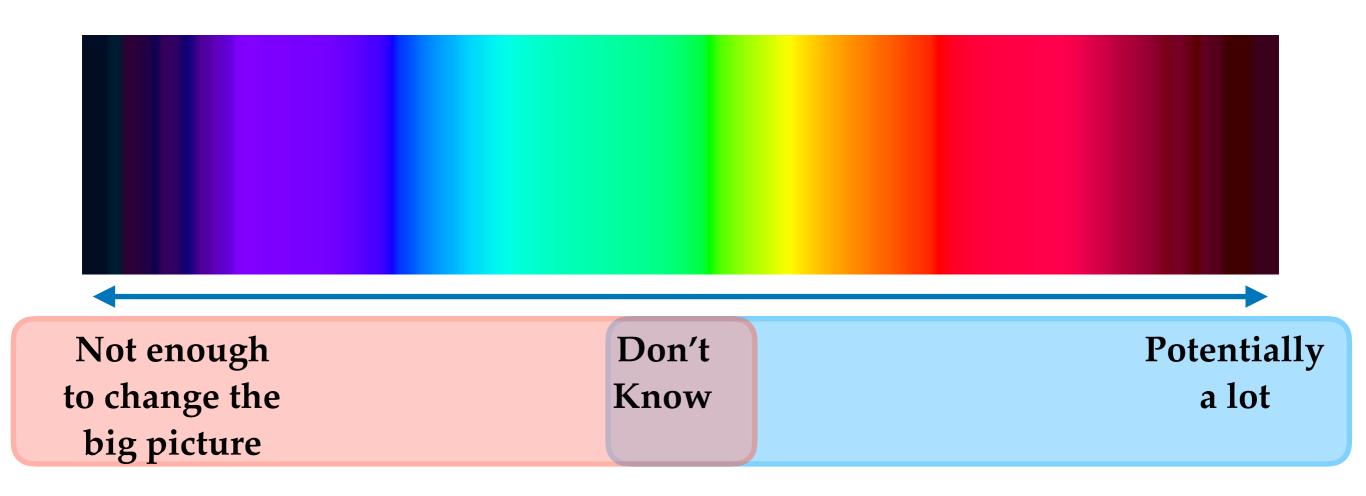
Pedigree-Informed Estimates of Abundance and Trends for the North Atlantic Right Whale

Timothy R. Frasier, *Kayla Fitzgerald*, Philip K. Hamilton, Moira W. Brown, Scott D. Kraus, Bradley N. White

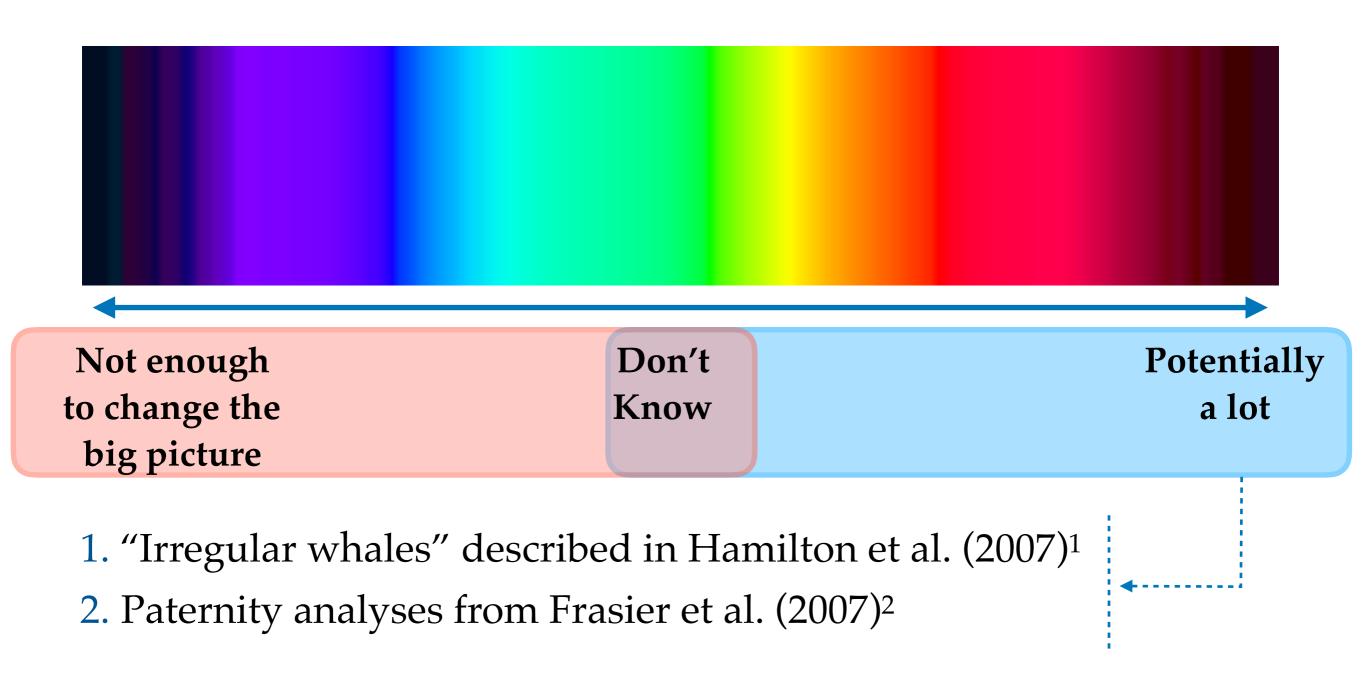
How Many North Atlantic Right Whales Are There?

- How "complete" is the photo-identification catalogue?
- How well do we understand distribution, movement patterns, and everything else?

How many individuals are not photo-identified?



How many individuals are not photo-identified?



- 1. Hamilton et al. (2007) p. 75-104 In: The Urban Whale (Kraus SD, Rolland RM, eds.) Harvard University Press.
- 2. Frasier et al. (2007) *Molecular Ecology* **16**: 5277-5293.

How can we incorporate the genetic inference of individuals in a statistically robust way?





Ecology and Evolution

Open Access

Using pedigree reconstruction to estimate population size: genotypes are more than individually unique marks

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²Zambian Carnivore Programme, Box 80, Mfuwe, Eastern Province, Zambia

$$\widehat{N} = N_s + N_{in} + N_{iv}$$

$$\widehat{N} = N_s + N_{in} + N_{iv}$$

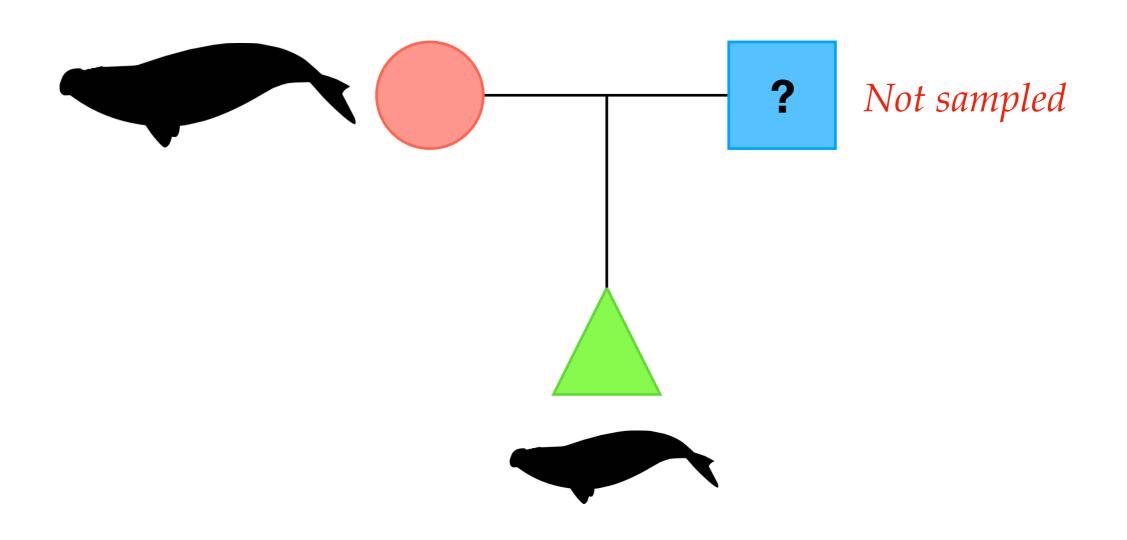
Number of individuals sampled

• Just a count

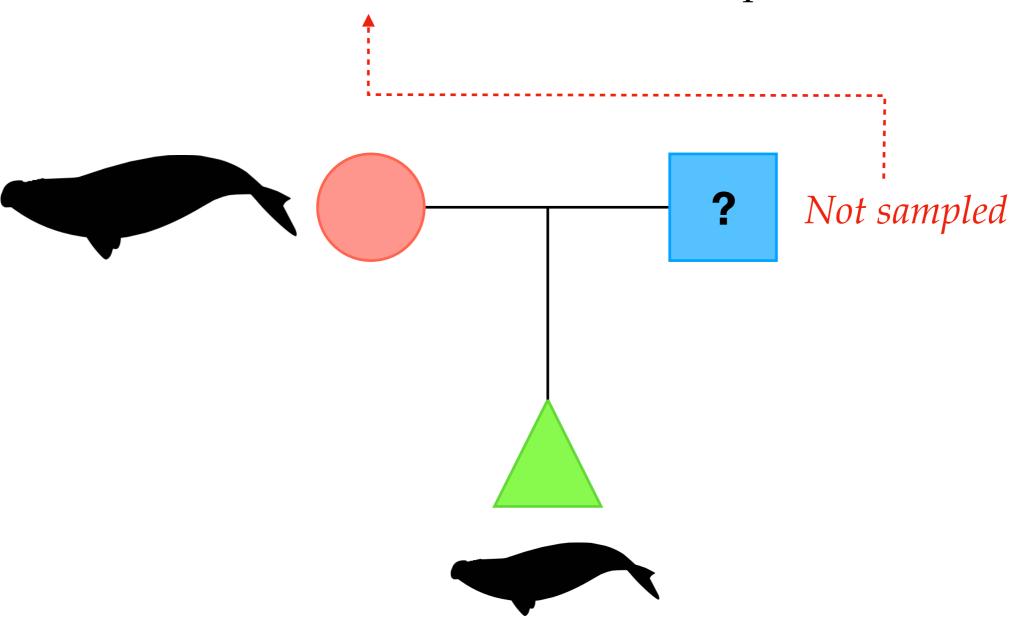
$$\widehat{N} = N_s + N_{in} + N_{iv}$$

Number of individuals inferred

- Based on pedigree data
- Also a count

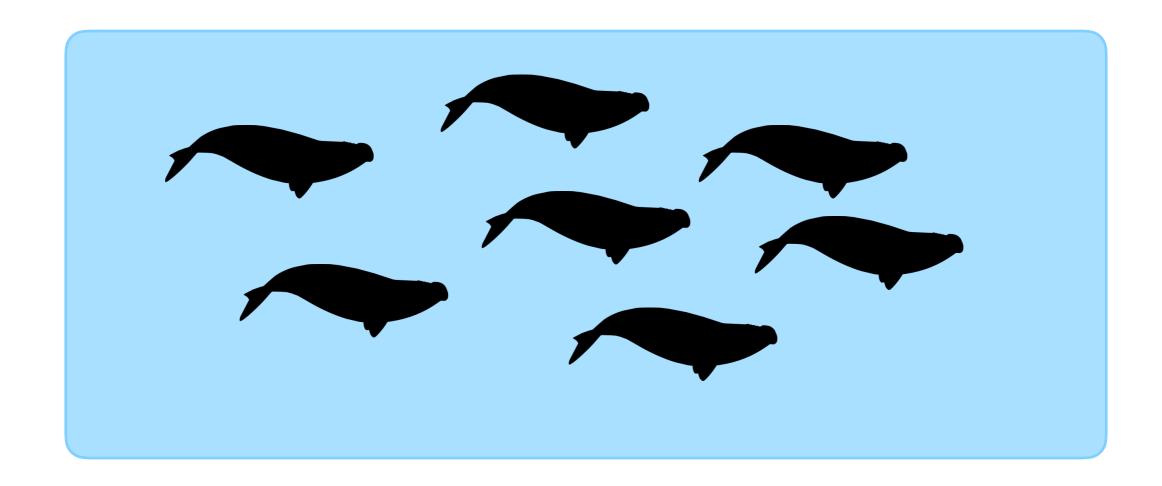


Infer 1 male? Not so simple



Calves without sampled fathers (suppose n = 7)

- DadShare by Bill Amos
- How related are they?
- How related would we expect them to be if:
 - Fathered by 7 males?
 - Fathered by 6 males?
 - etc?



$$\widehat{N} = N_s + N_{in} + N_{iv}$$

Number of individuals *inferred*

- Based on pedigree data
- Also a count
- Can be used to infer both males and females

$$\widehat{N} = N_s + N_{in} + N_{iv}$$

Number of individuals that are *invisible* to the pedigree analyses

- Where things get interesting!
- 1. Non-sampled non-breeders (N_{nsnb})
 - Adults that aren't sampled and haven't bred
 - Juveniles and calves that aren't sampled
- 2. Breeders who are not sampled and not inferred (N_{bnsni})

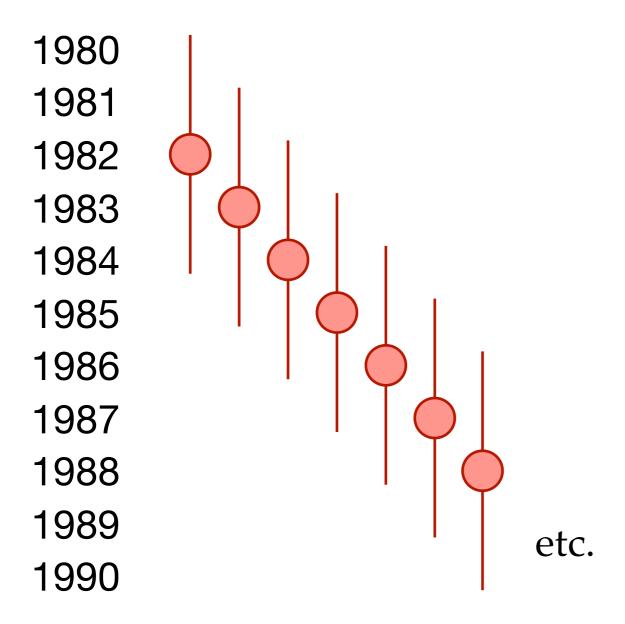
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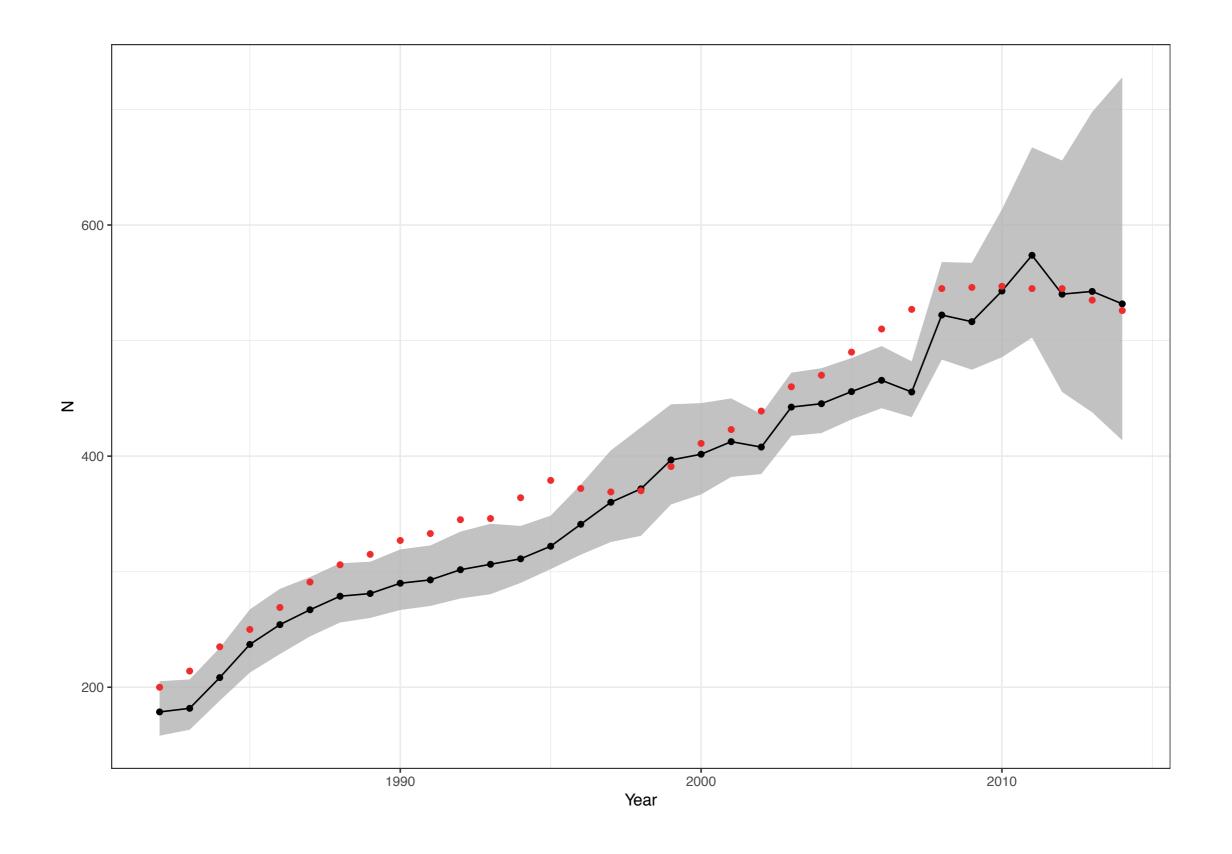
- Where things get interesting!
- 1. Non-sampled non-breeders (N_{nsnb})
 - Adults that aren't sampled and haven't bred
 - Juveniles and calves that aren't sampled
- 2. Breeders who are not sampled and not inferred (N_{bnsni})
- Require estimating:
 - Probability of being sampled ($P_{sampled}$) Bayesian estimation
 - Probability of being a breeder ($P_{breeder}$)

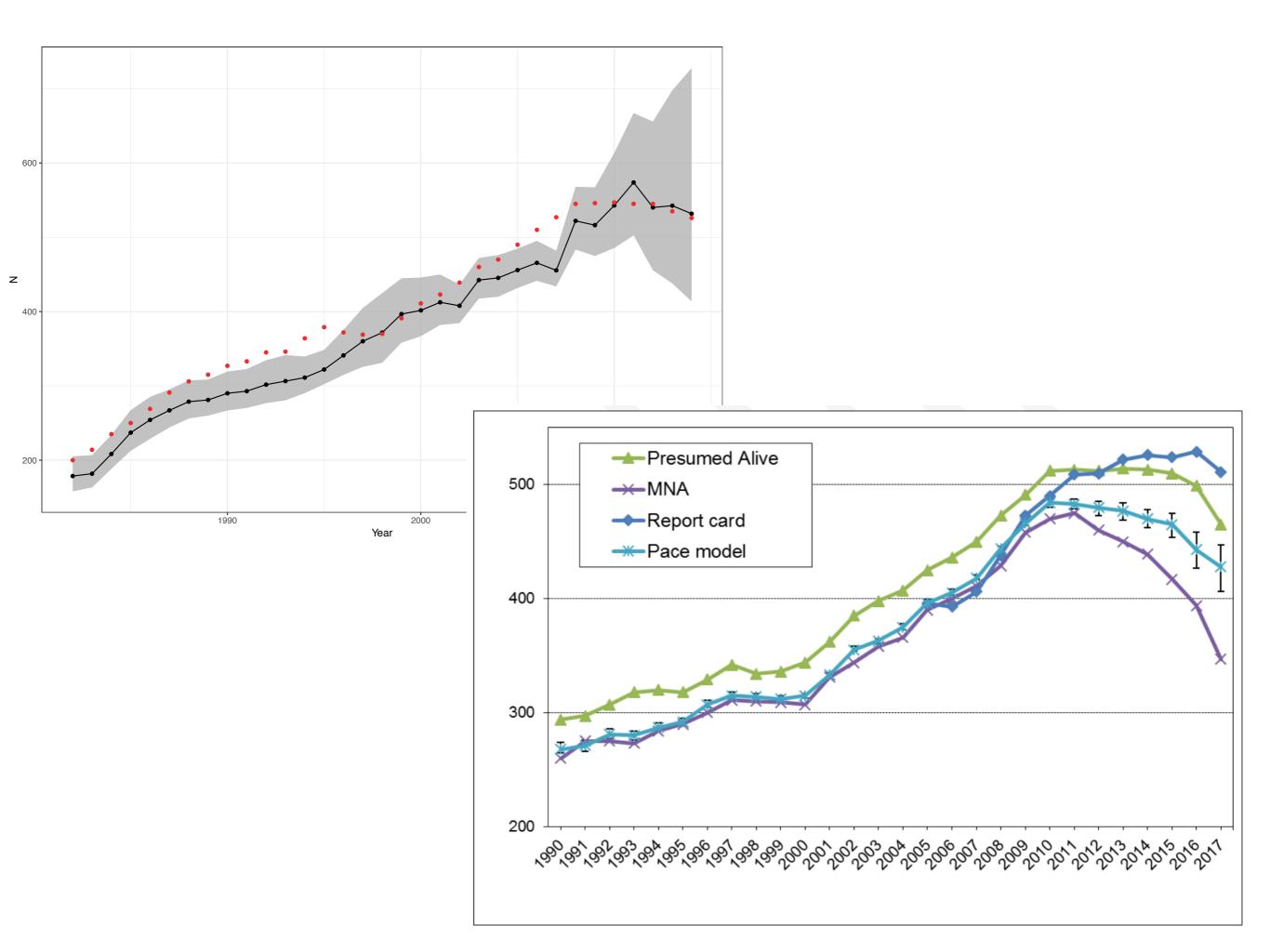
with Stan

Enough already, what about right whales?

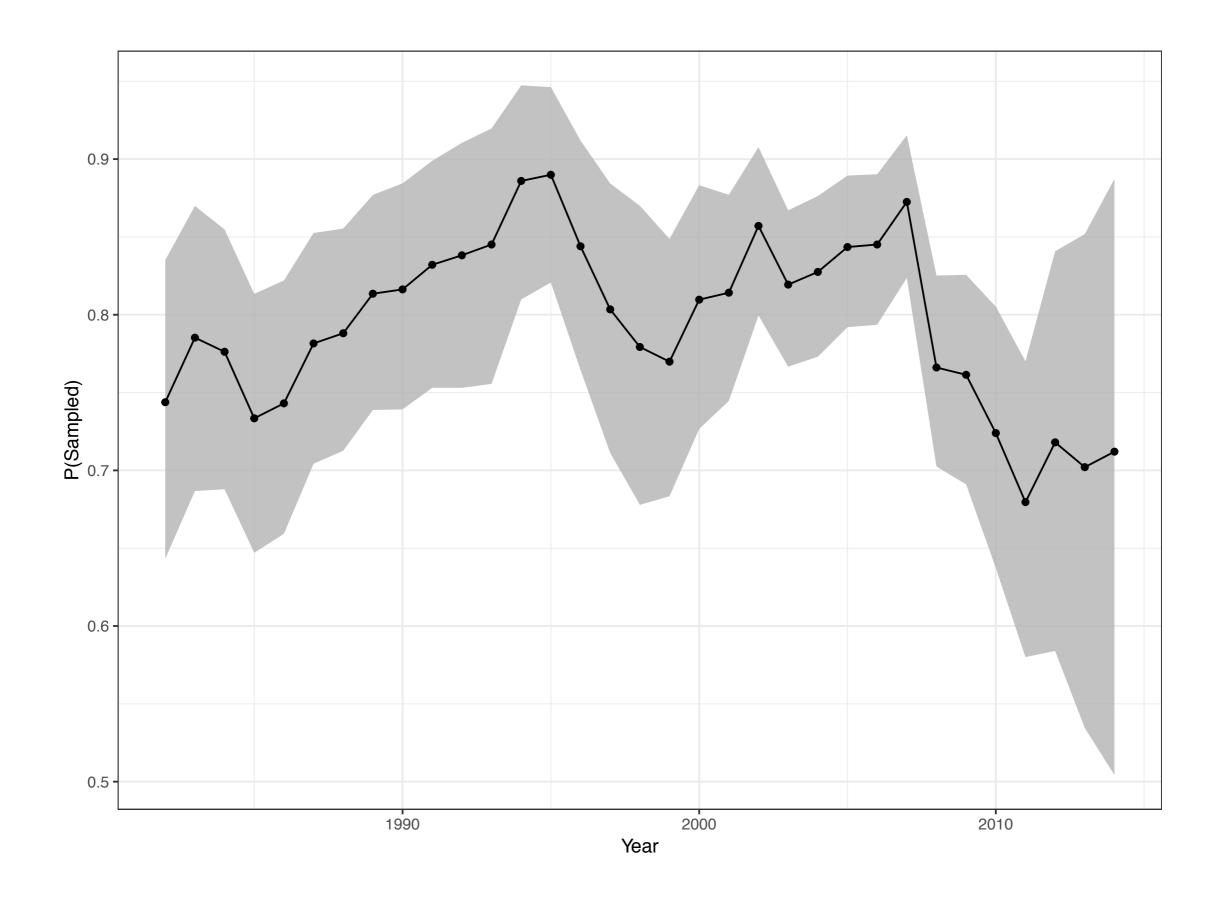


Abundance

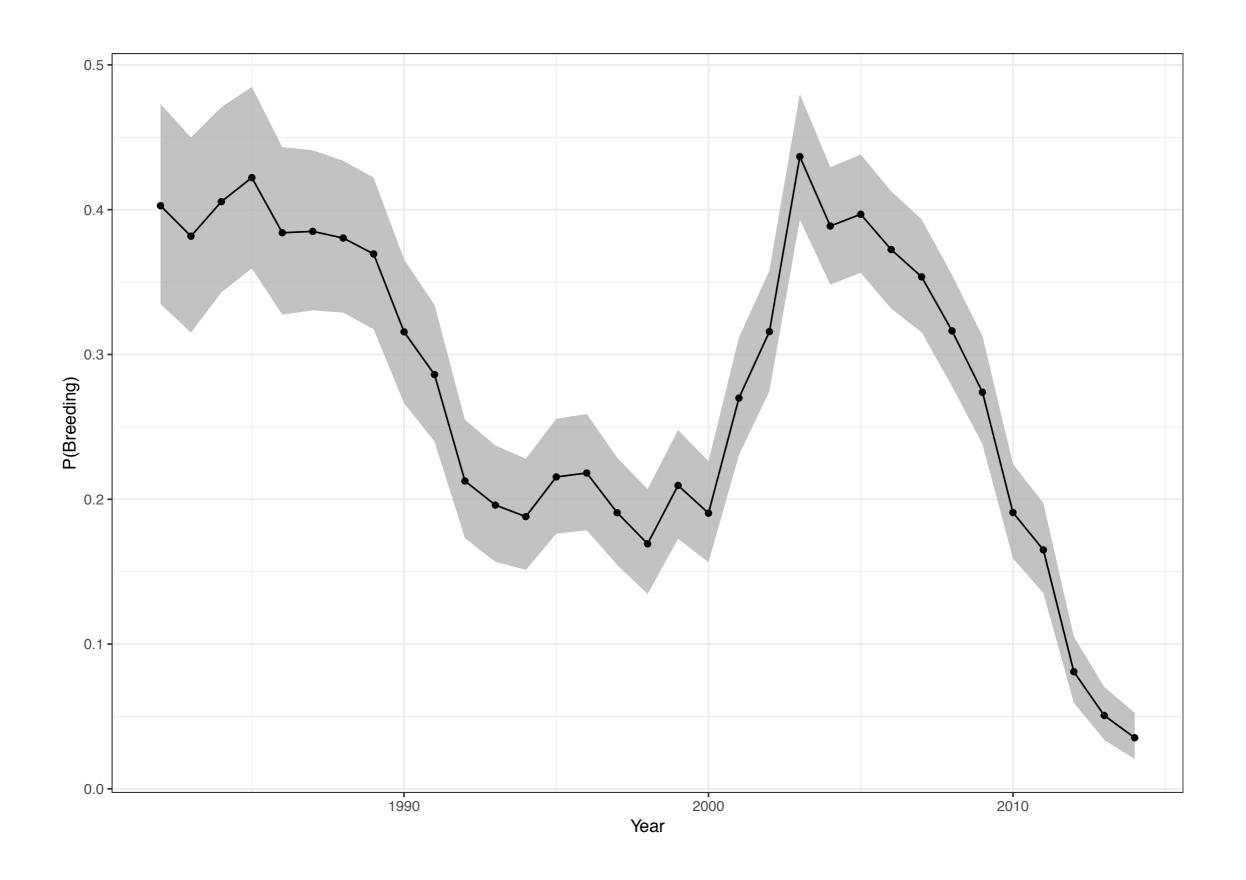




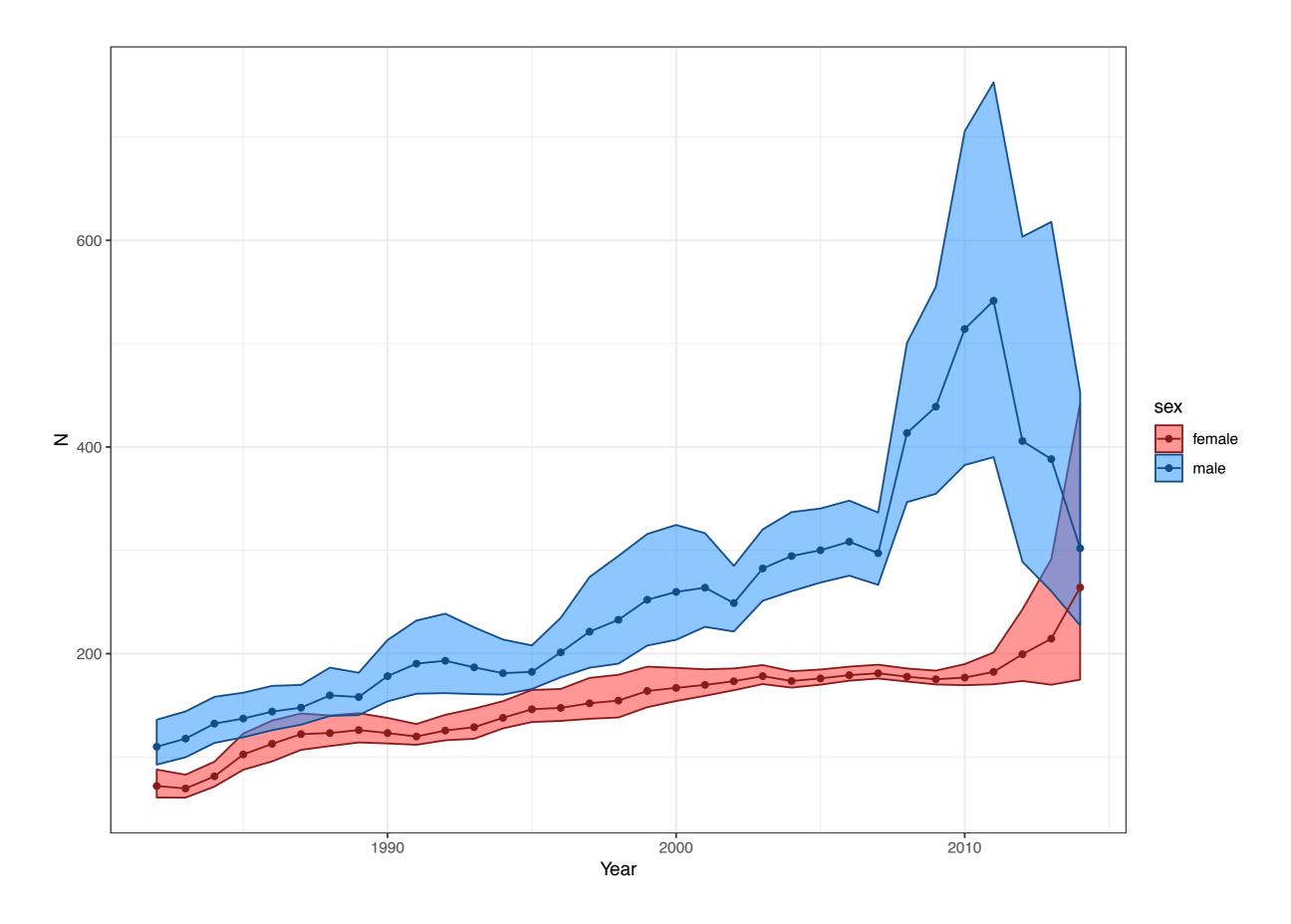
Probability of Being Sampled

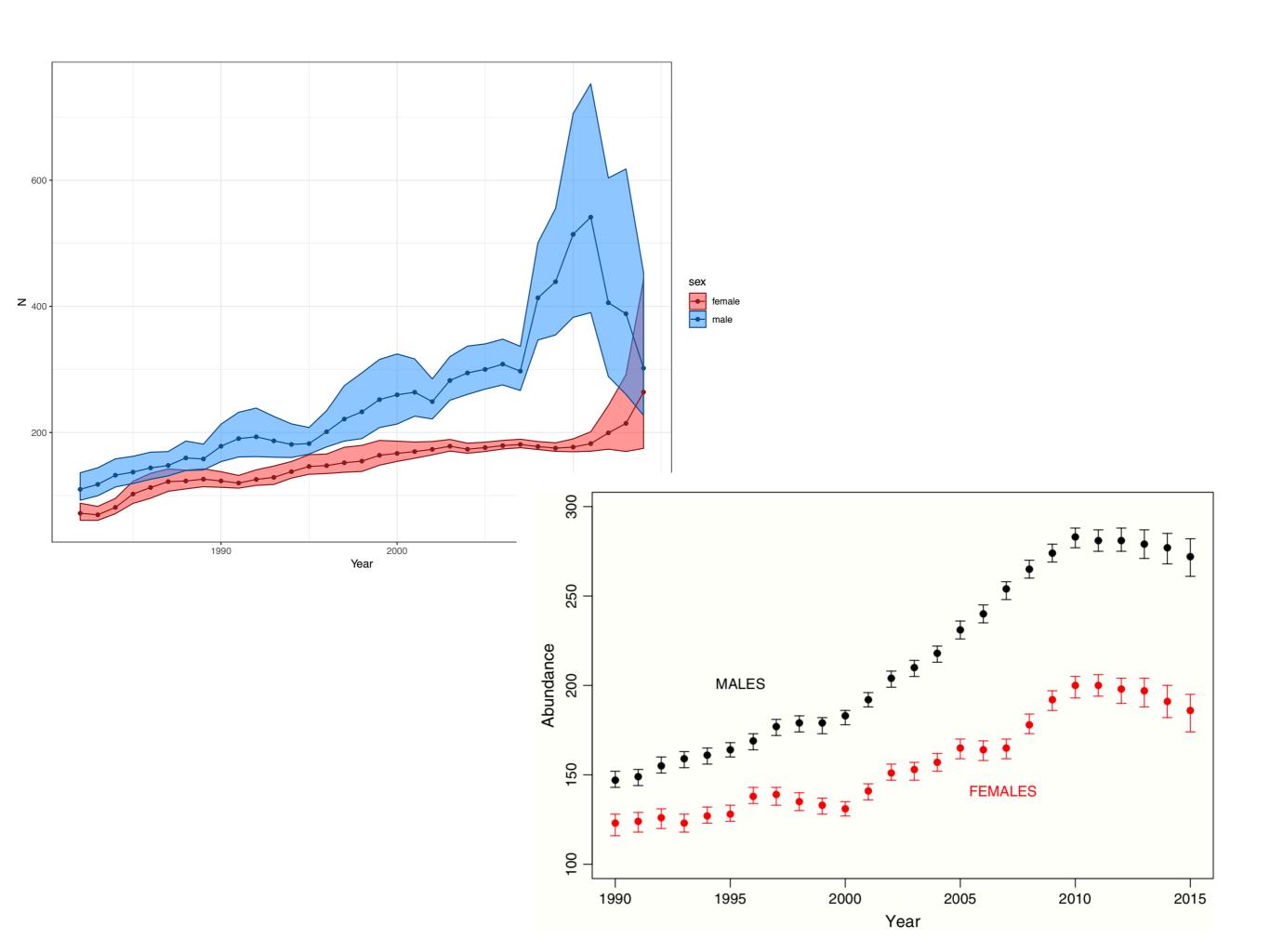


Probability of Being a Breeder

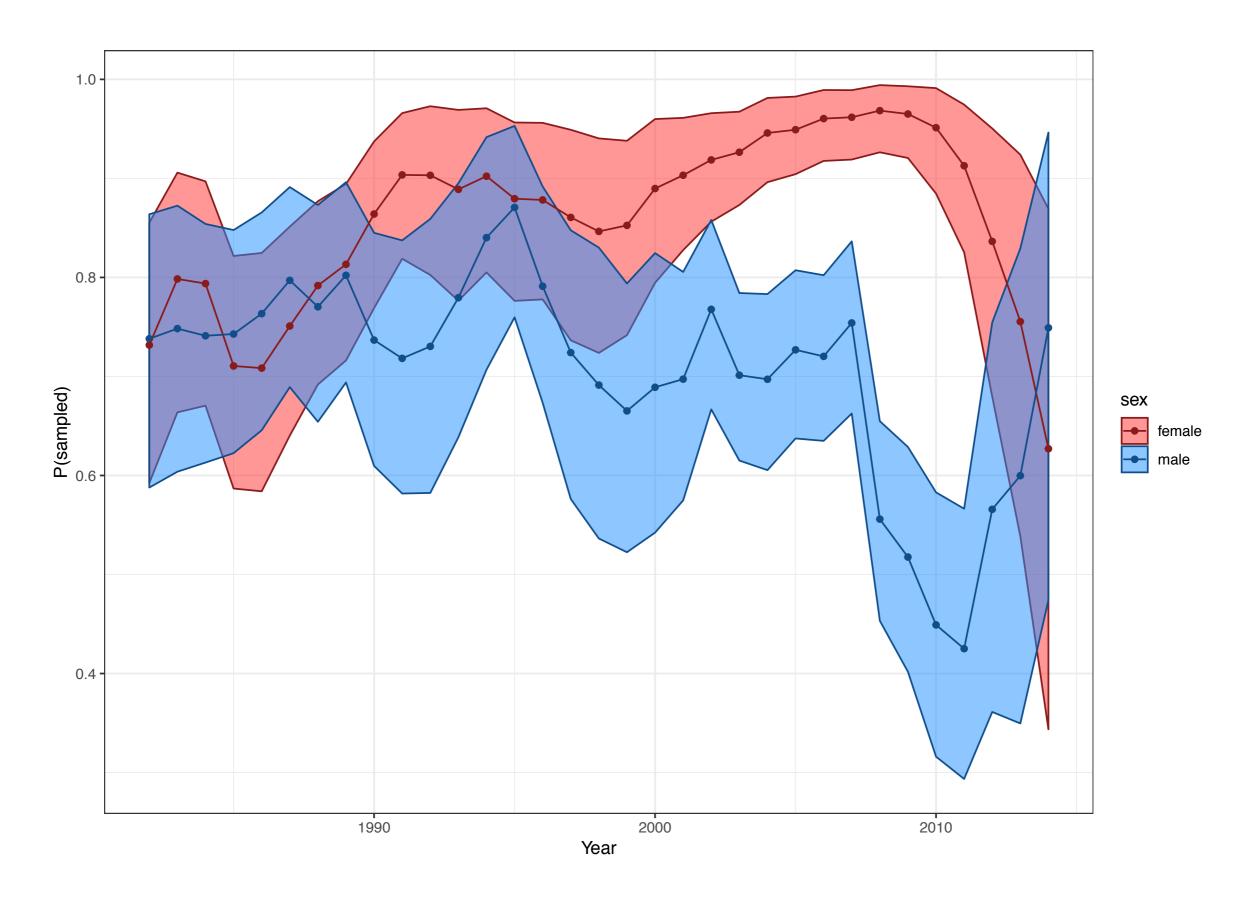


Abundance

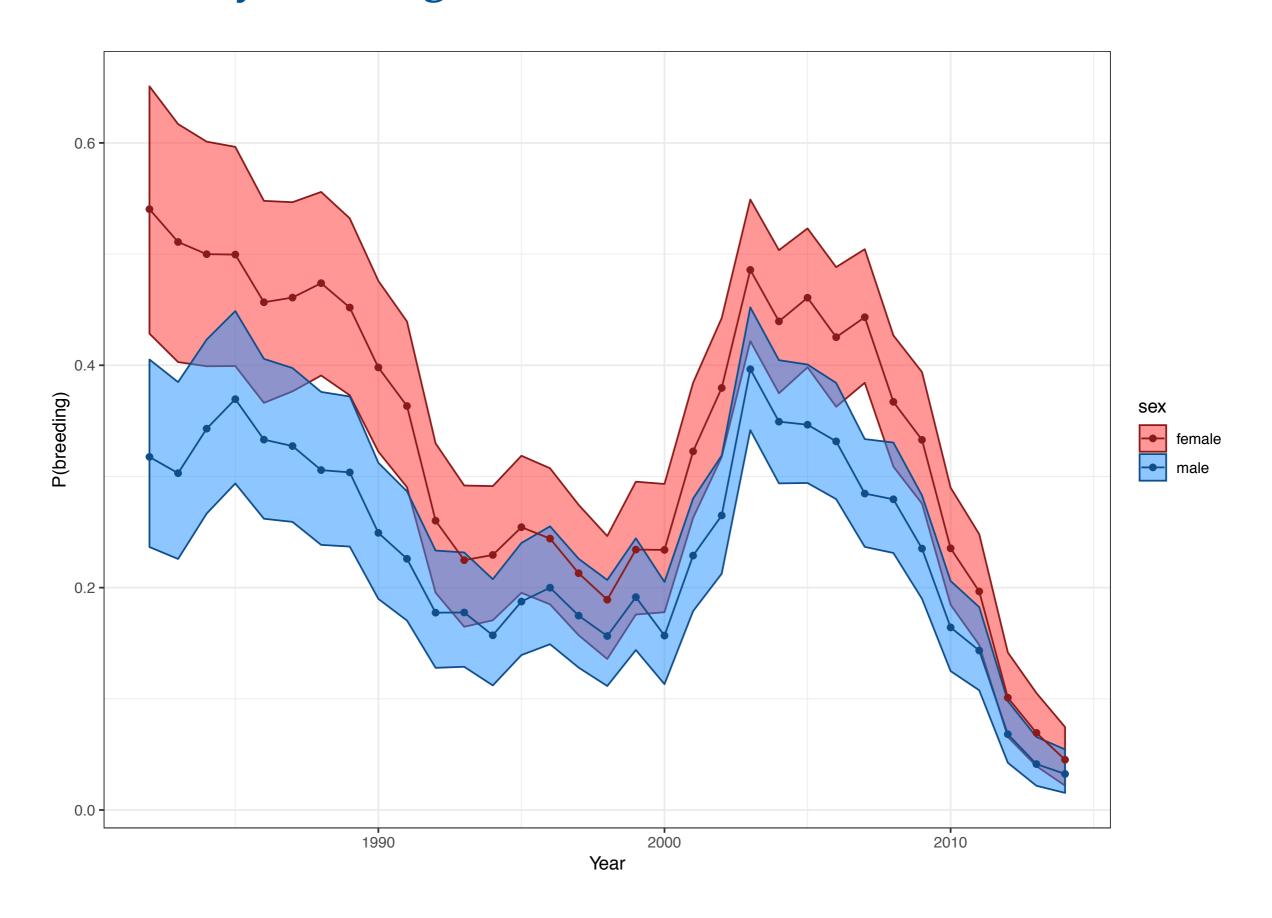




Probability of Being Sampled



Probability of Being a Breeder

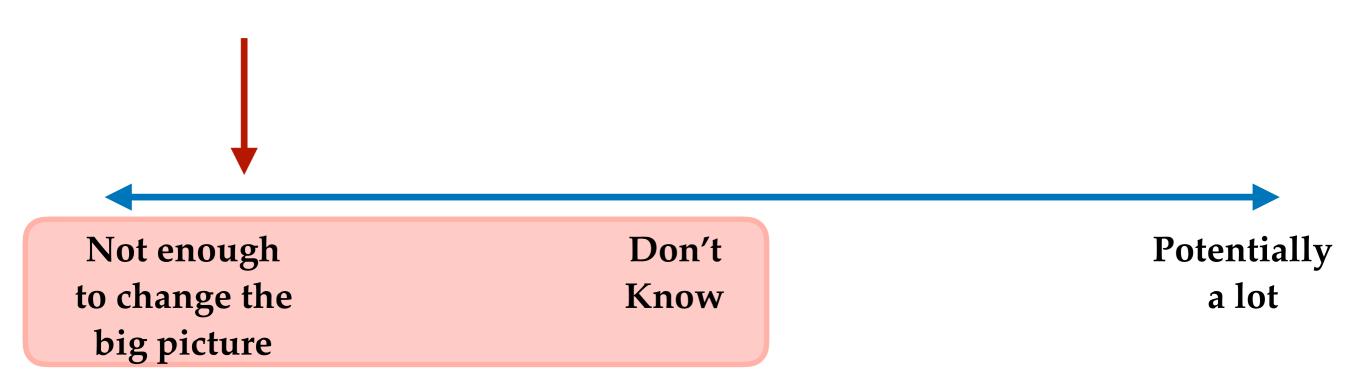


Interpretation

- 1. A valuable tool for "checking in" on the photo-ID data
 - a. A fairly independent method of abundance estimation
 - b. Pedigree estimates slightly lower than photo-ID
 - Seems OK:
 - Presumed alive an over-estimate
 - Model of Pace et al. does it too!!

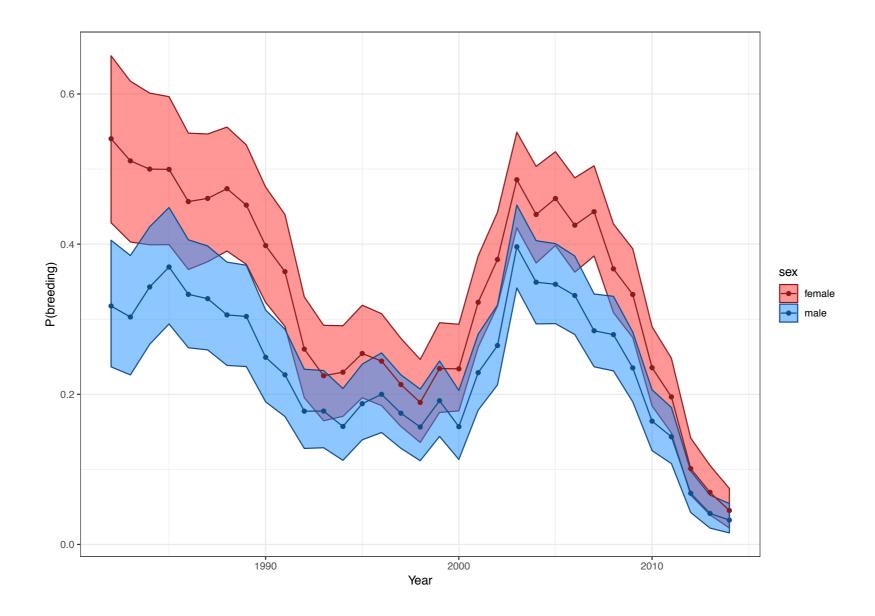
Interpretation

2. Does not appear to be a large number of "missing" whales



Interpretation

- 3. Great way to assess & monitor patterns of reproductive success
 - a. Peak in mid-2000s was similar to 1980s
 - b. Reproduction, on a per-whale basis, declining



Thank you!

- North Atlantic Right Whale Consortium
- All sample collectors and collaborators!!!!!!
 - Thanks for your help, persistence, and patience

Lisa Conger = CITES ninja!

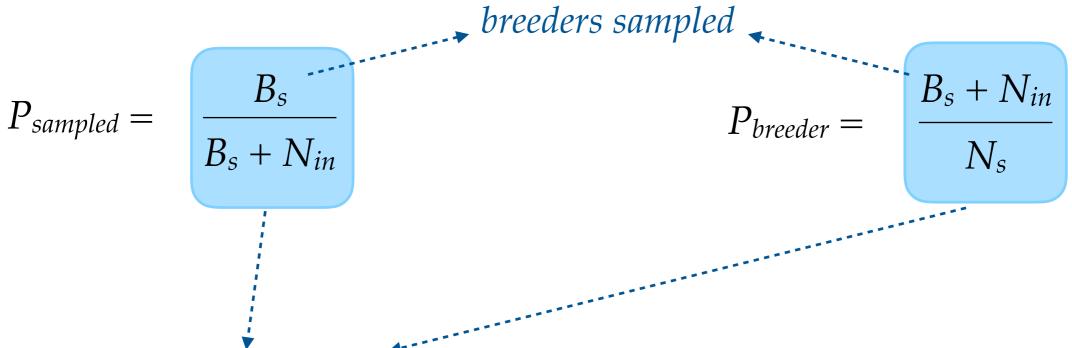
Phil Hamilton, Brenna Frasier, & Lisa Conger = Keeping samples & info organized

Nguyen Nguyen - laboratory assistance

1. Non-sampled non-breeders (N_{nsnb})

$$P_{sampled} = \frac{B_s}{B_s + N_{in}}$$
 $P_{breeder} = \frac{B_s + N_{in}}{N_s}$

1. Non-sampled non-breeders (N_{nsnb})



- A fair amount of uncertainty here
- Account for this via Bayesian estimation with Stan
 - Logistic regression



$$P_{not\text{-}sampled} = 1 - P_{sampled}$$

$$P_{not\text{-}breeder} = 1 - P_{breeder}$$

1. Non-sampled non-breeders (N_{nsnb})

$$\hat{N}_{not-sampled} = \frac{N_s}{P_{sampled}} - N_s$$

$$\hat{N}_{nsnb} = \hat{N}_{not-sampled} \times P_{not-breeder}$$

2. Breeders who are not sampled and not inferred (N_{bnsni})

$$\hat{N}_{bns} = \hat{N}_{not-sampled} \times P_{breeder}$$

$$\hat{N}_{bnsni} = \hat{N}_{bns} - N_{in}$$

$$\widehat{N} = N_s + N_{in} + N_{iv}$$

Number of individuals that are *invisible* to the pedigree analyses

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