

TDW 2024



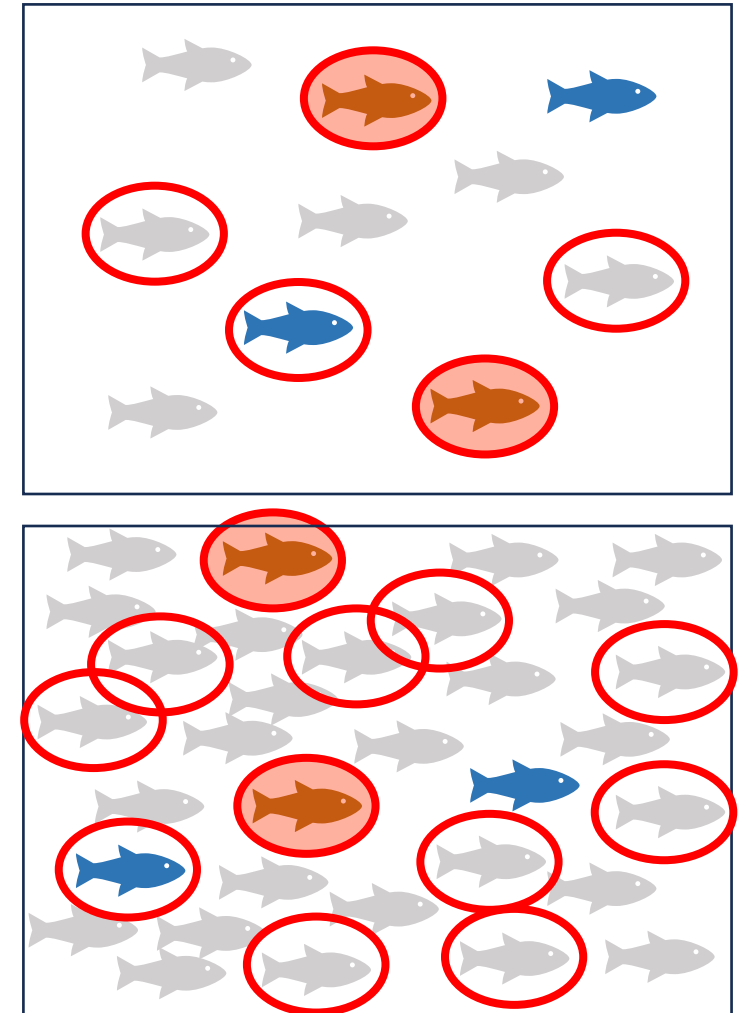
Close Kin Mark Recapture as applied to South Pacific albacore

8-12 April, Noumea, New Caledonia

Giulia Anderson on behalf of many collaborators

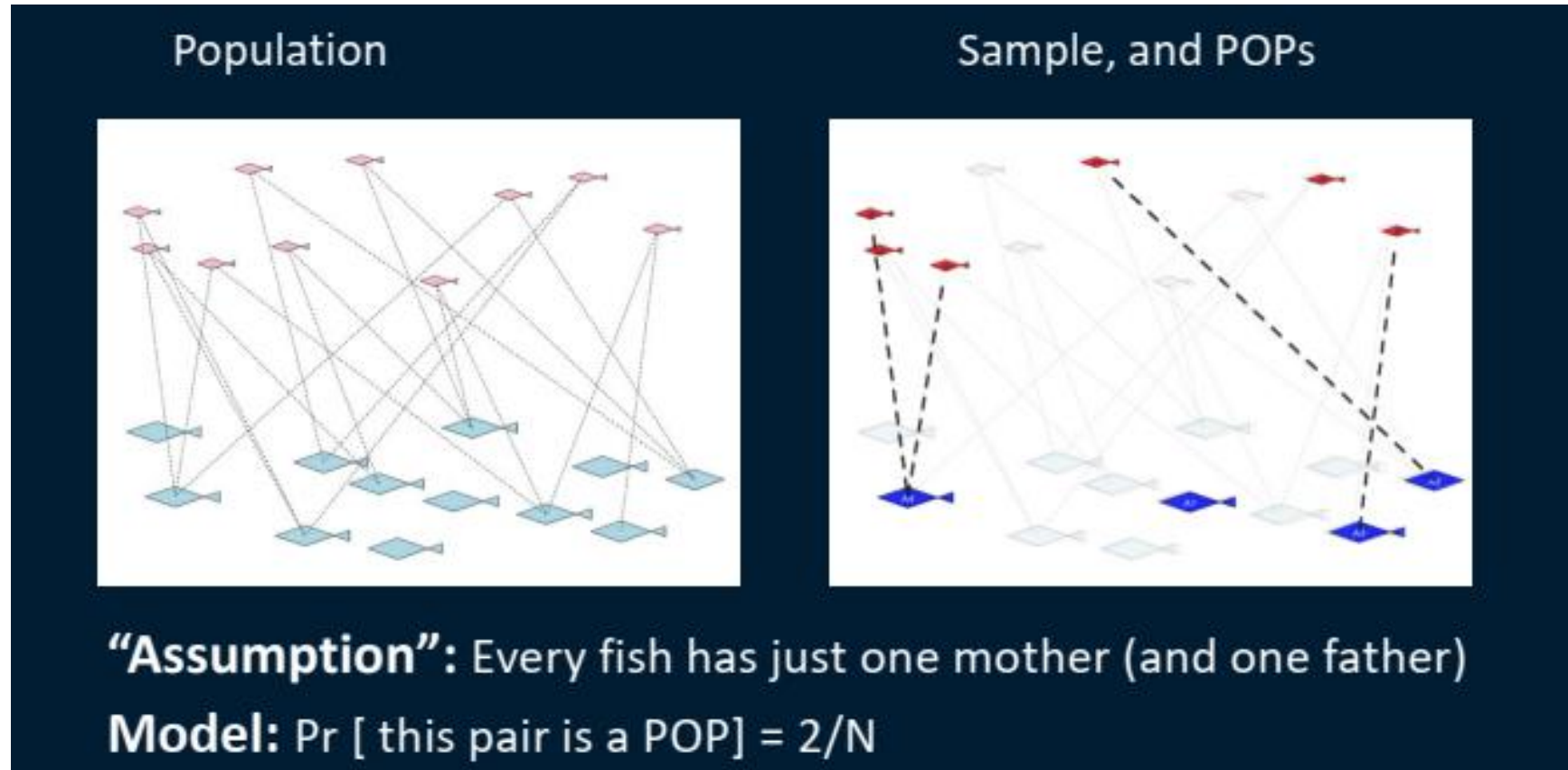
What is CKMR?

- A fisheries-independent assessment to estimate absolute population abundance/total reproductive output, and/or mortality
- A variation on mark-recapture studies that 'marks' fish genetically and 'recaptures' related individuals
- Basic concept: a ratio between fish sampled and kin found
 - the bigger the population, the less likely you are to randomly sample related individuals
 - the more samples you need to take to find 1 kin pair, the bigger the population must be



Some basics

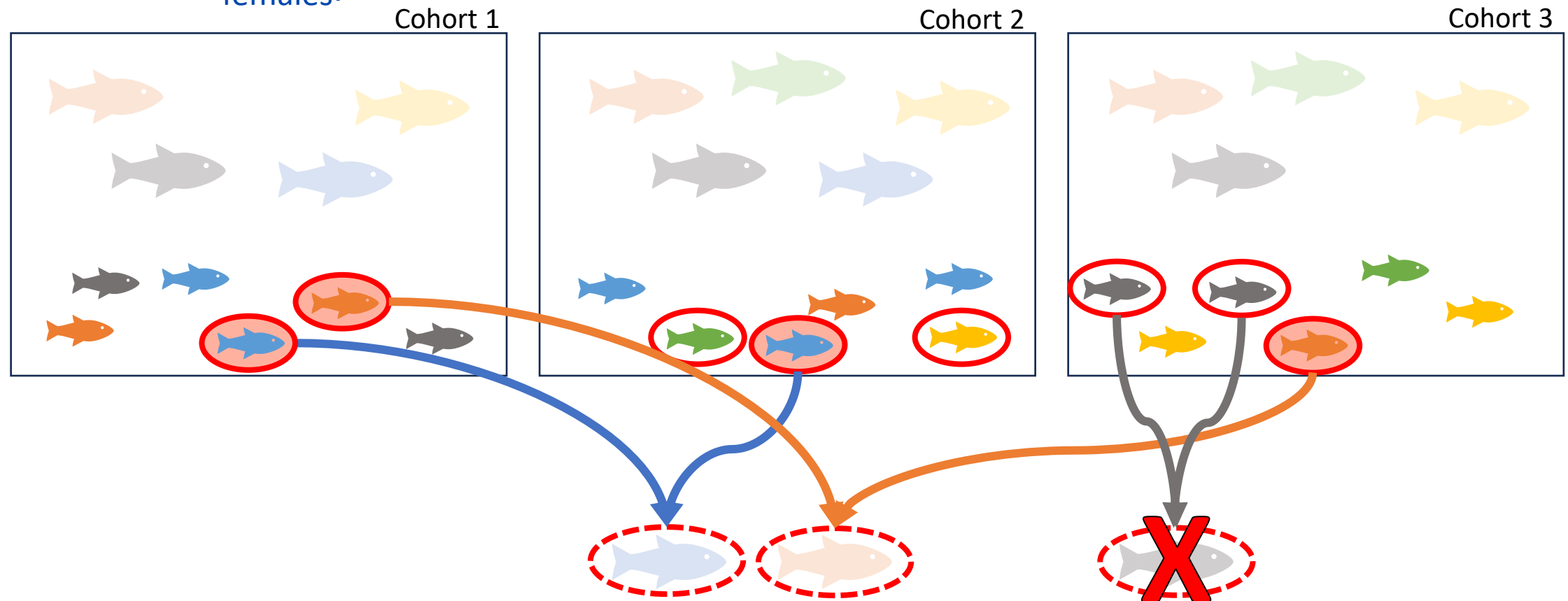
Original concept used parent-offspring pairs



$$\frac{\text{Number of kin pairs found}}{\text{Number of possible pairs}} = \frac{2}{\text{Number of adults in pop}}$$

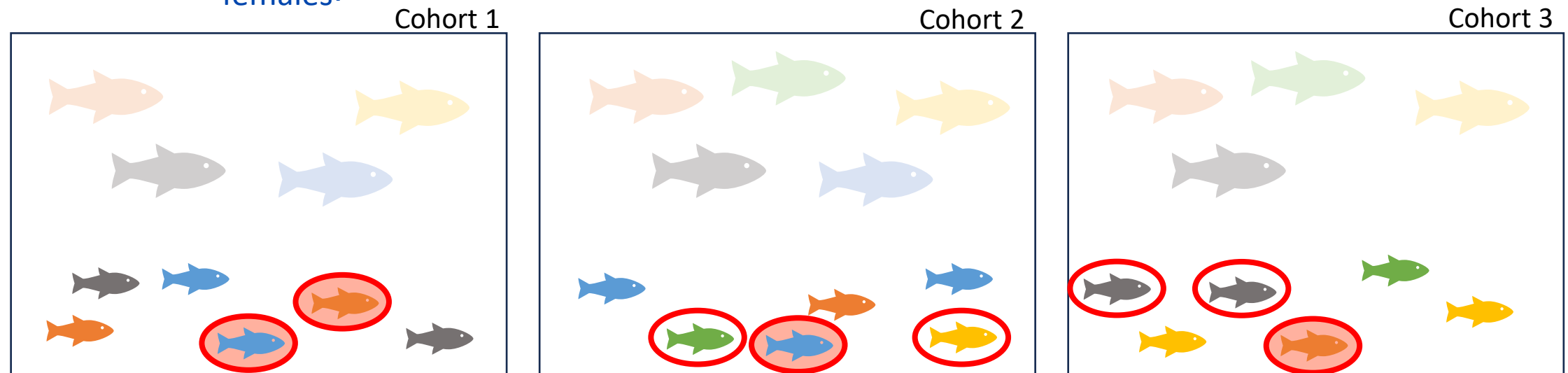
Some basics

Theory has been expanded to use cross-cohort half sibling pairs, since the ratio still holds (chances that two individuals have the same mother is still $1/N_{\text{females}}$)



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But now with more covariates

- Mother's survival between offspring
- Growth/changing fecundity
- Range of probable genetic relatedness

More technical bits

- “CKMR is a new source of data provided to an integrated population model, which computes a likelihood that compares observations to expectations”
- Quality of result depends on accuracy of population model and biologically-appropriate sampling scheme
 - Distribute samples across ages, sexes, spatial range, population substructure
- Different kinship types inform different metrics
 - Parent-offspring presence informs total abundance
 - Half-sib presence informs mortality rate
- Precision of estimate improves by finding more kin pairs
 - Baseline of 50 kin pairs to reach CV of 15-20%
 - Estimates are relevant to the birth year of sampled offspring

Data to collect

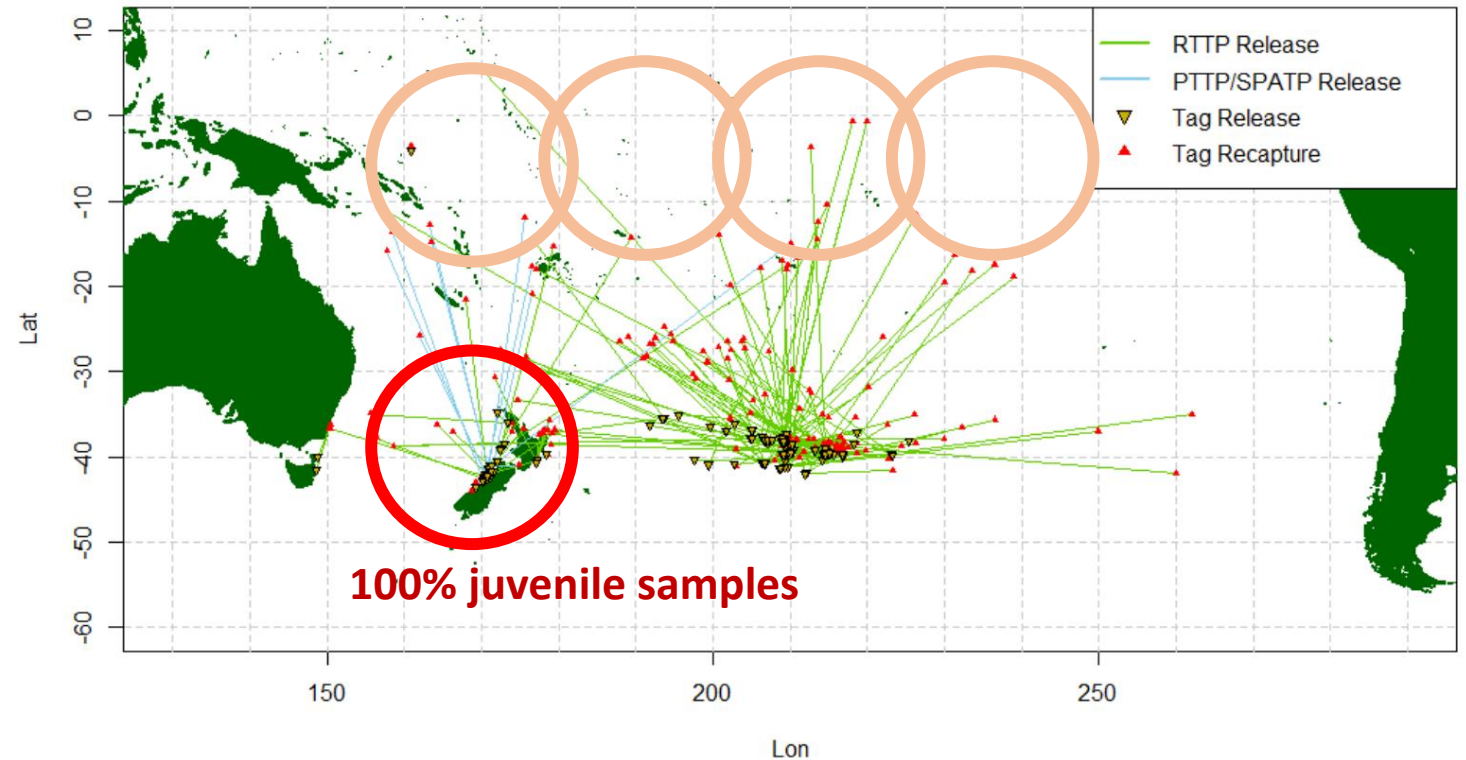
- Muscle tissue
 - Tiny amount of tissue needed, taken with the CSIRO widget
 - Used for genetic relatedness analyses
- Age
 - Currently using length-to-age conversions
 - Hopefully soon to augment with higher confidence epigenetic age estimates
- Other metadata
 - Location and time of catch (low-precision data is okay)
 - Sex
 - Some details about sampling conditions (flagging if best practices couldn't be followed)

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Albacore goals

- Initial modelling says we need...
- ~30,000 individuals
- Sampled evenly across all size classes
- Sampled evenly across the geographic range



How are we doing?

- 10000+ samples collected so far
- CKMR training events in Fiji*, Tonga and Marshalls, Samoa, and Solomons later this month
 - 28 collaborators from 10 countries **fully** trained
 - Protocols specialized at 6 ports
- Sampling kits for 26000 fish distributed to 8 countries
- Countries can start sampling independently once staff are trained and LOAs in place
- Starting to sample other species, too





Other considerations

- Deciding how to transport samples out of each country will likely require port-by-port assessments
- Still establishing quality control protocols to help flag sample quality issues. This could impact number of samples needed, and/or flag samples that are already collected
- Still working to incorporate epigenetic aging. Once rolled out, sampling should get still faster/more inclusive, and results should be more confident

Outlook

- This is still the ‘upfront investment’ phase. Once all pieces are in place, CKMR sampling should be a low-maintenance system that can be maintained across years
- Will create incredibly powerful temporal datasets that only gets more valuable as they mature
- Most of the site-specific protocols established for albacore (sampling, transporting, etc) are directly applicable to other species flagged for future CKMR studies

Questions?

