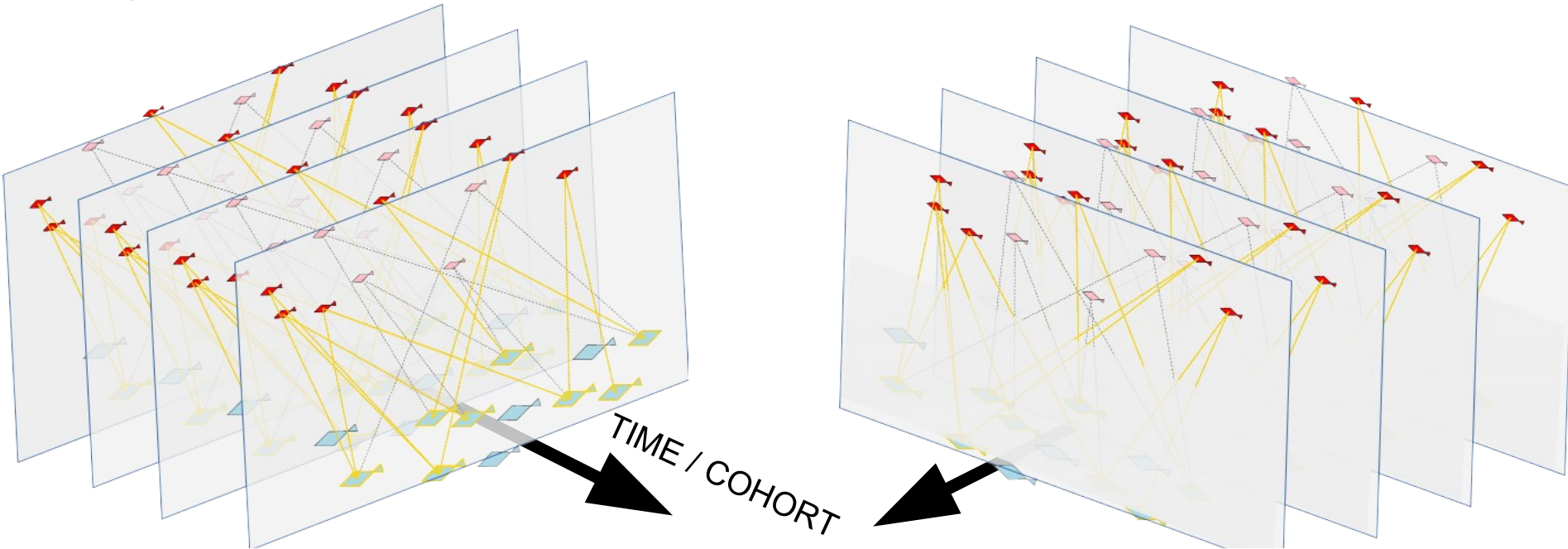
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Genetics tells us the *outcome* for each pair

CKMR in practice

Lots of different (juvenile) cohorts; **time series**

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NB: it's OK to be dead !

Use all samples together, in one single model

Compare each sample to every^[*] other sample: lots of pairs

A priori prob of POP/♀HSP/♂HSP varies from pair to pair: depends on "N" etc
... though it is not *compulsory*...

Genetics tells us the *outcome* for each pair

Fitting a CKMR model

Chassis: a standard-ish Age- and Sex- structured Pop Dyn model

PARAMETERS: "populate" the Pop Dyn Model

$$N_{a+1,t+1,s} = N_{ats}e^{-z} ; a \geq 8, t \geq 2002$$

$$\log N_{8t} \sim N(\mu, \sigma^2)$$

$$\log N_{2002,a} \sim N(\mu e^{-z'(a-8)}, \sigma^2)$$

COVARIATES: for each pair of samples (eg "Mary" and "Simon"),

use ERRO to work out POP and HSP probabilities, e.g.

Pr[Mary is Simon's mother | Mary's covariates, and Simon's]

RESPONSE DATA: the kinship of each pair: POP, HSP, UP (unrelated)

inferred from their genotypes

LOG-LIKELIHOOD: *lots* of Bernoulli (yes-no) comparisons

Can put in other data too

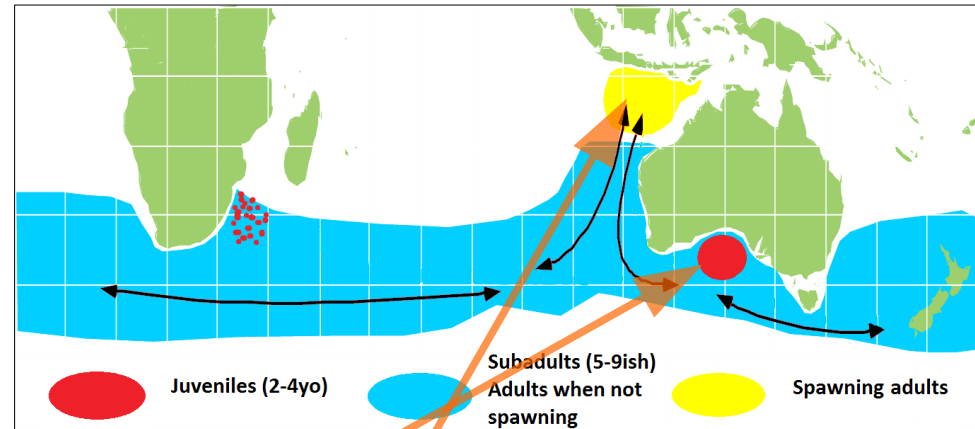
CKMR core assumptions

1. Every animal was born with 1 mother and 1 father
2. You can reliably detect POPs and HSPs via genetics

*Everything else is "just"
maths and logistics...*

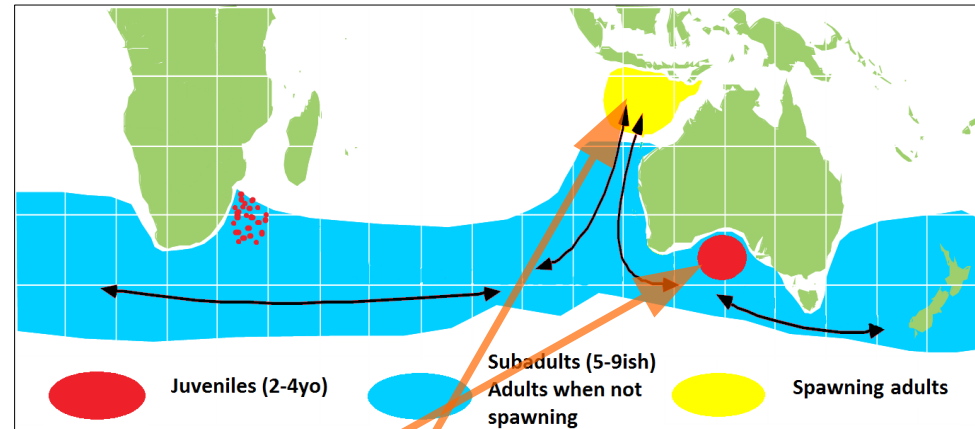
Example: Southern Bluefin Tuna

- Main catch:
 - juveniles (Australia)
 - subadults (Indian ocean)
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- "Challenging" conventional data



Example: Southern Bluefin Tuna

- Main catch:
 - juveniles (Australia)
 - subadults (Indian ocean)
- Maturity age ~ 10
- "Challenging" conventional data
- Heavily depleted, but no idea of absolute N



- 2006-2010: *genotyped 8000 juveniles (age 3) and 5000 adults* 25 usats
 - 45 POPs from 38,000,000 comps between juves and adults
- ... and after 2010...

SBT: results [2012 version]

- 38,000,000 comps; 45 POPs (+/-1)
- No sibs or half-sibs among POPs

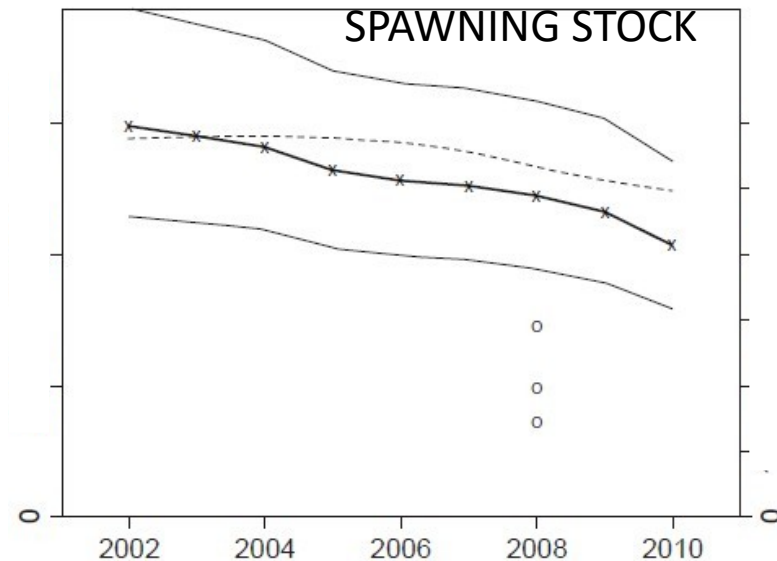
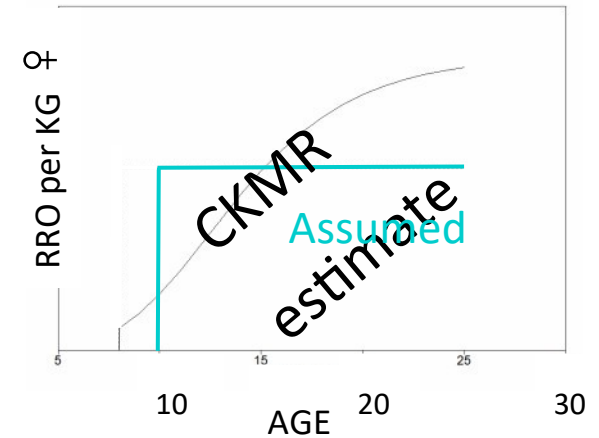
Skip-spawning in young adults

| Age | Gap-> | 1 | 2 | 3 | 4 | 5 | 6 | 7 |
|-------|-------|-----|-----|-----|-----|-----|-----|-----|
| 6-12 | Obs | 1 | 6 | . | 2 | . | 4 | . |
| | Exp | 1.6 | 2.3 | 2.7 | 2.6 | 1.9 | 1.1 | 0.6 |
| 13-25 | Obs | 7 | 5 | 10 | 7 | 2 | 1 | . |
| | Exp | 4.3 | 6.8 | 7.4 | 6.2 | 4.5 | 1.8 | 1.0 |

PRECISION:

17% CV on $N_{10+,2008}$ -- mostly driven by #POPs=45

Cartoon: need $10\sqrt{N_{adult}}$ to get 50 POPs, 15% CV



SBT: so good we did it twice

2017: 76 POPs, 140 HSPs +4 FSPs
(21,000 samples; ~80M and ~60M pairwise comps)

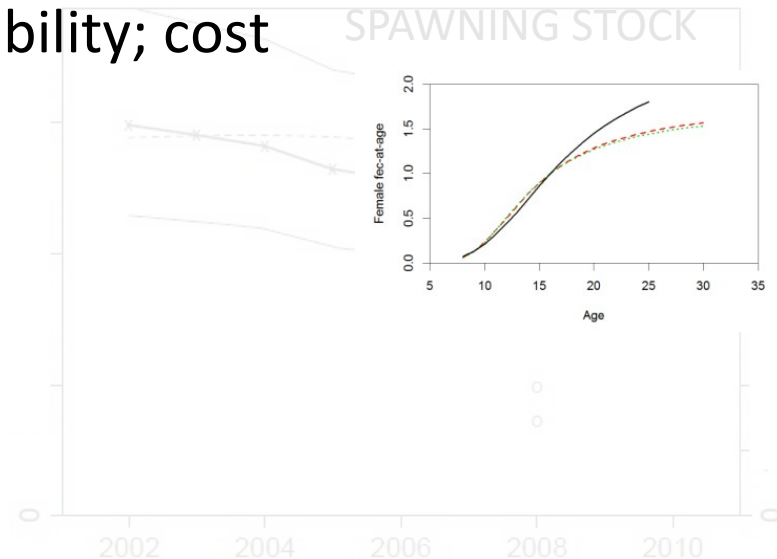
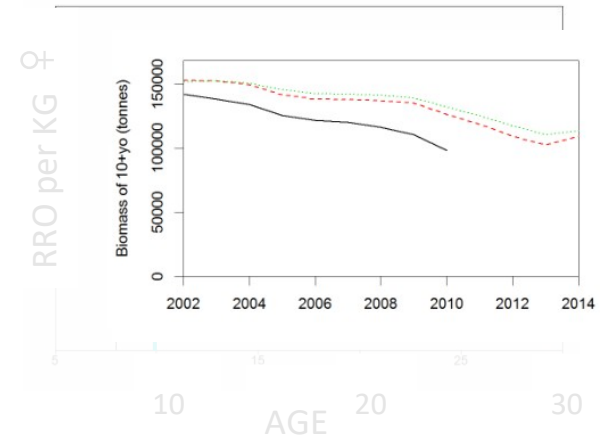
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 - Motives: HSPs as well as POPs; reliability; cost

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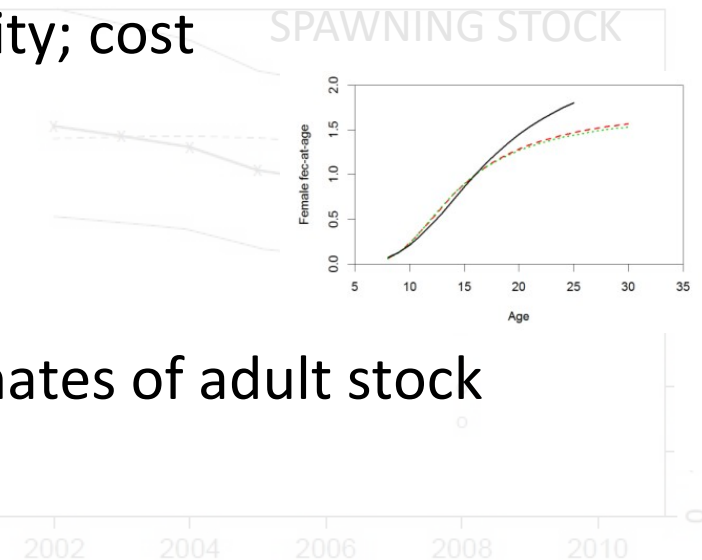
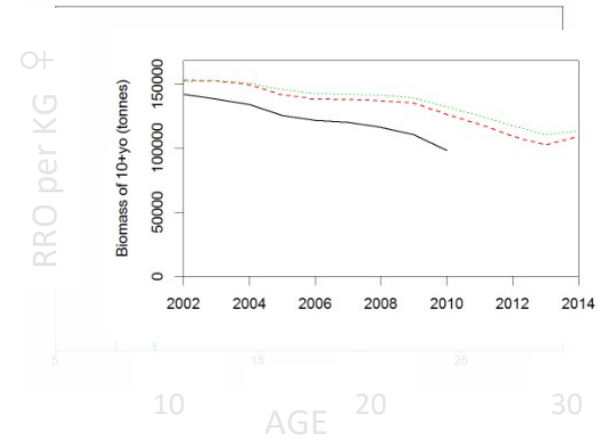
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- Motives: HSPs as well as POPs; reliability; cost

- 2018: updated with HSPs

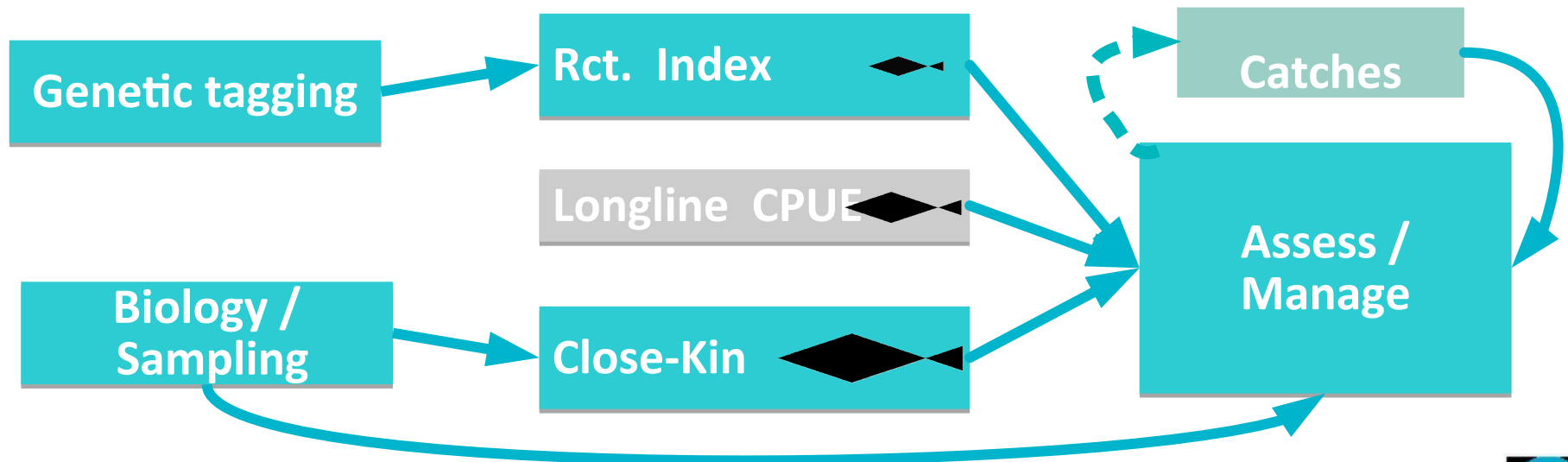
- now nearly **fishery-independent** estimates of adult stock

- ongoing, built directly into TAC-setting



SBT: from pariah to paradigm

- ~10 years ago: international basket-case
- Now: apparently the "gold standard" for tuna management !
- Runs on *fishery-independent* data: CKMR + genetic-tagging
- Not just due to science (certainly not just due to CKMR), but still ...



Completed CKMR at CSIRO, Sep 2018

| Species | | Source | Geno | Motive | POP | HSP | Model | "Stocks"? | N_{adult} | #Samples |
|-------------------------|---|--------|------|------------|-----|-----|--------------|-----------|--------------------|----------|
| SBTuna | 1 | Dead | usat | \$ | ✓ | — | Full pop-dyn | — | ■, 000, 000 | 15,000 |
| | 2 | D | Cap | | ✓ | ✓ | | | | 20,000 |
| School Shark | | D | Cap | \$ (choke) | (—) | ✓ | " | — | ■00,000 | 3,000 |
| White Sh. | E | Live+D | Seq | ! | — | ✓ | N, z, ρ | — | ■00 | 200 |
| | W | L+D | Seq | | (—) | ✓ | | — | ■000 | 200 |
| Grey Nurse Sh. | | L+D | Seq | ! | ✓ | ✓ | Stable-age | — | ■000 | 400 |
| Spertooth Sh. | | L | Cap | !? | — | ✓ | N, z, ρ | (✓) | ■000 | 300 |
| Different spertooth Sh. | | L | Seq | !? | — | ✓ | N, z, ρ | (✓) | ■000 | 300 |

| | |
|--------------|---|
| Cap | DARTCap™— based on ddRAD with capture probes for specific loci |
| Seq | DARTSeq™— based on ddRAD |
| N, z, ρ | exponential trend: $N_{\text{adult},t} = N_{\text{adult},0}e^{\rho t}$; $\mathbb{P}[\text{adult survives } y \text{ years}] = e^{-zy}$ |
| Stable-age | like N, z, ρ , plus assuming long-term stability of adult age compo |

It took a lot of work

| People (at CSIRO except as noted) | Organizations (Aus. except as noted) |
|--|---|
| Jorden Aulich Shane Baylis Russ Bradford Barry Bruce Paul Conn: NOAA Scott Cooper Campbell Davies Bill de la Mare: AAD Eric Anderson: NOAA Paige Evesson Jess Farley Pierre Feutry Peter Grewe Rasanthi Gunasekara Peta Hill | Rich Hillary Paavo Jumppanen Andrzej Kilian: DART Emma Lawrence Luke Lloyd-Jones Pete Kyrne: CDU Matt Lansell James Marthick: Menzies Inst. Toby Patterson Richard Pillans Craig Proctor Robin Thomson Robin Waples: NOAA David Westcott |

All[*] now continuing, for monitoring
--- CKMR is hard to start, but easy to update

| Project collaborators | Methods in Ecology and Evolution |
|--|---|
| White Shark Malcolm Francis Clinton Duffy Jonathan Werry David Harasti Charlie Huveneers Andrew Fox Andrew Wright Rory McAuley Paul Rogers Kent Stannard | Grey Nurse Shark Deborah Foote Carley Kilpatrick David Harasti Roger Laird Brett Loudon Peter Gibson Jo Williams Tom Davis Kenneth Goldman |



ARTICLE
Received 17 Nov 2015 | Accepted 8 Sep 2016 | Published 14 Nov 2016
DOI: 10.1038/ncomms14024 OPEN
Absolute abundance of southern bluefin tuna estimated by close-kin mark-recapture

Mark V. Bravington¹, Peter M. Greve² & Campbell R. Davies¹
Southern bluefin tuna is a highly valuable, severely depleted species, whose abundance and productivity have been difficult to assess with conventional fishery data. Here we use large-scale genotyping to look for parent-offspring pairs among 14,000 tissue samples of juvenile and adult tuna collected from the fisheries, finding 45 pairs in total. Using a modified mark-recapture framework where recaptures are for rather than individuals, we can estimate adult abundance and other demographic parameters such as survival, without needing to use contentious fishery catch or effort data. Our abundance estimates are substantially higher and more precise than previously thought, indicating a much healthier, more productive stock. More broadly, this tool can be used to estimate the absolute abundance of adults—wherever they live—of any species with a reproduction strategy or tag-release programme, and the interpretational problems of fishery catch rates.

SCIENTIFIC REPORTS

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

R. M. Hilary¹, M. V. Bravington¹, T. A. Patterson¹, R. Grewe², R. Bradford¹, P. Feutry¹, R. Gunasekara¹, V. Poddemann¹, J. Werry¹, M. P. Francis¹, C. A. Duffy¹ & B. D. Bruce¹
Conservation concerns exist for many sharks but robust estimates of abundance are often lacking. Improving population status is a fundamental measure for species under conservation or recovery plans, yet the lack of data permitting estimation of population size creates the difficulty of management actions can be difficult to assess, and achieving the goal of removing species from conservation listing (including the potentially dangerous species, like the white shark, following conservation and public safety demands) is frequently an elusive objective. Here, we report on a study of white shark population status. This increases the need for robust information to inform policy decisions. We developed a novel method for estimating the total abundance of white sharks in eastern Australia and New Zealand using the genetic relatedness of juveniles and applying a close kin mark-recapture framework and large-scale genotyping. We found numbers of adults are similar to 100,000, which is a total abundance estimate that is substantially higher than previous estimates. This tool can be used to estimate the absolute abundance of adults—wherever they live—of any species with a reproduction strategy or tag-release programme, and the interpretational problems of fishery catch rates.

Publications are still a bit behind...

Close-Kin Mark-Recapture
Mark V. Bravington, Hans J. Skaug and Eric C. Anderson

Abstract. Mark-recapture (MR) methods are commonly used to study wildlife populations. Taking advantage of modern genetics one can generalize from "recapture of self" to "recapture of closely-related kin". Abundance and other demographic parameters of adults can then be estimated using, if necessary, only samples from dead animals (live-release is optional). This greatly widens the scope of MR, e.g. to commercial fisheries where large-scale tagging is impractical, and enhances the power of conventional MR studies where live release and tissue sampling is possible. We give explicit formulae for kinship (i.e., recapture) probabilities in general and specific cases. These yield a pseudo-likelihood based on pairwise comparisons of individuals in the sample. It is shown that the pseudo-likelihood approximates the full likelihood under sparse sampling of large populations. Experimental design is addressed via the principle of maximizing the Fisher information for parameters of interest. Finally, we discuss challenges related to kinship determination from genetic data, focusing on current limitations and future possibilities.

Key words and phrases: Demography, genetics, kinship, mark-recapture, pseudo-likelihood.

1. INTRODUCTION
Mark-recapture (MR) methods allow population size and demographic parameters such as mortality rates to be estimated from an appropriately designed mark-

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not CSIRO!

ARTICLE
Genetic-Based Estimates of Adult Chinook Salmon Spawner Abundance from Carcass Surveys and Juvenile Out-Migrant Traps
Daniel J. Rawding, Cameron S. Sharpe,¹ and Scott M. Blankenship^{2*}
Washington Department of Fish and Wildlife, 600 Capitol Way North, Olympia, Washington 98501-1091, USA

Completed CKMR at CSIRO, Sep 2018

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| | |
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Mark V. Bravington¹, Peter M. Greve² & Campbell R. Davies¹
Southern bluefin tuna is a highly valuable, severely depleted species, whose abundance and productivity have been difficult to assess with conventional fishery data. Here we use large-scale genotyping to look for parent-offspring pairs among 14,000 tissue samples of juvenile and adult tuna collected from the fisheries, finding 40 pairs in total. Using a modified mark-recapture framework where recaptures are for rather than individuals, we can estimate adult abundance and other demographic parameters such as survival, without needing to use contentious fishery catch or effort data. Our abundance estimates are substantially higher and more precise than previously thought, indicating a much more productive stock. More broadly, this tool can be used to estimate the abundance of adults—where the data are lacking—for a wide range of fisheries and wildlife conservation programs, and the interpretational problems of fishery catch rates.

SCIENTIFIC REPORTS

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

R. M. Hilary¹, M. V. Bravington¹, T. A. Patterson¹, R. Grewe², R. Bradford¹, P. Feutry¹, R. Gunasekara¹, V. Faddam¹, J. Werry¹, M. P. Francis¹, C. A. J. Duffy¹ & B. D. Bruce¹
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Methods in Ecology and Evolution

PROFESSOR DANIEL RUZZANTE (Orcid ID: 0000-0002-8536-8335)

Article type : Research Article

Validation of close-kin mark-recapture (CKMR) methods for estimating population abundance

Daniel E. Ruzzante¹, Gregory R. McCracken¹, Brage Forland², John MacMillan¹, Daniela Notti³, Colin Baharwal⁴, Joanna Mills Flemming¹, Hans Skog¹

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All[*] now continuing, for monitoring
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quite similar to N Atl mako situation

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ARTICLE
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DOI: 10.1038/ncomms40002 OPEN
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Mark V. Bravington¹, Peter M. Greve² & Campbell R. Davies¹

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SCIENTIFIC REPORTS

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

R. M. Hickey¹, M. V. Bravington¹, T. A. Patterson¹, A. Grew¹, R. Bradford¹, P. Feutry¹, R. Gunasekara¹, V. Paddamoni¹, J. Werry¹, M. P. Francis¹, C. A. J. Duffy¹ & B. D. Bruce¹

Conservation concerns exist for many sharks but robust estimates of abundance are often lacking. Improving population status is a fundamental measure for species under conservation or recovery plans, yet the lack of data preventing estimation of population size creates the difficulty of management actions can be difficult to assess, and achieving the goal of removing species from conservation listing (including the potentially dangerous species, like the white shark) following conservation and public safety demands is frequently an elusive objective, often leading to significant uncertainty about their population status. This increases the need for robust information to inform policy decisions. We developed a novel method for estimating the total abundance of white sharks by using genetic data and these data used to estimate the genetic relatedness of juveniles and applying a close kin mark-recapture framework and a novel mark-recapture model. Using 10,000 tissue samples of juvenile and adult white sharks collected from commercial fisheries and public safety programs, we estimated the total abundance of white sharks in the eastern Australian and New Zealand waters. Our results show that the total abundance of white sharks is much higher than previously estimated, indicating a much healthier, more productive stock. More broadly, this tool can be used to estimate the absolute abundance of adult—where the data are available for population surveys or tag-release programmes, and the interpretational problems of fishery catch rates.

Received: 19 Jan 2017
Accepted: 10 Jan 2018
Published online: 08 February 2018

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

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Example: School shark



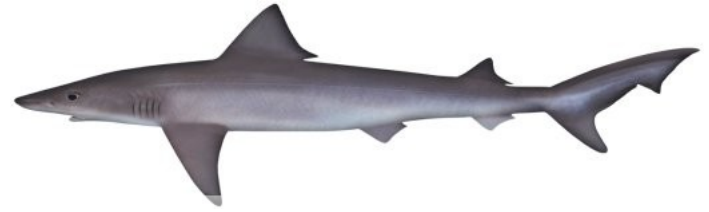
- Demography: a bit like makos
 - and, few adults are caught
- Target species: *heavily* depleted in 1990s
- Now *bycatch*: strong catch restrictions

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- CPUE series no longer informative--- if it *ever* was
- *Anecdotal* recovering--- but how can we tell ?

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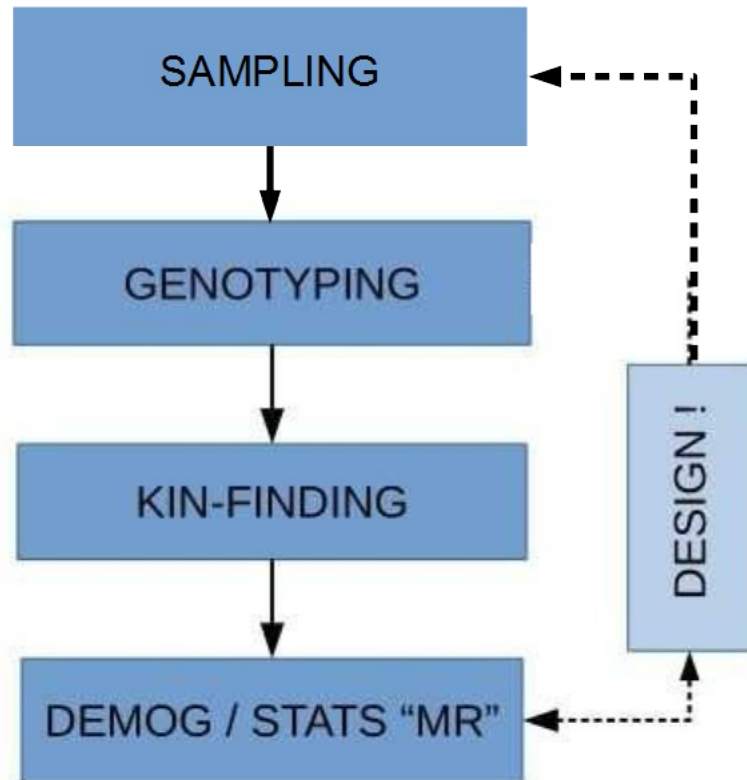


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- Now *bycatch*: strong catch restrictions
- CPUE series no longer informative--- if it *ever* was
- *Anecdotal* recovering--- but how can we tell ?

- Full age-based assessment using CKMR
- 3000 samples; vertebral ages with error; 65 HSPs
- Abundance: lower than CPUE-based "assessment"
- Trend: not yet significant
- Sampling is continuing; will update

CKMR: 5 steps to success

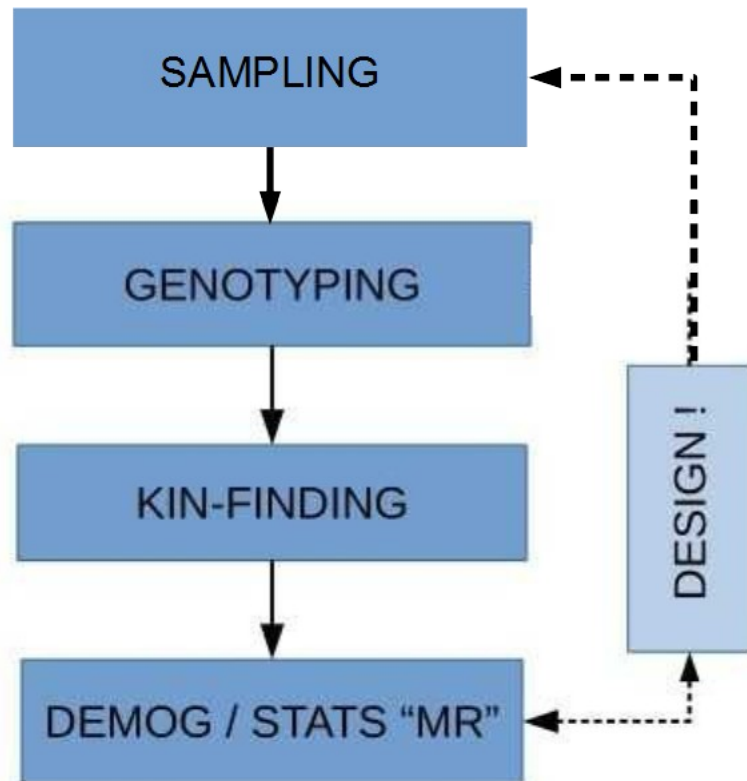
CKMR is a 4-letter word...



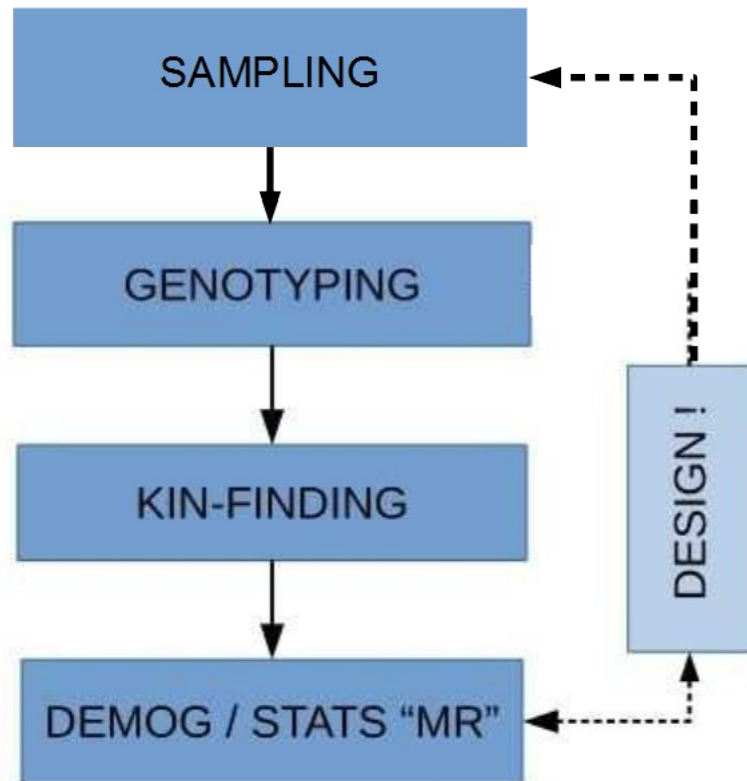
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easy



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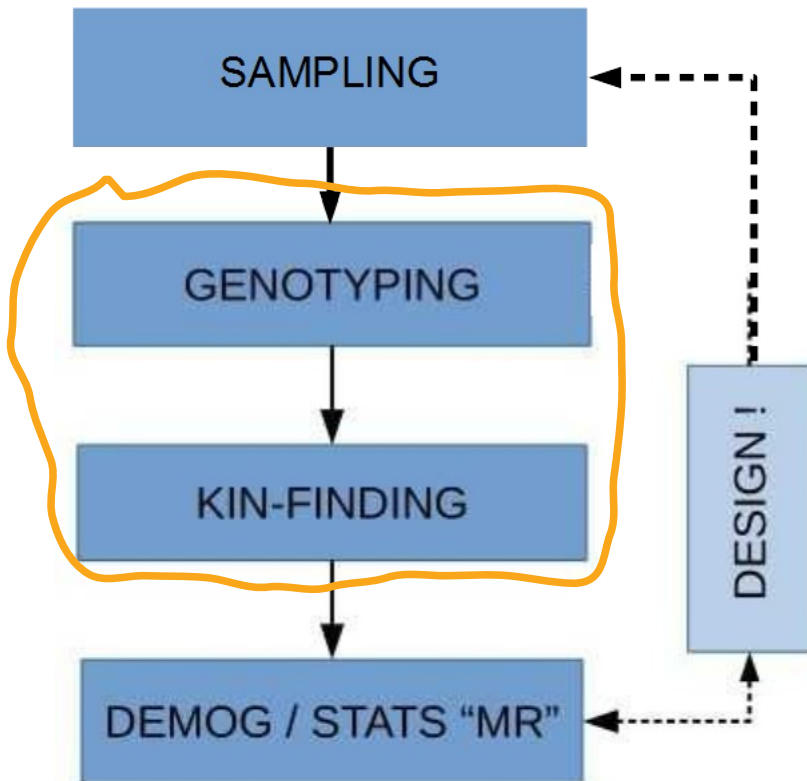
To cover all these,
you need a **team**

CKMR: 5 steps to success

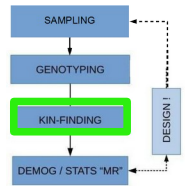
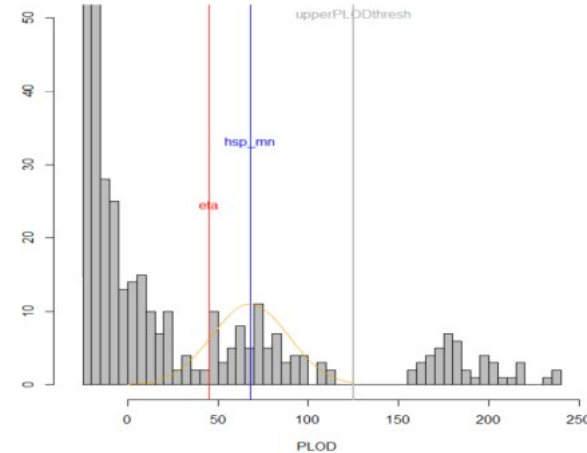
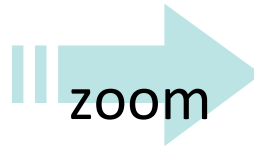
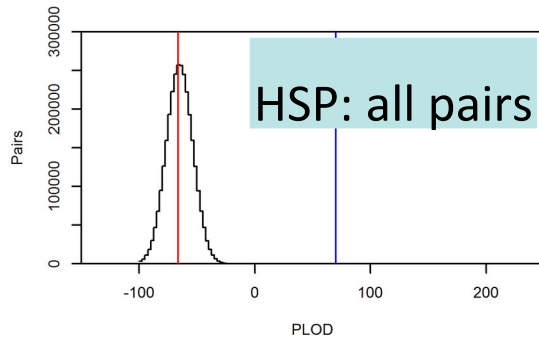
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KIN-FINDING

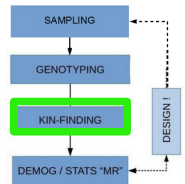
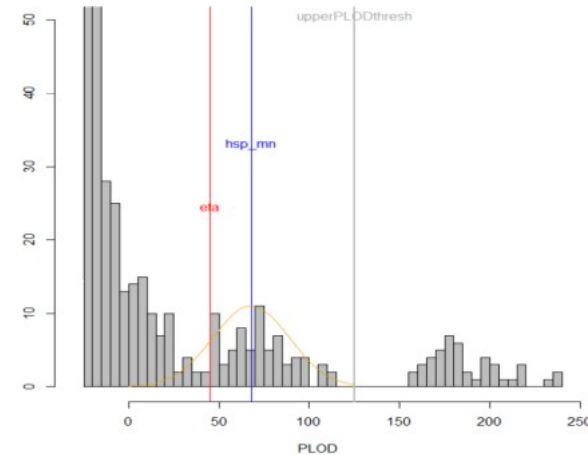
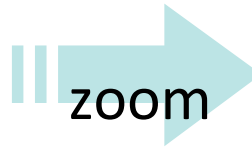
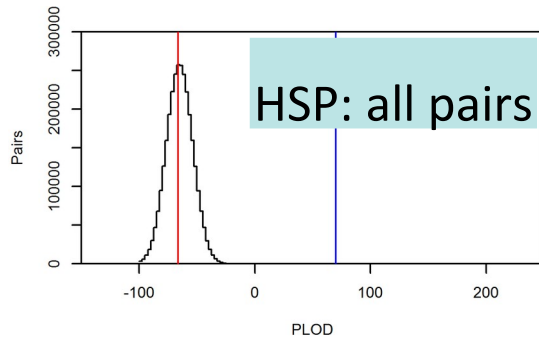


- False positives: must control strictly, eg 1 in 100,000,000
- False negatives: must estimate ppn. and allow for it

Genotyping and kinference for HSPs

- It *can* be done--- and quite cheaply
- But, if you pick the *wrong* technique: disaster !
- Doesn't need to be decided at the outset
- Every country *does* have to do it the same way...

KIN-FINDING



- False positives: must control strictly, eg 1 in 100,000,000
- False negatives: must estimate ppn. and allow for it

Genotyping and kinference for HSPs

- It *can* be done--- and quite cheaply
- But, in CSIRO: we use DartCap™ (from DArT plc)
- Does not require a reference genome
- Every year we release a new version

Reliable; cheap

Always working to improve it...

CKMR for makos : DESIGN

Needs:

- *adequate* sample size
- *adequate* spread of cohorts
- *adequate* age info maybe from length
- *adequate* spatial coverage
- [*adequate* genotyping/kin-finding]

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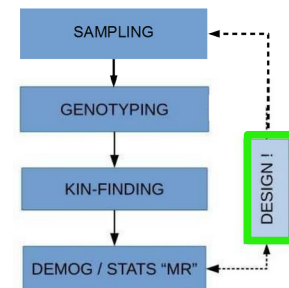
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Sample size etc, and true pop dyn, fixes likely number/pattern

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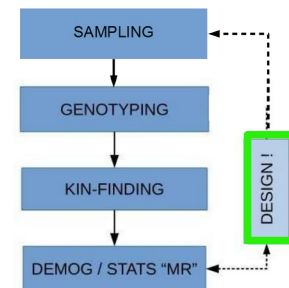
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- Start with demographic parameter estimates
- Build CKMR-based assessment model
- Get CVs of things-of-interest by "simulation"
- Explore different sampling setups until CV and feasibility is OK

DESIGN

Precision eg CV is set by number and pattern of HSPs found
Sample size etc, and true pop dyn, fixes likely number/pattern



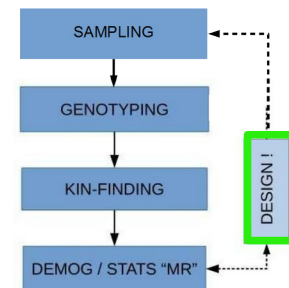
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CKMR assessment model for makos

- Main parameters: N_{1950} ; m ; "steepness"
 - m assumed *constant* across sex, age

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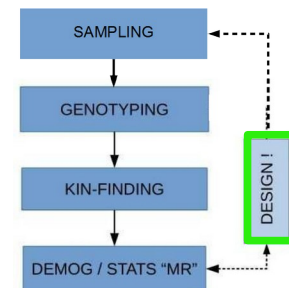
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CKMR assessment model for makos

- Main parameters: N_{1950} ; m ; "steepness"
 - m assumed *constant* across sex, age
- Details of age-from-length uncertainty
- No CPUE etc used just catch-at-age series

Design: North Atlantic

Parameter values assumed:

from ICCAT SMA_SA_2019 -- stock assessment

Options to consider:

- number of years
- total sample size
- mostly large <200cm, or mostly small?
- proportion aged via vertebrae (dead)

Things of interest:

- current SSF or, number of adult females
- depletion rel to 1950
- 10-year trend 2015--2025
- **SPRR** lifetime-spawning-per-recruit-ratio

Design: North Atlantic preliminary results

| Scen | NY | SS_small | SS_big | paged | E_HSP_XC | N_FAd2020 | depl_2020 | logtrend_10yr | m | SPRR |
|----------|----|----------|--------|-------|----------|-----------|-----------|---------------|-------|-------|
| Assessed | | | | | | 135,000 | 0.39 | -0.31 | 0.08 | 0.21 |
| V_n1 | 5 | 1774 | 3026 | 0.90 | 83 | 0.17 | 0.13 | 0.054 | 0.030 | 0.082 |
| V_n2 | 5 | 1774 | 3026 | 0.10 | 89 | 0.16 | 0.12 | 0.063 | 0.027 | 0.099 |
| V_n3 | 3 | 1774 | 3026 | 0.10 | 85 | 0.15 | 0.12 | 0.084 | 0.025 | 0.133 |
| V_n4 | 5 | 3660 | 1140 | 0.10 | 97 | 0.17 | 0.16 | 0.050 | 0.038 | 0.073 |
| V_n5 | 5 | 324 | 3876 | 0.10 | 88 | 0.15 | 0.11 | 0.078 | 0.025 | 0.123 |
| V_n6 | 5 | 24 | 1816 | 0.10 | 88 | 0.16 | 0.11 | 0.067 | 0.025 | 0.125 |
| V_n7 | 10 | 2733* | 1851* | 0.46 | 77 | 0.19 | 0.11 | 0.050 | 0.027 | 0.067 |
| V_n8 | 10 | 1774 | 3026 | 0.10 | 93 | 0.18 | 0.12 | 0.049 | 0.030 | 0.064 |
| V_n8×2 | 10 | 3548 | 7052 | 0.10 | 372 | 0.09 | 0.06 | 0.024 | 0.015 | 0.032 |

DON'T try to read all these numbers !!!

Design: North Atlantic preliminary results

| Scen | NY | SS_small | SS_big | paged | E_HSP_XC | N_FAd2020 | depl_2020 | logtrend_10yr | m | SPRR |
|-----------------|----|----------|--------|-------|----------|----------------|-------------|---------------|-------------|-------------|
| Assessed | | | | | | 135,000 | 0.39 | -0.31 | 0.08 | 0.21 |
| V_n1 | 5 | 1774 | 3026 | 0.90 | 83 | 0.17 | 0.13 | 0.054 | 0.030 | 0.082 |
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| V_n3 | 3 | 1774 | 3026 | 0.10 | 85 | 0.15 | 0.12 | 0.084 | 0.025 | 0.133 |
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| V_n5 | 5 | 924 | 3876 | 0.10 | 88 | 0.15 | 0.11 | 0.078 | 0.025 | 0.123 |
| V_n6 | 5 | 924 | 3876 | 0.70 | 84 | 0.16 | 0.12 | 0.067 | 0.027 | 0.105 |
| V_n7 | 10 | 2733* | 1851* | 0.46 | 77 | 0.19 | 0.11 | 0.050 | 0.027 | 0.067 |
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double the sample size

Design: North Atlantic preliminary results

| Scen | NY | SS_small | SS_big | paged | E_HSP_XC | N_FAd2020 | depl_2020 | logtrend_10yr | m | SPRR |
|-----------------|----|----------|--------|-------|----------|----------------|-------------|---------------|-------------|-------------|
| Assessed | | | | | | 135,000 | 0.39 | -0.31 | 0.08 | 0.21 |
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Design: North Atlantic preliminary results

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- 5000 samples: CV ~16% on *absolute* spawning stock

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Design: North Atlantic preliminary results

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Design: North Atlantic preliminary results

| Scen | NY | SS_small | SS_big | paged | E_HSP_XC | N_FAd2020 | depl_2020 | logtrend_10yr | m | SPRR |
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| V_n8x2 | 10 | 3548 | 7052 | 0.10 | 372 | 0.09 | 0.06 | 0.024 | 0.015 | 0.032 |

These results are a *starting point* for

- detailed conversations about logistics, goals, etc
- 5000 samples: CV ~16% on absolute spawning stock
- Similar results for most options except sample size
 - even for proportion-aged
- Short ie 3yr study is worse for trend but you can always extend it!
- What if assessment is **wrong** ? See later...

Design: South Atlantic based on catch-at-length series

- No assessment !!! Where to start ?

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- Design *as if* current F-pattern is *just about* OK
 - e.g. if current SPRR = 0.7
 - *If* this is the truth, we'd want to have reasonably precise estimates

Design: South Atlantic based on catch-at-length series

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- Design *as if* current F-pattern is *just about* OK
 - e.g. if current SPRR = 0.7
 - *If* this is the truth, we'd want to have reasonably precise estimates
- IE: try some value for N_{1950} ;
 - project to 2015 using catches;
 - check current SPRR;
 - adjust N_{1950} and repeat

Design: South Atlantic based on catch-at-length series

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- Design *as if* current F-pattern is *just about* OK
 - e.g. if current SPRR = 0.7
 - *If* this is the truth, we'd want to have reasonably precise estimates
- Reconstruction to hit $\text{SPRR}_{\text{now}} = 0.7$ is very sensitive to m
 - so, try four values from 0.06 to 0.12
 - pick a design that will cope with all of them

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What if assumptions are *wrong* ?

- Reconstruction to hit $\text{SPRR}_{\text{now}} = 0.7$ is very sensitive to *m*
 - so, try four values from 0.06 to 0.12
 - pick a design that will cope with all of them
- If **pessimistic**, then *few* HSPs--- **vague good news**
- If **optimistic**, then *many* HSPs--- **precise bad news**

Design: South Atlantic based on catch-at-length series

Table 2: South Atlantic: *if* current F-pattern is just about sustainable (70% SPRR)

| Scen | m | NY | SS_small | SS_big | paged | E_HSP_XC | N_FAd2020 | depl_2020 | logtrend_10yr | m | SPRR |
|--------|------|----|----------|--------|-------|----------|-----------|-----------|---------------|-------|-------|
| "True" | | | | | | | 780,000 | 0.78 | -0.10 | 0.06 | 0.70 |
| V_s1 | | 5 | 972 | 3828 | 0.1 | 15 | 0.42 | 0.188 | 0.40 | 0.076 | 0.209 |
| V_s2 | 0.06 | 5 | 922 | 9078 | 0.7 | 63 | 0.20 | 0.094 | 0.20 | 0.038 | 0.101 |
| V_s3 | | 5 | 6159 | 3841 | 0.1 | 68 | 0.21 | 0.114 | 0.17 | 0.046 | 0.108 |
| "True" | | | | | | | 470,000 | 0.75 | -0.10 | 0.08 | 0.70 |
| V_s1 | | 5 | 972 | 3828 | 0.1 | 22 | 0.34 | 0.169 | 0.37 | 0.066 | 0.141 |
| V_s2 | 0.08 | 5 | 922 | 9078 | 0.7 | 92 | 0.16 | 0.084 | 0.19 | 0.033 | 0.068 |
| V_s3 | | 5 | 6159 | 3841 | 0.1 | 100 | 0.18 | 0.102 | 0.16 | 0.040 | 0.080 |
| "True" | | | | | | | 400,000 | 0.75 | -0.09 | 0.10 | 0.70 |
| V_s1 | | 5 | 972 | 3828 | 0.1 | 30 | 0.29 | 0.15 | 0.30 | 0.050 | 0.150 |
| V_s2 | 0.10 | 5 | 922 | 9078 | 0.7 | 125 | 0.14 | 0.076 | 0.18 | 0.030 | 0.053 |
| V_s3 | | 5 | 6159 | 3841 | 0.1 | 136 | 0.15 | 0.092 | 0.15 | 0.036 | 0.065 |
| "True" | | | | | | | 210,000 | 0.71 | -0.09 | 0.12 | 0.70 |
| V_s1 | | 5 | 972 | 3828 | 0.1 | 40 | 0.25 | 0.138 | 0.36 | 0.056 | 0.092 |
| V_s2 | 0.12 | 5 | 922 | 9078 | 0.7 | 164 | 0.12 | 0.069 | 0.18 | 0.028 | 0.045 |
| V_s3 | | 5 | 6159 | 3841 | 0.1 | 179 | 0.13 | 0.082 | 0.15 | 0.033 | 0.055 |

DON'T try to read all these numbers either !!!

Design: South Atlantic based on catch-at-length series

Table 2: South Atlantic: *if* current F-pattern is just about sustainable (70% SPRR)

| Scen | m | NY | SS_small | SS_big | paged | E_HSP_XC | N_FAd2020 | depl_2020 | logtrend_10yr | m | SPRR |
|--------|------|----|----------|--------|-------|----------|----------------|-------------|---------------|-------------|-------------|
| "True" | | | | | | | 780,000 | 0.78 | -0.10 | 0.06 | 0.70 |
| V_s1 | | 5 | 972 | 3828 | 0.1 | 15 | 0.42 | 0.188 | 0.40 | 0.076 | 0.209 |
| V_s2 | 0.06 | 5 | 922 | 9078 | 0.7 | 63 | 0.20 | 0.094 | 0.20 | 0.038 | 0.101 |
| V_s3 | | 5 | 6159 | 3841 | 0.1 | 68 | 0.21 | 0.114 | 0.17 | 0.046 | 0.108 |
| "True" | | | | | | | 470,000 | 0.75 | -0.10 | 0.08 | 0.70 |
| V_s1 | | 5 | 972 | 3828 | 0.1 | 22 | 0.34 | 0.169 | 0.37 | 0.066 | 0.141 |
| V_s2 | 0.08 | 5 | 922 | 9078 | 0.7 | 92 | 0.16 | 0.084 | 0.19 | 0.033 | 0.068 |
| V_s3 | | 5 | 6159 | 3841 | 0.1 | 100 | 0.18 | 0.102 | 0.16 | 0.040 | 0.080 |
| "True" | | | | | | | 300,000 | 0.73 | -0.09 | 0.10 | 0.70 |
| V_s1 | | 5 | 972 | 3828 | 0.1 | 30 | 0.29 | 0.153 | 0.36 | 0.060 | 0.109 |
| V_s2 | 0.10 | 5 | 922 | 9078 | 0.7 | 125 | 0.14 | 0.076 | 0.18 | 0.030 | 0.053 |
| V_s3 | | 5 | 6159 | 3841 | 0.1 | 136 | 0.15 | 0.092 | 0.15 | 0.036 | 0.065 |
| "True" | | | | | | | 210,000 | 0.71 | -0.09 | 0.12 | 0.70 |
| V_s1 | | 5 | 972 | 3828 | 0.1 | 40 | 0.25 | 0.138 | 0.36 | 0.056 | 0.092 |
| V_s2 | 0.12 | 5 | 922 | 9078 | 0.7 | 164 | 0.12 | 0.069 | 0.18 | 0.028 | 0.045 |
| V_s3 | | 5 | 6159 | 3841 | 0.1 | 179 | 0.13 | 0.082 | 0.15 | 0.033 | 0.055 |

- Perfunctory examination only ! **more work needed**
- Low- m case hardest
- Samp size needs to be bigger than NA, eg 10000
 - or less, if SPRR=70% is "too precautionary"
- In SATl_f, may be worth "seeing what you get"

Design: Spatial coverage

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- But, "spatial fidelity" even if non-heritable, plus uneven sampling *could* cause bias in CKMR, for some species

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- Makos move a lot, but tend to stay either E or W for a few years
- Given *reasonable* sample sizes in E and W
 - then you will see any important pattern...
 - ... and can adjust model accordingly

Norwegian minke whale DNA-register

- 1000 sampled individuals
- Sparse sampling!

- 10 microsat markers

Detection of relatives by

- n = 3300 (years 1997-2002)

- 21 pairs detected

Stage I design

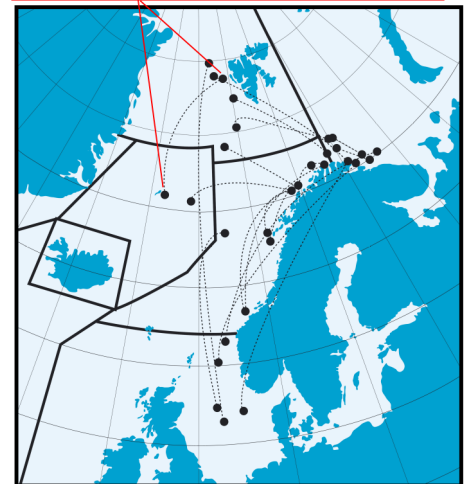
Stage I (screening, n = 3300)

- 10 microsats
- LOD scores, FDR = 50%

Stage II (validation, n = 73)

- 15 independent markers
- LOD scores, sign. lev. = 0.02

Sampling locations of a pair of related individuals



Design: Spatial coverage

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- But, "spatial fidelity" even if non-heritable, plus uneven sampling *could* cause bias in CKMR, for some species
- Makos move a lot, but tend to stay either E or W for a few years
- Given *reasonable* sample sizes in E *and* W
 - then you will see any important pattern...
 - ... and can adjust model accordingly
- **Do *not* have to sample everywhere or evenly**

Norwegian minke whale DNA-register

- 100 sampled individuals
- Sparse sampling!

- 10 microsat markers

Detection of relatives by
Skaug et al, 2010, Mol. Ecol. Res.)

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Stage design

Stage I (screening, n = 3300)

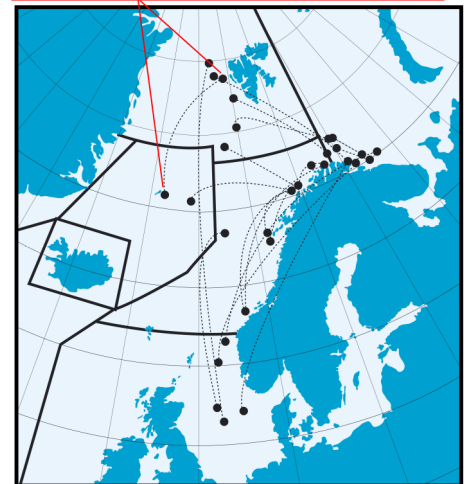
- 10 microsats

Stage II (validation, n = 173)

- 15 independent markers

LOD scores, sign. lev. = 0.02

Sampling locations of a pair of related individuals



CKMR: what do you need, what do you get?

"Fish" eg most teleosts

- POPs -- adults vs juves
- HSPs -- juves vs juves
- Range of adult ages & juve cohorts
- Adequate spatial coverage
- **ADEQUATE** sample data, eg length
- **ENOUGH SAMPLES !!**

"Mammals" eg most sharks

- HSPs -- juves vs juves
 - POPs nice, but not essential !
- Range of juve cohorts
- Adequate spatial coverage
- **ADEQUATE** sample data, eg length
- **ENOUGH SAMPLES !!**

other key biol / demog
parameters

For *adults* (only):

Absolute abundance: time series
Total / natural mortality

"I have read and accept the terms and conditions"



CKMR: what do you need, what do you get?

Also...

Total catch: useful not essential

CPUE: not required

CKMR data is "tamper-proof"

"Mammals" eg most sharks

- HSPs -- juves vs juves
 - POPs nice, but not essential !
- Range of juve cohorts
- Adequate spatial coverage
- **ADEQUATE** sample data, eg length
- **ENOUGH SAMPLES !!**

other key biol / demog
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Discussion #1 following ICCAT Shark WG presentation, Sep

- Results would be *very useful* for mako management:
 - anchor current assessments
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 - anchor current assessments
 - monitor status / response to future measures
- Looks do-able "on paper"
 - sample size OK eg 5000 *total* vs annual catch of ~90,000
 - age *not* essential; length would be OK *if accurate enough*
- Logistic issues still to sort out...
 - Which countries ?
 - ? Samples from live-releases ? or just dead landings?
 - CITES listing: *a problem for sampling !*

Discussion #1

- Results would be *very useful* for mako management:

9.2 Interactions with the CITES Secretariat

The Group chairman reported that the Secretariat had sent a letter to the CITES Secretariat regarding the difficulties encountered by CPC scientists to collect and ship biological samples due to CITES regulations requesting that they facilitate sampling of CITES-listed species for scientific research conducted under the auspices of ICCAT research programs. The letter identified "introductions from the sea" as one of the main difficulties encountered and that a possible solution would be that a permit be issued directly to ICCAT, which would cover and be distributed to the Contracting Party institute(s) participating in a specific project. However, the US objected to this citing bad precedent-setting. CITES has not yet replied to the ICCAT request, though it is expected an answer will be provided later this year. The goal is to establish non-detrimental findings (NDF) - yet this task requires excessive work. ICCAT has confirmed that CITES does not want to present an obstacle to science and was made aware of a shark working group within CITES where this issue can be taken up.

- CITES listing: *a problem for sampling !*

Next steps

- Continue engagements:
 - ICCAT SHK: mid 2020
 - tRFMO: Dec 2019

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- Continue engagements:
 - ICCAT SHK: mid 2020
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- Identify partners around Atlantic
 - Develop a full CKMR program design in 2020
 - ... maybe start sampling !
- Interest in CKMR worldwide: pelagic sharks and more
 - develop the tools for more general use

Close-Kin Mark-Recapture

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Thank you !

