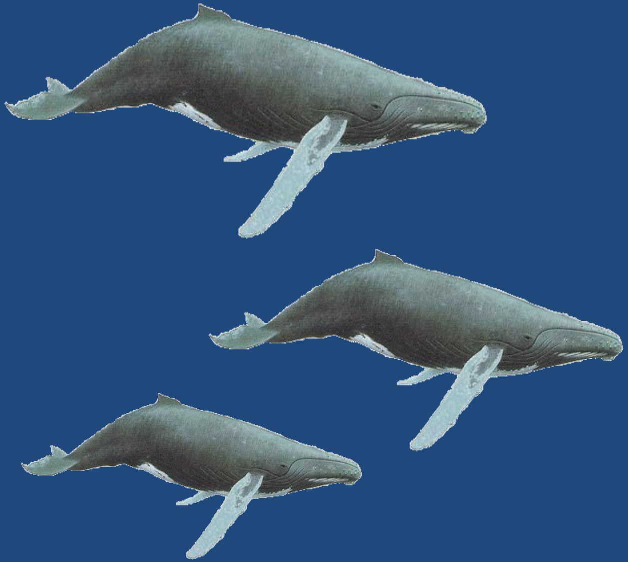
Humpback whale abundance in Oceania



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Introducing the Datasets

French Polynesia, New Caledonia, Tonga, Cook Islands, American Samoa, Vanuatu, Fiji, Samoa

Fluke photo-identifications (1999-2004)

SPLASH QC criteria for photographic quality: >782 photographs of 660 individuals

Microsatellite genotypes (1999-2005)

Biopsy or sloughed skin

1305 successful amplifications of 12-16 microsatellites, matches at >8 loci: 843 individual genotypes

Microsatellite- a highly variable DNA sequence of variable length. The chromosomal location of a microsatellite is it’s locus. Differences between microsatellites are defined by differences in DNA sequence lengths at each locus.
At each locus, because cetacean genomes are diploid (2 copies) there are two copies of the microsatellite (two alleles). If these differ in length, they are ‘heterozygous’, if they are the same length they are homozygous
A set of microsatellite loci described for an individual is it’s genotype

ook
moa
pes

SPLASH criteria
Each photo coded for quality (1*-5):
Proportion visible
Vertical Angle
Lateral Angle
Focus/sharpness
Exposure

Error checking and correction
Identification of null (non-amplified) alleles
Excluded loci with high error rates
All genotypes differing by over 4 loci considered ‘different’- every 4/5 loci mismatch evaluated case-by-case
Use haplotype information as additional comparative data

Previous abundance estimates

- Non QC fluke Photo-IDs 1999-2004
- 1148 sightings of 1021 individuals across Oceania
- Presented at Hobart IWC Comprehensive Assessment meeting in 2006 (Doc #SC/A06/HW51)

- Closed model (time and heterogeneity)
- Combined New Caledonia, French Polynesia, Tonga, Cook Islands
- N (2004) = 3827 CV 0.12

Analysis of recaptures

Fluke Photo ID- synoptic regions

	99	00	01	02	03	04
# I	108	124	132	114	150	110
Total I	108	226	338	434	551	627
	Year of recapture					
	99	00	01	02	03	04
99	X	6	13	5	8	6
00		X	7	8	10	10
01			X	5	7	8
02				X	8	2
03					X	8
04						X

#I: number of individual flukes captured
Total I: total individual flukes to date
X: Year of initial capture

Genotypes- synoptic regions

	99	00	01	02	03	04	05
# I	50	115	181	130	214	79	154
Total I	50	162	332	445	623	689	807
	Year of recapture						
	99	00	01	02	03	04*	05
99	X	3	7	3	6	2	2
00		X	4	5	9	3	6
01			X	9	17	4	8
02				X	4	2	8
03					X	2	8
04						X	4
05							X

* No data from Tonga this year

Analysis of recaptures

Genotypes- males

	99	**00**	**01**	**02**	**03**	**04**	**05**
# I	25	70	112	78	114	24	82
Total I	25	92	197	265	358	377	**436**
	Year of recapture						
	99	00	01	02	03	04*	05
99	X	3	4	0	3	0	1
00		X	3	3	6	2	6
01			X	7	10	2	5
02				X	2	0	4
03					X	1	5
04						X	2
05							X

Genotypes- females

	99	**00**	**01**	**02**	**03**	**04**	**05**
# I	25	41	58	45	76	26	51
Total I	25	66	120	158	219	228	**277**
	Year of recapture						
	99	00	01	02	03	04*	05
99	X	0	3	3	3	2	1
00		X	1	2	3	1	0
01			X	2	7	2	3
02				X	2	2	4
03					X	0	2
04						X	2
05							X

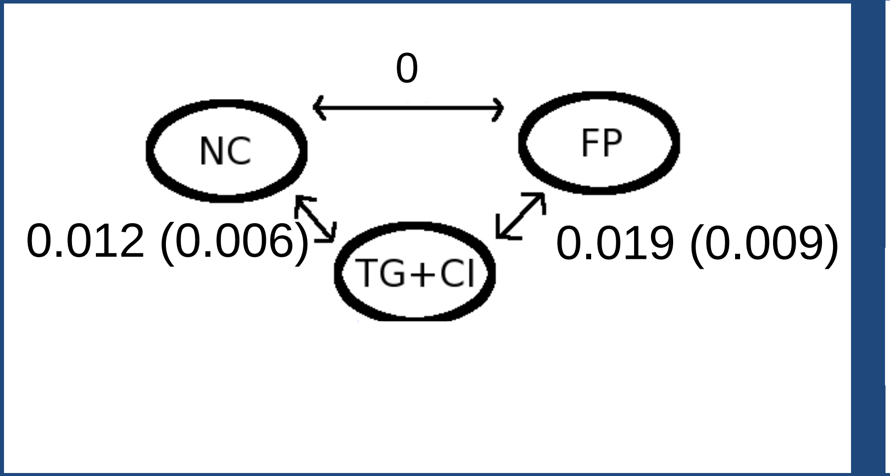
#I number of individual flukes
Total I total individual flukes to date
X Year of initial capture

Sex ratio: 1.57: 1 males : females

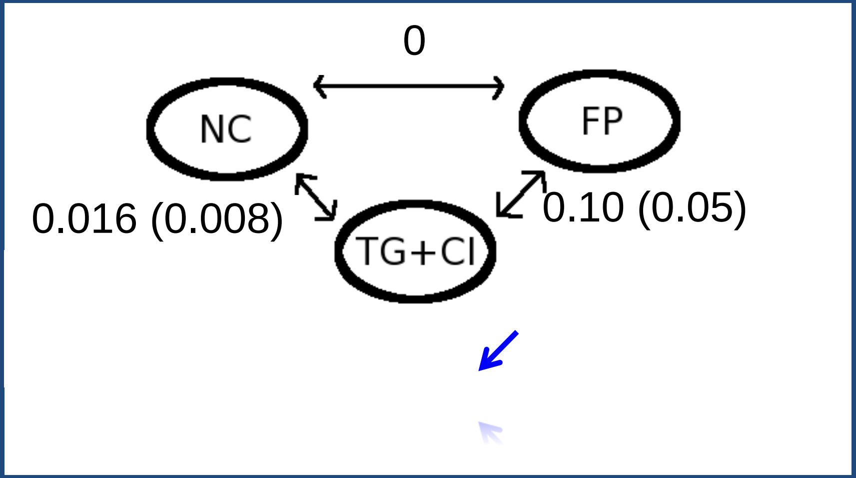
* No data from Tonga this year

Movement rates between regions: Multi-strata models (Ψ)

Photo-ID



Genotype



- Slightly higher movement probabilities from genotype dataset
- Estimated movement probabilities are similar between NC and other regions for datasets (all $p < 0.02$)
- Differing (but non significant) sex-specific movement rates between TG/CI and FP

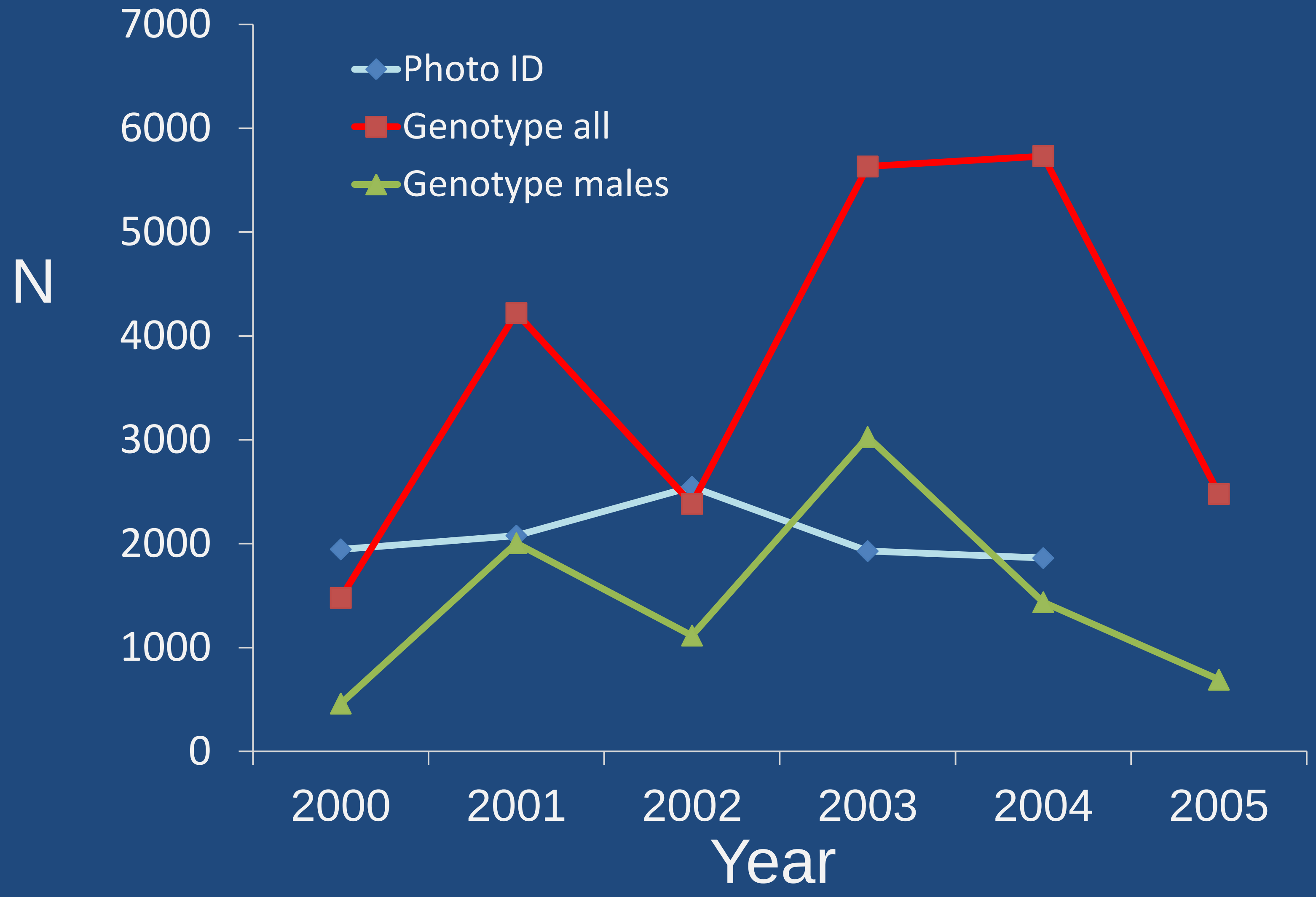
Ψ probability of movement between regions, conditional on survival

Is Oceania a 'closed' population?

- Closure assumes births, deaths, immigration and emigration are negligible
- Survey area and effort constant over time
- Some evidence of occasional movements between east Australia/Colombia
- Data collected over 6/7 years, are births really negligible?

- Test for trends in abundance (PRADEL)
  - Photo-ID
    - λ = 1.09, CI 0.08-0.15
    - Φ = 0.96, CI 0.39-1.00
  - Genotype
    - λ = 0.97, CI 0.26-1.00
    - Φ = 0.92, CI 0.62-0.99
  - Not significantly worse fit to the data than no trend
- Specific closure tests (Stanley and Burnham 1999)
  - Not significant
- NO significant closure violations

Lincoln-Petersen estimates of N: large variability in genotype data



CLOSED MODELS: exploring the impact of time, heterogeneity and behaviour after capture

- Closed models assume capture probabilities not biased by variable effort
- Parameters p (capture), c (recapture) and additionally π (mixture)

- **Mt**: p varies over time, i.e. p1-p6 over 1999-2004

- **Mh**: p varies across the population, i.e. proportion π_A of the population has p_A, proportion π_B has p_B

- **Mb**: p and c differ.

“Best” closed and open models

- •Minimum AIC values- fit of model to data, penalized by number of parameters
- •Model averaging: models weighted by AIC support levels, estimates of abundance also similarly weighted across models

Photo ID	Genotype
With heterogeneity	
N: 1417 CV 0.13	Nm: 1409 CV 0.11 Nf: 889 CV 0.13
No heterogeneity	
N: 1337 CV 0.14	Nm: 1457 CV 0.09 Nf: 929 CV 0.09
Mh Jacknife	Mth Chao
N: 1808 CV 0.04	Nm: 2202 CV 0.15 Nf: 1045 CV 0.17
POPAN: all individuals present in the ‘super’-population	
N: 2039 CV 0.10	Nm: 1657 CV 0.12 Nf: 1013 CV 0.12

What is the true abundance?

- Photo-ID < genotype abundance estimates, but no known error contribution

•Significant signal of ‘transience’ in both photo ID and male genotype datasets: excess of first captures that are never recaptured. Much stronger in genotype dataset

•Significant ‘trap-shy’ effect detected in female (and overall) genotype dataset, marginally ‘trap-happy’ effect in photo-ID data

Direction of Bias in N

Photo	Genotype
+	+
−	+

Conclusions

1. If females are trap-shy of biopsy sampling, recapture rates of females are biased low, therefore total (and female) genotype abundance may be biased high

N = 3827 CV 0.12

1. Effect does not explain skewed sex r to be captured in order to exhibit trap shy effect

2. Male 'transience'- recaptures biased low and therefore total genotype abundance biased high. No strong differences in sex specific movement rates for multi-strata models. Transience may also explain lower estimates of survival (0.92) from genotype data... but where are they going and should they be excluded?

Is POPAN best?

Nm: 1657 CV 0.12 Nf: 1013 CV 0.12

Onward to the Oceania population assessment...

	2009	2010
Corrected catch record and allocation of catches to ‘stocks’	✓	
Current abundance		Incorporate encounter histories – directly estimate abundance and trend
Trend information (east Australia)- none discernable in Oceania		
Stock structure	✓	
Number of haplotypes (*Nmin*)	✓	

Questions of interest

- How many whales were there prior to whaling?

- How fast is their population growth?

- How strongly are they recovering?

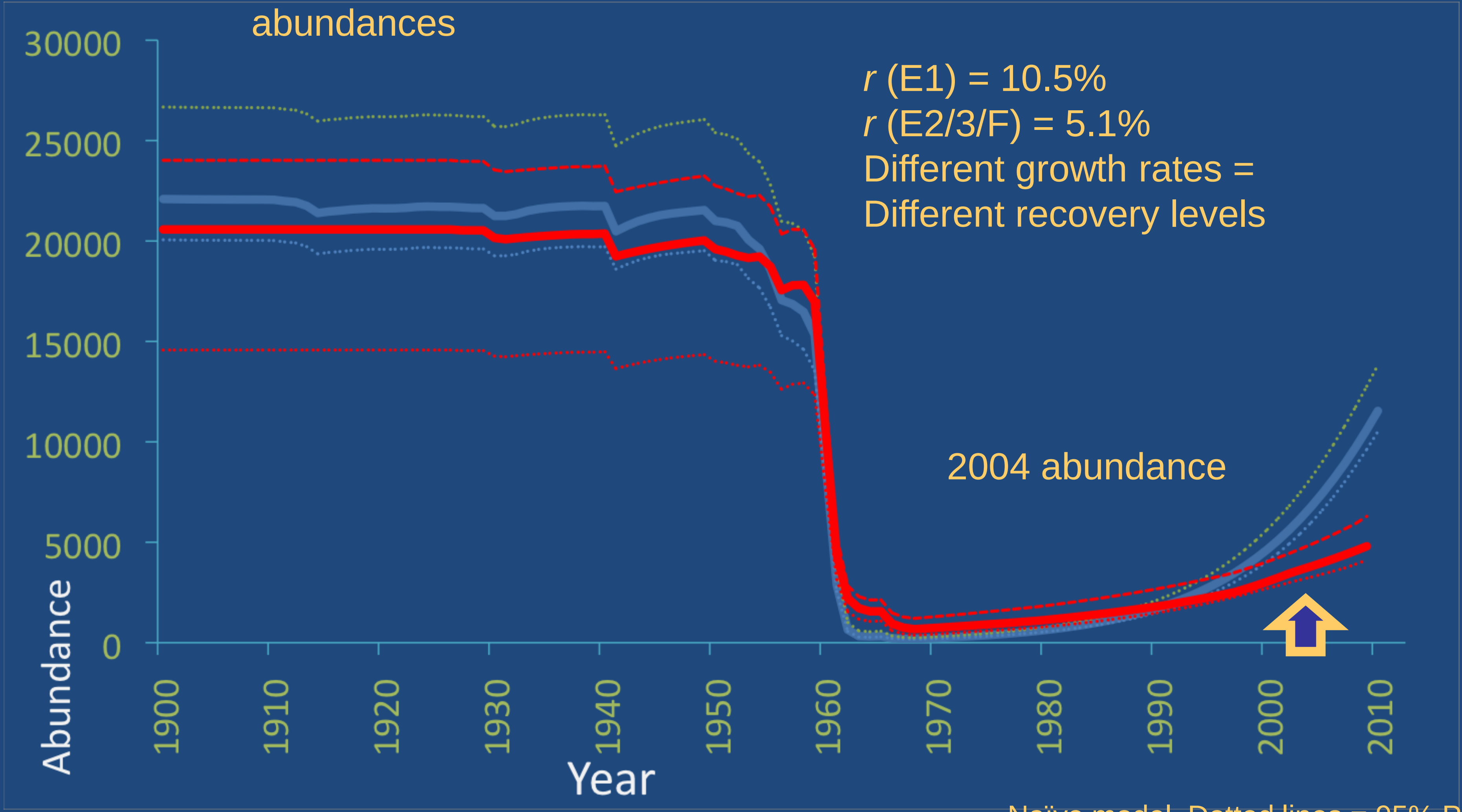
New two-stock population model

- Bayesian Logistic ‘HITTER’ model - to ‘hit’ using appropriate mark recapture model of abundance

- Trend weighted by Mark Recapture data

- Age and sex aggregated
- Density-dependent catch allocation between stocks
- Constrain minimum abundance (N_{min}) using surviving maternal lineages (mtDNA haplotypes, Jackson et al 2007)

Population reconstruction for east Australia (red) and Oceania (blue)



Similar pre-exploitation abundances

r (E1) = 10.5%
r (E2/3/F) = 5.1%
Different growth rates = Different recovery levels

2004 abundance

Naïve model, Dotted lines = 95% PI

Population assessment of south Pacific humpbacks

- How many whales were there prior to whaling?
  - East Australia: 22,000-25,700
  - Oceania: 17,800-20,600
- How fast are these populations growing?
  - East Australia: 10.4-10.5% PA
  - Oceania: 5.1-6.4% PA
- What is the current level of recovery (2009)?
  - East Australia: 44-46%
  - Oceania: 23-30%

Next Steps

Mark recapture models with transience – deriving N

SimSPLASH simulations: test the sensitivity of abundance estimates to behavioural effects

Incorporate abundance model into population dynamic framework

Comprehensive Assessment for IWC 2012

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