Including CKMR in stock assessments: The SBT experience

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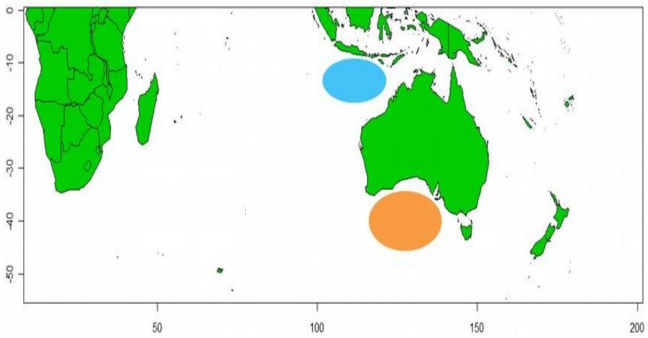
SBT biology & fishery

- Southern bluefin tuna (SBT) 1 of 3 global pop^{n}s
- Reasonably fast growing *and* long-lived (30+)
- Late maturing (50% between 8 to 10 y.o.)
- Caught from 2 y.o. onwards by variety of gears/fleets
- Distributed across SEIO, South Atlantic, Tasman Sea

SBT spawning behaviour

- Spawning (blue), summer ages 2 to 4 (orange):

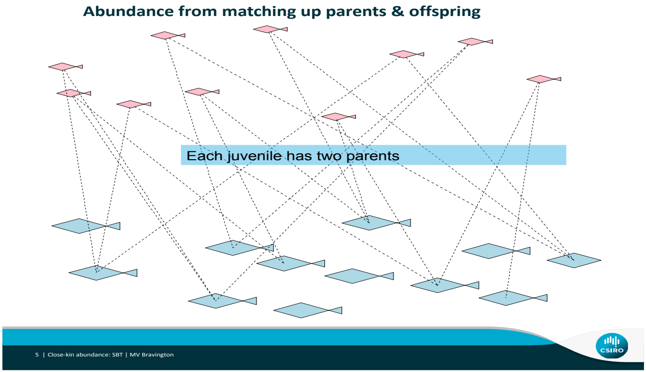


Why did we choose SBT for CKMR?

- Status of stock in 2006:
  1. Spawning stock biomass (SSB) at 5% of unfished
  2. Fishing mortality too high for SSB to increase
  3. Weakest recruitments ever seen 1999–2002
  4. Substantial historic catch misreporting revealed
- Estimates of SSB_{2006} **highly** uncertain
- Catch uncertainty essentially unresolvable
- No other plausible data sources to inform on SSB
- CKMR proposed as a viable way to resolve this

Parent-Offspring Pairs (POPs)

- Adult-juvenile comparisons (looking for POPs)



Parent-Offspring Pairs (POPs)

- Cartoon population dynamics: N_A is adult abundance
- Genotype m_A adults & m_J juveniles
- Chance of finding a parent (mother or father):

$$\mathbb{P}(POP) = \frac{2}{N_A}$$

- You find R POPs (recaptures basically...)
- Estimate of abundance: $\widehat{N}_A = 2m_A m_J / R$
- Precision: CV will be approximately $1/\sqrt{R}$
- **Bonus point**: CV scales with $m_A + m_J$ (not square root)

Parent-Offspring Pairs (POPs)

- Reality more complex than cartoon...
- Bigger/older adults more successful at reproducing
- Factor age (size) into POP probabilities
- Key covariates in SBT case:
  1. Juvenile's year of birth/cohort
  2. Adult's sampling year
  3. Adult's sampling age/size

Half-Sibling Pairs (HSPs)

- Juvenile-juvenile comparisons
- You never see the adult
- "Mark": birth of older juvenile
- "Recapture": detection of HSP
- Cartoon: $N_{\male} = N_{\female} = N_A/2$, mortality M_A
- HSP with a 5 year gap between birth years:

$$\mathbb{P}(HSP) = \frac{e^{-5M_A}}{N_{\male}} + \frac{e^{-5M_A}}{N_{\female}} = 4 \times \frac{e^{-5M_A}}{N_A}$$

- HSPs have mortality *and* abundance information

Half-Sibling Pairs (HSPs)

- Again, the cartoon gives way to reality...
- Juvenile-juvenile comparisons:

  1. Juvenile cohort, c, when spawned
  2. Covariates: $\{i, i'\}$, $z_i = \{c_i\}$ and $z_{i'} = \{c_{i'}\}$
  3. **Don't** do within-cohort $(c_i \neq c_{i'})$

- Factors accounted for in $\mathbb{P}\left(K_{ii'} = HSP \,|\, z_i, z_{i'}\right)$:

  1. Unknown adult ages $(y = c_{\min} = \min\{c_i, c_{i'}\})$
  2. Cumulative **total** mortality $(y = c_{\min}, \ldots, c_{\max})$
  3. Increased reproductive output $(y = c_{\min}, \ldots, c_{\max})$
  4. Time-varying nature of adult abundance

- Eqn^s more complex than POP case (see me later...)

Why POPs **and** HSPs?

- Can't do it all with just POPs
- Disentangling abundance, mortality and age/size
- Having both can undo this demographic Gordian knot
- Able to test key assumptions (e.g. pop^{n} structure)
- Reduce sample sizes (you already have the juveniles...)
- Question really is why *wouldn't* you do both

SBT CKMR "timeline"

- Idea proposed in late 2000s
- **Phase 1**:
  - Use microsatellites; POPs only
  - Incorporated in SBT assessment 2012
- **Phase 2**:
  - Move to SNPs; both POPs & HSPs
  - Both incorporated in SBT assessment 2017
- CKMR included in revised Management Procedure (2020)

Sample sizes

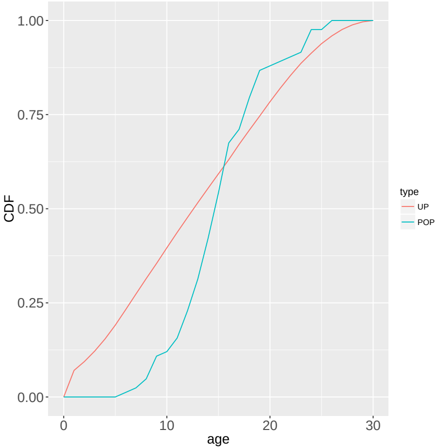
- Number required depends on pop^n size
- Also depends on what you want from the data
- Since 2006:
  - **Adults**: almost 10,000 genotyped
  - **Juveniles**: just over 15,000 genotyped
  - Around 25,000 fish in total: 89 POPs; 115 HSPs
  - Data covers over 10 years of adult dynamics
  - Current rate: about 1,000 adults, 1,000 juveniles *p.a.*
- Sample harder early: accrue matches slowly then quickly
- Later on modify according to needs/resources

SBT stock assessment structure

- Data sources:
  1. Age/length catch composition
  2. Longline CPUE index (mostly on sub-adults)
  3. Multi-year mark-recapture (juveniles $a = 2, \ldots, 5$)
  4. Juvenile (ages 2–4) relative biomass survey
  5. Gene-tagging 2 year old absolute abundance index
  6. CKMR (POPs and HSPs)
- Model structure: "standard" age and seasonal model
- Key parameters:
  1. Annual recruitment
  2. Time-varying fishery selectivity
  3. Age-dependent natural mortality
  4. Length-specific reproductive output (ψ)

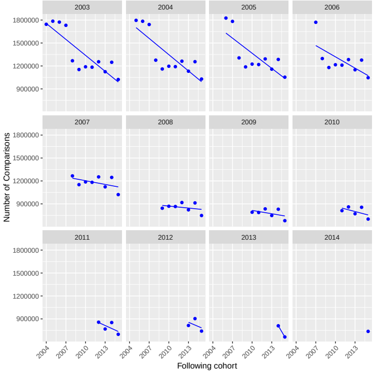
Summary of the POP data

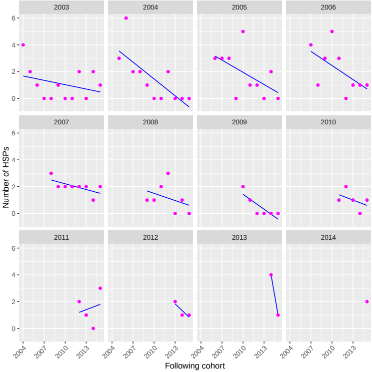
1. Years (2006–2018), cohorts (2002–2015), age (5+)
2. Around 112 **million** comparisons; 89 POPs



Summary of the HSP data

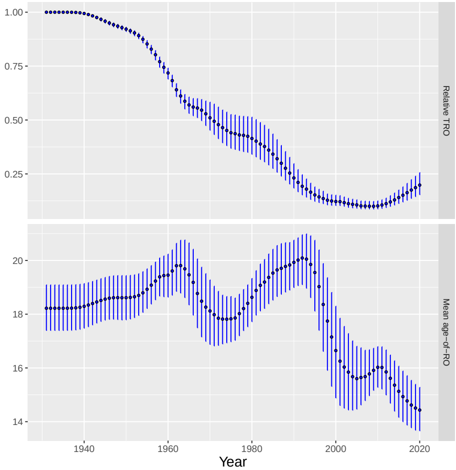
1. Cohorts (2003–2012)
2. Around 88 **million** comparisons; 115 HSPs





Key reproductive pop^n variables

- Relative TRO (top) & mean age in spawners (bottom):

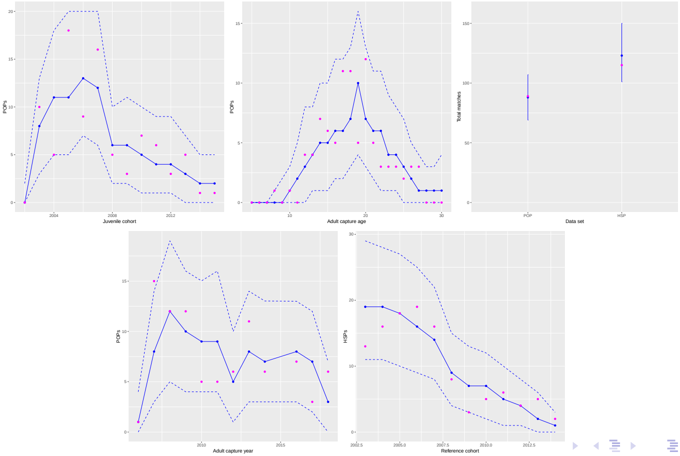


Fits to the CKMR data

- Data (esp. POPs) basically sparse MR data
- Aggregate data/predictions across covariates
- POP data aggregation:
  1. Adult capture age & year (cohort level)
  2. Adult capture age & juvenile cohort (age level)
  3. Adult capture age and cohort (adult sampling year level)
- HSP data aggregation:
  1. Following juvenile cohort (initial cohort level)

Fits to the CKMR data

- POP cohort (TL), age (TM), year (BL) level; HSP (BR) initial cohort and finally total matches (TR):



What did the CKMR change/tell us?

- Spawning population larger, less depleted
- Current depletion: 0.2 (0.16–0.24)
- Sustainable yields essentially unchanged
- Adult mortality lower than previously thought
- Successful sizes/ages of reproduction bigger/older
- However, Big Fecund Female hypothesis not supported

Oversight & engagement

- Original project had expert steering committee
- Move from microsats to SNPs reviewed by experts
- Get buy-in from stakeholders, SC and Commission
- Particularly on genetics - topic of least familiarity

Lessons learned & future work

- Unsurprisingly, this takes time...
- Takes a dedicated inter-disciplinary team
- Important to explore role of length/sexual dimorphism
  - SBT seems OK; exception not the rule?
- Spend **a lot** of time bringing people along
- CCSBT funded CKMR as ongoing monitoring program
- CKMR data used in CCSBT Management Procedure

Acknowledgements

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