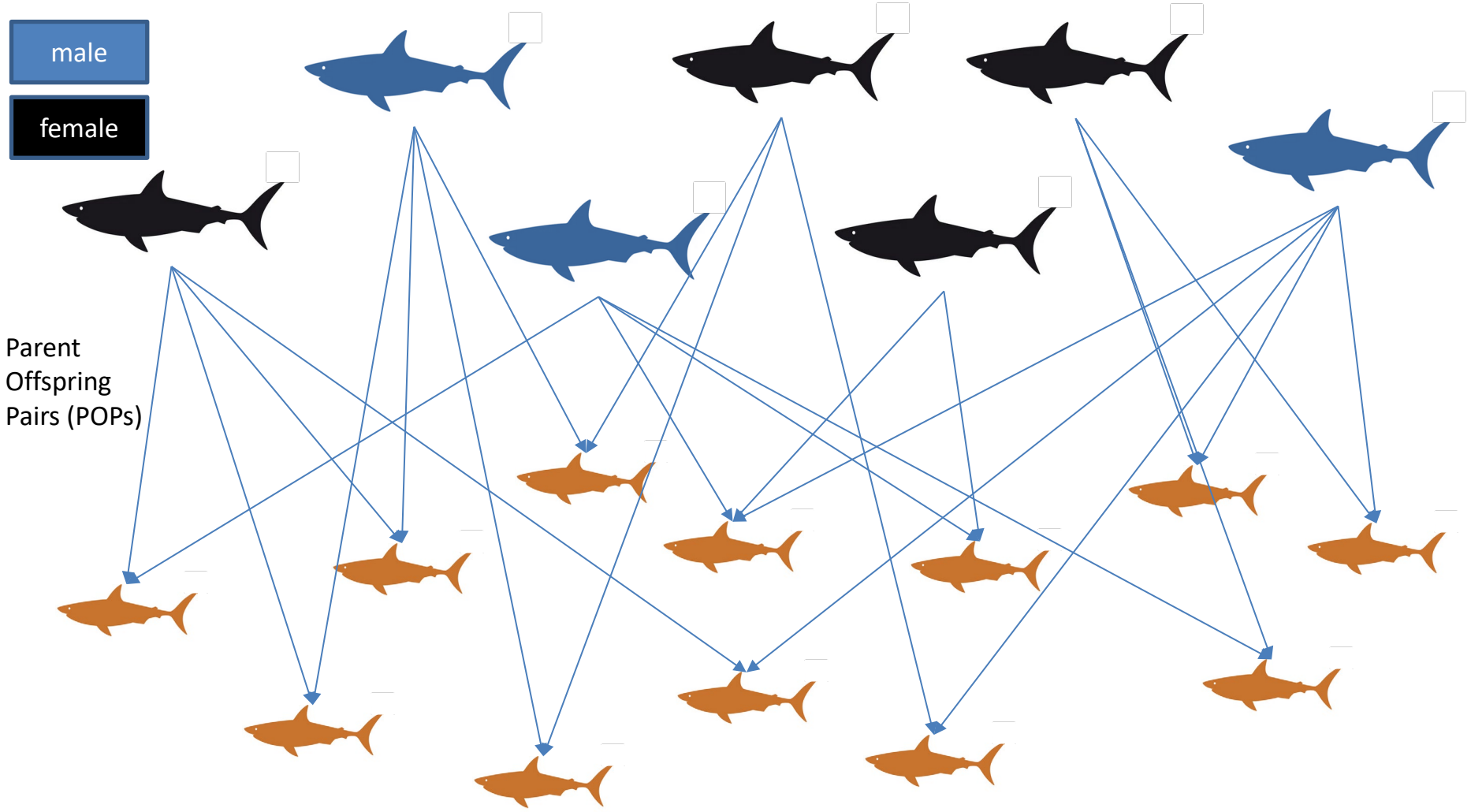
Marine and Coastal

National Environmental Science Program

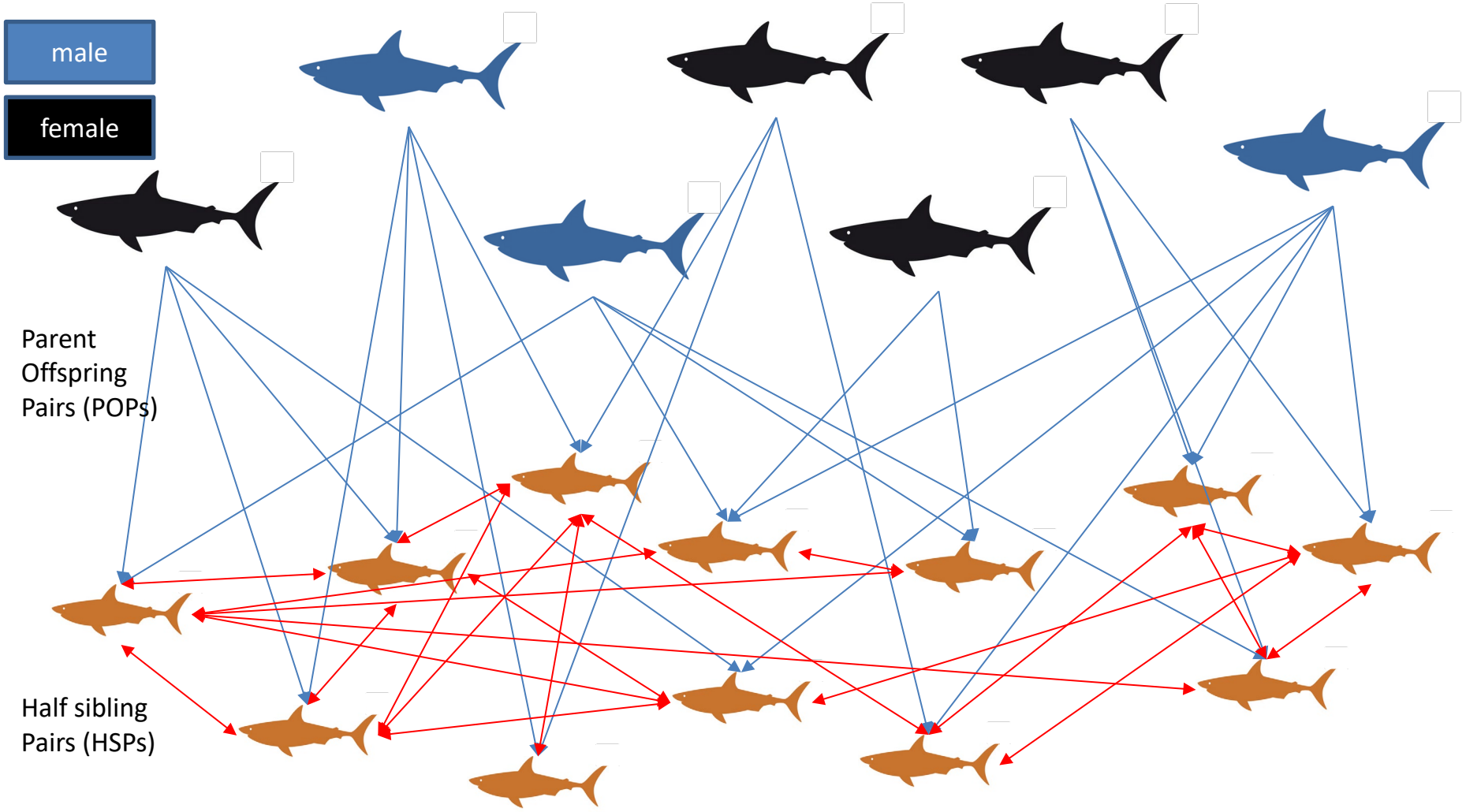
White shark population update

Maugean skate population and habitat

Presenter: Toby Patterson, CSIRO Environment Research Unit



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



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

White shark population update:

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Updated on previous estimates Bruce et al (2018)

Investigate stock structure in white sharks at southern hemisphere scale:

- **Eastern Australia / New Zealand / Southern—Western Australia, South Africa**

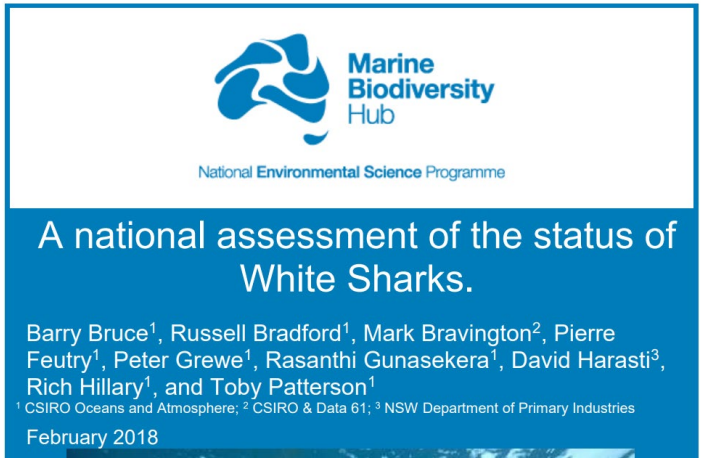
CSIRO: Toby Patterson, Russ Bradford, Richard Hillary, Pierre Feutry, Paige Eveson

WA DPIRD: Mike Travers

Flinders University: Charlie Huveneers

SARDI: Michael Drew

NSW DPIRD: Paul Butcher



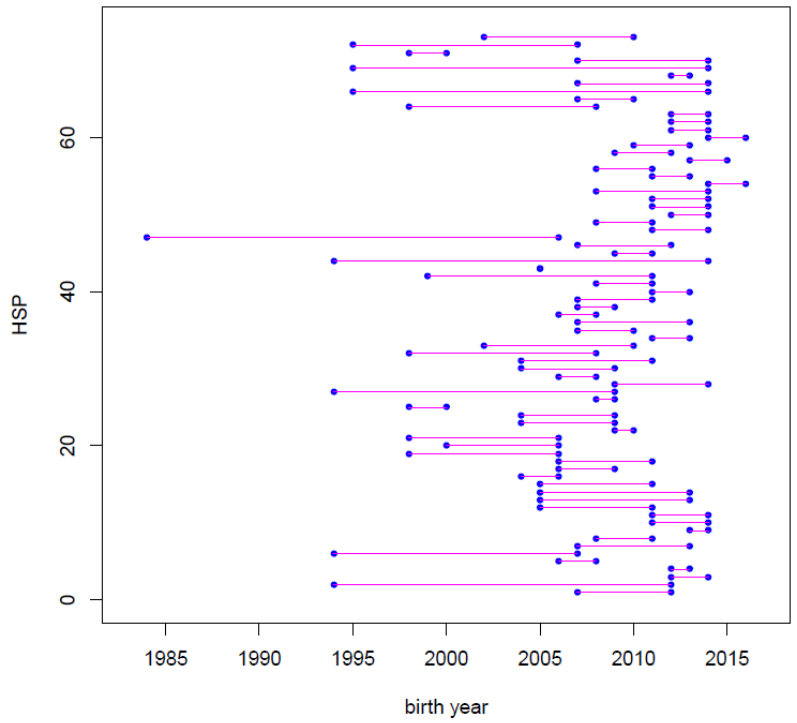
https://www.nespmarine.edu.au/document/national-assessment-status-white-sharks

Eastern population

Initial N_{samp}=281
(considered >14k loci)

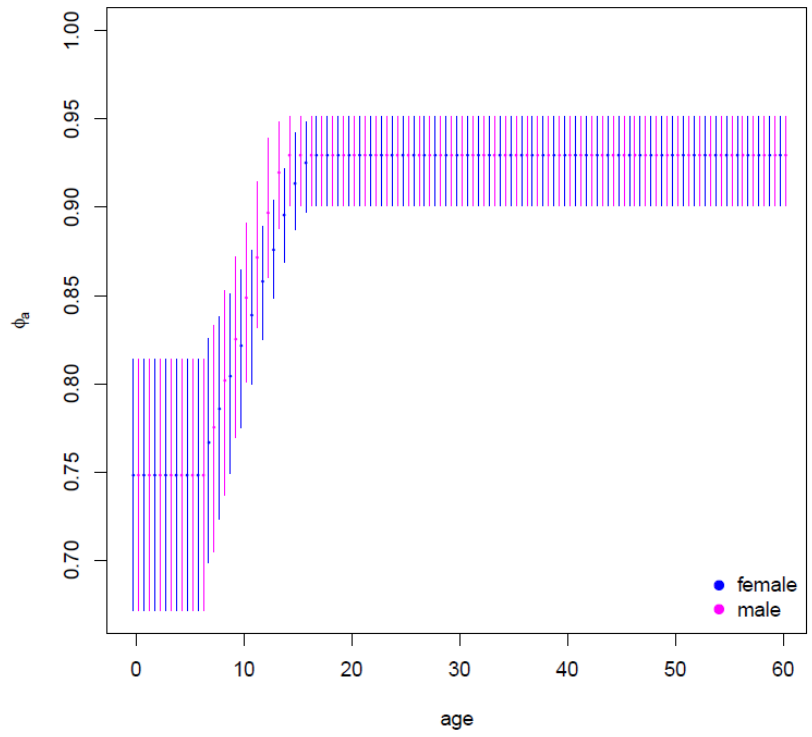
QC checks

N_{samp}=214 / 3097 loci



- 73 HSP / 23 FSP
- Mean cohort difference – 5.5 years (1 HSP -22 yr difference)
  - => High adult survival.
- mtDNA:
  - 36% share a haplotype/ 64% did not
  - => ♂ bias

Eastern population



Adult population size: 700-750
Adults (CV: 0.2)
Overall adult survival: 0.93 (SD: 0.03)
Sex ratio : 60/40
Population growth rate: -0.03 (n.s. from 0.0)
-> Stable adult population
-> Strong evidence against increase

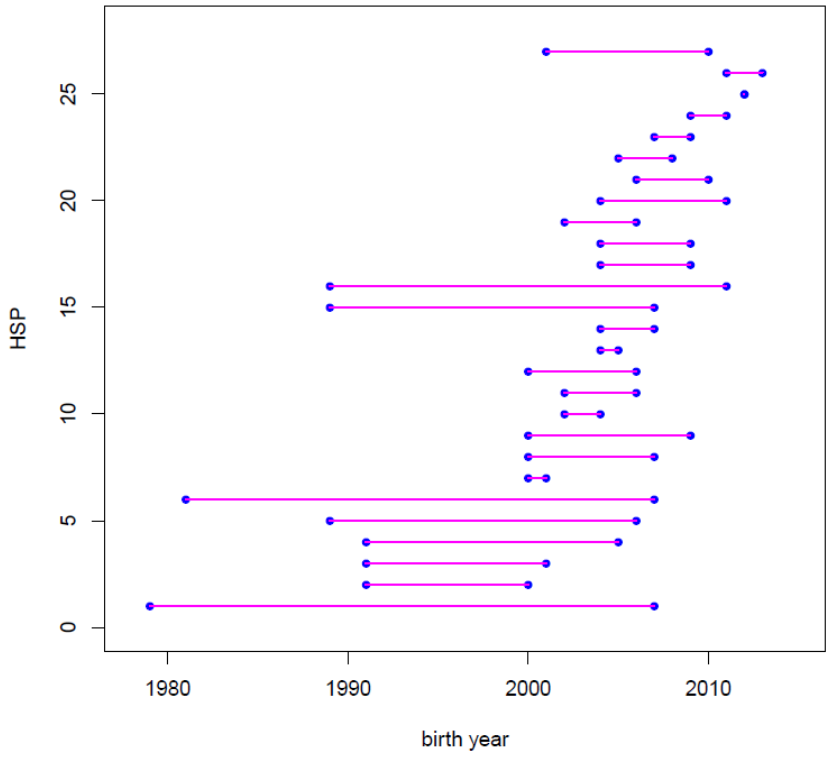
Combined with juvenile survival estimate (0.73 from acoustic tracking data
-Estimate of total population size: N_{total} = **5460 (2909-12802)**

Southern-Western population

Initial N_{samp}=271
(considered >14k loci)

QC checks

N_{samp}=175 / 3185 loci



- 27 HSP / 14 FSP
- Mean cohort difference – 8.4 y
- 1 HSP -30 yr difference
  - => High adult survival.
- mtDNA:
  - 40% share a haplotype/ 59% did not
  - => ♀bias (uncertain)

Maugean skate

CSIRO – Toby Patterson, Paige Eveson, Shane Baylis, Pierre Feutry, Karen Wild-Allen, Richard Thomson.

IMAS – Jayson Semmens, David Moreno, Kwan Tzu

Aims:

Close kin Mark Recapture

Use tissues samples from IMAS sampling (2012 – present; N=4-500 samples) to attempt an estimate of adult abundance and trend over 20 years.

- Initial sequencing conducted by IMAS. Evidence of kin pairs but new sequencing being undertaken to provide more accurate characterisation of kin pairs.

- Investigate whether CKMR can be used to track adult abundance as a monitoring tool.

Habitat Modelling

- Use IMAS telemetry data from skate coupled with CSIRO biophysical models of Macquarie Harbour

- Map extent of likely habitat throughout Macquarie harbour and examine variability in habitat

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Thank you

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