

Evaluating how sample size and spatial scale affect estimating the effective number of breeders for Cisco in Lake Ontario



Joseph Sweeney and Dr. Nick Sard

Biological Sciences Department, SUNY Oswego, Oswego, New York

Background

- Cisco (*Coregonus artedii*) were **once abundant and ecologically significant prey fish in Lake Ontario.**
- Due to overfishing and habitat degradation, Cisco **populations have been declining since at least the 1950s**¹
- Conservation efforts include using hatchery fish in population supplementation as well as habitat restoration.¹
- Understanding Cisco reproduction is essential to their conservation—**despite this little is known about the effective population size (N_e) or number of breeders (N_b) in Lake Ontario.**
 - N_e can be understood as the ideal population where **the effect of genetic drift is the same as the actual population.**²
 - N_b can be understood as the N_e **surrogate for one reproductive cycle.**³
- These parameters are especially important in the management of a species that has been supplemented with hatchery fish.
 - Large releases of genetically similar captive-bred individuals can inflate population size but reduce N_e by diluting the wild gene pool.
 - Known as the **Ryman-Laikre effect**⁴

Objective

- We aim to estimate N_b for cisco in Lake Ontario as well as investigate the effects of sample size and sample location on estimates.

General methods

- Cisco larvae ($n > 2000$) were collected from Chaumont Bay, NY in 2023 using ichthyoplankton tows and emergence traps.
- DNA from samples was extracted using a glass-fiber protocol.⁵
- Using a species diagnostic GT-seq panel we genotyped the samples at 302 of loci across the genome.⁶
- To estimate N_b we used sibship pedigree reconstruction with the program COLONY (Jones & Wang, 2010).⁷

Preliminary results

Ichthyoplankton tows ($n = 51$) collected larvae throughout the bay

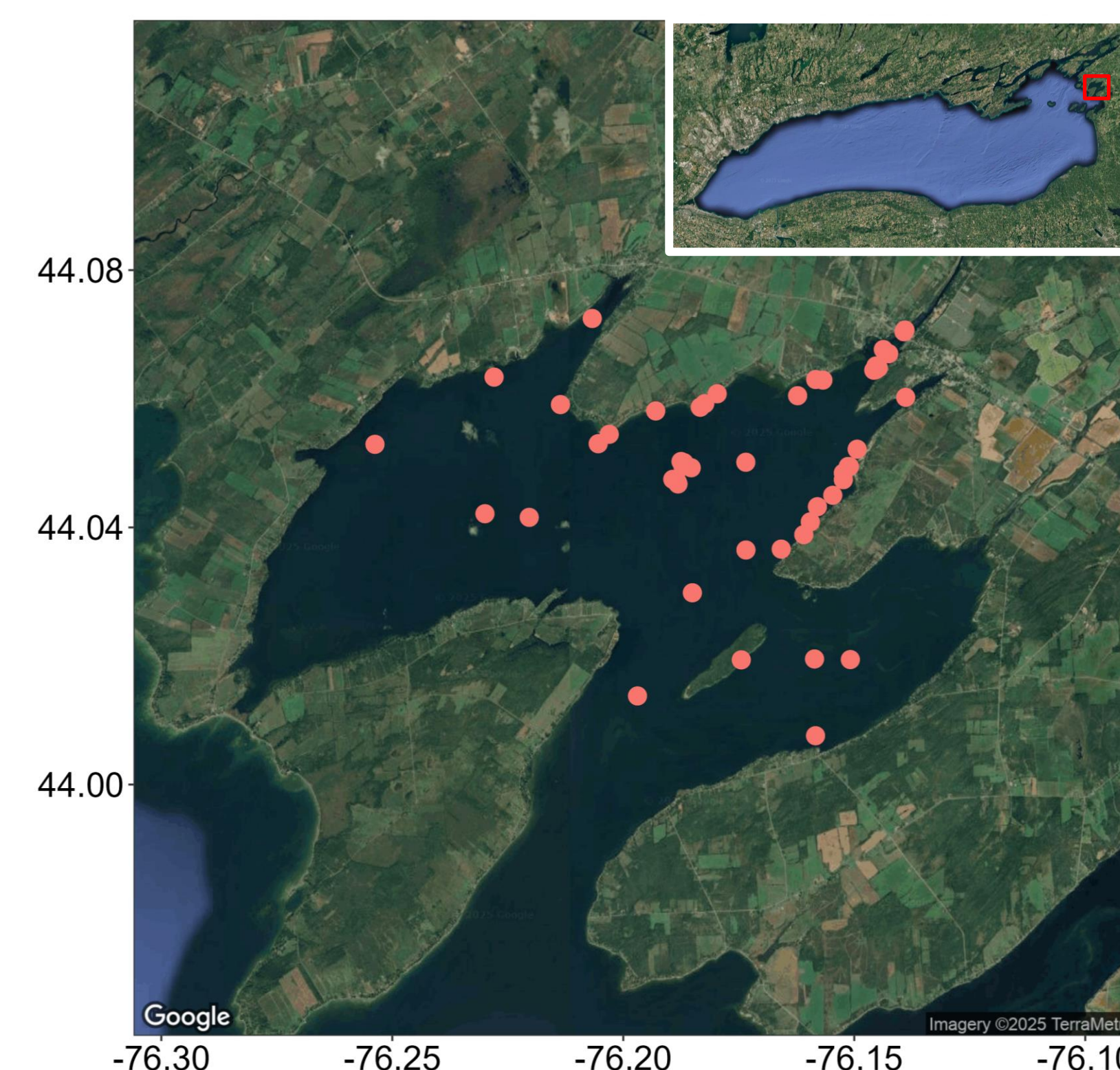


Figure 1. A map of the study site, Chaumont Bay. Dots represent locations where tow samples were collected.

A sample size of > 1000 is needed to estimate N_b

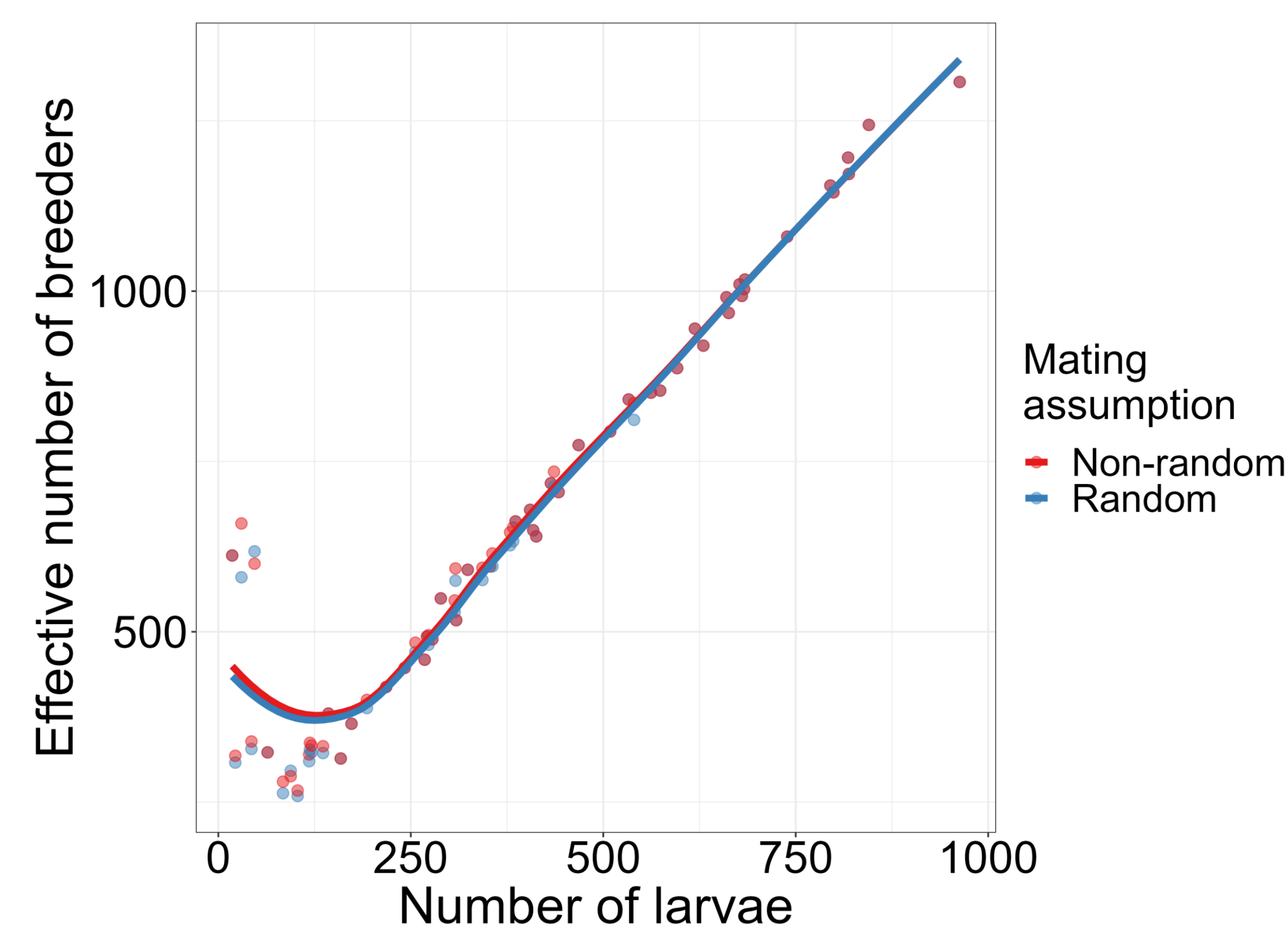


Figure 2. Larvae randomly sampled (without replacement) with varying sample sizes plotted against their corresponding N_b estimates.

Individual tows aren't enough to estimate N_b

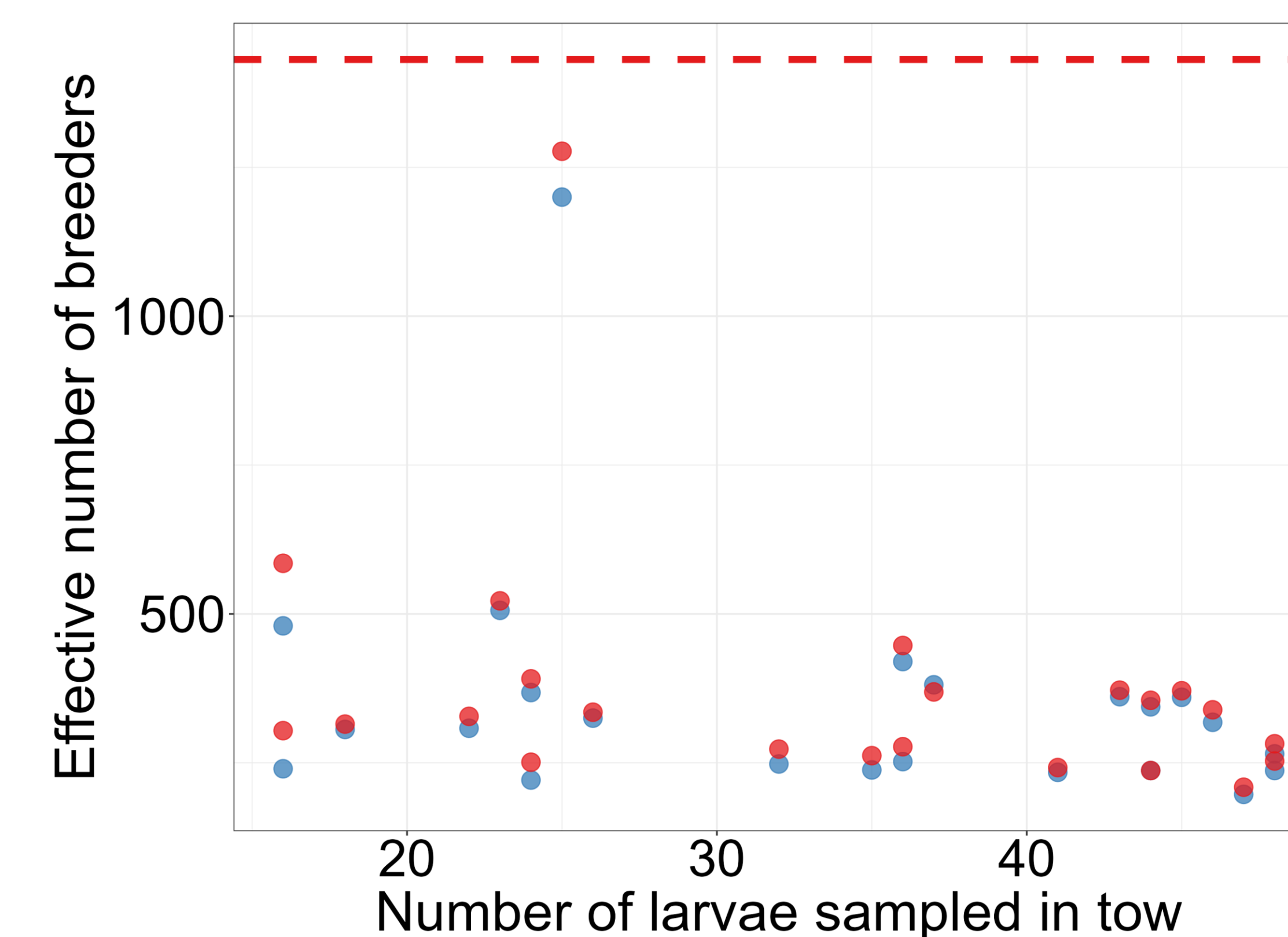


Figure 3. The number of larvae in each tow plotted against the estimated N_b calculated from that tow. The red dashed line indicates the estimated N_b from all the tows collectively.

Discussion

- Need even greater sample size to estimate N_b
 - Will incorporate larvae collect in emergence traps to increase sample size
- Mating type assumption (random or non-random) makes no difference in estimates.
- Sample sizes < 100 have significantly decreased accuracy.
 - Individual tows can't be used to accurately estimate N_b .

Future work

- Using linkage disequilibrium to estimate N_b might mitigate the effects of a small sample size.
- Adults caught in Chaumont Bay can be used in reconstruction to get more accurate estimates.



Figure 4. A painting of a Cisco by Ellen Edmonson.



Corresponding author:
nicholas.sard@oswego.edu

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