



Australia's National Science Agency

Understanding whale shark populations through kinship



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Overview

- Estimating local Ningaloo whale shark abundance:
 - Challenges
 - Resight data approaches
 - Resight population model results from CSIRO data
- The broader view:
 - How do we look across whale shark generations?
 - How do we examine population at large scales?
 - Kinship and close-kin mark recapture



Whale shark abundance

- Anthea Donovan and Colby Bignell talks have given the background in detail.
- **Recap:**
 - Ningaloo aggregations have been studied via individual mark resight data.
 - Data uploaded to Wildbook photo-ID
 - This project has collected significant new resight data (~600 encounters)



Estimating local abundance

Simple "open" population model following Peel et al (2015)

$$N_t = N_0(1 + r)^t$$

- where:
- N_t are the total numbers at time t . Here timesteps are annual.
- N_0 is the initial population size
- r is the logistic/ intrinsic rate of increase.
- Population allowed to increase/decrease through the term r .
 - Examined model with growth rate r fixed at 0 (=>Population ~constant) to
 - Model with estimated r (population allowed to increase/decrease through time).
- Model includes **apparent** mortality rate M (i.e. will include true mortality + departures)
 - Included in likelihood function used in estimation of model parameters

Number of sharks encountered

- Annual encounters

Year	total encountered
2016	23
2017	66
2018	99
2019	107
2021	103
2022	133



- M-array format for model fitting
- Numbers from year y_i encountered in y_{i+n}

	qtab	2016	2017	2018	2019	2020	2021	2022
2016	23	0	1	3	2	0	0	0
2017	66	0	1	14	8	0	5	6
2018	99	0	0	0	15	0	12	7
2019	107	0	0	0	0	0	10	11
2020	103	0	0	0	0	0	0	0
2021	133	0	0	0	0	0	1	13
2022	23	0	0	0	0	0	0	0

Model limitations:

No population structure (age, sex, connectivity etc).

Note 2022-23 data not incorporated yet

Model estimates of Ningaloo abundance

Constant population size model ($r=0$)

Parameter	$\hat{\theta}$	Lower 95% CI	Upper 95% CI
$\hat{N}_{2016}^{constant}$	494	284	784
\hat{M}	0.751	0.592	0.942

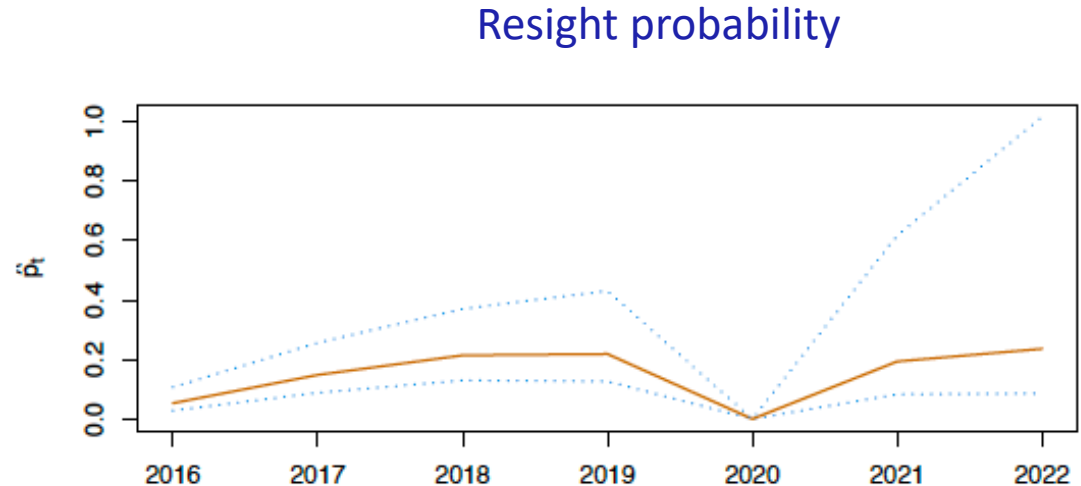
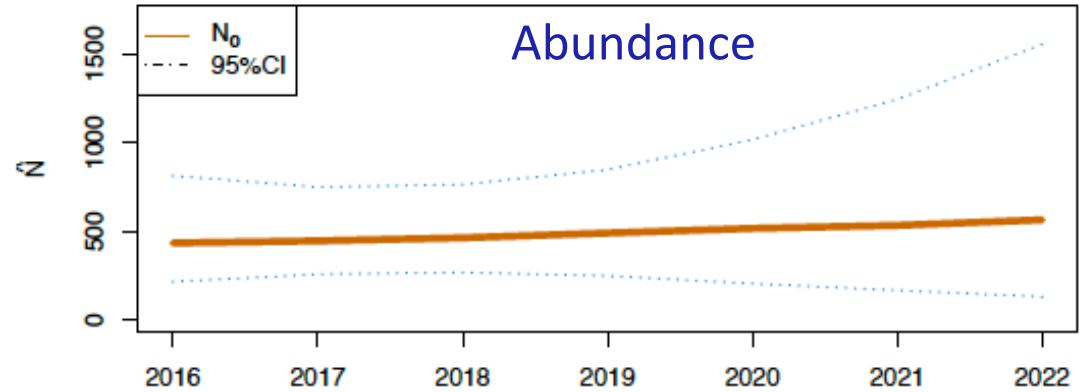
Varying population size model (r estimated)

Parameter	$\hat{\theta}$	lower 95%CI	upper 95% CI
\hat{N}_{2016}	426	188	985
\hat{M}	0.742	0.591	0.936
\hat{r}	0.0377	-0.218	0.291

- Abundance
 - Models estimating ~4-500 animals in 2016
- Apparent Mortality
 - $M = 0.75 \text{ y}^{-1}$
- Population growth r
 - Nominally around +3-4% per year.
 - However wide confidence
 - => Can't say if different from $r=0$.
 - Potential for effort effects ?

Model predictions

- Note wide confidence intervals through time
- COVID sampling gap
- Most confident in the middle of the time series.
- Will investigate time-varying population growth. Initial results mixed.
- Resight probability estimated around 20%



Comparison to previous studies

- Various earlier estimates from previous studies
 - **Abundance:**
 - E.g Meekan (2006) N=300-500 individuals estimated depending on open / closed model variant.
 - **Apparent survival rates**
 - Holmberg (2007): 0.55-0.85 year⁻¹.
 - **Trend**
 - Bradshaw (2007): 0.87 year⁻¹ (decline)
 - Holmberg (2008): 1.12 year⁻¹ (increase)
- Trends of this magnitude unlikely?
Our recent data shows agreement with Meekan et al estimates from 18 years ago.
- CSIRO data suggests broad agreement with previous studies on abundance.
- **Limitations mark-resight data methods:**
 - Broader Spatial structure unclear
 - Estimating long term trends happens in real time (slowly)
 - Can't estimate key quantities – Breeding stock abundance
 - Effects of biases in the aggregation? More males, smaller individuals

Close Kin Mark Recapture

- Resight data can estimate local abundance.
- But unless:
 - Resights across ocean basins -> **connectivity unresolved**
 - Within generation only -> **takes many years of data for long lived species**
 - Population genetics: Panmictic pacific + IO populations
 - **Very low gene flow can mask structure at demographic scales**

- CKMR uses prevalence of related individuals (parent/offspring, siblings) in a sampled population.
- Allows estimate of :
 - Adult population size
 - Mortality rates
 - Generational connectivity

CKMR

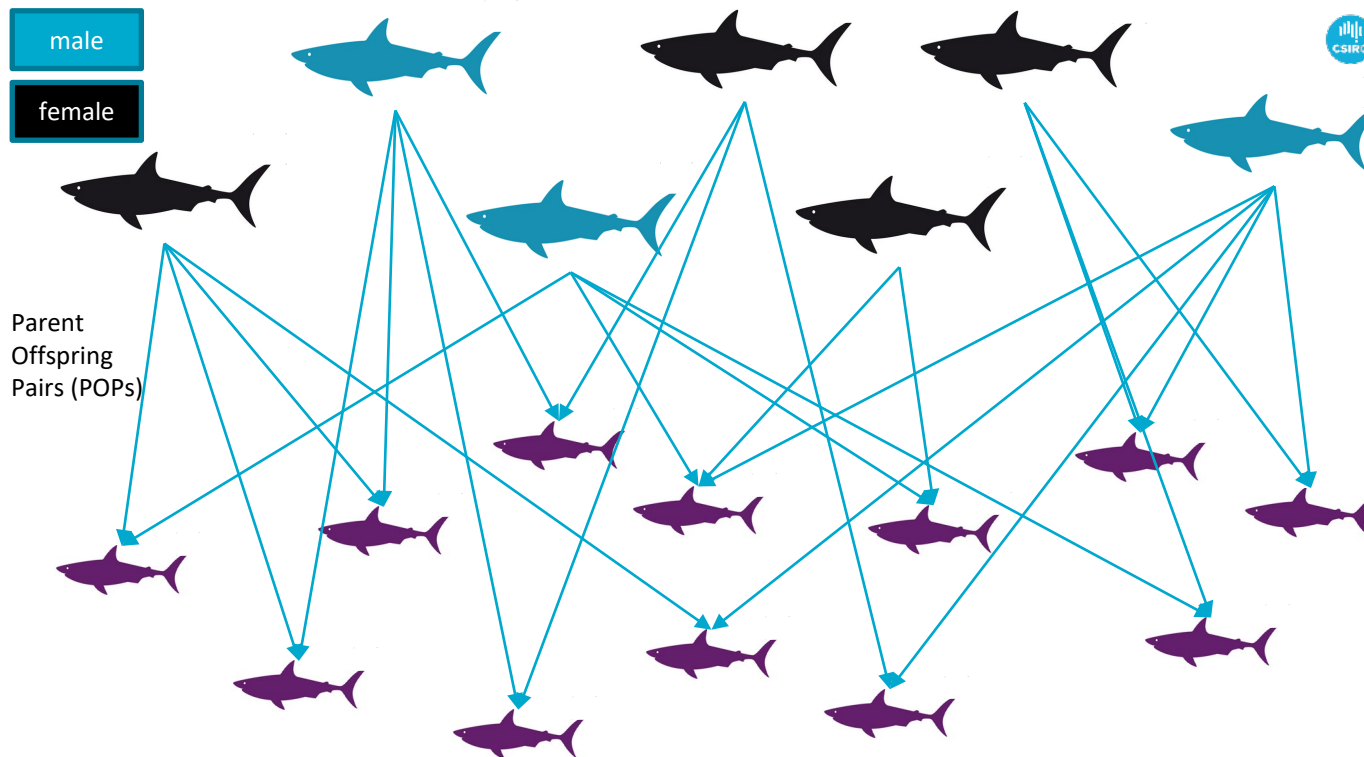
- We would expect largely to have half-sibling pairs as we don't sample too many mature animals
- Offspring “tag” their parents through their inherited DNA
- mtDNA allows us to determine if two siblings are related maternally or paternally
- Knowing the age gap between siblings informs on parent (i.e. adult survival rate).



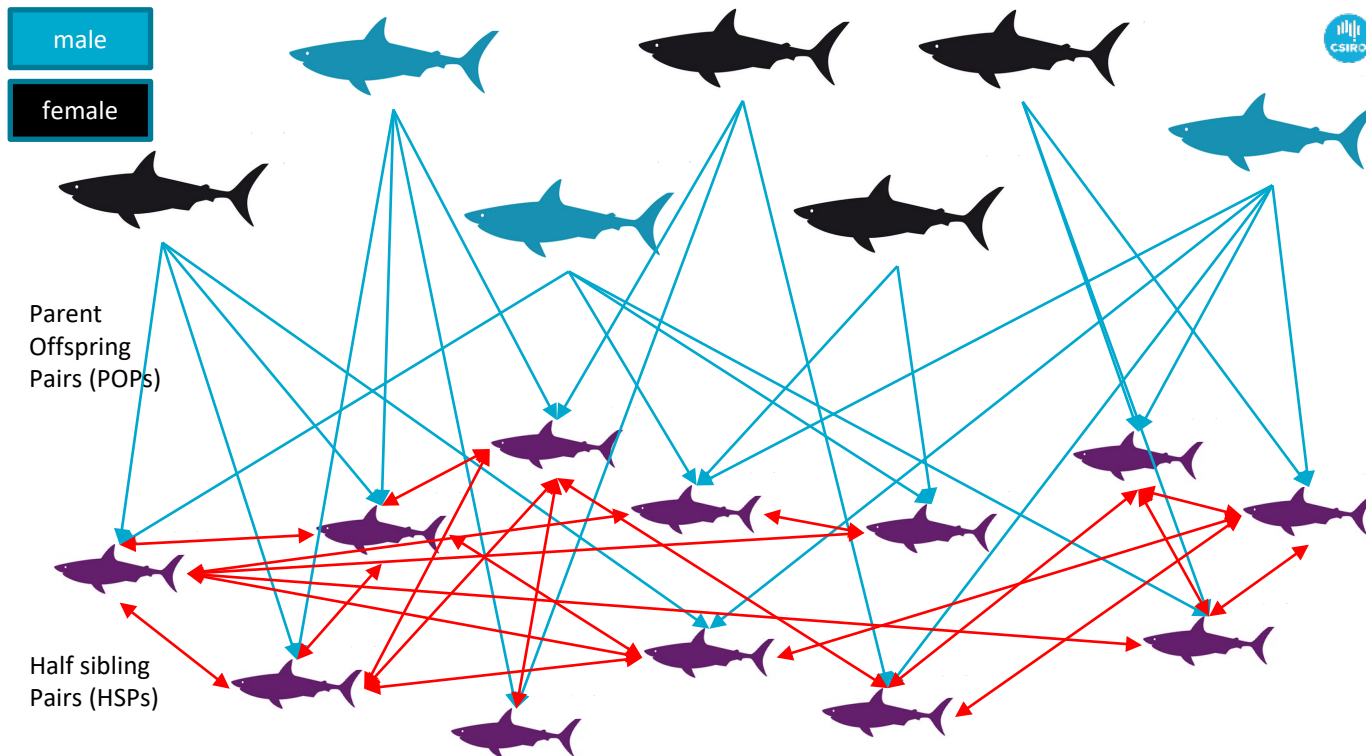
The CKMR Process

1. Sampling
2. Genotyping (DART)
3. “Kinference” -> related pairs
4. Age estimates from length or epi-genetic ageing
5. Population model fitted to data on number of related vs unrelated pairs





See Bravington, Skaug, Anderson (2016) Stat. Sci.

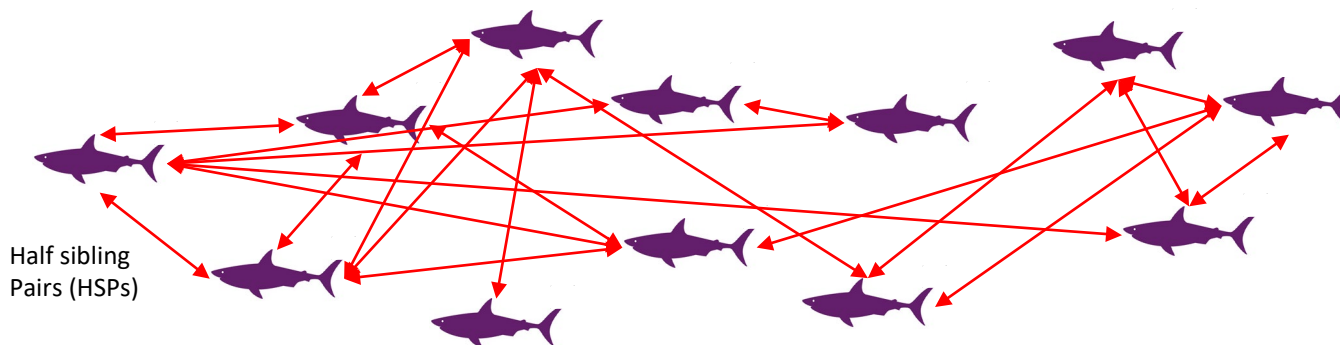


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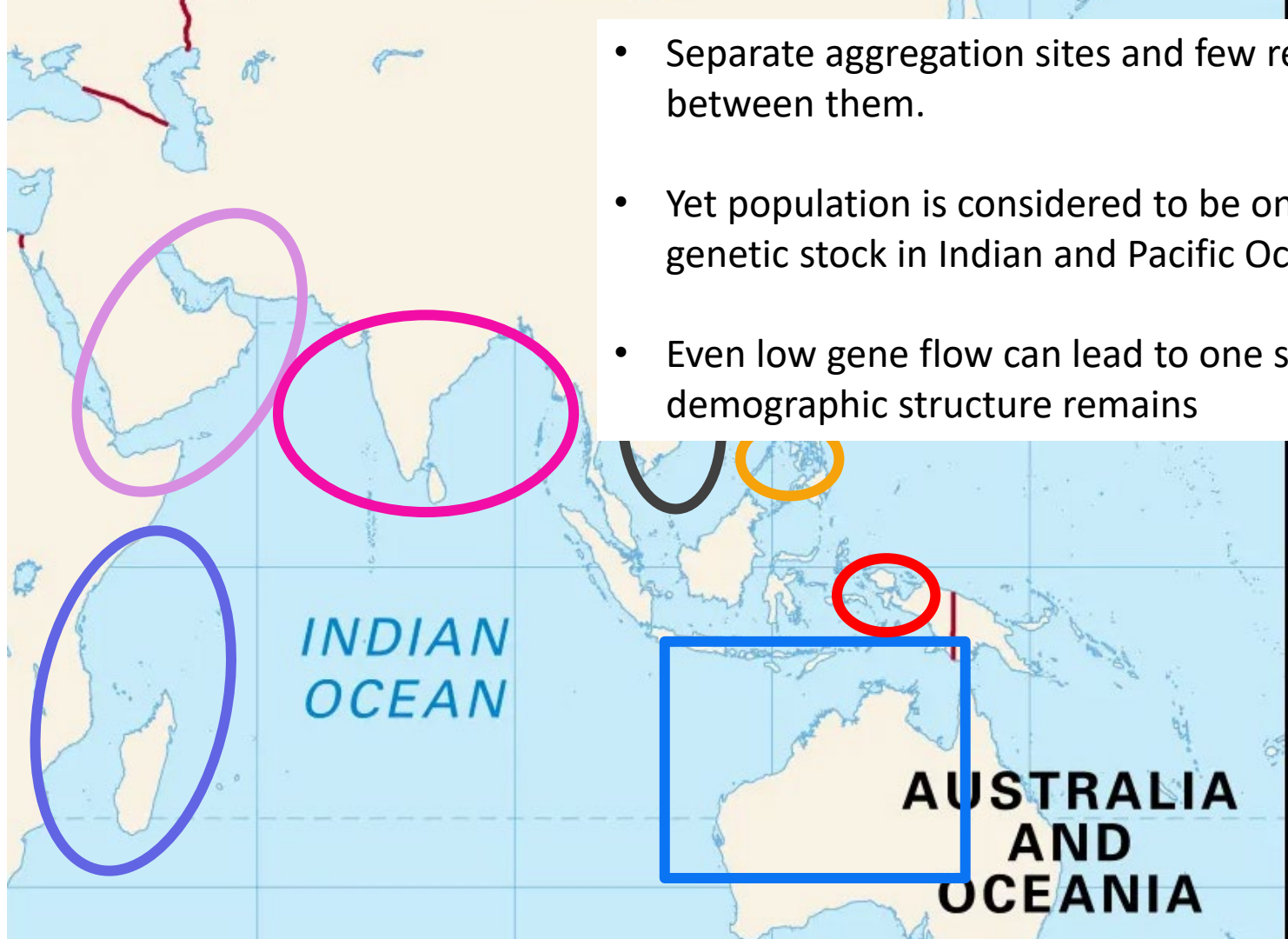
male

female

Not observed
(Only juveniles sampled)



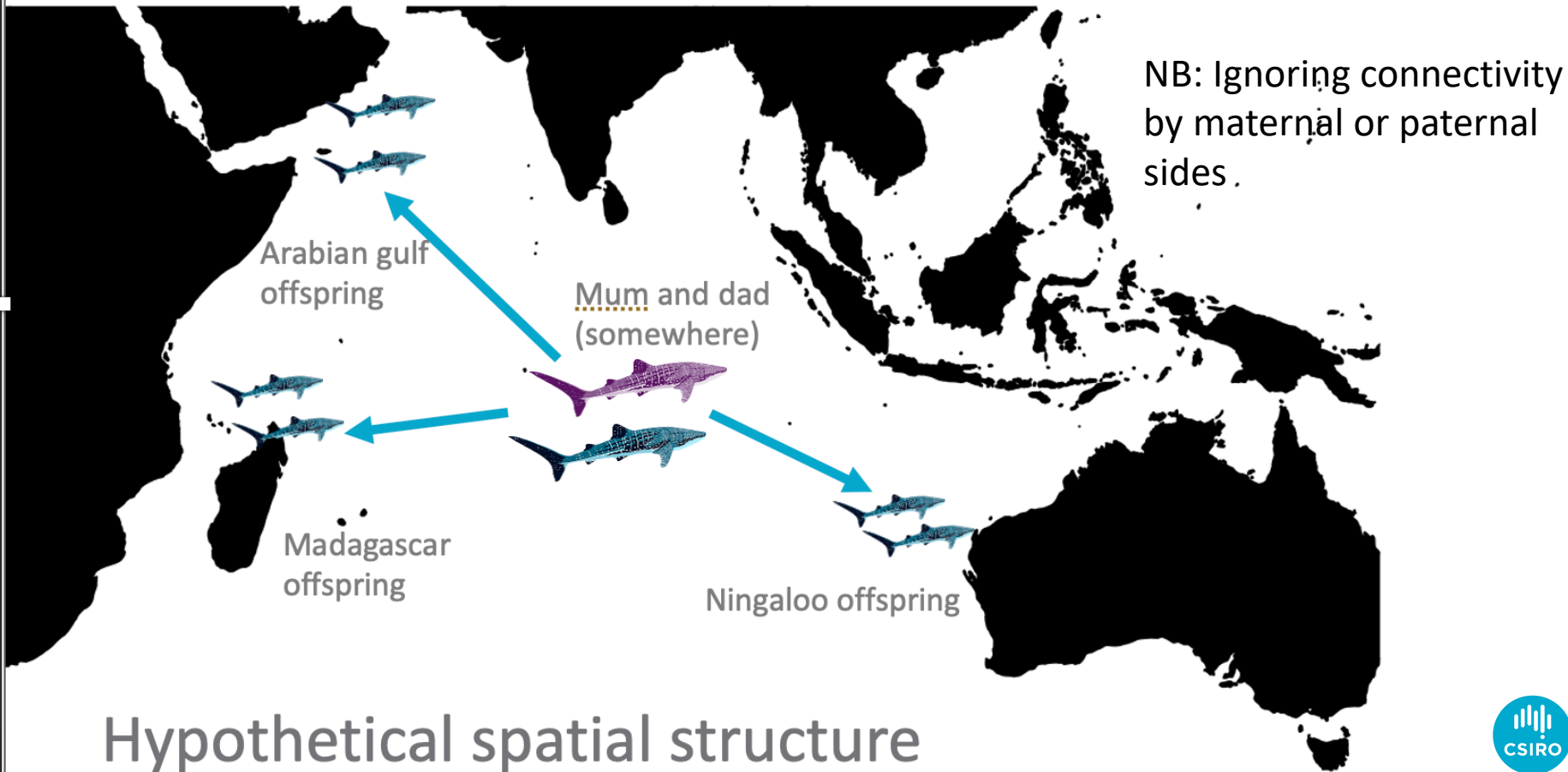
Never have to sample adults to estimate breeding stock abundance



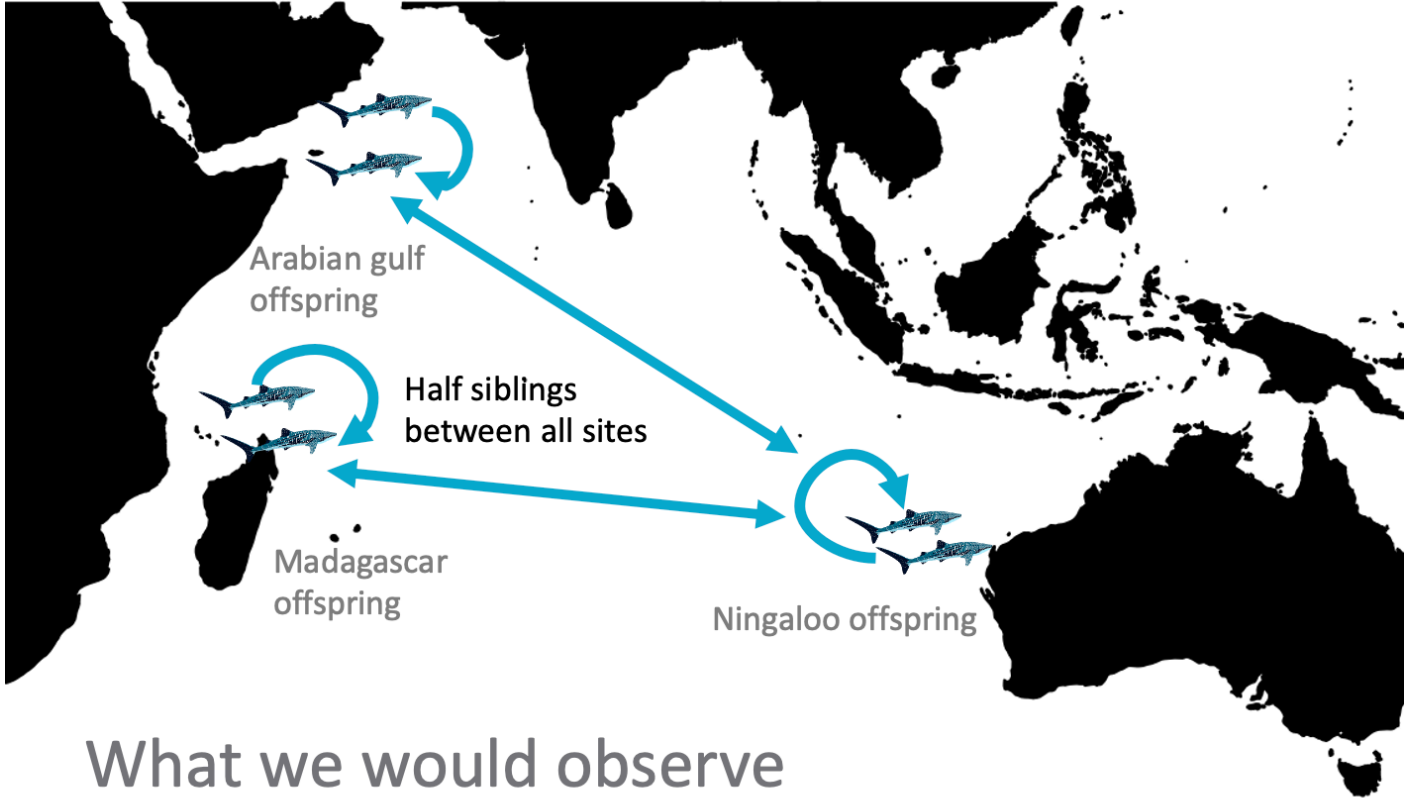
- Separate aggregation sites and few resights between them.
- Yet population is considered to be one genetic stock in Indian and Pacific Oceans
- Even low gene flow can lead to one stock but demographic structure remains

Connectivity from CKMR

Spatial patterns of relatedness informs on connectivity over a generational scale

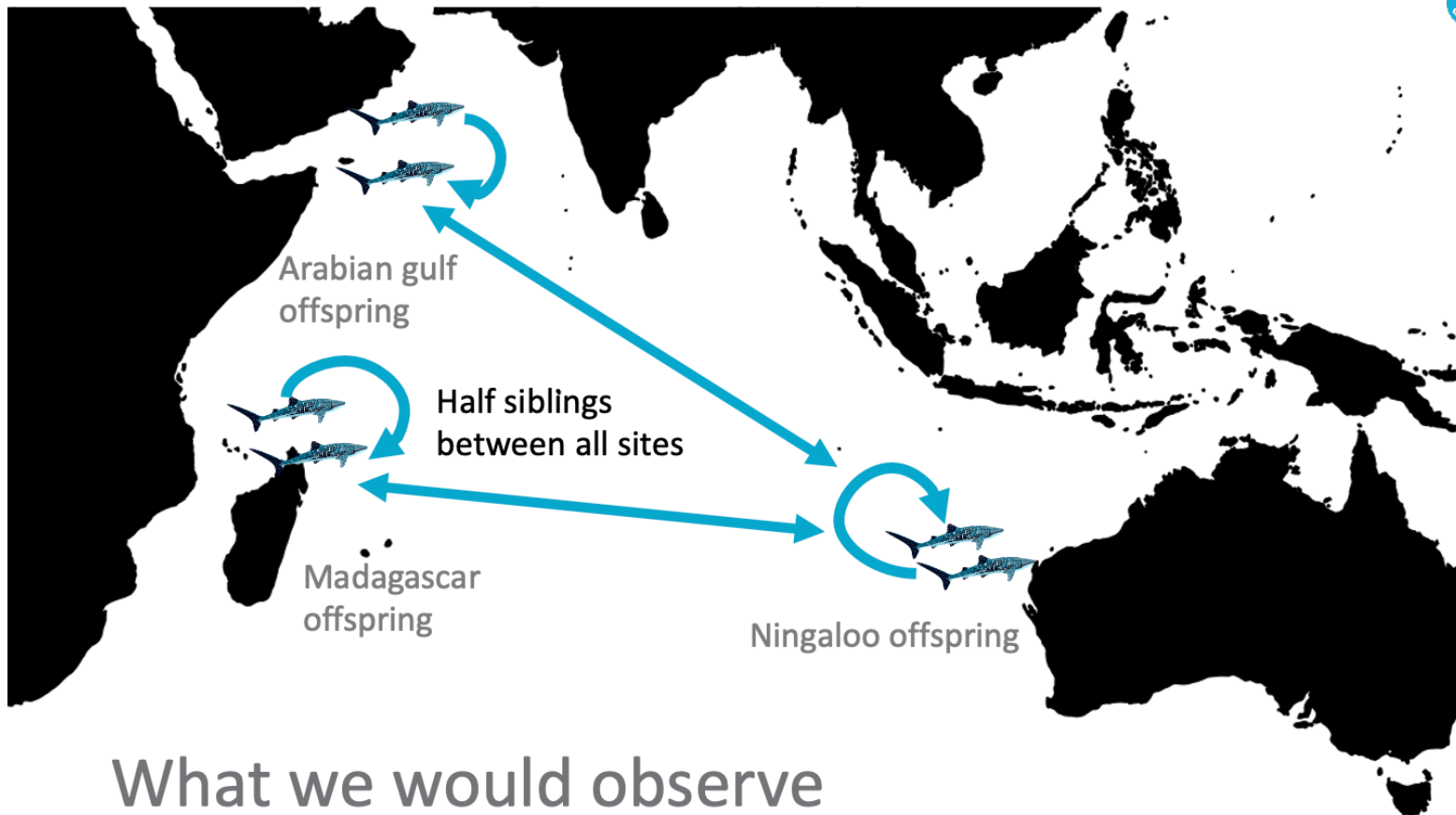


Data if single parental stock supporting all aggregations



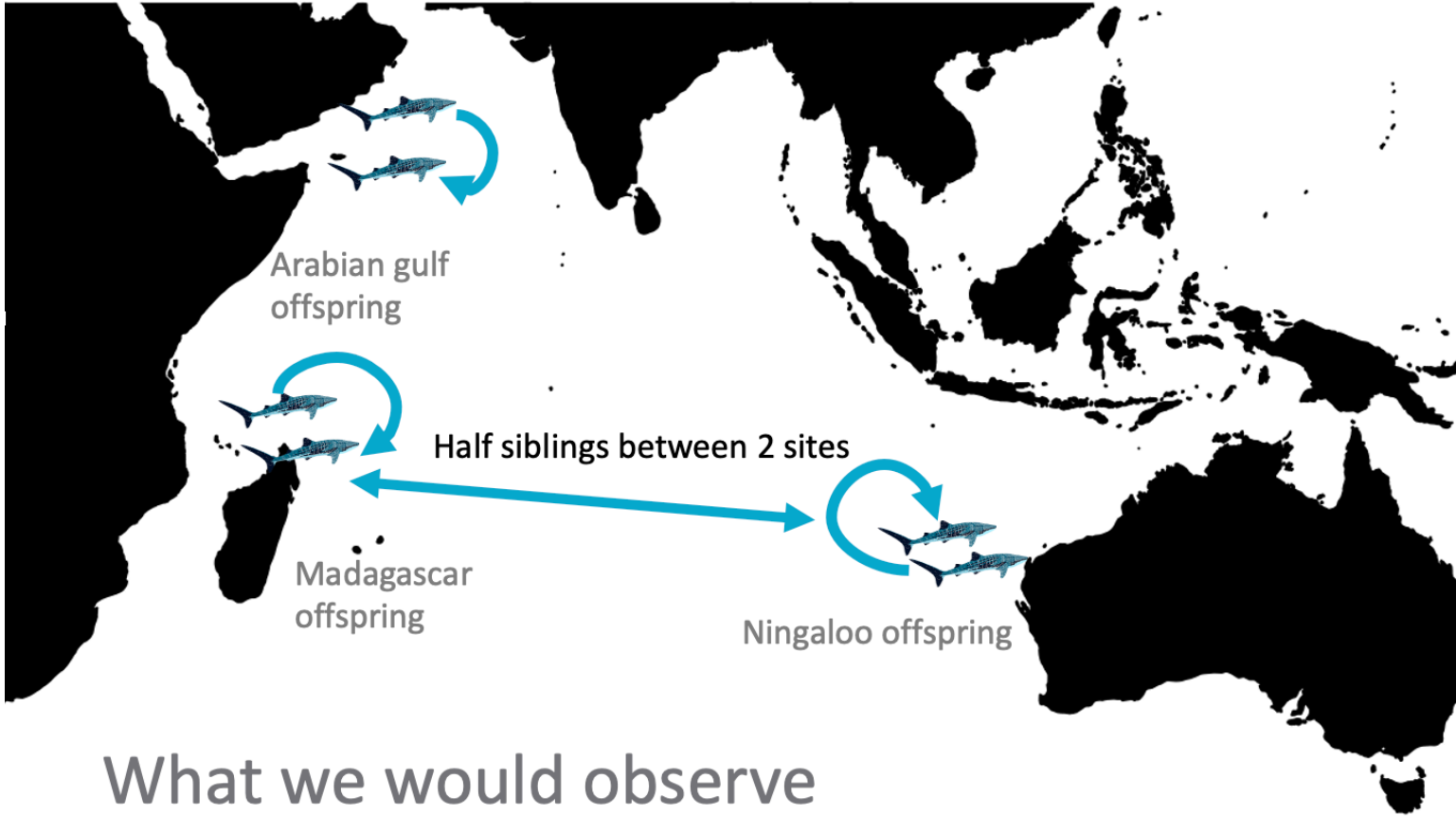
What we would observe

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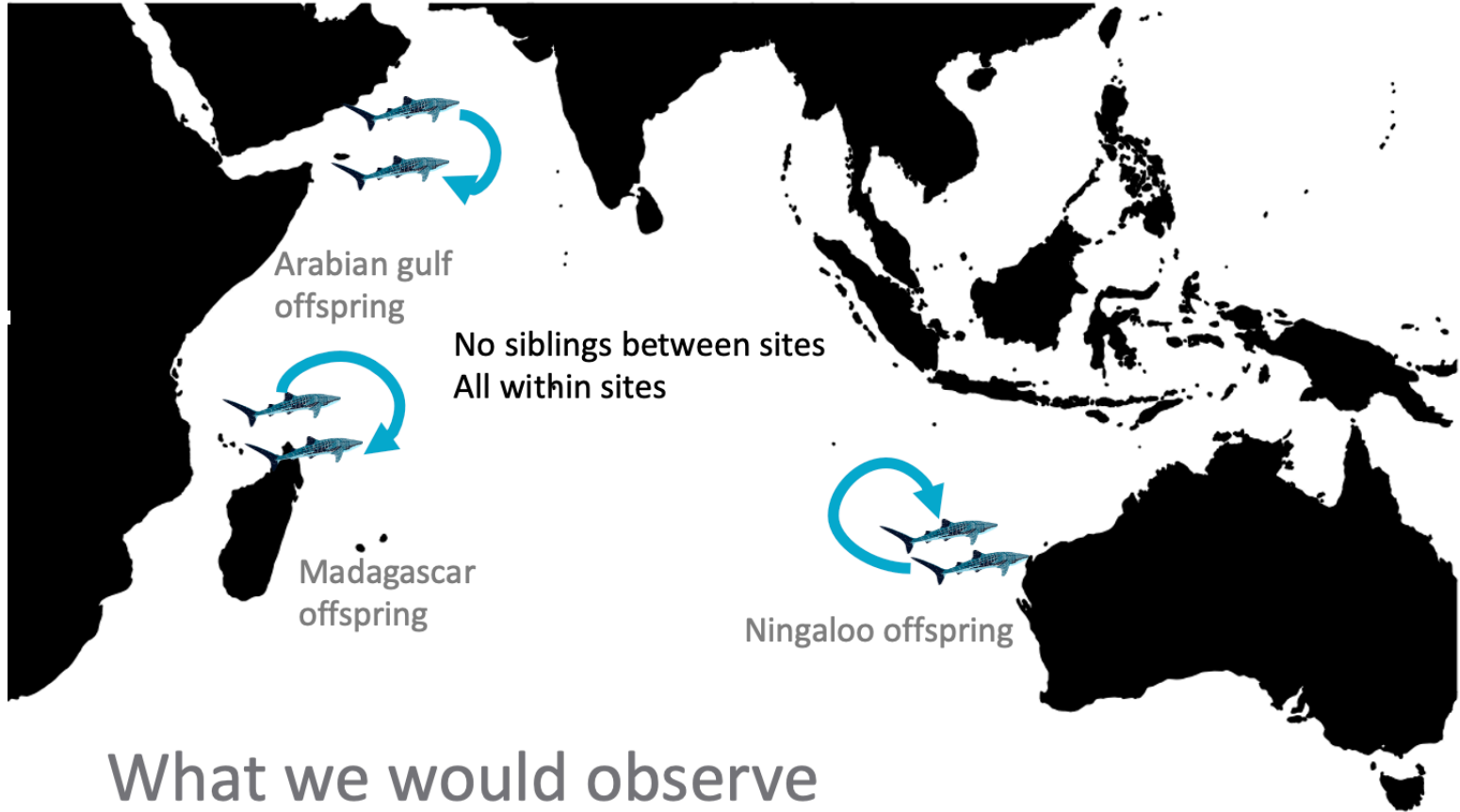


What we would observe

Data if single parental stock some but not all aggregations



Data if aggregations are separate



Data sources:

- Samples from Indian Ocean

- CSIRO worked with Marine Megafauna foundation (Stella Diamant) to access 50 samples from Eastern IO
- Collaborating with Clare Prebble and Alexandra Watts (MMF) to obtain further samples Tanzania after detailed CITES importation process completed
- Working on access to a broader spatial distribution of samples with data holders in United Kingdom (Alexandra Watts)
- Includes samples from sites around the Indian Ocean and the Pacific

- Prevalence of kin pairs within Ningaloo samples informative

- If local population unconnected to other aggregations => highly related
- Informs on size of the parent population supporting Ningaloo aggregation even if connectivity unresolved

Thank you



CSIRO Environment

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