

# Estimating the historical size of the southern resident killer whale population

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# Why do we want to know?

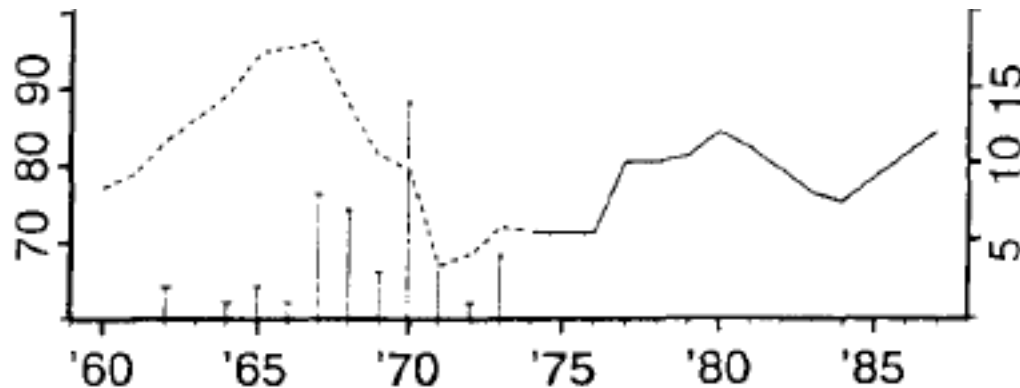
- Panel question:
  - Perhaps the SRKW population has always been small?
  - How does the density of SRKW compare to the densities of KW in other areas – NRKW, Alaska, other?
- Context for recovery goals
- Context for carrying capacity question

# Ways of addressing this question

- Reconstruct largest known size of population
- Compare to size range and 'density' of other killer whale populations
- Estimate parameters from population genetic models

# Reconstruct largest known size of population

- Population size in 1974 = 71
- Peak size reconstructed from life-tables = 96 (in 1967). (Obs peak size of 97 in 1996)
- 5 captures from 1962-1966
- = 101 whales if all captures had lived
- Wiles (2004) obtained a similar number (117) by adding all captures to population size in 1971



Olesiuk et al 1990

# Compare to size range of other killer resident whale populations

Whales/1000 km<sup>2</sup>

– SR: 0.9

– NR: 1.7

– SE AK R: 0.9

– SAR R: 10.7

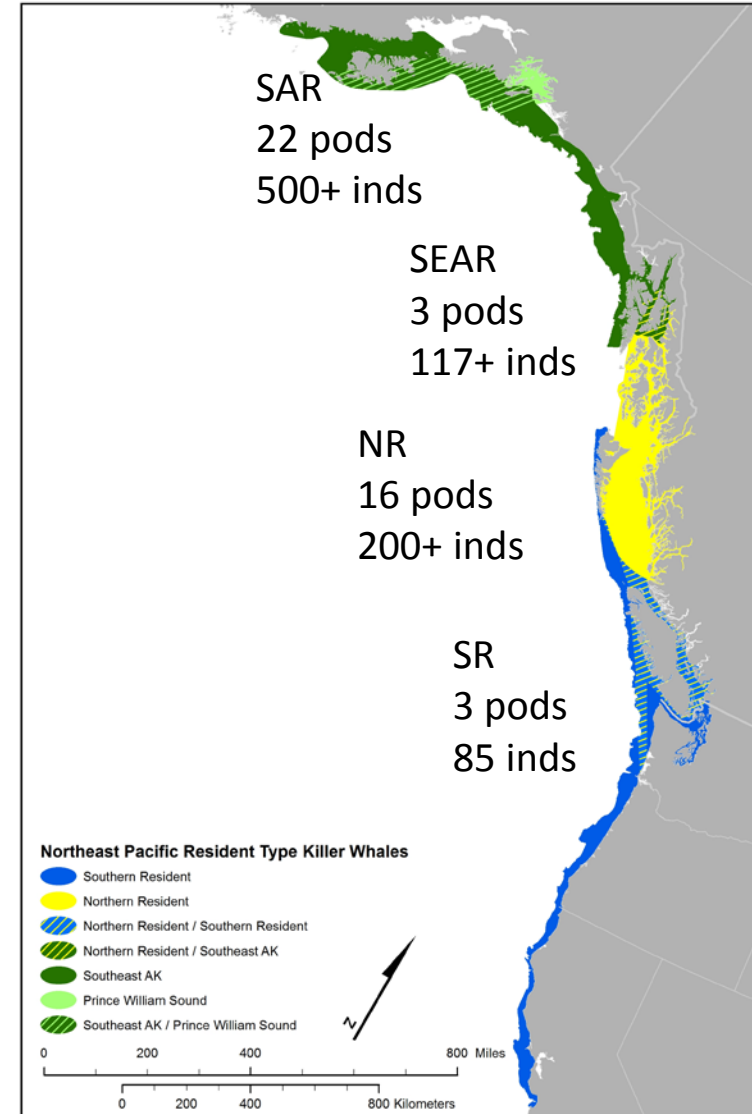
– Kenai/E Aleutians:  
6-29 \*

– Norway 6.1-6.5

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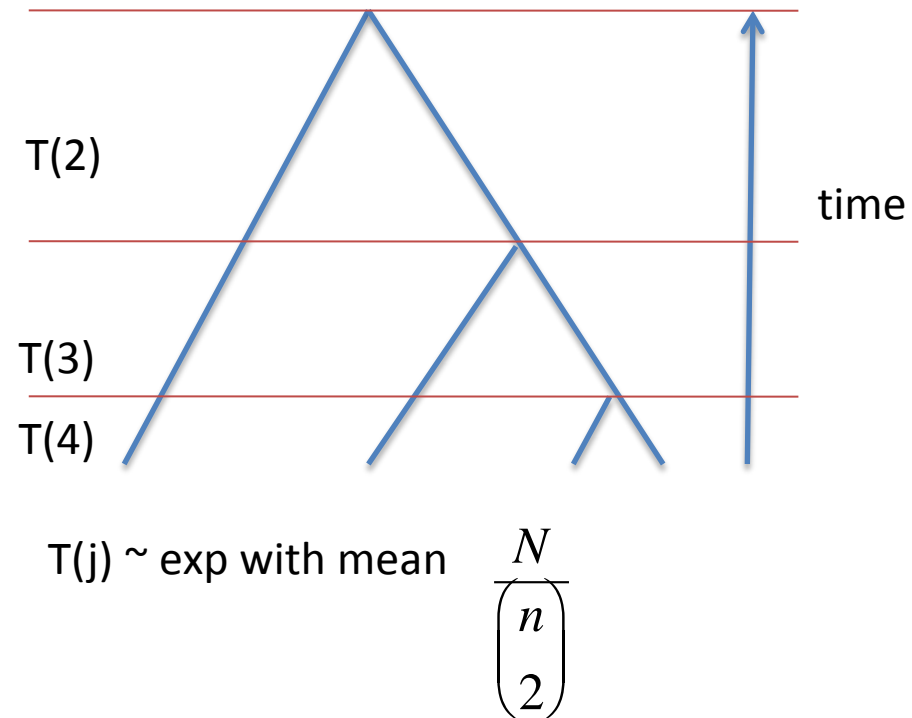
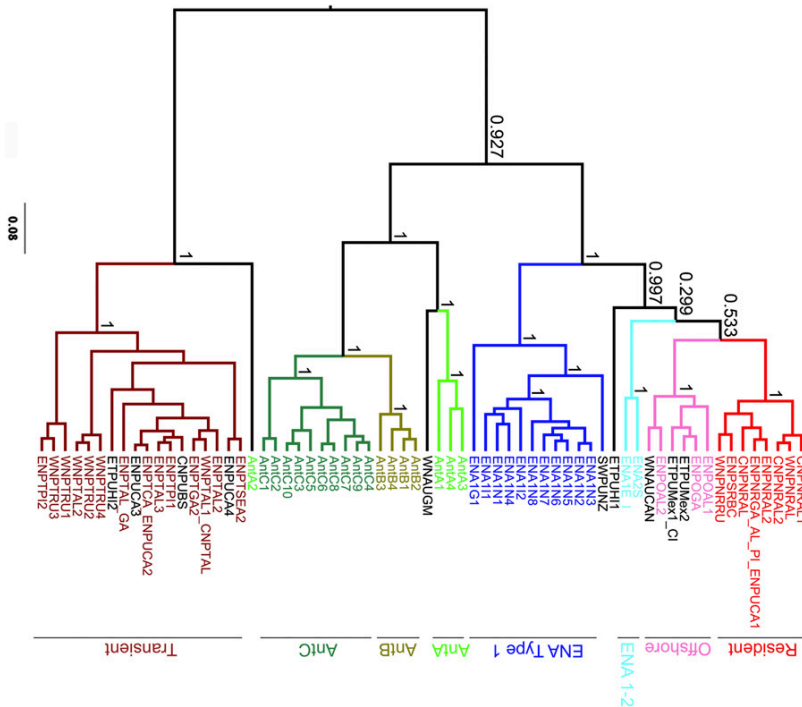
\* Zerbini et al. Mar Biol (2007)

\*\* reviewed by Forney and Wade (2006)



# Estimate parameters from population genetic models

- Most models based on coalescent theory:

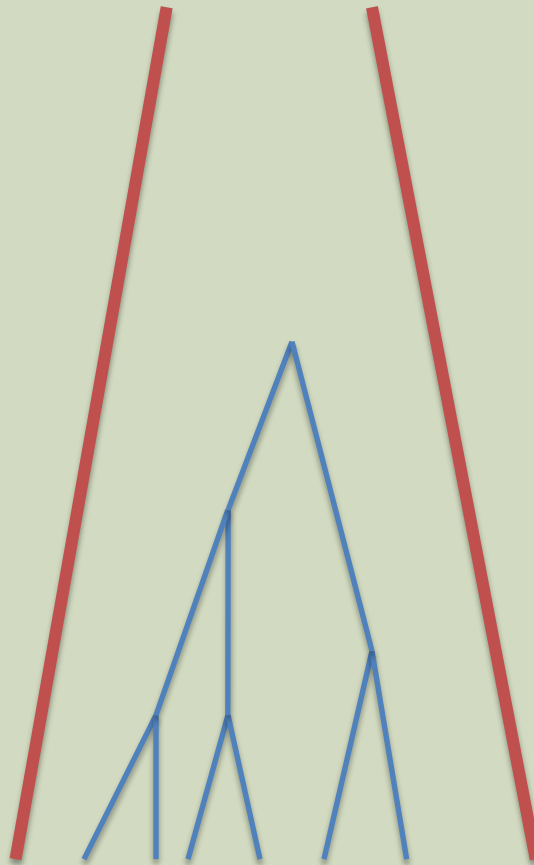


# Gene trees changed by changing population size

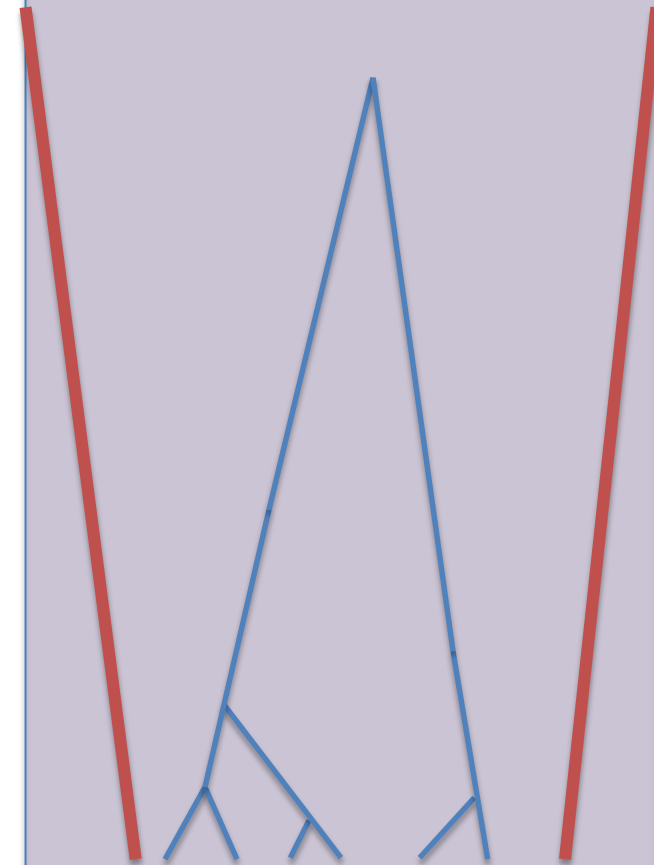
Constant population



Expanding population

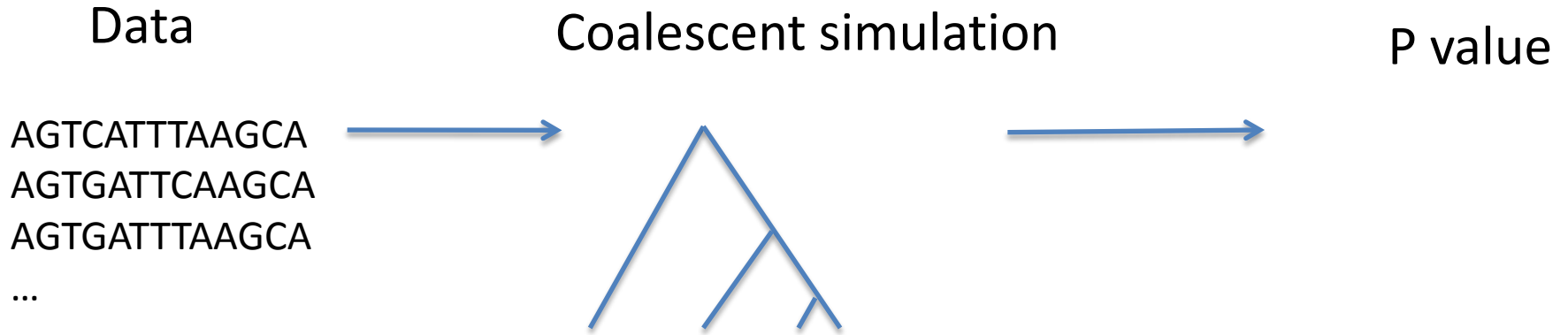


Contracting population



# Two basic modeling approaches

Hypothesis testing (e.g, Cornuet and Luikart 1996, Tajima 1986)

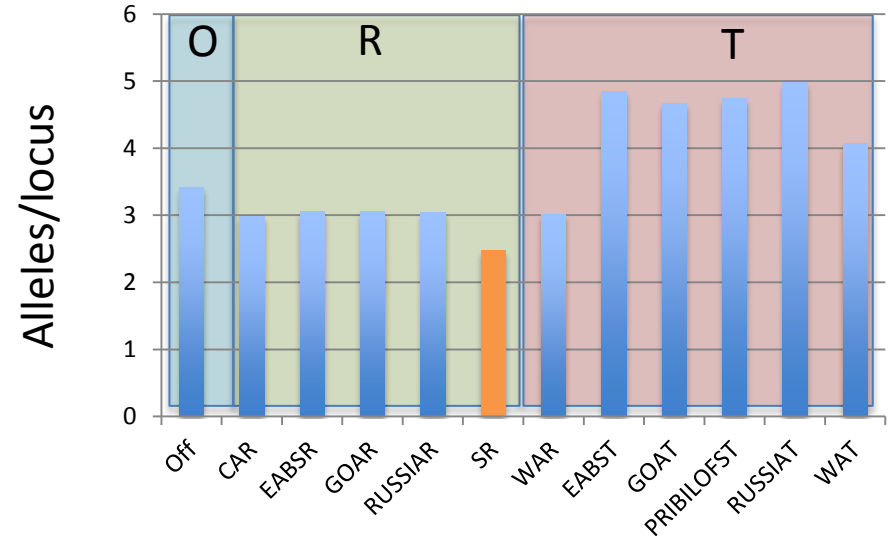
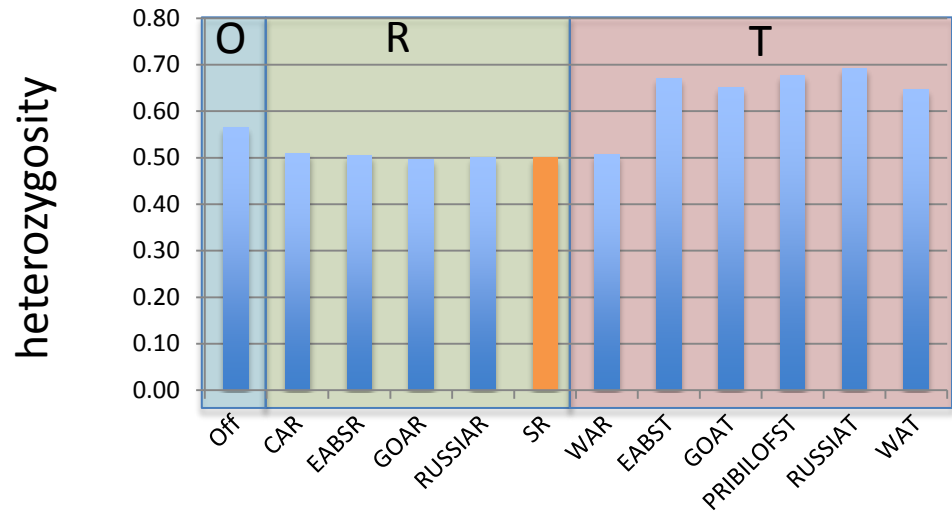


Parameter estimation (e.g. Hey & Nielsen 2007, Drummond et al. 2005)





# Results – hypothesis testing

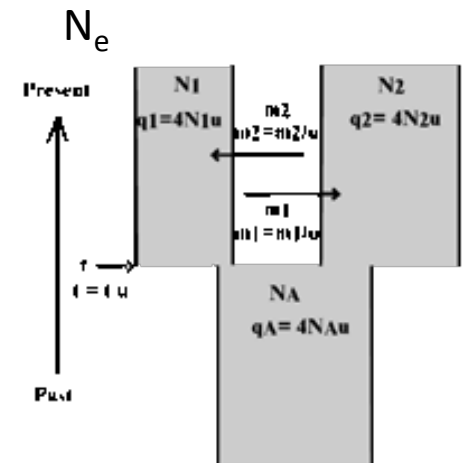
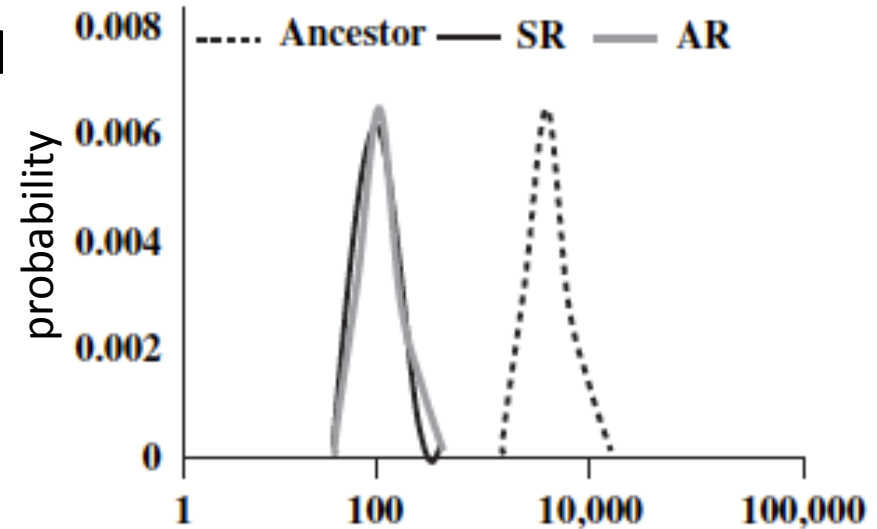


Southern residents have same heterozygosity as other residents, but fewer alleles.

- BOTTLENECK method (Corneut and Luikart 1996)
  - Allele frequencies more intermediate than expected by chance (highly significant)
  - Consistent with population bottleneck
  - No information on timing, but  $\gg 1$  generation ago
  - Other populations do not generally show this pattern

# Parameter estimation methods

- Two population models (Hoelzel et al. 2007)
  - 30-40X smaller than ancestral population
  - Similar pattern for all populations
  - Timing 10,000s of years
  - Conclusion: estimating size of an very ancestral population – not historical size of the SRKWs
- Single population models (Ford, preliminary)
  - Somewhat similar results
  - Population reduction time estimate more recent (4-10 generations ago)
  - Population size estimates poorly defined



Ima2 model - Hey and Nielsen 2007

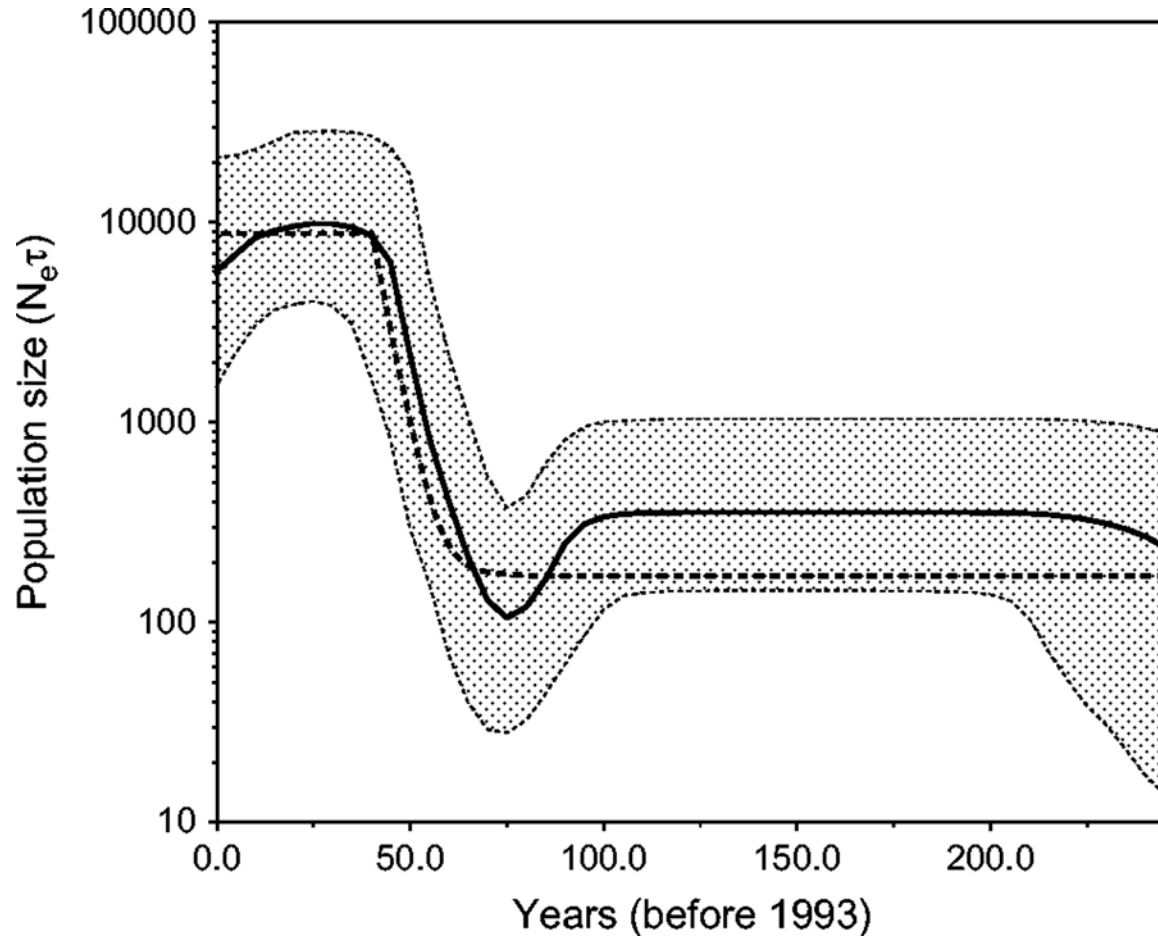
# Summary

Years ago	Generations ago	Approx Population size	Comment
0-40	0 - 3	71-100	Current/recent size
100-300	5-15	Bigger	BOTTLENECK results
10,000-40,000	500 – 2000	6000 – 30,000	IMA results: Ancestral N Pacific Resident population

# New information / analysis

- Complete mtDNA genomes from all matrilineal lines (collaboration with Phil Morin, John Ford and others).
  - Much better bounds on the 'age' of the SRKW population
  - Potential for better historical size analysis
- New nuclear sequence
  - ~50,000,000 base pairs of sequence from 2 individuals (K13, J26)
  - 10,000+ variable sites
- Microsatellite models recently added to BEAST package (Wu and Drummond 2011)

# Bayesian Skyline Plot



Drummond A J et al. Mol Biol Evol  
2005;22:1185-1192