

Estimating escapement of Chilkat River Chinook salmon using trans-generational genetic mark-recapture (tGMR)

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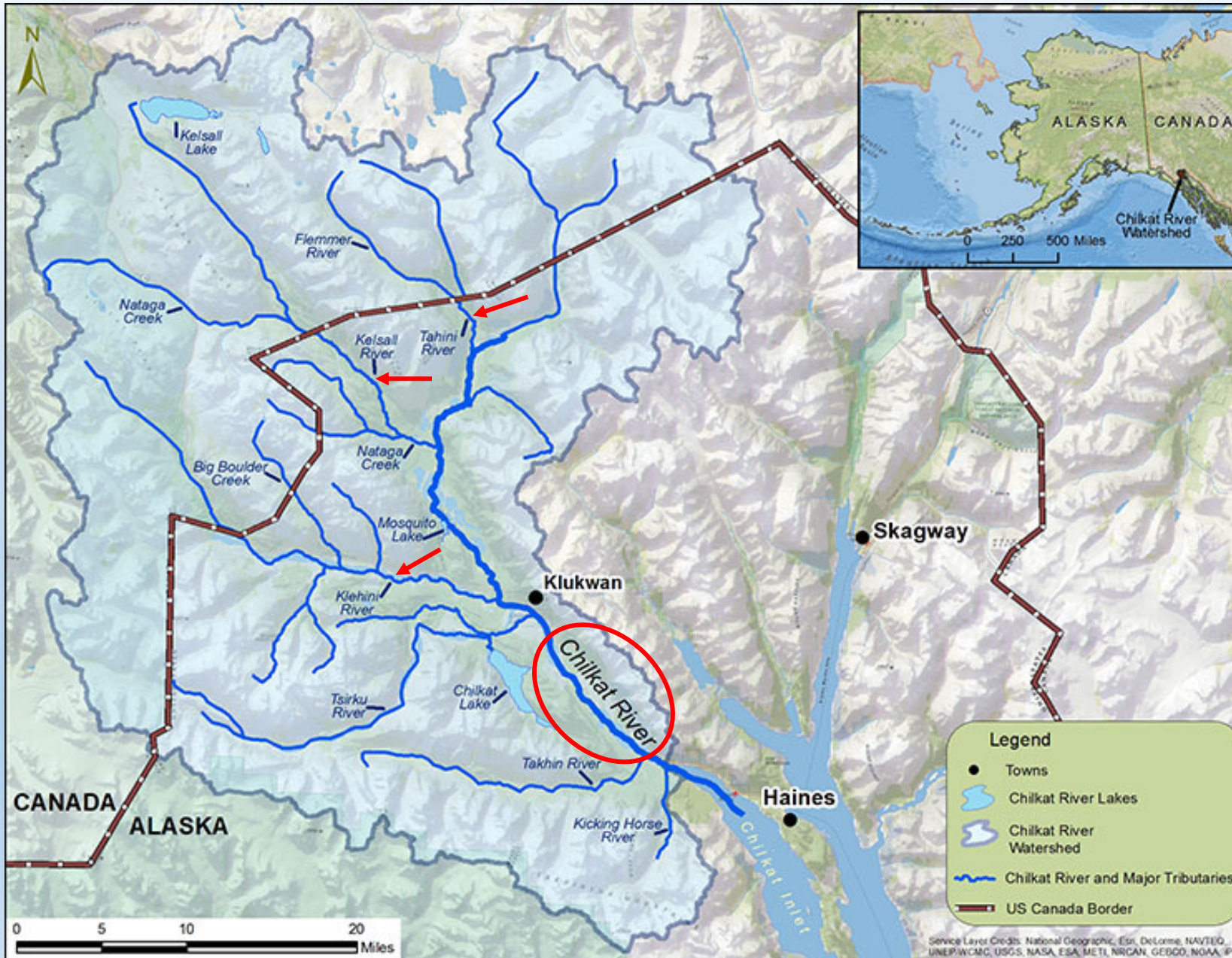
Acknowledgements

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- **ADF&G Collaborators:** Kyle Shedd, Randy Peterson, and Brian Elliot
- **Funding:** Alaska Sustainable Salmon Fund, Pacific Salmon Treaty, Alaska NSF EPSCoR, AFS Genetics Section
- **Land:** Ancestral home of the Klukwan people



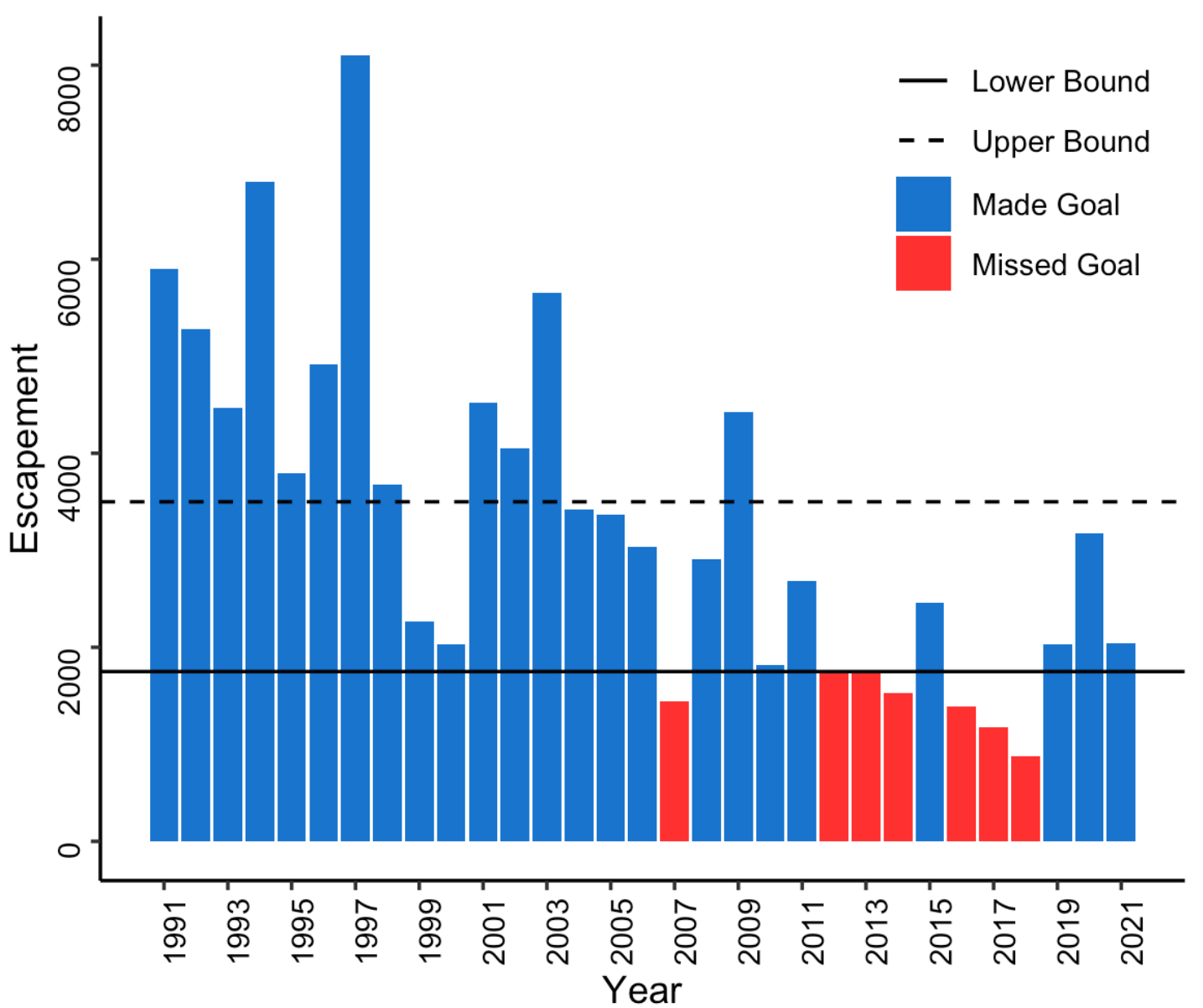
Chilkat River Watershed

3rd largest producer of Chinook salmon in SEAK



PSC exploitation rate and escapement indicator stock

Stock Trends



“Stock of Management Concern” designation in 2017

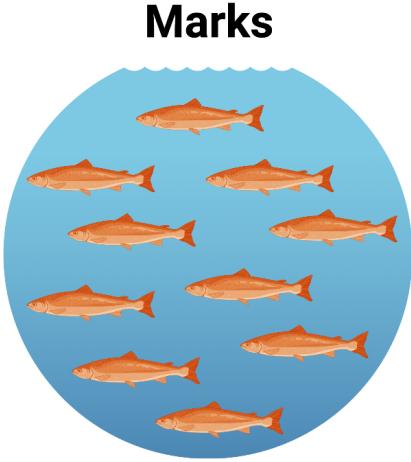
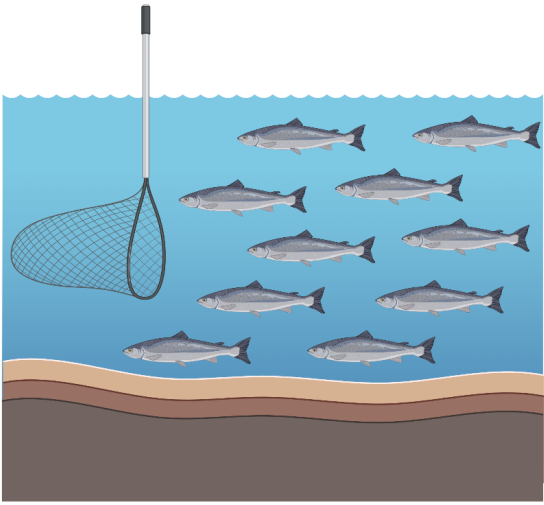
Halted subsistence harvest

Objectives

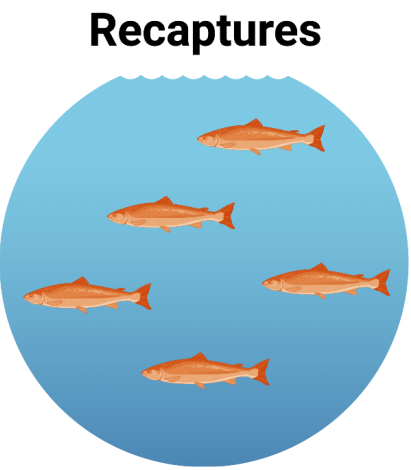
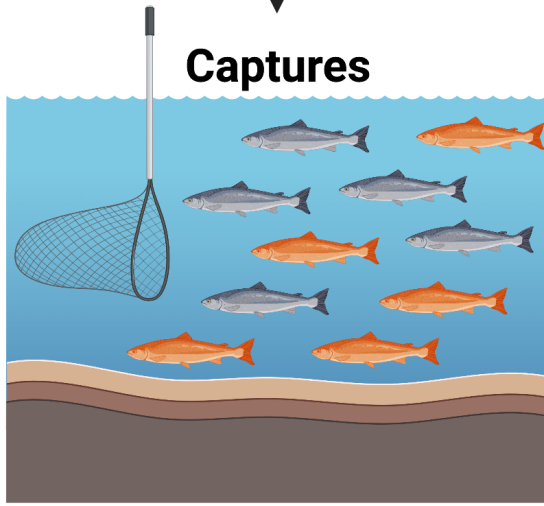
A wide, shallow river flows through a valley. The water is clear, revealing a rocky riverbed. In the background, there are large mountains, some with patches of snow. The sky is overcast with grey clouds. The overall scene is a natural, somewhat desolate landscape.

- Validate tGMR methodology in Alaska
- Compare accuracy and precision
- Determine feasibility of future tGMR projects

Mark-Recapture

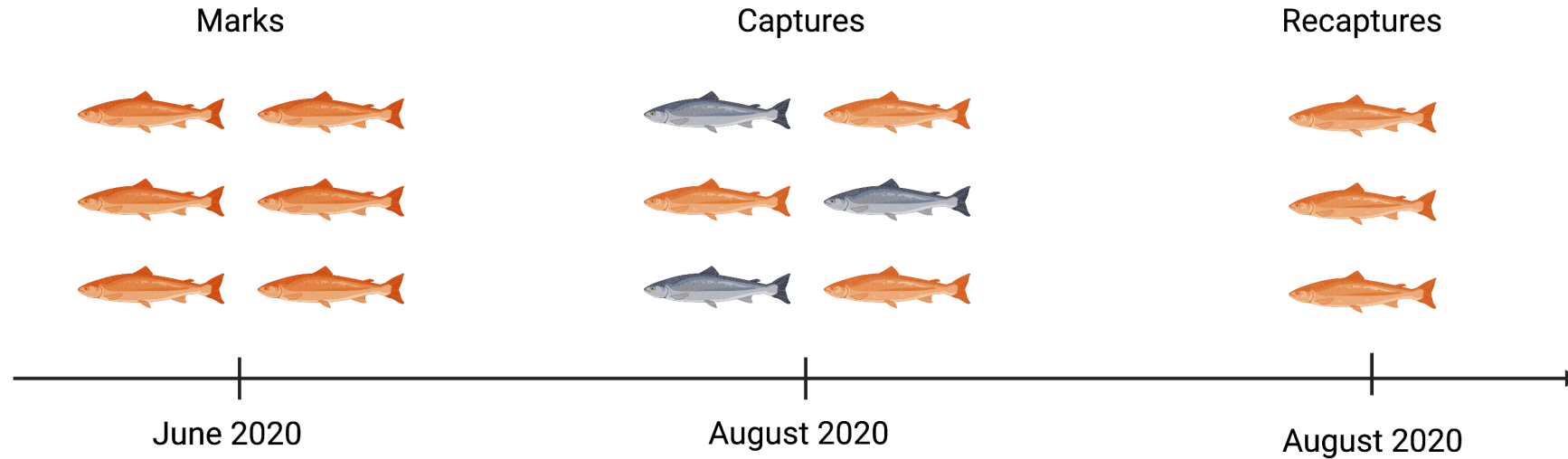


$$N = (\text{Marks} \times \text{Captures}) / \text{Recaptures}$$

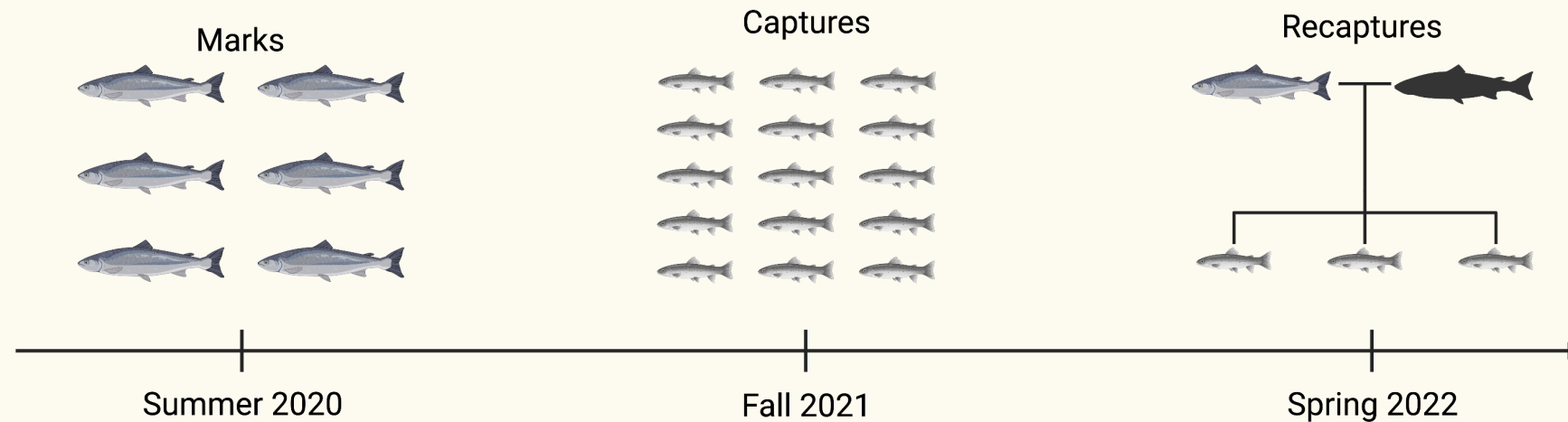


What is tGMR?

Traditional Mark-Recapture



Trans-Generational Genetic Mark-Recapture (tGMR)

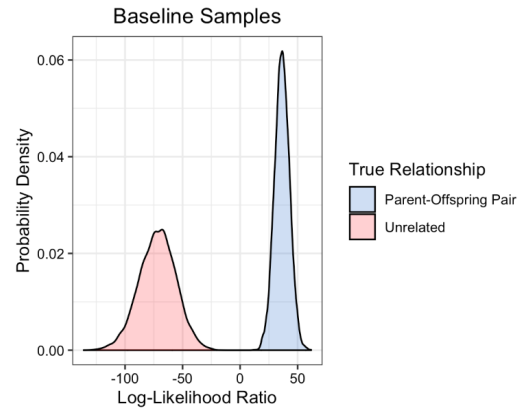


tGMR Assumptions

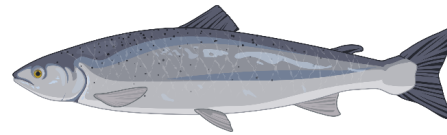
1. Marks are retained
2. Marks are correctly identified
3. Closed population
4. Marking does not affect behavior
5. Equal probability of being marked in the first sample

tGMR Workflow

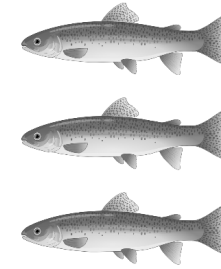
1 Panel Simulations



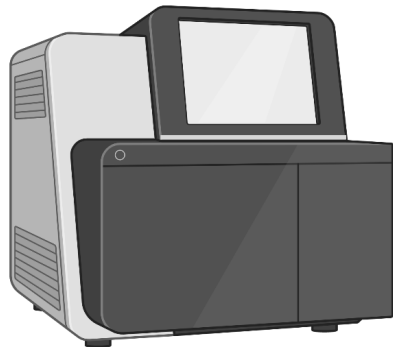
2 Adult Sampling



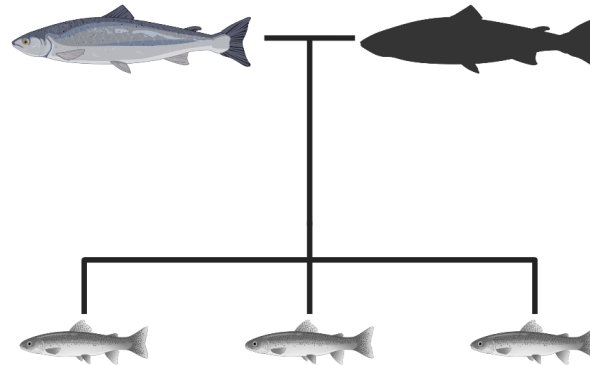
3 Juvenile Sampling



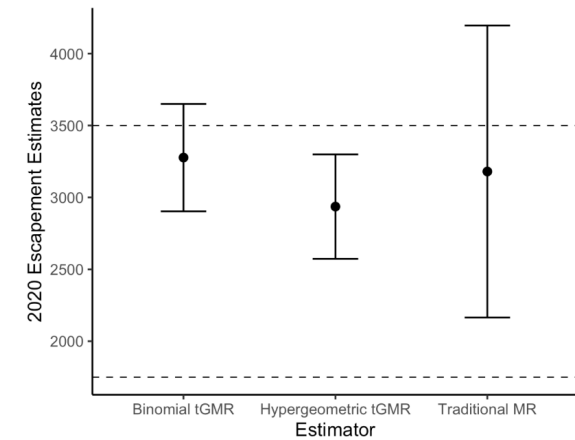
4 Sequencing



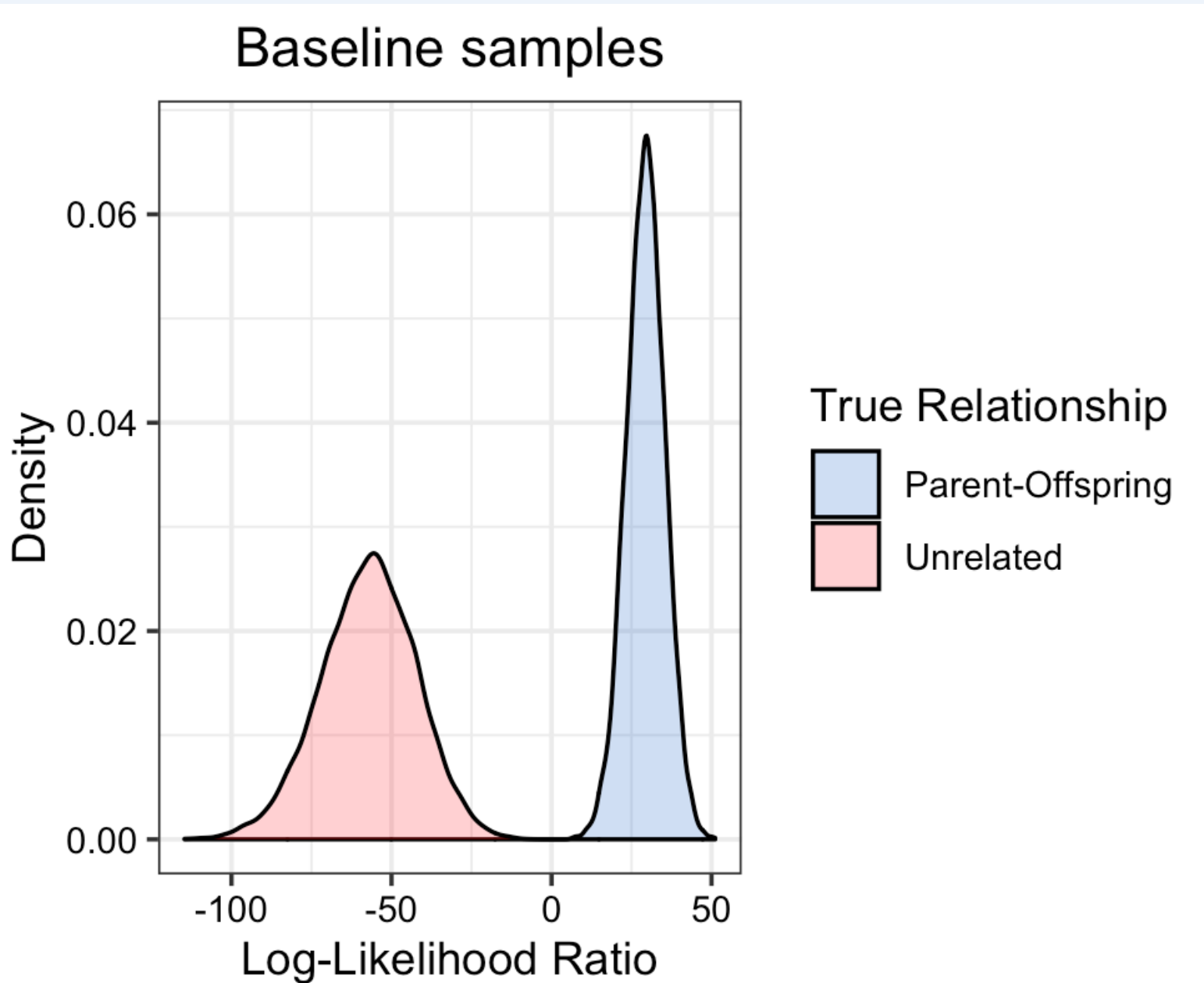
5 Parentage Analysis



6 Calculate Estimates



Marker Panel Simulation

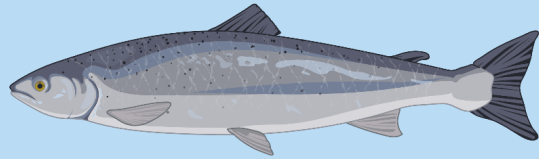


Tissue Sampling

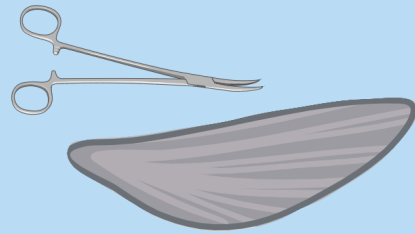
Event 1

Summer 2020

641 Adults



Fin Clips



Event 2

Fall 2021

700 Juveniles

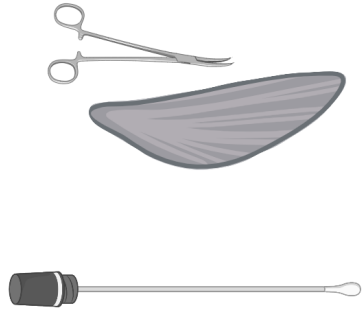


Omni Swabs

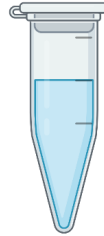


Genotyping

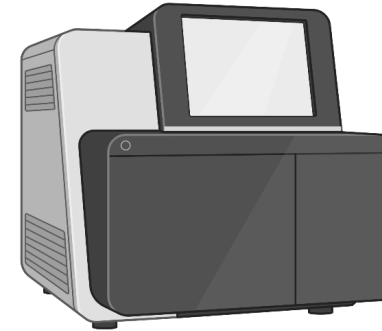
1. Sample Collection



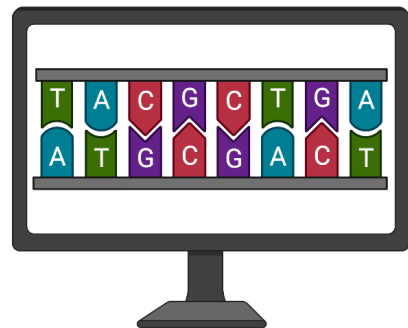
2. DNA Extraction & Library Preparation



3. Next-Generation Sequencing



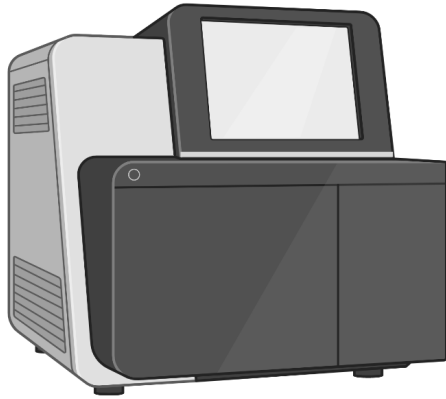
4. QA/QC



5. Genotypes

Loci	Adults	Juveniles
278	581	682

Step 1:
Procure Genotypes

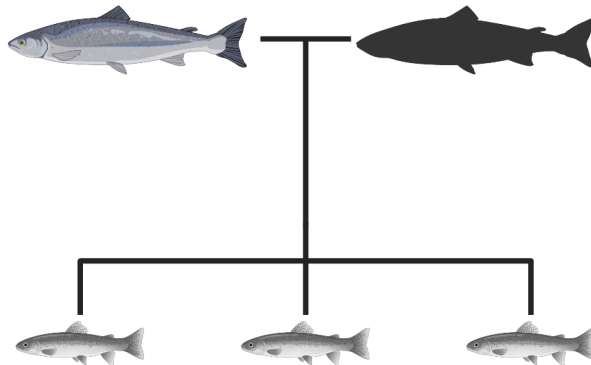


Step 2:
Run COLONY



Parentage Analysis

Step 3:
Generate Pedigree



Step 4:
Obtain Parameters

Parent-Offspring Pairs	Parent-Offspring Triads	Unique Sampled Parents	Unique Inferred Parents
221	20	148	751

Binomial vs Hypergeometric tGMR Models

Basic Equation

$$N = (\text{Marks} \times \text{Captures}) / \text{Recaptures}$$

Binomial

Sampling with replacement

Marks = adult genotypes
Captures = juvenile genotypes x 2
Recaptures = parent-offspring pairs

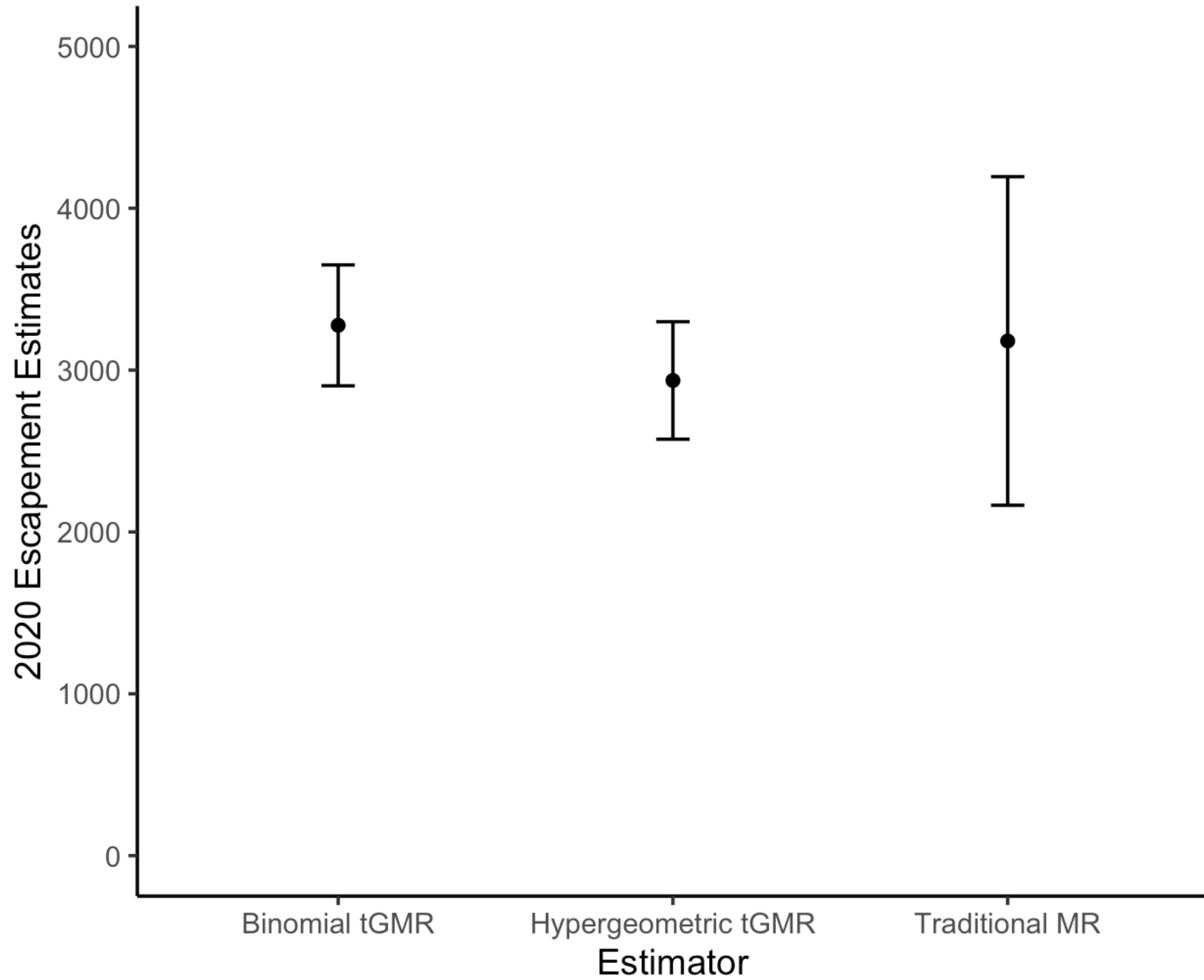
Hypergeometric

Sampling without replacement

Marks = adult genotypes
Captures = unique inferred parents
Recaptures = unique sampled parents

Estimators

Estimator	2020 Escapement Estimate	Coefficient of Variation (CV)
Binomial tGMR	3,277	0.06
Hypergeometric tGMR	2,936	0.06
Traditional MR	3,180	0.16



Key takeaways

- Validated tGMR in SEAK
 - Accurate and more precise
 - Lower uncertainty
- Potential for being:
 - More cost-effective
 - Less invasive



Next steps

- What happens when the equal probability of capture assumption is violated?
- Use simulation models to evaluate bias under varying scenarios



Questions?

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