

Chinook Salmon Carcass Mark-recapture Methods



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Objectives

- Reliable estimates of escapement without marking live fish, use of traps/weirs/device counters
 - Logistically feasible in times of large numbers
 - Also works when numbers are small
 - Potential to account for differences between sex/size/origin

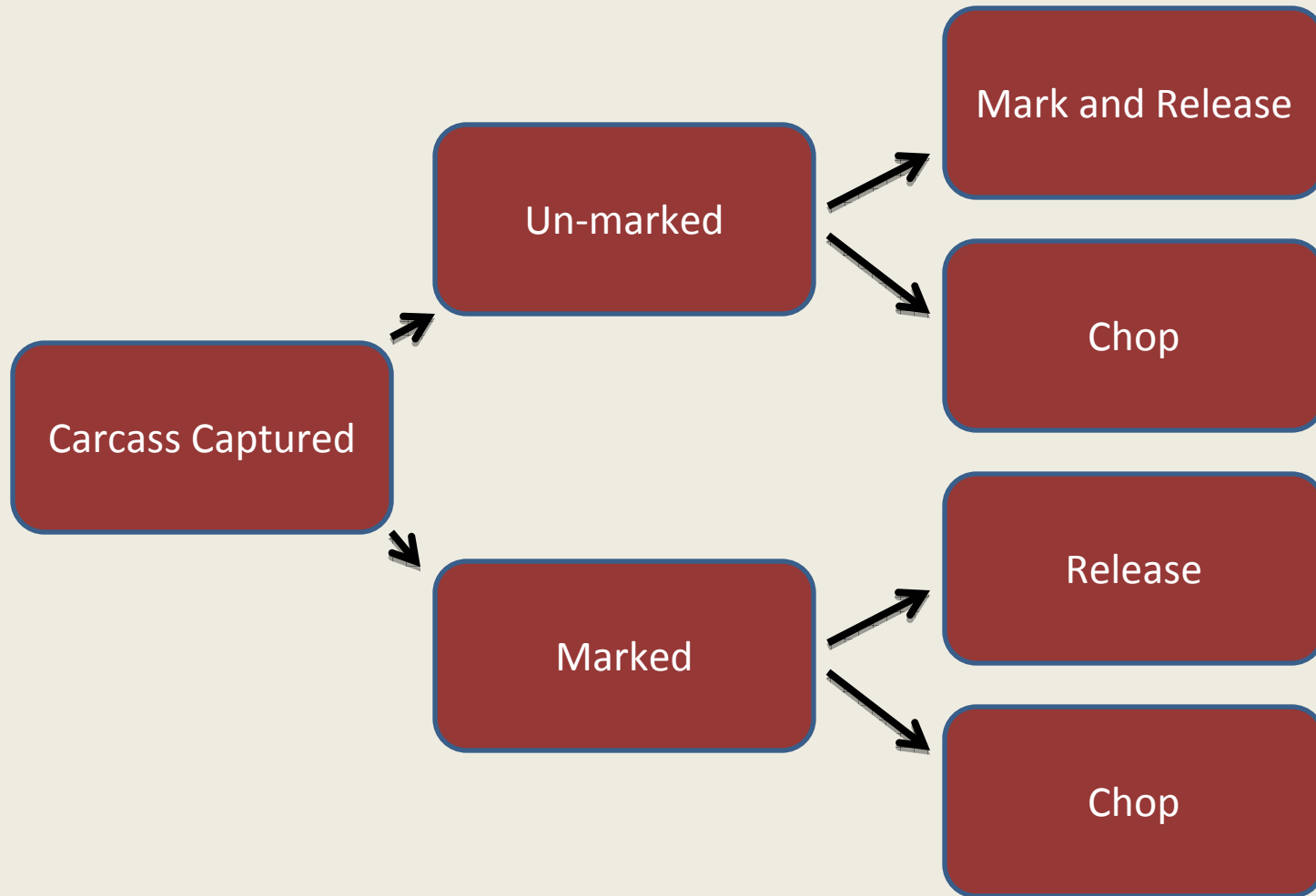
Sampling Situation

- Spawning areas have been identified
- Multiple surveys (mark & recapture occasions) conducted with a spawning season
- Surveys begin when first spawners appear and carcasses are just beginning to enter system
- Surveys end after no 'new' carcasses are found

Sampling Situation

- Tags are used to identify when the carcass was marked
- Additional biological information is also collected for each carcass captured

Sampling Situation



Analysis Options

- Past analysis methods have included
 - Pooled-Petersen
 - Modified Schaefer
 - (modified) Jolly-Seber

Pooled-Petersen/Schaefer

- Pooled-Petersen
 - A simple, closed population analysis
 - Begins with a stratified Petersen
 - Data pooled across multiple marking/recovery periods, and stratification is ignored
 - Chapman modification is recommended although it usually has little influence
 - Requires:
 - Population remains constant (no births or deaths)
 - Mixing (i.e., equal $P[\text{capture}]$ between marked and unmarked)
 - No lost tags

Pooled-Petersen/Schaefer

- Schaefer
 - Understood to (usually) have the same general performance and requires the same conditions as the pooled-Petersen, so it is no longer recommended (citations available)
- Both Pooled-Petersen and Schaefer can handle some violation of 'closure'
 - When violation is similar across strata, and is similar for marked and un-marked
 - Thus, can probably handle 'deaths' in some situations
- But, cannot account for 'births' (new carcasses)
 - because 'births' are ALWAYS un-marked

Modified Schaefer

- ‘Modified’ Schaefer (subtracting $\sum_2^s R_j$)
 - Citations are a mystery

Pooled-Peterson vs. Modified Schaefer

Some Simulation Results (in a nutshell)

- When population is closed and there are sensible strata...
 - Pooled-Petersen and Schaefer work similarly and OK
- When population is not closed but deaths and movement among strata occur...
 - Pooled-Petersen and Schaefer work similarly but positive bias
 - Modified Schaefer works similarly
- When population experiences births...
 - Pooled-Petersen and Schaefer can be TERRIBLE
 - Modified Schaefer not good either, but a bit better

Pooled-Peterson vs. Modified Schaefer

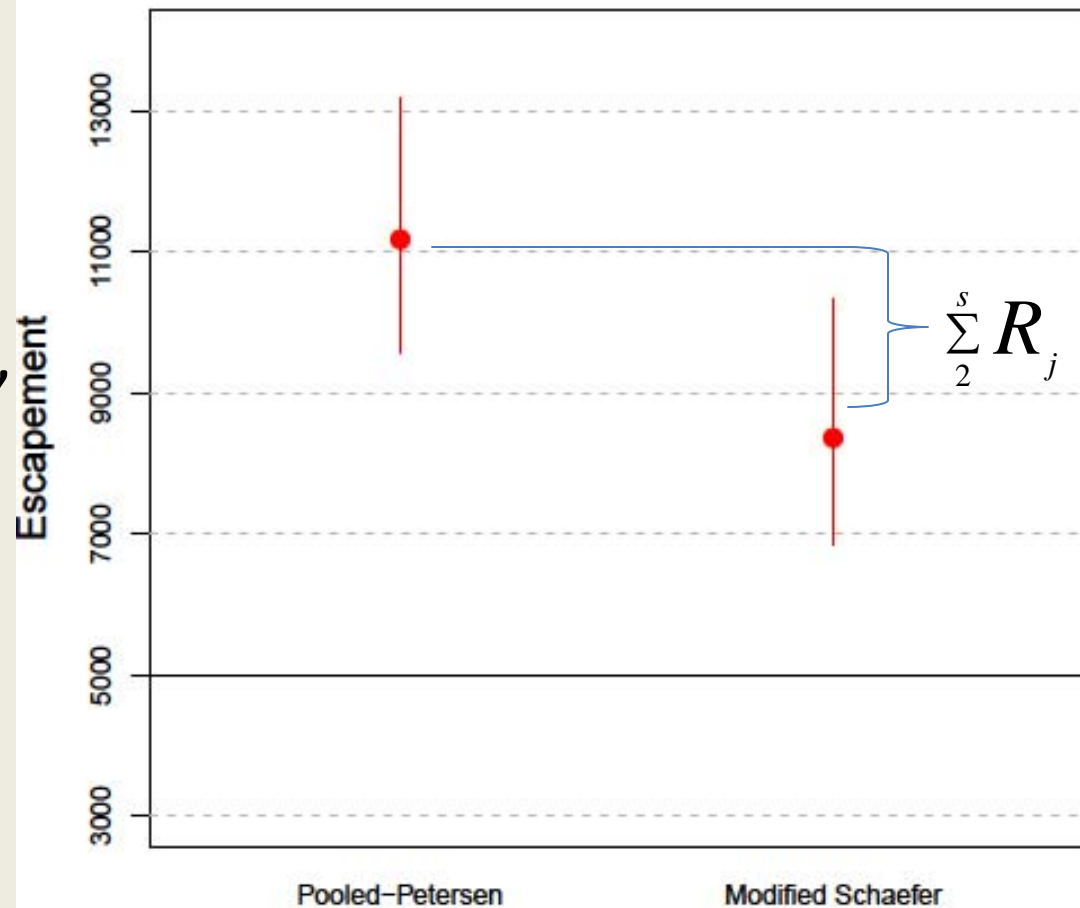
5 survey periods

$P[\text{capture}] = 0.5$

Births = 500, 1000,
2500, 1000, 0

$N = 5000$

$P[\text{survival}] = 0.8$



Pooled-Peterson vs. Modified Schaefer

- Other, more complex, simulations sometimes show a closer agreement between the 2 methods
 - But they are still biased high
- These techniques are not meant to handle 'births'

Jolly-Seber

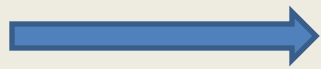
- Open population model
- Closed form MLE available that includes (derived) estimates of \hat{N}_j (more on this later)
- Requires:
 - no lost marks
 - emigration is permanent
 - equal survival and detection probabilities for marked and un-marked (i.e., mixing)
- Heterogeneity in capture probabilities (e.g., small vs. big fish) can result in negative bias

Jolly-Seber

- \hat{N}_j for survey periods estimate total number in the population during that time
 - Final estimate is an average of the \hat{N}_j values
- The superpopulation reparameterization was developed to handle a situation similar to what is experienced in the salmon surveys (i.e., lots of births and some deaths)
 - Crosbie and Manly 1985, Schwarz et. al 1993)
 - Estimates births between surveys i and $i+1$ and adjusts for those that died before having a chance to be sampled
 - Escapement = sum of births
 - Provides an estimate of the total number of unique carcasses ever in the system and available to be detected during the study

Analysis Options

- Can we improve on the (modified) Jolly-Seber?
 - Specifically, what about...
 - Equal survival and detection probabilities for marked and un-marked (i.e., mixing)
 - Heterogeneity in capture probabilities (e.g., small vs. big fish)



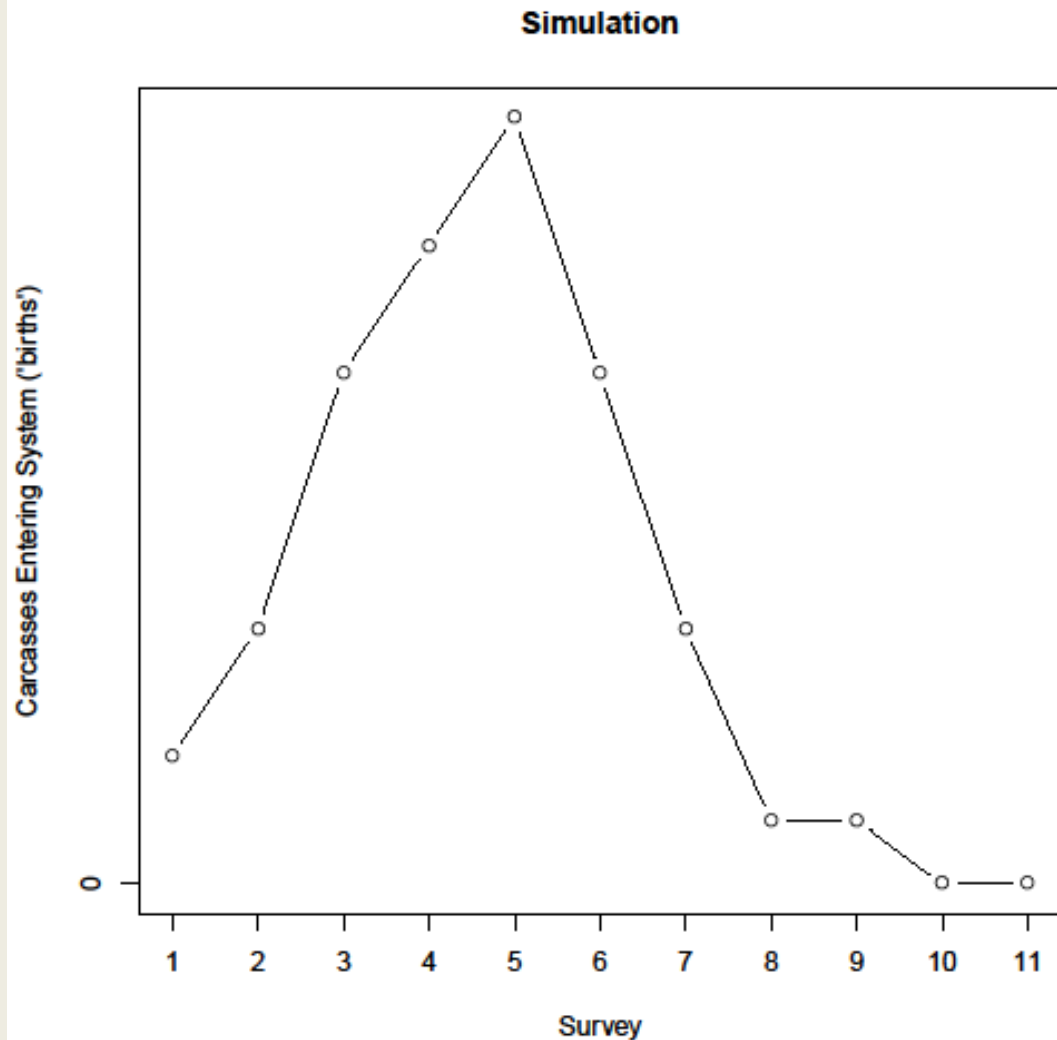
Cormack-Jolly-Seber

Cormack-Jolly-Seber

- Differences to the Jolly-Seber
 - Conditions on initial capture, thus does not require equal catchability between marked and un-marked carcasses
 - Likelihood is a bit different
 - Can handle complicated covariates (e.g., sex, size)
 - Still requires $P[\text{capture}] > 0$ and the right covariates
 - More robust

A Few Simulations

- 1,000 iterations
 - Unique ID tags
 - All fresh fish marked
 - Chopping
 - 11 sampling periods
 - Small N
 - Low survival
 - Low P[capture]
 - Focus on JS and CJS only
- only



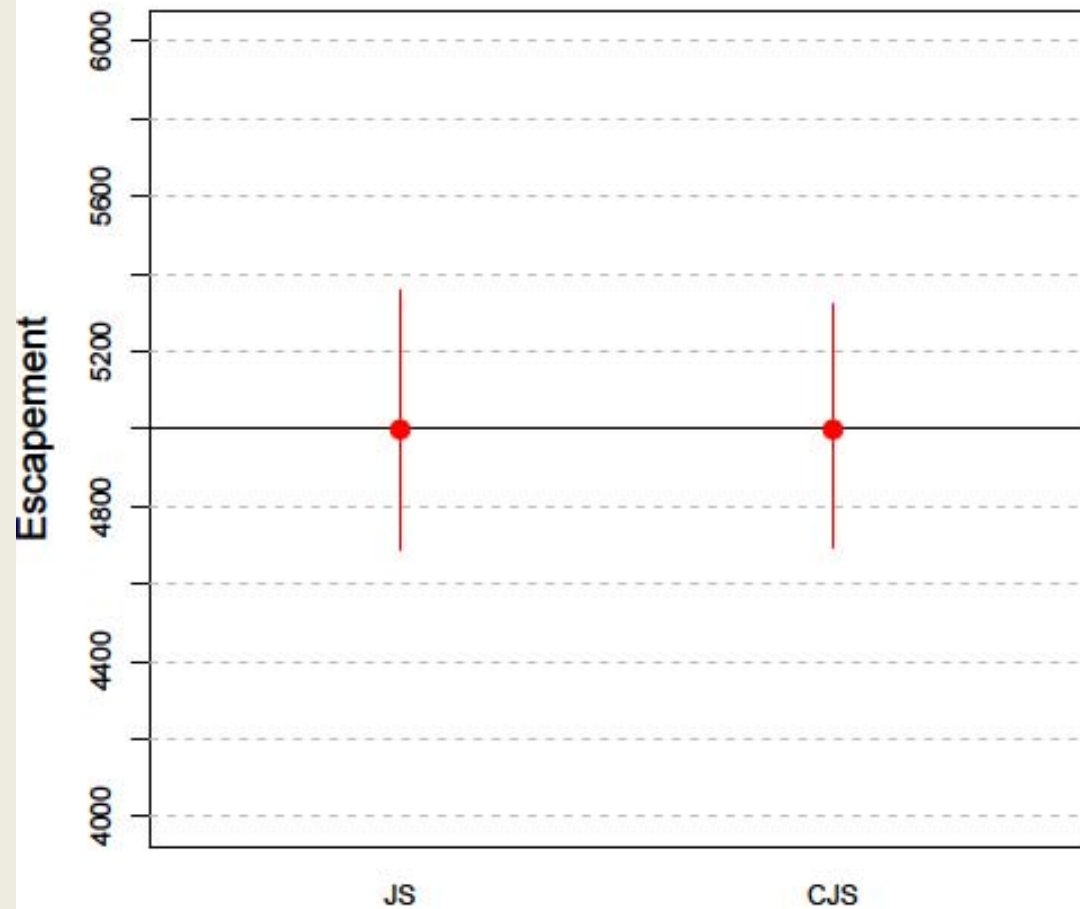
Simulation 1

Survival from
period i to $i+1 = 0.6$

$P[\text{capture}] = 0.3$

$N = 5000$

90% estimates within
8% of true
escapement



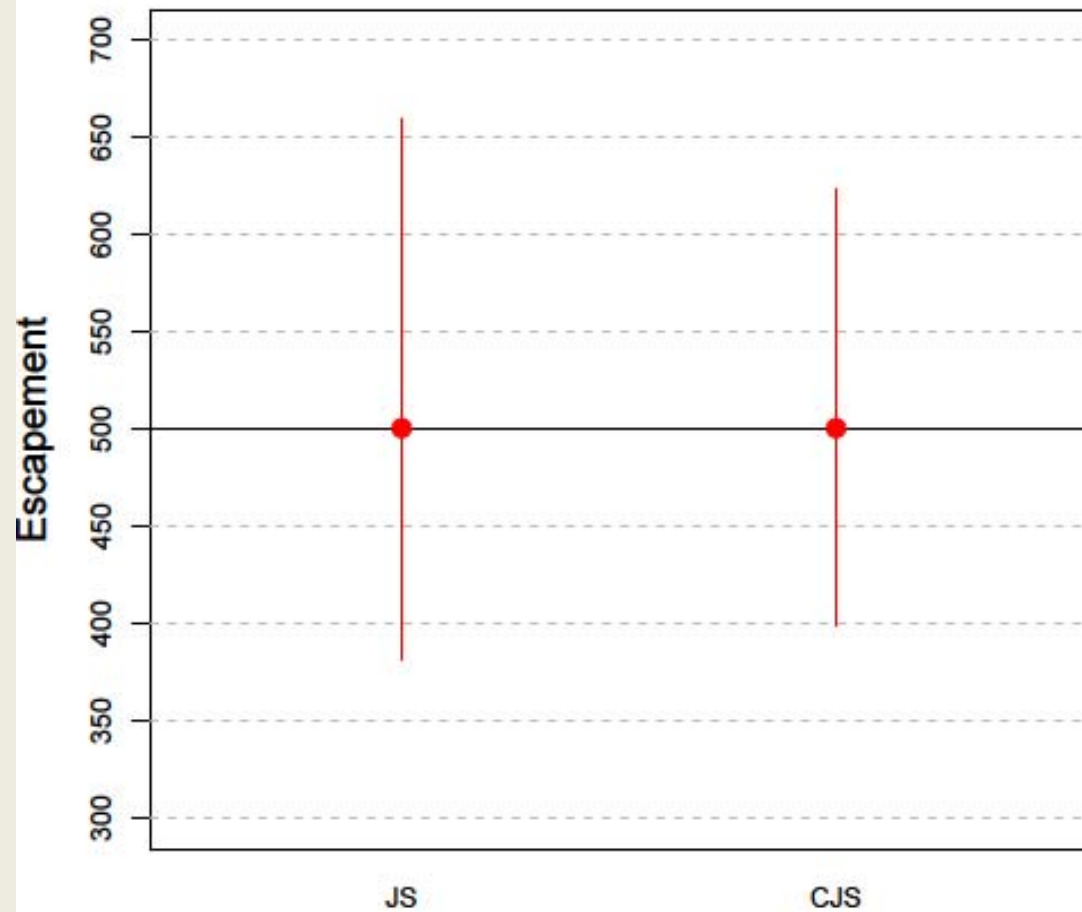
Simulation 2

Survival from
period i to $i+1 = 0.6$

$P[\text{capture}] = 0.3$

$N = 500$

90% estimates within
20% of true
escapement



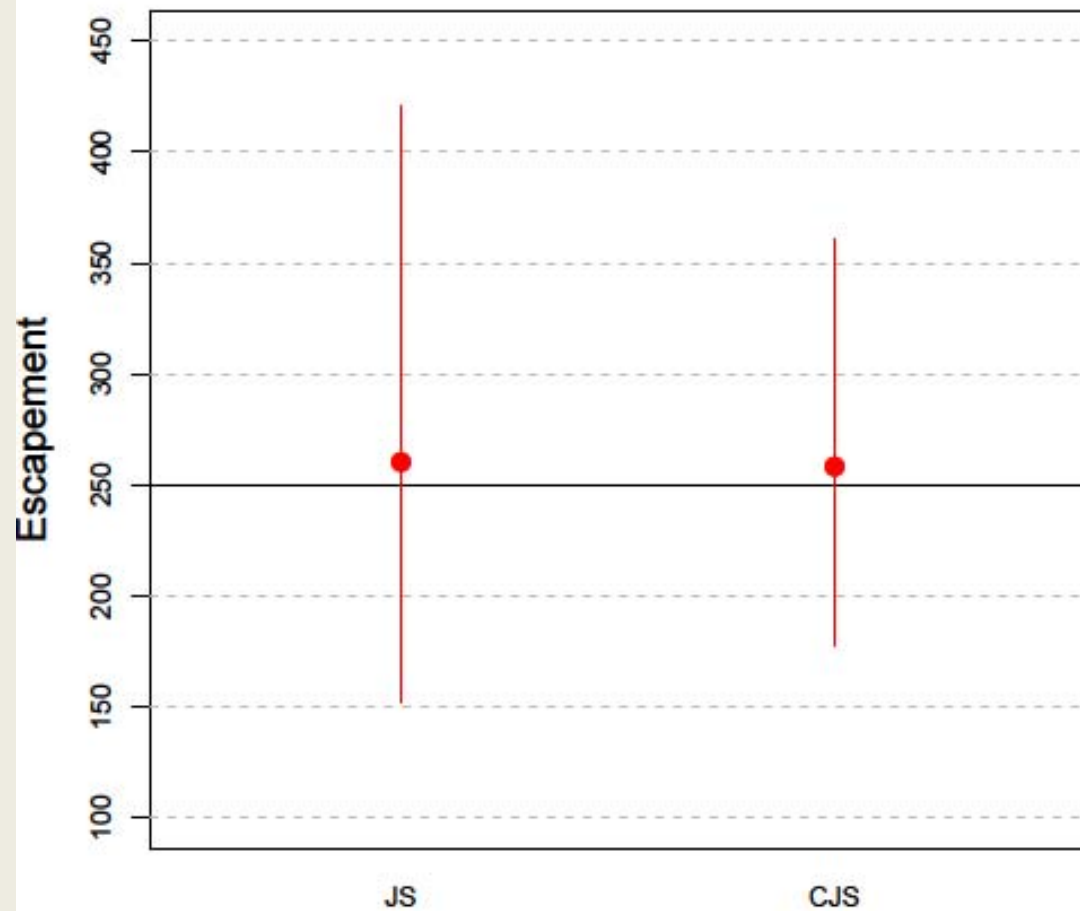
Simulation 3

Survival from
period i to $i+1 = 0.6$

$P[\text{capture}] = 0.3$

$N = 250$

90% estimates within
60% of true
escapement

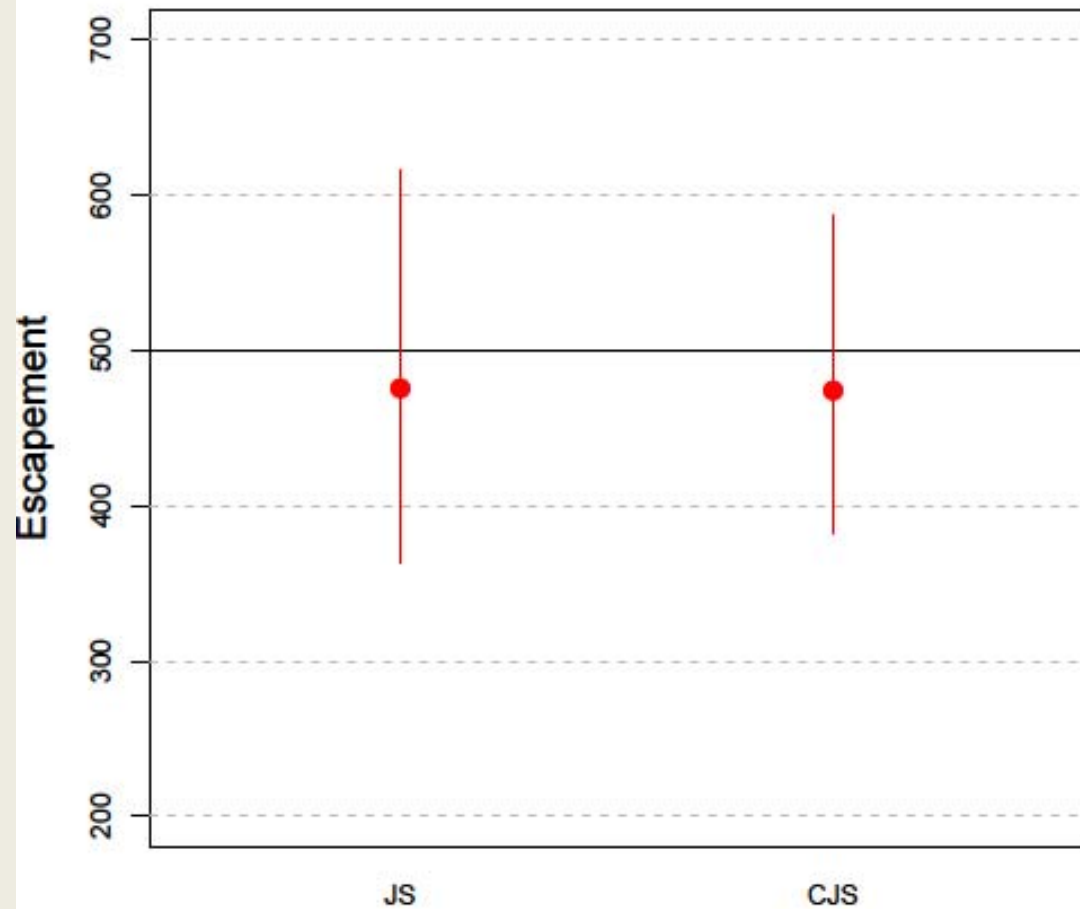


Simulation 4 - Heterogeneity

Survival from
period i to $i+1 = 0.6$

P[capture]
 $\sim \text{Unif}(0.15, 0.45)$

$N = 500$

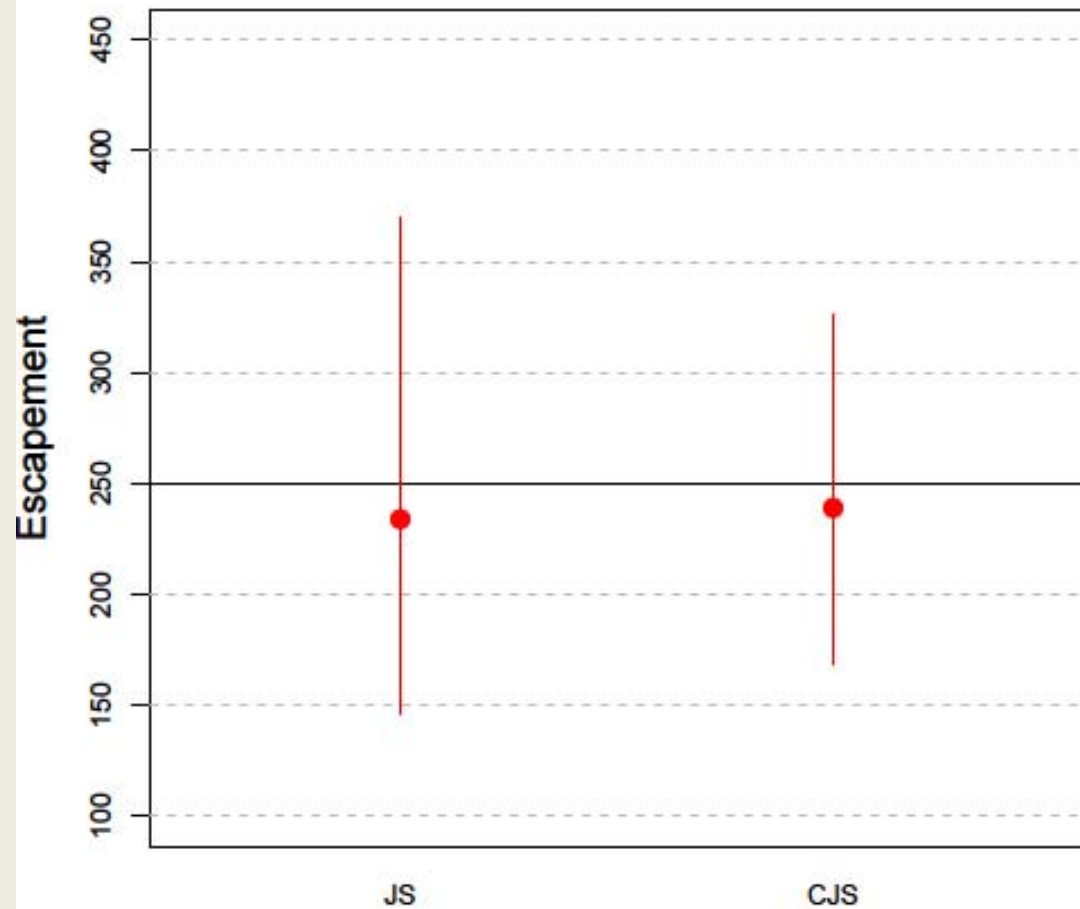


Simulation 5 - Heterogeneity

Survival from
period i to $i+1 = 0.6$

P[capture]
 $\sim \text{Unif}(0.15, 0.45)$

$N = 250$



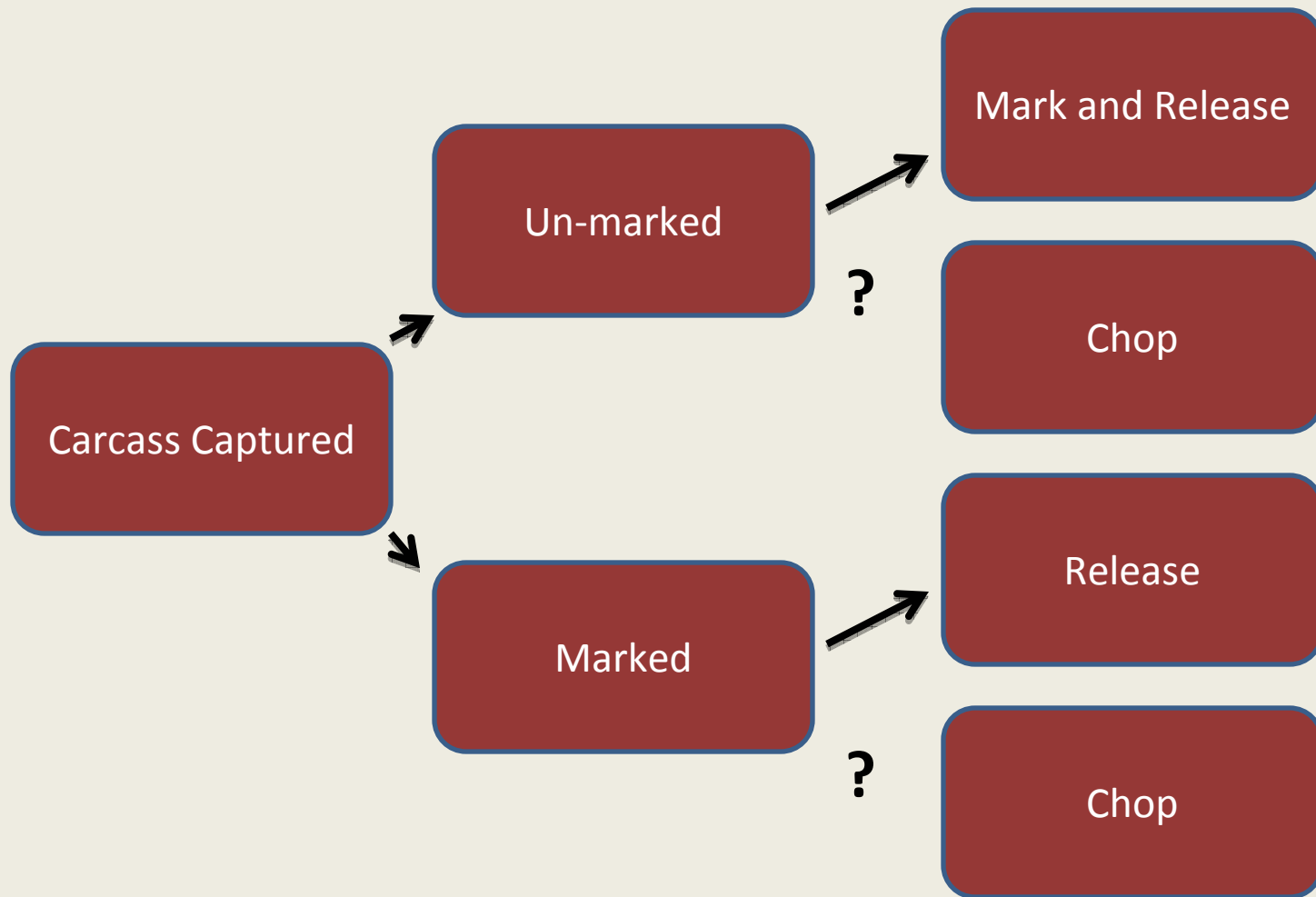
Conclusions

- CJS works a bit better than JS
 - We expected this
- CJS works well even when N , $P[\text{survival}]$ and $P[\text{capture}]$ are low
 - Superpopulation approach seems more robust than typical JS/CJS estimates
- Sampling protocol currently employed works
 - Can chop fish and focus on fresh
 - But we may need more data...

Discussion

- If we believe there is heterogeneity in the population, we can adjust for it using the CJS with covariates
- Testing covariates that may relate to $P[\text{capture}]$ and/or $P[\text{survival}]$ might require more data

Discussion



Discussion

- Unique tags
 - Lower jaw, so ad-clipped fish can be included
- Use the superpopulation modification to the CJS (see handout)
- Consider covariates that may relate to
 - $P[\text{capture}]$
 - $P[\text{survival}]$
- AICc can help determine 'best' model
- Confidence Intervals estimated via bootstrap

Future Work

- Workshop in winter of 2011 demonstrating analysis methods and use of 'mra' in R
 - Demonstrate installation and use of R
 - Modification of 'mra' for the superpopulation modification to CJS
 - Include code for comparing models using AICc and bootstrap for CIs
 - Include example data

Future Work

Collection of Future Data

- Record capture history for each carcass
 - E.g., 001020
 - '1' for when the carcass entered the marked population or was recaptured and released back into the marked population
 - '2' for when the carcass was removed from the marked OR unmarked populations: e.g., 002000
- Link biological information with each capture history