# A New Computer Program to Evaluate Biases in the Two-Sample Mark-Recapture Abundance Estimator 



## ABSTRACT

Two-sample mark-recapture sampling is a common method used to estimate stream fish abundance. The idea is to capture and mark fish in an initial sample. The fish are then released to mix randomly with the whole population. A second sample is obtained, and the number of marked and unmarked fish is recorded. The Chapman estimator uses the number of fish marked in the first sample, the total number of fish captured in the second sample, and the number of recaptured fish to estimate abundance. The assumptions are: 1) the population is closed, meaning no immigration, emigration, births, or deaths, 2) all fish are equally vulnerable to being captured during each sample, meaning marking does not change the behavior of fish, and 3) marks are not lost or overlooked. Violations of these assumptions can fish, and 3) marks are not lost or overlooked. Violations of these assumptions can happen frequently and examining bias when a combination of assumptions are
violated is difficult. To explore how simultaneously violating multiple assumption violated is difficult. To explore how simultaneously violating multiple assumptions Python software that allows the end user to assess bias by simulating a closed or open population, varying fish capture probabilities, and allowing fish to lose marks. open population, varying fish capture probabilities, and allowing fish to lose mark
The simulations allow the end user to experiment by intentionally violating any The simulations allow the end user to experiment by intentionally violating any
combination of model assumptions and determining the effect on estimator bias This software should be useful to fisheries managers that use the Chapman estimator or instructors that teach the two-pass mark-recapture sampling for abundance estimation.

## InTRODUCTION

- 2-sample mark-recapture is a commonly used method to estimate fish abundance.
- For statistical estimators to be valid, the sampling method must meet certain assumptions
- Violating model assumptions can result in bias, and assessing the resulting bias is often difficult.
- This computer software was developed to help users assess biases when assumptions of the abundance estimator are violated


Fig. 1. Main graphical user window to begin use of the software.

## MeTHODS

Upon start-up of software, a user can manipulate the following variables under the "Raw Simulation tab":
$>$ Total Fish Population in Study Reach: Know fish abundance.
$>$ Closed or Open Population: With a closed population, there are no births, mortality, or movement in and out of the study reach (Figure 2).
$>$ Capture Probability: The chance of capturing a fish. This can be equal between all sampling or varied. It can also be completely random for each fish.
> Tag Loss \& Misidentification Probability: The chance of a fish losing its tag or a user not seeing the tag.

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- Sub-reach Size: The percent of the study area being sampled.
- Number of Trials: The total number of times to repeat the simulation.


Fig. 2. The blue curve above shows a balanced beta distribution if a user decides to keep migration in and out of the reach equal. Upstream-biased movement is represented by the orange curve.

## Results

Results are available in a variety of formats:
$>$ A Histogram Plot.
$>$ Textbox showing statistical data
$>$ Table showing raw data for each trial run. $>$ CSV, PNG files if user desires to export results


Fig. 3. A histogram plot to display simulation results.


Fig. 4. The text box on the upper screen summarizes conditions of the most recent simulation as well providing statistical analysis.


Fig. 5. Filetypes available to users to save their simulation results.


Fig. 6 Additional tab so that the user can estimate abundance from a sample using the Chapman estimator.

## Technical Specirications

- Executable for Windows Platforms.
- Open-sourced code available on GitHub.
- Multiprocessing to speed up simulations.


## Future Improvemients

- Add visual simulation feature.
- Refactor code to add in data structures and algorithm to further speed up simulations.


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## References

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