Genetic bottlenecks and historical population estimates of Southern Hemisphere baleen whales

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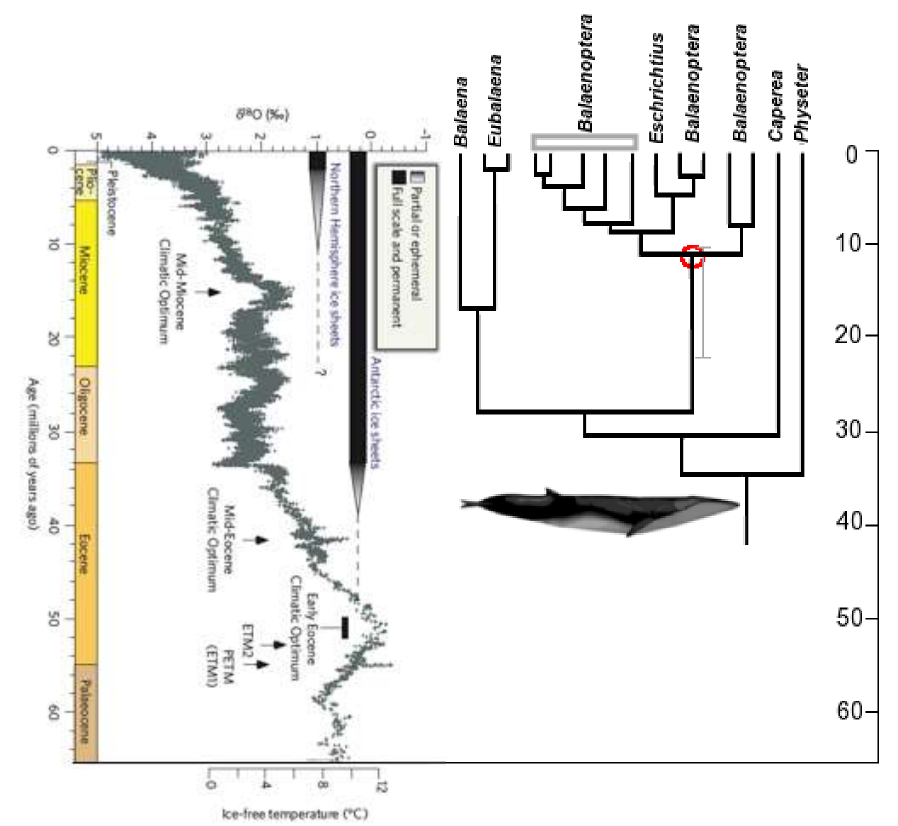
Molecular time travel

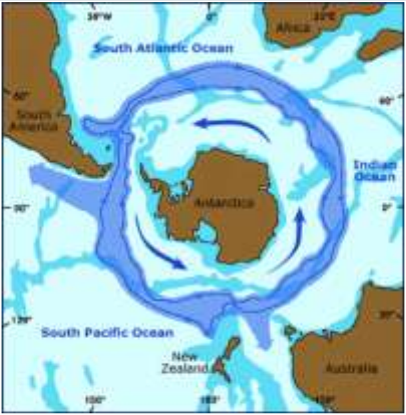
- Molecular tools for estimating:
  - long term population sizes (deep time)
  - minimum abundance during recent whaling bottlenecks (last 200 years)
  - Population dynamic changes in the future

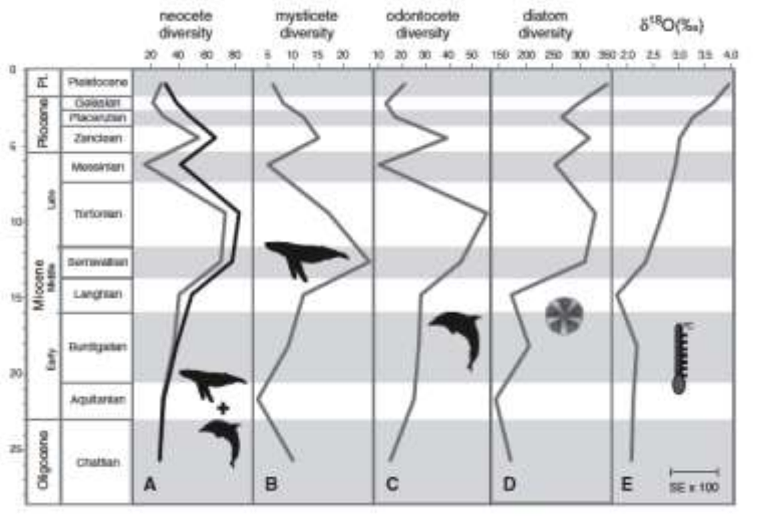
- Focus: humpback whales, blue whales, minke whales and southern right whales

Baleen whales and the Southern Ocean: a long history



Zachos et al. 2008 Fig 2.
Nature, **451**, 279-283

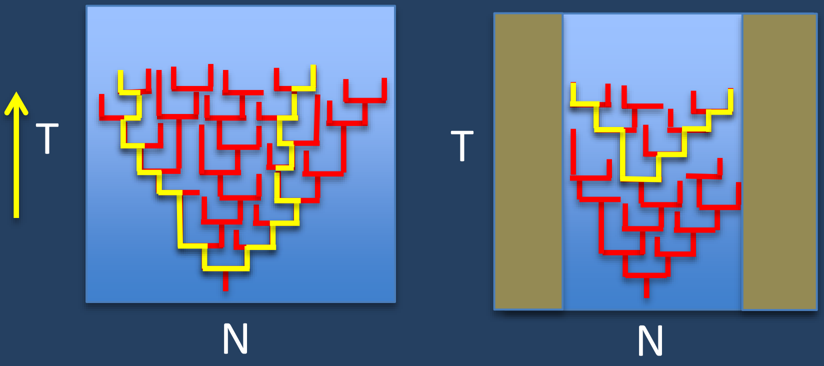




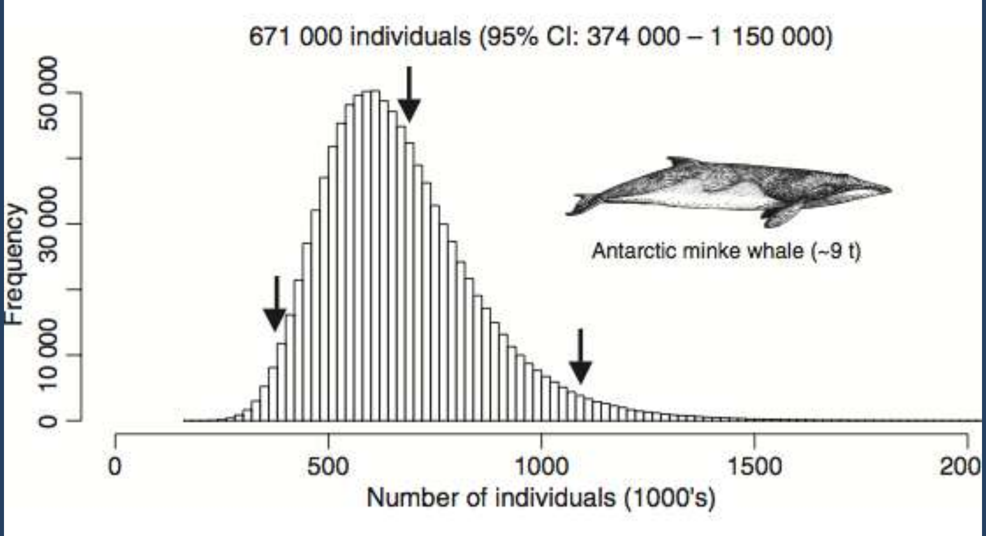
Deméré et al. (2008) Syst Biol **57**, 15-37, Fig 1
Marx and Uhen (2010) *Science* **327**, 993-996, Fig 1

Genetic diversity relates to long-term abundance

Genetic lineages through time



Diversity Θ measures the genetic distance among individuals in the population. Large Θ = large historical abundance $\Theta = 4Ne\mu$



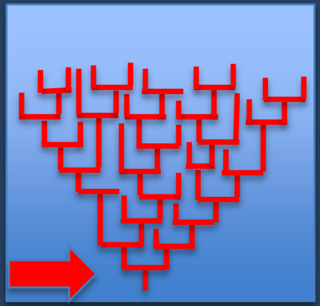
- Nucleotide diversity (accounting for population subdivision)
- Genetic substitution rate μ
- Generation times

$\Theta = 0.0071$, $\mu = 4.54\times10^{-10}$ bp / year
generation time= 17.65 years

Ruegg et al. Mol Ecol (2010) 19, 281–291

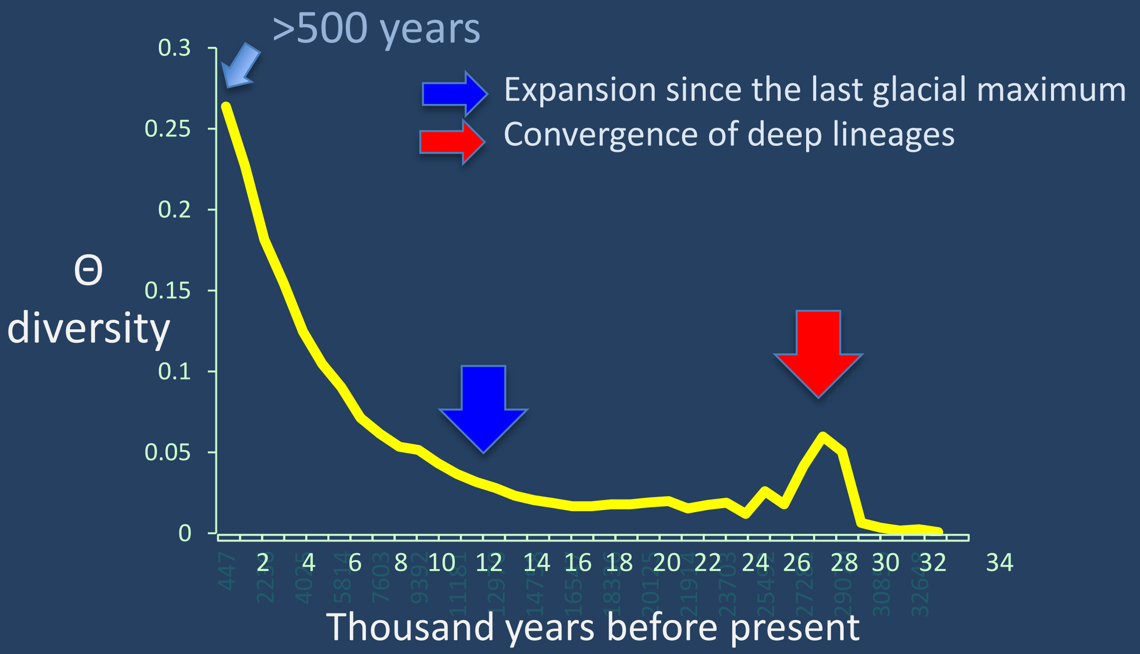
Population changes through time

- Molecular estimates of diversity can also contain signals of rapid past population change



- Segregated from northern ocean diversity
- ≈2,800 mitochondrial DNA control region sequences
- μ = 5.2% per million years
- Generation time 21.5 yr
- MIGRATE Bayesian analysis

Molecular ‘skyline’ of Southern Hemisphere humpback Θ diversity through time



20th century kills of Southern Ocean-associated baleen whales

Antarctic blue [a]	346,000
Pygmy blue [a]	13,000
Sei [b]	208,000
Fin [b]	723,000
Humpback [c]	220,000
Southern right [d]	>5,000
Minke [b,e]	117,000

H. Omura in Clapham, Modern Whaling 2001

[a] Branch et al. IWC SC/60/SH9, [b] Clapham and Baker 2001, [c] Allison IWC catch database, [d] IWC Comprehensive assessment of southern right whales, [e] IWC special permit catches 2001-2012

19th century baleen whale kills

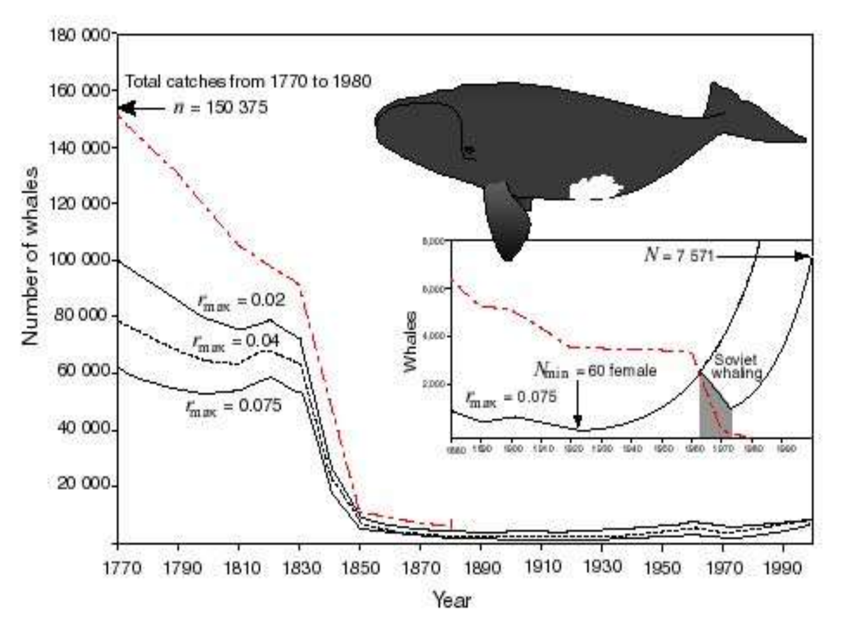
Species	Net: 1600s	Basque style: 1050s	American style shore: 1600s	American style pelagic: mid 1700s	Norwegian style shore: 1860s
Blue					SA, IO
Sei					SA, IO
Fin					SA, IO
Humpback	NZ	Brazil	Australia, Chile, Equatorial Guinea, Mozambique, New Hebrides, New Zealand, Norfolk Island, Tonga	SA, SP, IO	SA, IO
Southern right		Brazil, South Atlantic	Australia, Chile, New Zealand, South Africa	SA, SP, IO	

Reeves and Smith (2006) A taxonomy of world whaling *in* Estes et al. *Whales, whaling and ecosystems*

Genetics can aid population assessments of baleen whales

- Tool for individual ID, also sex specific abundance estimates
- Population mixing (i.e. assignment)
- Haplotype diversity relates to minimum bottleneck size (i.e. number of maternal lineages)

Population dynamics models are used to understand how whale abundance has changed in response to whaling



Baker and Clapham 2004, from IWC 2001 Comprehensive assessment of southern right whales

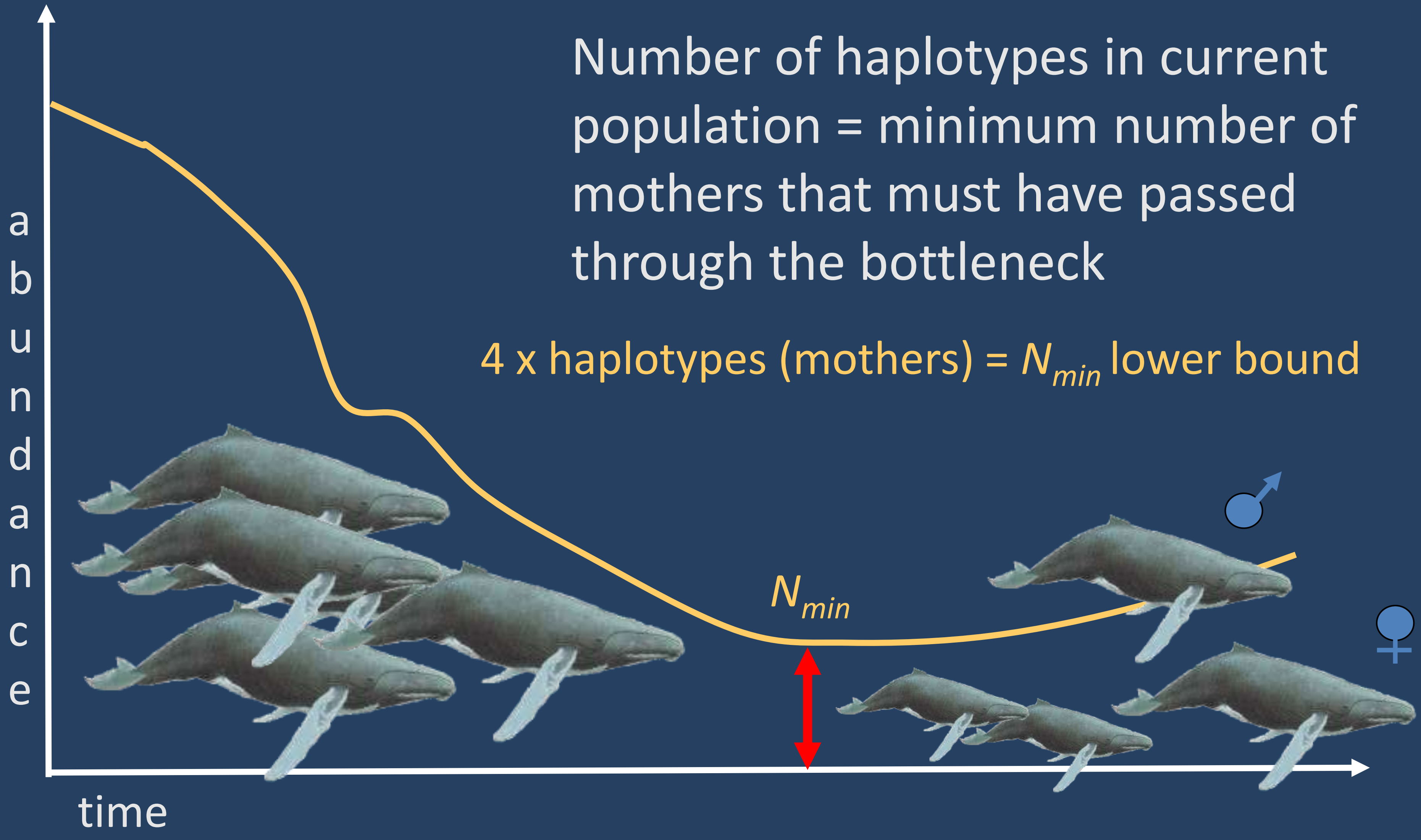
Logistic population models (HITTER and FITTER)

- Current abundance
- Trend in abundance
- Catch history
- Minimum bottleneck abundance
- Population sub-structure

Population model finds the initial (pre-exploitation) abundance value that most closely ‘fits’ the estimated trend and current abundance

Assumes static carrying capacity through time

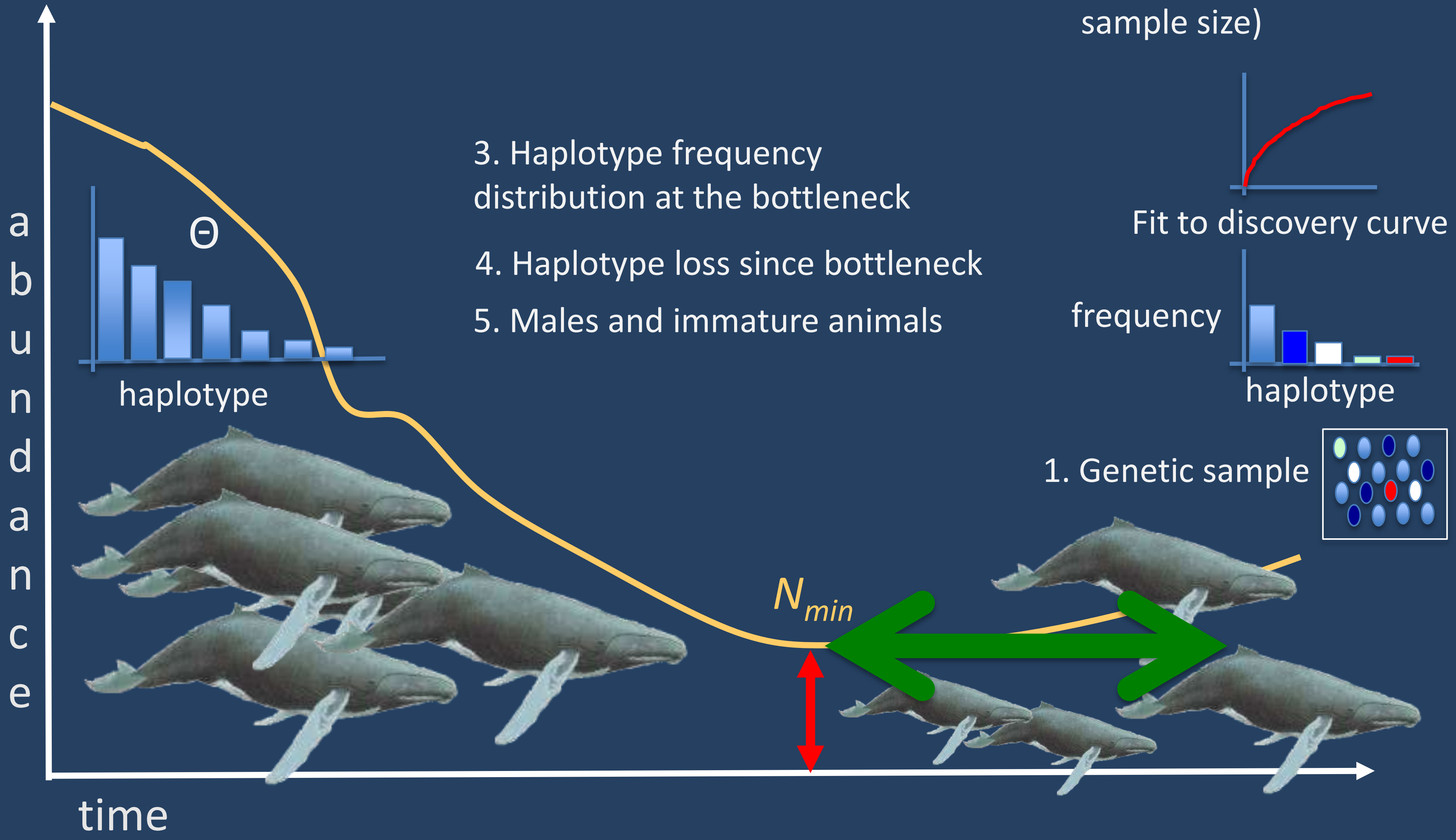
N_{min} derived from mitochondrial lineages (‘haplotypes’)



Number of haplotypes in current population = minimum number of mothers that must have passed through the bottleneck

4 x haplotypes (mothers) = N_{min} lower bound

Estimating bottleneck size



1. Genetic sample

2. Population sample (sequence length, sample size)

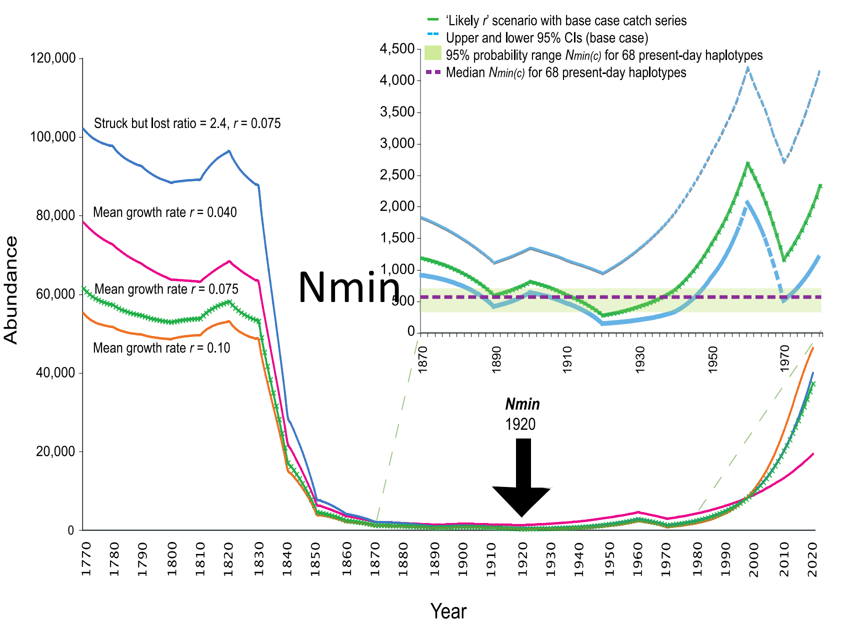
3. Haplotype frequency distribution at the bottleneck

4. Haplotype loss since bottleneck

5. Males and immature animals

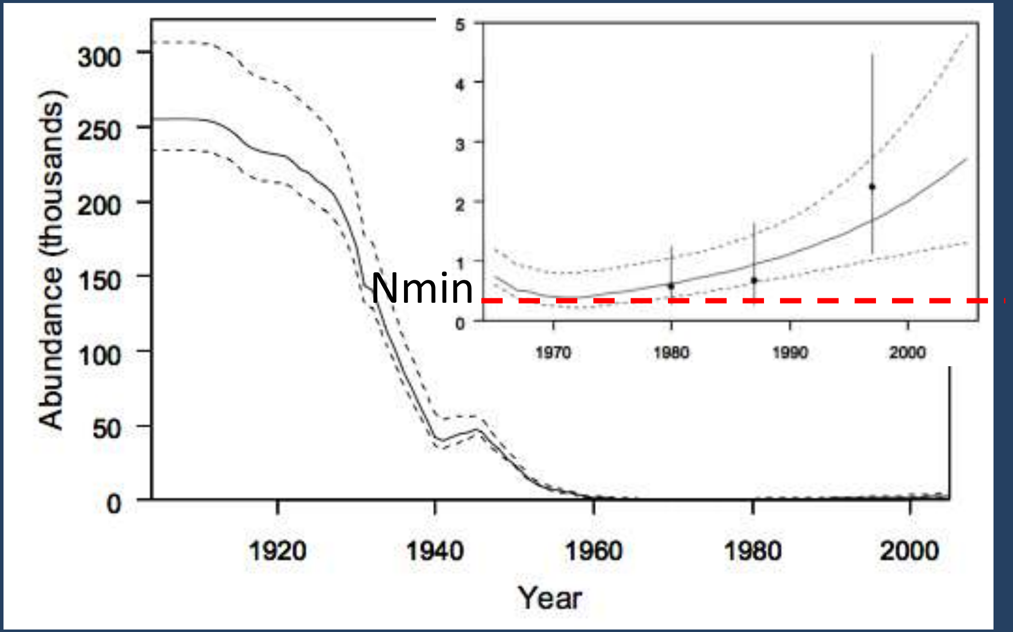
Southern right and Antarctic blue whales: less bottlenecked?

Haplotyes = 38 -> Nmin = 524



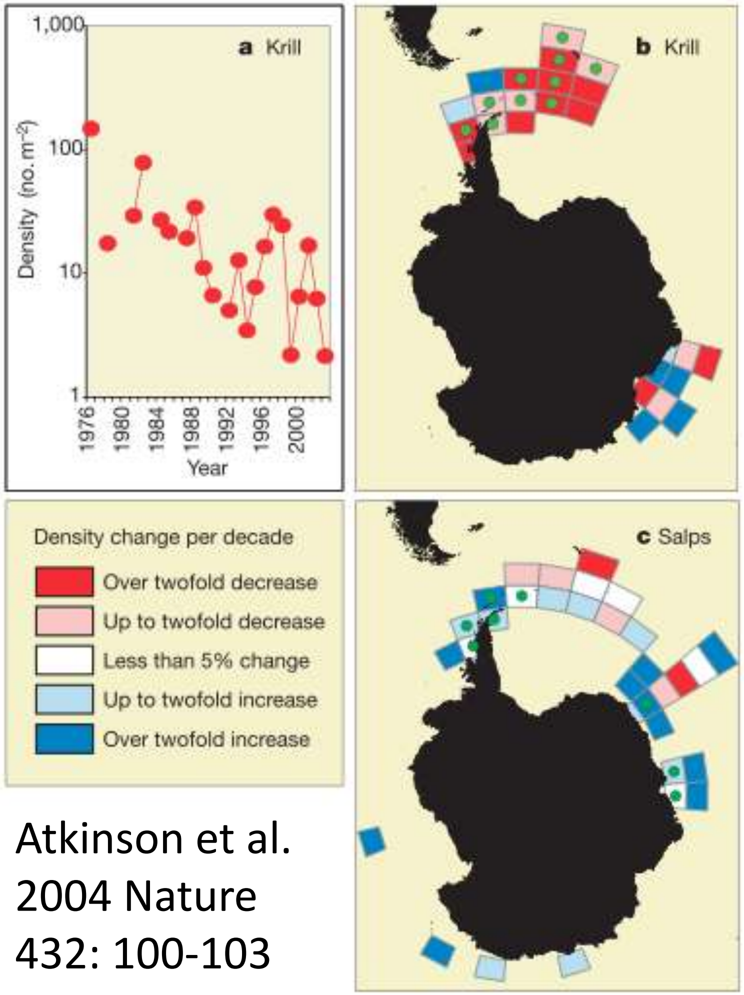
Southern right whales: IWC et al. (2001), Jackson et al. (2008) Mol Ecol 17, 236-251. Jackson et al. (2009) Mol Ecol 18, 4134-4135.

Haplotyes = 26 -> Nmin = 214



Branch (2008) IWC SC/60/SH7, Branch and Jackson (2008) IWC SC/60/SH10…. But see Sremba et al. 2012 PLoS One 7(3) e32579 as haplotypes = 52

Into the future: changing carrying capacity in the Southern Ocean?



Atkinson et al. 2004 Nature 432: 100-103

H. Omura in Clapham, Modern Whaling 2001

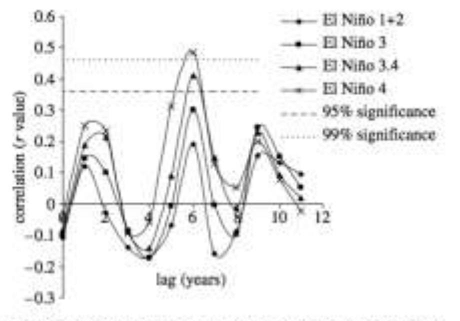


Figure 2. Correlation between deviation from expected calf output and lagged, mean June–May, El Niño SST anomalies, calving years 1971–2000.

Genetics to monitor future change

Genetic ‘baselines’ for large baleen whales complete or under way: humpbacks, blues, southern rights, minkes, fins

Population genomic markers: rapid evolution, detection of change in population abundance and connectivity over time, e.g. mark recapture, mixed stock analysis

Biopsy samples have multiple downstream uses, e.g. prey isotopes, pollutant measures, pathogen loads

Acknowledgements

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