



Estimating effective population size (N_e) of wild Delta Smelt using RAD-seq

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Background

Species

- *Hypomesus transpacificus* (Delta Smelt) is a small translucent estuarine fish endemic to the San Francisco Estuary
- Delta Smelt population abundances have been declining since the 1970s and have been protected under the federal and California Endangered Species Act since 1993
- Currently, Delta Smelt abundances are monitored through regular surveys¹
- Despite an intense amount of research into the species the population abundances continue to decline

Historical Techniques

- Previous studies have used temporal (N_{eV}) and linkage disequilibrium N_{eLD} methods to estimate N_e of the wild Delta Smelt population using 12-15 microsatellite markers²⁻³

Purpose

- The effective population size (N_e) of a population provides insights into demography history and extinction risk of species of interest and is an important parameter in conservation biology
- The purpose of this study is to develop techniques to sensitively estimate N_e in Delta Smelt using RAD-seq data
- Develop a bioinformatics pipeline to be used to monitor the genetic diversity of non-model organisms
- Determine if declining abundances of Delta Smelt has affected the species' genetic diversity

Contact



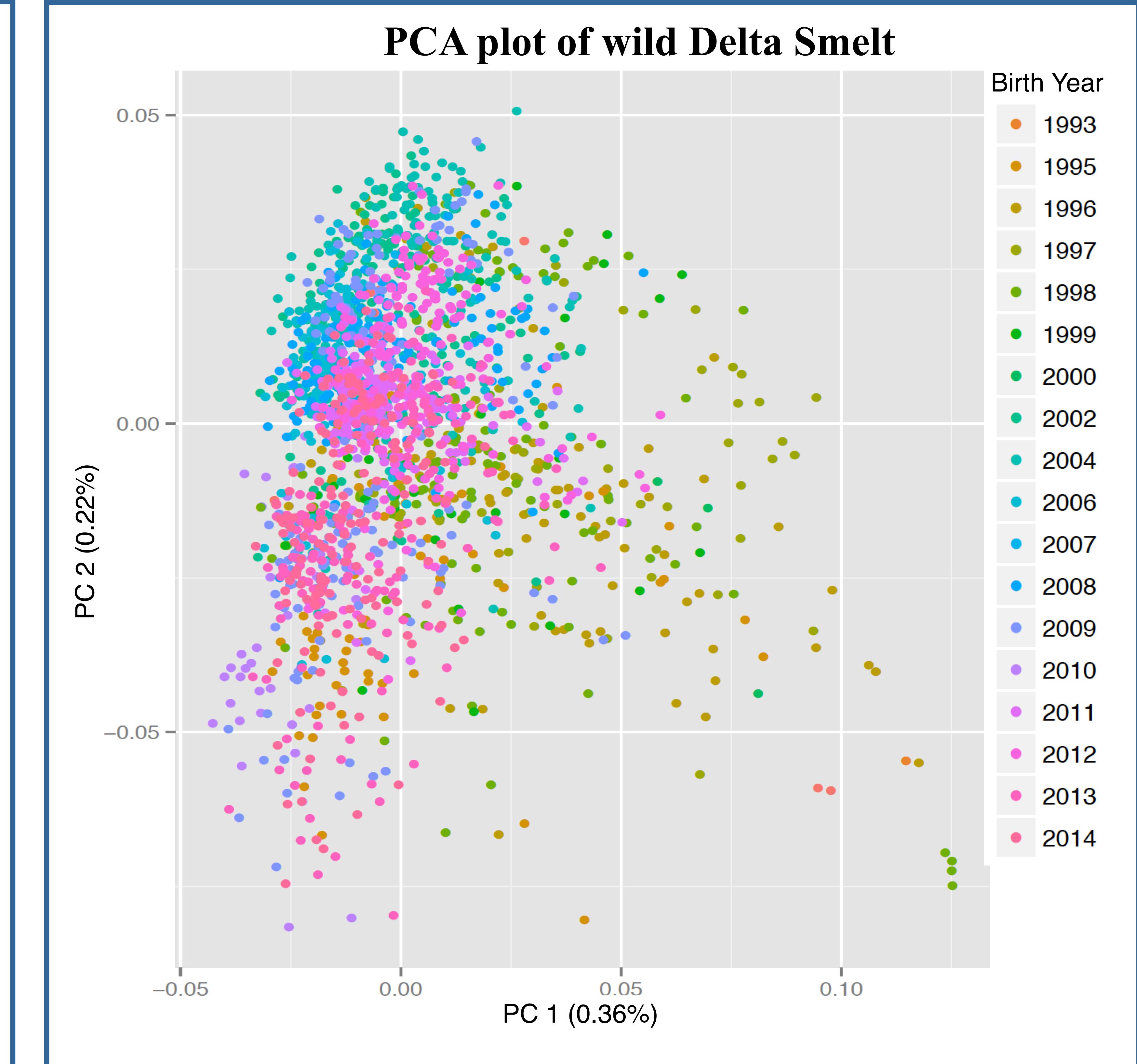
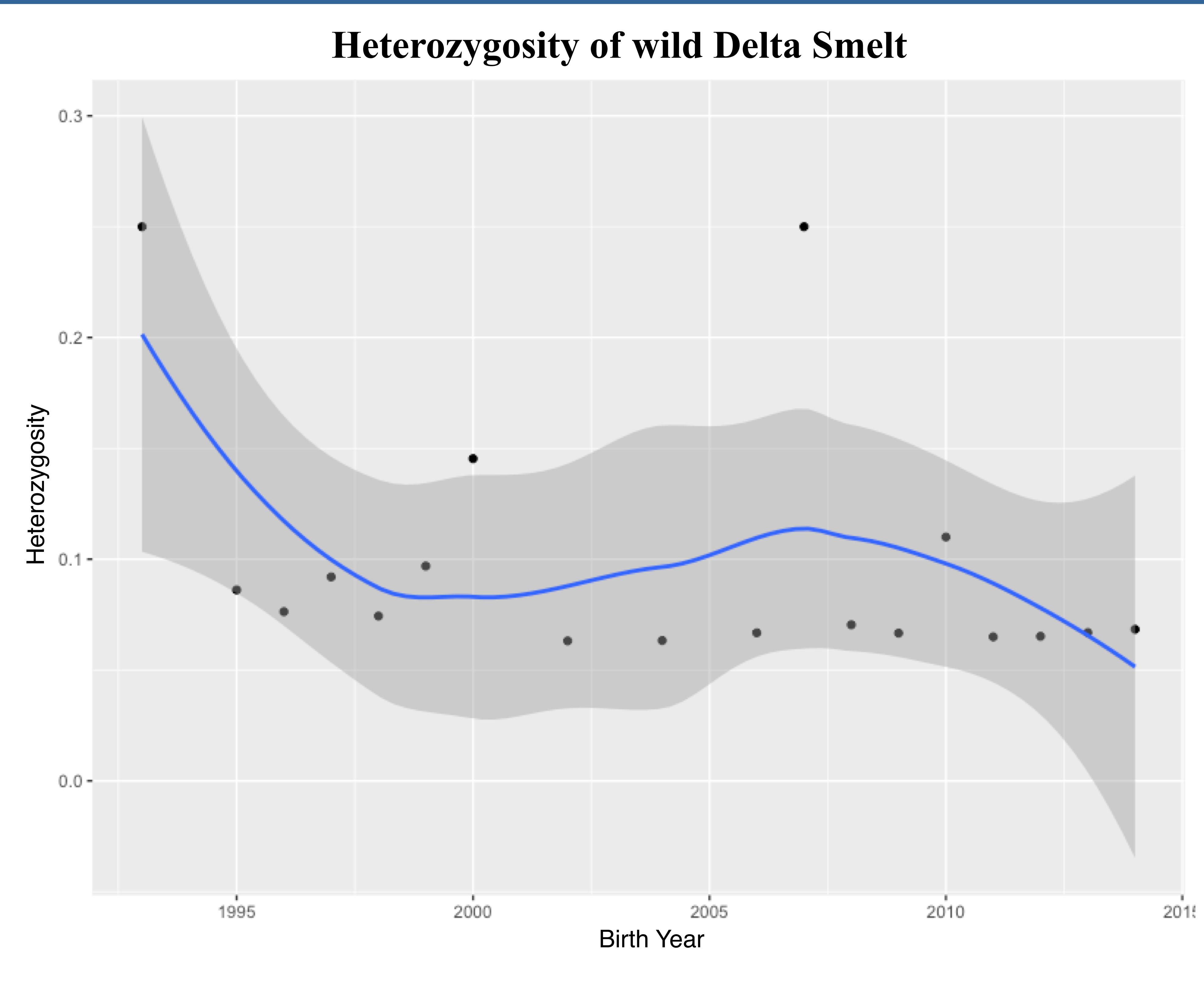
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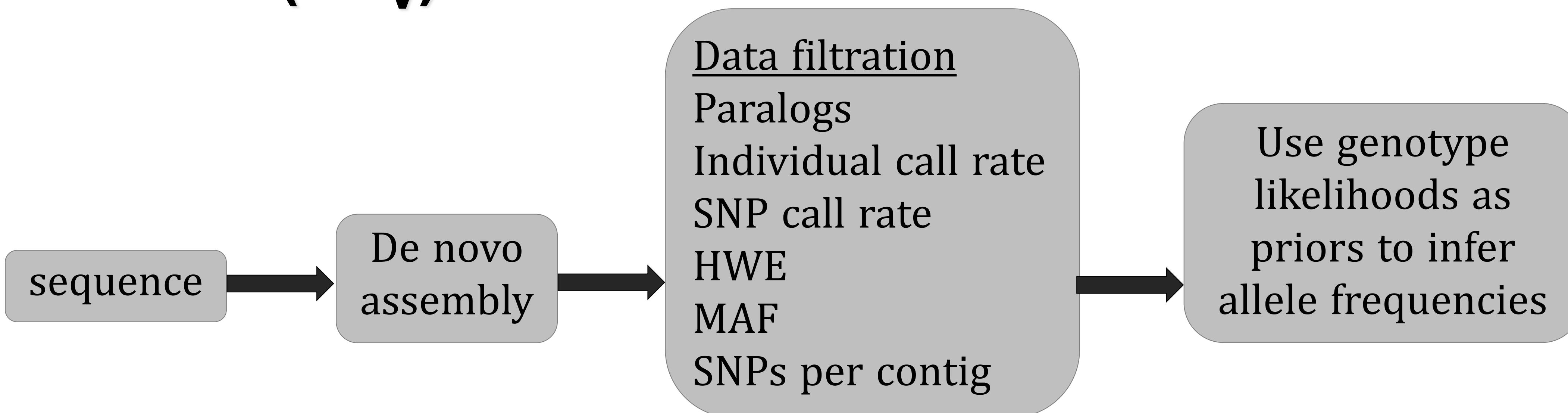
Okay to photograph



Research Questions:

- Are lower abundances of Delta Smelt negatively affecting the species genetic diversity?
- What is the most sensitive and accurate way to estimate the effective population size of Delta Smelt?
- Is the observed decline in heterozygosity a filtration artifact?
- Has there been a shift in allele frequencies over time?

Method (N_{eV})



References [1.] Baxter, R. *et al.* An updated conceptual model of Delta Smelt biology: our evolving understanding of an estuarine fish. 224 (2015). [2.] Nunziata, S. O. & Weisrock, D. W. Estimation of contemporary effective population size and population declines using RAD sequence data. *Heredity (Edinb)*. 1–12 (2017). doi:10.1038/s41437-017-0037-y [3.] Fisch, K. M., Henderson, J. M., Burton, R. S. & May, B. Population genetics and conservation implications for the endangered delta smelt in the San Francisco Bay-Delta. *Conserv. Genet.* 12, 1421–1434 (2011). [4.] Finger, A. J., Schumer, G., Benjamin, A. & Blankenship, S. Evaluation and Interpretation of Genetic Effective Population Size of Delta Smelt from 2011–2014. *San Fr. Estuary Watershed Sci.* 15, (2017). [5.] Lew, R. M. *et al.* Using Next-Generation Sequencing to Assist a Conservation Hatchery: a Single-Nucleotide Polymorphism Panel for the Genetic Management of Endangered Delta Smelt. *Trans. Am. Fish. Soc.* 144, 767–779 (2015).

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