SEDAR

Southeast Data, Assessment, and Review

South Atlantic Red Snapper Research Program

Review Workshop Report

February 13, 2026

SEDAR

4055 Faber Place Drive, Suite 201

North Charleston, SC 29405

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1 INTRODUCTION

1.1 WORKSHOP TIME AND PLACE

The South Atlantic Red Snapper Research Program (SARSRP) Review Workshop was held in

Charleston, SC

January 13-15, 2026.

1.2 TERMS OF REFERENCE

1. Evaluate the study designs used for developing estimates of absolute abundance of age-2+ red snapper in the U.S. South Atlantic region (Florida, Georgia, South Carolina, North Carolina).
    a. Assess the study design and sampling sufficiency as they pertain to the application of genetic close-kin mark-recapture methodology.
    b. Assess the study design and sampling sufficiency as they pertain to the application of hierarchical Bayesian abundance modeling.

2. Evaluate the statistical/modeling methods used to analyze the data, and to construct the absolute abundances estimates and their variances.
    a. Are the close-kin mark-recapture methods applied appropriately?
    b. Are the hierarchical Bayesian modeling methods applied appropriately?

3. Are the estimates of absolute abundance (age-2+ red snapper) and their variances reliable?
    a. For each of the two estimation approaches, are assumptions appropriate, given study design considerations?
    b. Are there potential sources of uncertainty that were not considered when developing the estimates of abundance?
    c. For each of the two estimation approaches, describe the magnitude and direction of any potential biases.

4. Provide future research recommendations.
    a. How could each of the methods used in this study be improved for more accurate estimates?
    b. Are there other sampling or survey methods that could be used to improve the accuracy of estimates of absolute abundance?

1.3 LIST OF PARTICIPANTS

Review Panel

Marcel Reichert (Chair)	SAFMC SSC
Luiz Barbieri	SAFMC SSC
Noel Cadigan	CIE Reviewer
Joe Powers	CIE Reviewer
Daniel Ruzzante	CIE Reviewer

Program Team

Will Patterson (Lead PI)	Univ of Florida
Nathan Bacheler	SEFSC
Jeffrey Buckel	NCSU
Nathan Hostetter	NCSU
David Portnoy	TAMUCC
Matthew Vincent	SEFSC

Staff

Julie A Neer	SEDAR
Chip Collier	SAFMC Staff
Judd Curtis	SAFMC Staff
Rachael Silvas	SAFMC Staff
Emily Ott	SEDAR

Workshop Observers

Chris Bradshaw	FLFWC
Wally Bubley	SCDNR
Chris Custer	NCSU
Amy Dukes	SCDNR
Liam Kehoe	UF
Ryan McMullen	SC Sea Grant
Emily Osborne	SC Sea Grant
Tracey Smart	SCDNR
Julie Vecchio	SCDNR
Jordy Wolfe	SCDNR

Workshop Observers via Webinar

Eric Anderson	
Jordan Bajema	FWC
Sydney Bates	SCDNR
Kristan Blackhart	NOAA
Jason Boucher	NOAA
Myra Brouwer	SAFMC Staff
Julia Byrd	SAFMC Staff
Jessica Carroll	FWC
David Chagaris	UFL
Kristin Cook	FWC
Ellie Corbett	FWC

Michael Drexler	Ocean Conservancy
Ben Dyar	SCDNR
Joseph Evans	SCDNR
Alena Figueroa	FWC
Margaret Finch	SCDNR
Kristin Foss	FWC
Dawn Franco	GA DNR
Elizabeth Ford	
Keilin Gamboa-Salazar	SCDNR
Brad Gentner	
Ben Goldstein	
Elizabeth Gooding	SCDNR
Amiee Griffin	FWC
Jenny Grossmann	COFC
Martha Guyas	ASA
Homer Hiers	SCDNR
Kathleen Howington	SAMFC Staff
Jeanette Huber	FWC
Allie Iberle	SAFMC Staff
Blaik Keppler	SCDNR
Kevin Kolmos	SCDNR
Genine McClair	FWC
Maria McGirl	FWC
Paul McLaughlin	FWC
Nikhil Mehta	NOAA
Trish Murphey	NCDEQ
Gabby Ocampo	FWC
Krishna Pacifici	NCSU
Chloe Ramsay	FWC
Brian Reich	NCSU
Scott Sandorf	NOAA
Mike Schmidtke	SAFMC Staff
Nick Smillie	SAFMC Staff
Wiley Sinkus	SCDNR
Kevin Spanik	SCDNR
Joesph Tarnecki	
Chris Taylor	NOAA
Miaya Taylor	UFL
Erik Williams	SEFSC
Olivia Wilms	FWC
Meg Withers	SAFMC Staff
Daniel Zapf	NCDEQ

1.4 LIST OF MATERIALS AVAILABLE TO THE REVIEW PANEL

Population Estimation of U.S. Atlantic Red Snapper: Final Report to the South Atlantic Red Snapper Research Program
Appendix I: Applying mark-resight, count, and telemetry data to estimate effective sampling area and fish density with stationary underwater cameras
Appendix II: An Integrated Approach to Estimating the Effective Sampling Area of Baited Underwater Camera Traps
Appendix III: Spatiotemporal dynamics and habitat use of red snapper (*Lutjanus campechanus*) on the southeastern United States Atlantic continental shelf
Appendix IV: Genetic Population Structure of Red Snapper, *Lutjanus campechanus,* in the U.S. Atlantic and Eastern Gulf of America
Appendix V: Sensitivity of CKMR population estimates to uncertainty in life-history parameters
Appendix VI: Incorporating Close-Kin Mark-Recapture Data into an Integrated Stock Assessment Model for Southeast United States Atlantic Red Snapper (*Lutjanus campechanus)*
Appendix VII: Estimating Reef Fish Exploitation Rates in Catch-and-Release Fisheries with Conventional and Genetic Tags
Appendix VIII: Stakeholder Insights Corroborate Habitat and Reef Fish Abundance on the Southeastern U.S. Atlantic Continental Shelf
Appendix IX: Discard mortality rates of Red Snapper after barotrauma and hook trauma: Insights from using acoustic telemetry in the U.S. South Atlantic
Appendix X: Post-release Mortality of Red Snapper, *Lutjanus campechanus*, in U.S. Atlantic Waters off Northeast Florida Estimated with Three-Dimensional Acoustic Telemetry

2 REVIEW PANEL REPORT

2.1 EXECUTIVE SUMMARY

The purpose of the review was to evaluate work conducted by the South Atlantic Red Snapper Research Project (SARSRP) following the provided Terms of Reference. The Review Panel reviewed the provided documents and received four presentations during the review. The Panel appreciated the enormous amount of work the project represented.

Close-Kin Mark-Recapture Methodology (CKMR)

The Review Panel concluded that the CKMR methodology and study design appears robust and the sampling effort sufficient for an initial estimate of population abundance, although the uncertainty associated with this estimate is likely to have been underestimated. The Panel further determined that the CKMR methods and analyses were developed consistent with theory and modeling experience and were applied appropriately. However, the Review Panel noted that insufficient information was provided to fully assess the reliability of the CKMR overall abundance estimate given the assumptions and appropriateness of the input data and parameters. CKMR methods are conditioned on life-history and demographic parameters. Census population size can be estimated using genetic data, but only if the estimation model is not misspecified in ways that bias the expected probabilities of observing CKMR kin pairs. The Review Panel also cautioned that the abundance estimate based on CKMR is not independent from the SEDAR 73U stock assessment information and this may be problematic. One concern is whether a CKMR abundance estimate that relies so heavily on SEDAR assessment(s) can be used as an independent estimate or input to the next stock assessment. The Panel had considerable discussions about the methods and data used in the analysis, in particular relative to how the simulation software CKMR*pop* was configured and parameterized for the sensitivity analyses (SARSRP Appendix V).The Review Panel recommends that the sensitivity analyses be redone using the CKMR model described in Chapter 3 and that the impact of different levels of the parameter overdispersion (reproductive skew) be considered. Until these analyses are completed the Review Panel is unable to assess misspecification of this parameter as a potential source of bias in the CKMR abundance estimate. Another potential source of uncertainty is the lack of consideration of fish sex. Significant differences between the sexes would lead to different Expected Relative Reproductive Output (ERRO) estimates depending on the sex of the unsampled parent of the half sibling pairs. The SARSRP Team presented several alternative model structures or sensitivity analyses to assist in the evaluation of the relative importance of the various model components on final estimates. These tests included assuming equilibrium population size over the sampling period versus allowing for an increasing trend. Also, alternative initial age structures were investigated. The Review Panel noted that further uncertainty in the estimate of total abundance for age 2+ red snapper is likely given that, as stated in Chapter 3, an unknown number of age 1 (and age 0) fish may have been included in the CKMR estimate.

Bayesian Hierarchical Integrated Model (BHIM)

The Review Panel concluded that sampling design and sampled locations were sufficient to estimate average camera counts of red snapper for the entire sampling frame of the Southeast Reef Fish Survey (SERFS). Paired sampling with SERFS video trap and remotely operated vehicle (ROV) to calibrate red snapper counts occurred in three areas. The Review Panel concluded this was sufficient for the purpose of calibration with video trap counts. Based on the ROV data, the SARSRP Team concluded that Red Snapper abundance over unconsolidated bottom was very low in the Atlantic SEUSA, and the Review Panel agreed with that conclusion. The two complementary studies conducted at Chicken Rock (North Carolina) and Turtle Mound (Florida) to estimate the effective sample area (ESA) of video trap gear were critical for estimating total red snapper abundance. The Review Panel did not review the Turtle Mound study in detail as estimates were considered unrealistic by the SARSRP team. The Review Panel noted that it was difficult to fully understand how the Chicken Rock study results were produced, but based on additional information by the SARSRP Team, the Review Panel has confidence in the study outcome. However, since this study was conducted in only one area over a limited time, the Review Panel had little confidence that the resulting ESA represents the overall ESA for the entire stock area. Another area of concern was that the SERFS video data and ROV density estimates were expanded to the entire study area using uncertain information of hard bottom habitat. The BHIM red snapper population estimate was sensitive to how bottom type was identified and classified, and this habitat uncertainty was not included in the overall CV of the BHIM red snapper population estimate. As with the CKMR methods, the Review Panel noted that the population estimate coming from the BHIM is not entirely independent from stock assessment data. Video trap data from the trap cameras have been used in previous assessments as a measure of relative abundance and were also used in the BHIM analysis. Because size and age information was not included in the BHIM analysis, the estimate of total abundance for age 2+ has some uncertainty as an unknown number of age 1 (and possibly age 0) may have been included in the estimate. As with the CKMR work, this is explored in the SARSRP report but should be taken into account when this estimate is included in, or compared with the assessment outcome. Overall, the Review Panel noted that it had little confidence in the BHIM population estimate because the estimate of ESA is based on data from one study in one area, and more importantly because of the uncertainty in the hard bottom habitat characterization.

The Panel provided 15 research recommendations that may lead to improving the accuracy of the red snapper population estimates.

2.2 INTRODUCTION

An independent peer review of the South Atlantic Red Snapper Research Project (SARSRP) was conducted during an in-person Review on January 13-15, 2026, in Charleston, SC. The Review Panel consisted of Drs. Marcel Reichert (Chair), Luiz Barbieri (South Atlantic Fisheries Management Council's Scientific and Statistical Committee), Daniel Ruzzante (Center for Independent Experts, CIE), Noel Cadigan (CIE), and Joe Powers (CIE). The Review Panel was assisted by Southeast Data, Assessment, and Review (SEDAR) staff Julie Neer and Emily Ott, and various South Atlantic Fisheries Management Council (SAFMC) staff. Prior to the review the Review Panel was provided with a SARSRP report and ten supporting appendices. During the review, the SARSRP team (led by P.I. Dr. Will Patterson) provided 4 presentations supporting information in the review documents.

The Review Panel much appreciated the very collegial nature of the review deliberations and the positive response of the SARSRP Team to the Panel's comments, questions, and requests for additional information. The Review Panel acknowledged the SARSRP team for the incredible amount of work, the project report, and the presentations during the review. The Review Panel also thanks SEDAR, SC Sea Grant, and SAFMC staff for their invaluable support during the review process.

This summary report addresses Terms of Reference (see page 3 above) and the report structure generally follows the TORs.

2.3 REVIEW PANEL SUMMARY REPORT

The purpose of the review was to evaluate work conducted by the South Atlantic Red Snapper Research Project (SARSRP). There were several opportunities for the public to provide comments, but no public comment was provided prior and during the review, either in person or in writing.

The Panel reviewed the provided documents and during the review received four presentations by Drs. Will Patterson (Report Chapters 1- Introduction, and 4 - Summary), Nathan Hostetter (Report Chapter 2 - Hierarchical Bayesian Abundance Modeling), and David Portnoy (Report Chapter 3 - Close-Kine Mark-Recapture Methodology). The discussions following the presentations are summarized below.

1. Evaluate the study designs used for developing estimates of absolute abundance of age-2+ red snapper in the U.S. South Atlantic region (Florida, Georgia, South Carolina, North Carolina).

1.a. Assess the study design and sampling sufficiency as they pertain to the application of genetic close-kin mark-recapture methodology.

Genetic mark-recapture methodologies are a modern variation of traditional mark-recapture with some important differences. A genetic mark is the composite genotype of an individual across some number of characterized loci and is natural and permanent. Therefore, it can be recovered from tissue whether the animal is alive or dead. Genetic marks are transmitted from parent to offspring, thus are partially shared between related individuals, considerably expanding the scope of what may be considered a “recapture” to closely related individuals (i.e., kin). Combining kin recaptures with models informed by life-history information to relate the number of kin to absolute population size is a recent technique of close-kin mark-recapture (CKMR). Note that these CKMR methods are always conditioned on life-history demographic parameters.

Preliminary simulations of population dynamics with hypothesized CKMR sampling were conducted to determine the required sampling regime prior to the implementation of the study. Results indicated a target annual sample size of 2,500 individuals per year would produce an accurate (±4.5%) red snapper population estimate with CV ≤0.3 for population sizes of 0.5-1.5 x 10^6 individuals. When the fin clip sample size was increased to 5,000 individuals per year, the accuracy of the CKMR estimate was ±4.4% with a CV ≤0.14.

Based on these results, a design was implemented in which red snapper fin clips were sampled from fisheries-independent and -dependent sources along the U.S. Atlantic Coast between Port St. Lucie, Florida and Cape Hatteras, North Carolina during 2021-2023. Metadata for all sampled individuals can be found at https://github.com/marinegenomicslab/Red-Snapper-CKMR. Sampling was carried out by a variety of academic, state and federal partners, with the majority of samples coming from randomized fishery-independent video/trap or vertical line surveys conducted by NOAA Fisheries, Beaufort Laboratory, South Carolina Department of Natural Resources (SCDNR), and the Florida Fish and Wildlife Conservation Commission (FWC). The sampling design and the realized sampling effort exceeded the recommendations implied by the sampling simulations.

The CKMR estimation of Atlantic red snapper population size was conditioned on an age-structured demographic model with parameters from the most recent stock assessment (SEDAR 73 Update) or from the Data Workshop of the ongoing SEDAR 90 stock assessment process providing existing age structure (ages 1-20+), survival rates, and fecundity. Age-specific relative reproductive output of males was assumed to scale with age the same as the fecundity of females. The proportion of females mature at age was assumed to be the same for males. A sex ratio of 1:1 was used throughout. By design, the CKMR estimates depend on the understanding of the demographic rates and proportions as they existed in 2019-2023. However, it is expected that estimates of the 2019-2023 demographic rates and proportions will evolve based on future stock assessments and/or future research. Thus, the CKMR estimates for this time period will also evolve. Nevertheless, the Review Panel concluded that the current design conditioned on the most recent assessment and Data Workshop are sufficiently adequate for estimation.

The Review Panel had considerable discussion relative to the methods and data used in the CKMR analysis, in particular relative to the metric of reproductive output (adult biomass-at-age vs. fecundity-at-age) used in different parts of the report (Chapter 3 vs. Appendix V). The Review Panel recommended adding text to an update of the report to clarify this (see also below).

The Review Panel noted that it is important to realize that the population estimate coming from the CKMR analysis is not entirely independent from population estimates coming from previous or ongoing SEDAR stock assessments. In particular, the demographic model was parameterized with age composition data for all age groups in years 2014-2023, and with year-specific annual survival rates estimated by the SEDAR 73 update assessment. Likewise, life-history characteristics and parameters (sex ratios, sexual maturity, mean lengths and weights at age, and instantaneous total mortality at age) were derived from the current SEDAR 90 Data Workshop report. Life-history parameters (i.e., vital rates) anchor all probabilities in CKMR, so if they are off (e.g., survival overestimated), the bias in census abundance (*Nc*) estimates compounds or sometimes partially offsets the age composition bias. This also raises concerns about the next planned step in this process (i.e., the incorporation of CKMR abundance estimates into the Beaufort Assessment Model used for SEDAR 90).

> From Appendix VI – Incorporating CKMR data into the S90 stock assessment:
> "*CKMR population estimation will be incorporated into the BAM as an additional likelihood component, specifically using a binomial pseudo-likelihood formulation (Bravington et al. 2016; Hillary et al. 2018). This binomial model utilizes kinship probabilities modeled as a function of abundance-at-age, spawning output, and survival probability.*"

The Review Panel finds it problematic if a CKMR abundance estimate that relies so heavily on a previous stock assessment (SEDAR 73 Update) is used as an independent input to the next stock assessment. It seems more appropriate to incorporate the CKMR data into the estimation of the next stock assessment (SEDAR 90), as the Appendix VI text above indicates, but should be clarified that probabilities are modeled as a function of BAM internal values. Hence, incorporating the CKMR data may affect BAM estimates of *abundance-at-age, etc*.

Overall, the study design appears robust and the sampling effort seems to have been sufficient for an initial estimate of population abundance, although given the issues described above, the uncertainty associated with this estimate is likely to have been underestimated. What is required to potentially increase accuracy and perhaps precision on the *Nc* estimate is the identification of the sex of the UNSAMPLED parent of the half sib pairs. A difference between the sexes in age at 50% maturity and in the relationship between fecundity and age would lead to differences in the ERRO estimation which would propagate to the *Nc* estimation.

1.b. Assess the study design and sampling sufficiency as they pertain to the application of the Hierarchical Bayesian abundance modeling

The Bayesian Hierarchical Integrated Model (BHIM) utilized data from the Southeast Reef Fish Survey (SERFS) video trap as well as from fish count estimates produced with remotely operated vehicle (ROV) video samples. BHIM predicted abundance throughout the stock area by utilizing modelled relationships with hardbottom (reefs, rocks, and areas of high relief) habitat and depth data. The SERFS video trap data were utilized to examine temporal and spatial trends in red snapper abundance and bottom habitat in areas of the southeastern U.S. Atlantic (SEUSA). ROV data also contributed abundance information in hard bottom regions and were also used to test whether red snapper could be found on unconsolidated habitats not targeted by the SERFS survey, which has been identified to occur in the Gulf of Mexico.

The SERFS video traps sampled reef fish across the SEUSA continental shelf and upper slope between Cape Hatteras, North Carolina, and St. Lucie Inlet, Florida, using baited chevron traps with two attached video cameras. For the purpose of the BHIM analysis, the number of red snapper were then quantified using the video analysis only. Red Snappers were counted in each of 41 snapshots spaced 30 seconds apart, beginning 10 minutes after the video trap reached the seafloor and spanning a total of 20 minutes. Trap catches of red snapper were not used in the BHIM for several practical reasons (e.g., uncertain effective sampling area; see research recommendation below). SERFS sampling locations were chosen via simple random sampling from approximately 4,300 potential sites assumed to have reef structure. An important factor to affect camera counts was current direction, which was qualitatively categorized at each location as “away”, “sideways”, or “towards” based on the movement of visible particles in the water relative to the view field of the video camera over the trap mouth. Sampling occurred during April-September in 2021 (n=1,384 video trap deployments) and 2022 (n=1,050 video trap deployments).

The Review Panel concluded that the sampling design and sampled locations were sufficient to estimate average video camera counts of red snapper for the entire SERFS sampling frame (i.e., approximately 25% of the 4,300 potential sites were sampled in 2021 and 2022) , but the Review Panel noted that no video trap data was available for the area south of St. Lucy, FL and North of Cape Hatteras, NC, as was acknowledged in the SARSRP Report.

The primary purpose of the ROV surveys was to estimate red snapper density over a variety of habitats, assuming that “area swept” could be estimated accurately. Importantly, ROV data were used to test whether red snapper occurs on unconsolidated habitats not targeted by the SERFS survey. Sampling was conducted during June-August 2021 (n = 262 samples) and June-October 2022 (n = 174 samples). Sites (n = 231) were either randomly selected for sampling (in 6 strata) or paired with SERFS camera-trap locations (n = 205). The stratified-random sampling area included the Florida Keys and the area north of Cape Hatteras that were not part of the SERFS sampling area.

Prior to the study, there was uncertainty about whether there was a significant Red Snapper abundance/biomass on unconsolidated habitat not sampled by SERFS, and thus not accounted for in (stock assessment based) abundance estimates. The ROV study concluded that Red Snapper abundance over unconsolidated bottom was very low in the Atlantic SEUSA, and the Review Panel agreed with that conclusion.

Additional sites (n = 205) were selected to pair with SERFS video trap locations to calibrate ROV red snapper counts with video trap counts. Paired sampling occurred in three areas. The Review Panel concluded this seemed sufficient for the purpose of calibration with video trap counts.

Two additional, complementary studies were conducted to estimate the effective sample area of video trap gear such that red snapper count data could be expressed as density (number per unit area), which was critical for estimating total population size. These complementary studies involved telemetry experiments at two sites (Chicken Rock, North Carolina and Turtle Mound, Florida). At Chicken Rock, 18 sites were selected for both baited underwater video and ROV surveys, while at Turtle Mound 36 sites were selected. At Chicken Rock, 21 acoustic receivers were deployed in a grid and 45 fish were tagged with acoustic transmitters and released. At Turtle Mound, 100 receivers were deployed and 65 fish were acoustically tagged. The telemetry data were used to provide information on the movement and relative distribution of fish around the video traps and the effective sampling area (ESA) of video traps. Estimates from the Turtle Mound study were considered unrealistic by the SARSRP team and the Review Panel did not review this study in detail. Therefore, the informative prior distribution for ESA used in the BHIM was based only on the Chicken Rock study, and the Review Panel concluded that this was insufficient to estimate video trap ESA for red snapper throughout the SEUSA Atlantic stock area. The Chicken Rock study was provided in Appendix II and was not reviewed and discussed by the Review Panel in great detail. Review Panel members noted that it was difficult to fully understand how the results were produced. The Review Panel recommends adding text from Appendix II to the main body of an updated SARSRP report to improve understanding of how this information was obtained (and integrated into the analysis). Additional information and the presentations by the SARSRP Team during the review resulted in some confidence by the Review Panel in the outcome of the Chicken Rock study. However, because this study was conducted in only one area over a limited time, the Review Panel had little confidence that the resulting ESA represents the overall ESA for the SEUSA (see also Research Recommendations under TOR #4 below).

SERFS video data and ROV density estimates were expanded to the SEUSA stock area using information on the extent of hard bottom habitat. There was important uncertainty about the locations of hard bottom habitat throughout the stock area. Analyses by the SARSRP Team demonstrated that the BHIM was sensitive to how bottom type was classified throughout the stock area. This included uncertainty about whether identified locations with hard bottom habitat were accurate, and whether the larger areas characterized as unconsolidated habitat could contain some hard bottom red snapper habitat. The Review Panel considered this an area of considerable concern.

As with the CKMR methods, the Review Panel noted that it is important to realize that the population estimate coming from the BHIM is not entirely independent from stock assessment data. Video trap data from the trap cameras have been used in previous assessments as a measure of relative abundance and were used in the BHIM analysis.

During the workshop the Review Panel requested several additional clarifications and analyses related to the parameterization of the BHIM. Clarifications were requested on 1) how well identified some of the BHIM parameters were and 2) about the N-mixture model detection probabilities. The SARSRP team provided this information during the meeting (see Addendum A). Posterior distribution correlations were high between camera trap ESA for the three current direction categories. Also, there was substantial correlation in estimates of the ROV offset parameter and the parameter for paired sampling design effects. However, overall, the Review Panel was satisfied that the BHAM parameters were not highly confounded. The SARSRP team provided the posterior distribution for the camera-trap detection probabilities, which had a mean of 0.19. This indicates that roughly 19% of the latent number of red snapper available at a sampling site are detected in one camera-trap frame, but this will vary between frames and sampling sites. The Review Panel appreciated these responses from the SARSRP teamAfter discussing the additional material, the Review Panel had no additional requests or comments.

Overall, the Review Panel concluded that the study design and sampling was sufficient, but noted that the fact that the ESA estimates were based on data from one study in one area only, and more importantly the uncertainty in the area of hard bottom habitat significantly increased the CV around the abundance estimate.

2. Evaluate the statistical/modeling methods used to analyze the data, and to construct the absolute abundances estimates and their variances.

2.a. Are the close-kin mark-recapture methods applied appropriately?

The Review Panel concluded that the CKMR methods were generally developed consistent with theory and modeling experience and the statistical and modeling methods were applied appropriately, but some details were difficult to evaluate (see also under TOR 1a).

The basic structure of the methods implemented was a standard CKMR pseudolikelihood using an age-structured model. Given numbers at age at different times, N, then the probability that a pair of samples with birth years b1 and b2 are half-siblings, i.e., P(HS|b1,b2,N,Θ) is calculated. This depends on other inputs, Θ, which includes: time-specific age composition, age-specific fecundity / reproductive output and age-specific total survival rates (S).

Ages of most red snapper samples (81.7%) were estimated via standard otolith-based ageing protocols. Age was estimated for samples that lacked otolith samples utilizing an age-length key (ALK) developed for SEDAR 90. The ALK provides the probability of being age (0 to 20) given length (in 10 mm bins) and month. However, the sum of all possible pairs over all ages within a strata would result in an infeasible number of categories of pairs that would need to be evaluated. Instead, ages were imputed based on the ALK probability and repeated 100 times, which reduced the number of category pairs to a feasible number of 8000.

The generalized CKMR model for half-sibling kinship probability of a half sibling occurring (with b1<b2 and d=b2-b1) is

$$P(\mathrm{HS}|b_1,b_2,N,\Theta) = 4\sum_{a^*=1}^{a*=20-d}\left[\frac{E_{b_1,a^*}E_{b_2,a^*+d}}{N_{b_2,a^*+d}}\prod_{a=a^*+1}^{a^*+d} S_a\right]$$

where the leading factor of 4 accounts for maternal and paternal half-siblings with an even sex ratio and similar survival and reproductive success between sexes. The probability of an HS pair occurring ***and*** being designated is: PHS(b1,b2 ,NSL) = P(HS|b1,b2,N,Θ)(1 – $\mathrm{FNR}_{\text{GT-seq}}$)(1 – $\mathrm{FNR}_{\text{ddRAD}}$). The probability that any pair (HS or unrelated) is not designated as an HS at the GT-seq stage is:

$PN(b1,b2\,,NSL) = 1 - P(HS|b1,b2,N,\Theta)(1 - FNR_{GT\text{-}seq})$, where FNR is the false negative rate and NSL is the number of shared loci.

Let #HS(b1, b2, NSL) and #N(b1, b2, NSL) be the number of identified HS pairs and non-HS pairs, respectively in a b1, b2 and NSL category. Then this category contributes #HS(b1, b2, NSL)log[PHS(b1,b2 ,NSL)] + #N(b1, b2, NSL)log[PN(b1,b2 ,NSL)] to the pseudo-log-likelihood. Then the full-pseudo-log-likelihood is a sum over the ~8,000 different b1, b2, and NSL categories. This constitutes the basic statistical method for half sibling CKMR maximum likelihood estimation of abundance at age for specified years. That formulation allows for the estimation of variance, as well. However, it must be remembered that this variance is conditional on having known ages and other known demographic parameters.

The report describes the demographic model used in the estimation (see under TOR 1a). However, the underlying equations were not explicitly given in the report. The Review Panel requested that the SARSRP Team provide those equations such that the communication of these complex models becomes more easily transparent. The SARSRP Team subsequently provided these equations during the review (see Addendum B of this report).

The Review Panel had considerable discussions about the simulation study using CKMR*pop* to conduct the sensitivity analyses detailed in the SARSRP report Appendix V. The SARSRP team provided a correction to this appendix during the meeting. Further, given the significance of the information in that Appendix, the Review Panel recommends integrating text from Appendix V into the main body of an updated SARSRP report to improve understanding of how this information was obtained and integrated into the analysis.

Additionally, several alternative model structures or sensitivity analyses were investigated to assist in the evaluation of the relative importance of the various model components on final estimates. These tests included assuming equilibrium population size over the sampling period versus allowing for a trend. Also, alternative initial age structures were investigated. Note that these alternative age structures were labeled as plus or minus 50% of the fishing mortality rate (F). The Review Panel thought that this label is a mischaracterization of the particular sensitivity being tested. The plus/minus F was just an ad hoc way of generating an alternative steady-state age distribution for the estimation and thus, this scenario did not adjust the survival rates.

Also, there were a number of investigations of the basic CKMR mark data to examine if assumptions are likely to be violated because of insufficient mixing, the possible movement of reproductive fish from the west coast of Florida and others. However, the Review Panel agreed that the current available information would make it difficult to evaluate this.

2.b. Are the hierarchical Bayesian modeling methods applied appropriately?

The Review Panel concluded that the BHIM methods were applied appropriately. This model integrated Red Snapper density information from two surveys (video trap and ROV) using well-reasoned observation models. This included a novel (for fisheries surveys) N-mixture model component that the Review Panel concluded was a strength of the BHIM. Parameter priors were usually uninformative, except when other data provided information. Hence, the Review Panel felt the BHIM used objective priors, which is a strength of the approach. The possible exception was the priors used for ESA based on the Chicken Rock telemetry study, which represented a small fraction of the stock area. A prior variance inflation factor could have been used to account for possible differences in ESA in other regions of the stock. However, the Review Panel recognized that the choice of variance inflation will be subjective, and a better approach to deal with this uncertainty is to do additional ESA telemetry studies (see TOR 4 - Research Recommendation).

3. Are the estimates of absolute abundance (age-2+ red snapper) and their variances reliable?

Close-Kin Mark-Recapture

The Review Panel concluded that insufficient information was provided to fully assess the reliability of the CKMR abundance estimate given the assumptions and appropriateness of the input data and parameters (*see comments elsewhere in this report*). Further, the uncertainty associated with this estimate is likely to have been underestimated. For example, the estimate of total abundance for age 2+ has some uncertainty relative to the true 2+ estimate as an unknown number of age 1 (and age 0) may have been included in the estimate. This is explained in the SARSRP report, but this uncertainty should be taken into account when this estimate is compared with the assessment outcome. There is also an added degree of uncertainty related to potential sex differences in age at 50% maturity and fecundity at age (or size) relationship. There is a need to identify the sex of the unsampled common parent of the HSP members.

Bayesian Hierarchical Integrative Modeling

There was transparency in the SARSRP Report and presentations concerning the uncertainties. However, the Review Panel concluded that the BHIM CV's are likely too low given the uncertainty in bottom habitat information that was not propagated into BHIM CV's for absolute abundance estimates.

Because size and age information was not included in the BHIM analysis, the estimate of total abundance for age 2+ has some uncertainty as an unknown number of age 1 (and possibly age 0) may have been included in the estimate. This is explored in the SARSRP report (see also slide 62 of the BHIM presentation) and is, relative to other uncertainties, a minor factor, but should be taken into account if this estimate is compared with the assessment outcome.

The Review Panel concluded that the ESA estimate and more importantly, the bottom habitat information, was too uncertain to provide a sufficiently reliable BHIM based absolute population abundance estimate of red snapper in the SEUSA area at this time.

3.a. For each of the two estimation approaches, are assumptions appropriate, given study design considerations?

Close-Kin Mark-Recapture

The Review Panel concluded that the assumptions were generally appropriate, but there were concerns regarding life history information used as inputs to the CKMR model (*see also discussion in above sections*). The CKMR estimates are conditioned on age proportions and age-specific demographic rates that were derived from the most recent assessment (SEDAR 73 Update) and the Data Workshop for SEDAR 90. These represent implicit assumptions integral to the estimation. To some extent the impact of misspecification was evaluated through sensitivity analysis of alternative age structures and trends in abundance. Additional sensitivities were conducted (Appendix V); however, these tests were using a CKMR demographic structure that was parametrized differently than the final structure used in the report. Nevertheless, those results indicated that generally the estimates were robust to alternative specifications of adult M, recruitment variability and maturity. But the overall fecundity relationship was found to be more sensitive.

This sparked discussion among the Panel about the assumptions about reproductive output. The fecundity/reproduction output relationship is used to convert an observation of a “marked fish” to the number of eggs that a female produces and the subsequent offspring that transition through their life history. Because the ratio of subsequent offspring to the reproductive output is the basis of CKMR estimates, understandably this relationship is important. The underlying assumption was that a female fecundity was proportional to its weight at age. This relationship is commonly the “first hypothesis” used in fisheries assessments (that the number of eggs is proportional to SSB). Thus, typically SSB is used as a surrogate for eggs in a stock-recruitment curve. Note that because the estimation is concerned with ratios, the exact proportionality constant is not important. However, there is evidence in other some stocks (including Gulf red snapper) that fecundity is proportional to weight at age with an exponent greater than one. Because of how this enters into the estimation model, this could be an important assumption and should be explored further when implementing this into future evaluations.

Additionally, the current CKMR model assumes that male contribution to the probability of successful reproduction mimics the female fecundity weight at age relationship. This has not yet been evaluated and deserves consideration in future implementations. But at this stage, the current assumptions are appropriate given study design considerations.

Bayesian Hierarchical Integrative Modeling

The Review Panel concluded that the assumptions for the BHIM were generally appropriate. The BHIM estimated spatial stock size at a fine mesh grid with 14,658,041 cells of approximately 90 × 90 m. Absolute abundance was estimated by summing spatial stock size across all these grid cells. The Review Panel concluded this basic approach was appropriate. The BHIM included factors for depth, bottom type (hard bottom or not), and number of hard bottom neighbors. The last effect and depth were highly significant and BHIM produced substantially different estimates of density depending on bottom type. The analysts demonstrated that the absolute abundance estimates were highly sensitive to how the bottom type was classified.

A primary measure of model uncertainty is characterized by the posterior distributions of the estimates, which provide a comprehensive quantification of uncertainty. This was primarily characterized by the CV, which the Review Panel considered appropriate. However, the posterior distribution did not include uncertainty in bottom type classification and therefore the posterior CV is an under-estimate of true uncertainty. The prior distribution for ESA was only based on one study. This informative prior distribution may also have important impacts on the posterior distribution of absolute abundance; therefore, the Review Panel also concluded for these reasons that the posterior CV is an underestimate of true uncertainty.

Overall, the Review Panel concluded that bottom type was a major source of uncertainty, and that there is enough uncertainty in bottom type classification in the SEUS Atlantic region that the absolute abundance estimate was not reliable (see also discussions above). In addition, absolute abundance estimation relied on an estimate of effective sampling area (ESA) from a small part (i.e., Chicken Rock) of the stock area. While the Review Panel concluded that this estimate seems reliable, the Review Panel was uncertain whether this value reflected ESA through the entire stock area. See research recommendation under TOR 4 for additional comments.

3.b. Are there potential sources of uncertainty that were not considered when developing the estimates of abundance?

Close-Kin Mark-Recapture

A potential source of uncertainty in the analysis is the lack of consideration of sex differences in age at 50% maturity, in the fecundity @ age or fecundity @ size relationship. Significant differences between the sexes in these metrics would lead to different ERRO estimates depending on the sex of the unsampled parent of the HSP.

The CKMR estimate of abundance is based on HSP, the parents of which remain unsampled. Analysis of mtDNA haplotype composition is needed to assess whether the HSPs share a common father or a common mother. A difference in the mtDNA haplotype between the HSP members would indicate the common parent is a male. The same haplotype suggests the common parent is likely a female but this depends on the frequency of the haplotype. If the haplotype is common, two different females with the same haplotype could have contributed to the HSP and the common parent is a male.

The SASRP report states (Page 79, under Discussion) that "*the results of the study described in Appendix V demonstrate CKMR is fairly robust to errors in demographic data*." However, the Review Panel noted that the sensitivity analyses described in Appendix V were conducted using Atlantic red snapper fecundity-at-age estimates that were found to be unreliable by the SEDAR 90 DW Life History Working Group. This is particularly problematic because these CKMR estimates are not directly comparable to the ones produced by a different CKMR demographic model used to develop the estimates provided in Chapter 3. These were conducted using fish mass (mean weights-at-age as a proxy for fecundity-at-age). Under "Research Recommendations" below the Review Panel recommends that the sensitivity analyses described in Appendix V be redone using weight-at-age in place of fecundity-at-age and that the impact of different levels (low, medium, and high) of the parameter overdispersion (i.e., reproductive skew) be also considered. Until these additional analyses are completed the Review Panel is unable to properly evaluate the impact of incomplete or misspecified demographic data on CKMR model results.

Bayesian Hierarchical Integrative Modeling

The uncertainty in the area and location of hard bottom habitat was not (fully) accounted for in the population estimate (see also above).

The Review Panel also discussed current velocity as a potential source of unaccounted uncertainty.

There is no video trap data available in the areas north of Cape Hatteras, NC, and south of the St. Lucie. FL, areas as they are currently outside the sampling area. The Review Panel agreed with the SARSP team's conclusion that the impact on the overall abundance estimate is likely small. The ROV data showed no Red Snapper detections north of Cape Hatteras and a relatively low number of Red Snapper detections in the Florida Keys.

3.c. For each of the two estimation approaches, describe the magnitude and direction of any potential biases.

Close-Kin Mark-Recapture and **Bayesian Hierarchical Integrative Modeling**

The Review Panel was unable to properly evaluate a potential bias in the CKMR census population estimate since it appears that the parameter "overdispersion" (reproductive skew) was not included in the estimation model. In highly skewed species, the same "super-reproducers" may contribute across multiple years. That introduces correlations that a poorly specified skew model won't capture, even in cross-cohort pairs. Recognizing that overdispersion in most–if not all–CKMR applications rely on assumed or indirectly inferred levels of reproductive skew, sensitivity analysis of this critical parameter becomes essential rather than optional.

4. Provide future research recommendations.

4.a. How could each of the methods used in this study be improved for more accurate estimates?

4.b. Are there other sampling or survey methods that could be used to improve the accuracy of estimates of absolute abundance?"

Review Panel research recommendations in order of priority for improving the population estimates.

Genetic close-kin mark-recapture methodology

1. Continue sampling and genotyping with the goal of providing a time series of *Nc* (CKMR) estimates.
2. Revise and expand the simulations and sensitivity analyses conducted in Appendix V as follows:
    a. Conduct the simulation in CKMR*pop* using adult fish mass (mean weights-at-age) instead of just using fecundity-at-age.
    b. Evaluate the sensitivity of CKMR abundance estimates over a range of overdispersion (i.e., reproductive skew) values; perhaps low, medium and high, to address conditioning the overdispersion to the same set of individuals being super-successful at reproducing in different years.
    c. Collection of additional data to inform the fecundity-age (or size) relationships for males and females, and spawning season duration for individual fish can considerably improve the population size estimate.
3. Conventional tagging, including double tagging to estimate tag shedding rates.

4. Use the epigenomic aging clock to estimate the age of as many individuals as feasible, including all those identified as members of HSPs and a subset of the U (unrelated) individuals); rerun the CKMR model.
5. Provide the chromosome level genome sequence to assess the degree of linkage among the ~ 1755 multiallelic haplotypic loci used to obtain the current estimate.
6. A recommendation regarding the population structure analysis upon which the CKMR work relies: Instead of running hierarchical AMOVAs grouping samples by state (a political boundary) The Review Panel suggested that samples be grouped by hardbottom aggregations. Samples from hardbottom locations within a 5-10 km radius should be grouped together and separate from samples collected from hardbottom locations located 50s or 100s km apart from each other. The Review Panel found it somewhat surprising for a fish species that uses natural reefs or is associated with hardbottom substrate and is not otherwise a long-distance migratory species not to show any sign of meta-population structure over a few thousand kilometers.

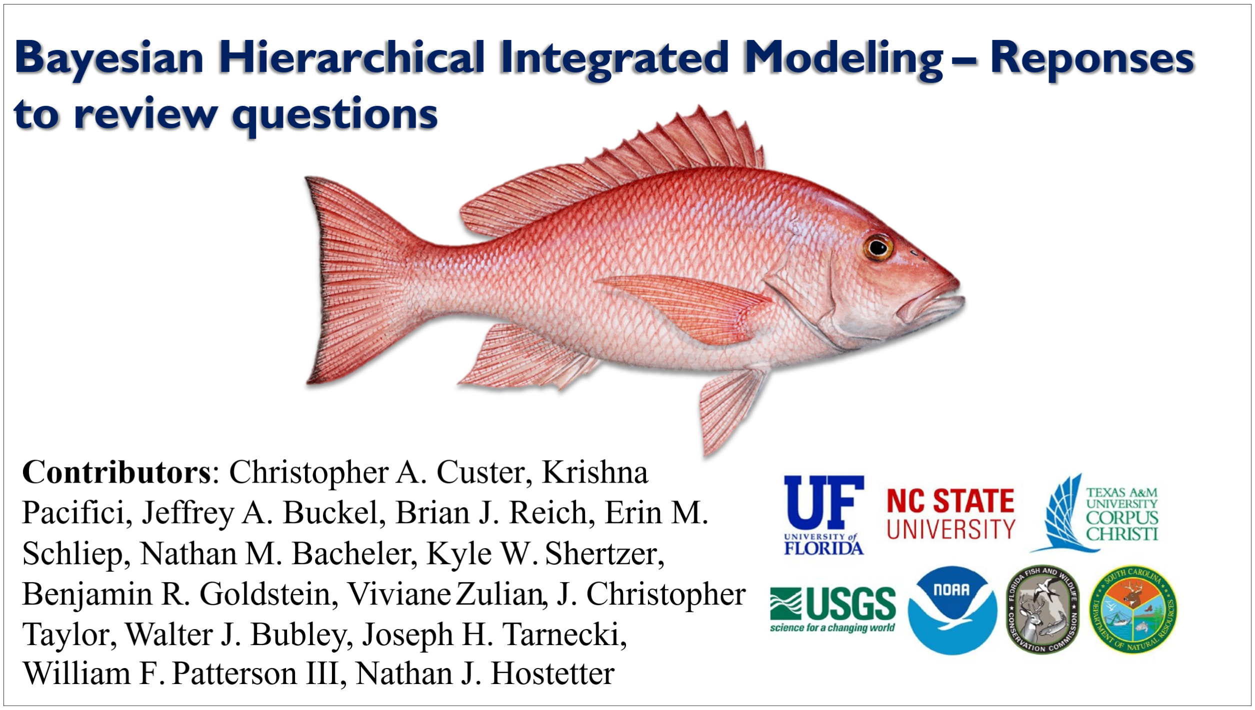
Bayesian Hierarchical Integrative Modeling

1. There is substantial uncertainty in the bottom classification in the Atlantic SEUS. This uncertainty may have substantial impacts on the BHIM estimates of red snapper total abundance, and the uncertainty of the estimates. The Review Panel recommends increasing the accuracy of bottom type/habitat classification by mapping or other methodologies. This will provide a more reliable habitat covariate for use in the BHIM to estimate red snapper total abundance.
2. The BHIM estimate of red snapper total abundance used information from SERFS and ROV surveys. The BHIM also required information on the effective sampling area for the SERFS video camera counts. This was derived from a telemetry/camera/ROV study in a small region (Chicken Rock). The Review Panel recommends repeating the “Chicken Rock” telemetry project/analyses in other areas to assess spatial variation in effective sampling area and to gain more understanding about the factors that affect ESA.
3. In addition to #1 above, investigate assigning a probability of hard bottom based on other sources of information (modeling) and include this major uncertainty in the BHIM abundance estimation.
4. Determine effective sampling area of trap catches (vrs video).
5. Explore integrating trap catches into the Bayesian Hierarchical Integrated Modeling (BHIM).
6. Measure water current velocity at video trap locations to improve estimation of ESA.
7. Analyze recordings from both trap video cameras for fish abundance. Currently only the recordings from one of the cameras is used for BHIM (and other) analyses.
8. Expand video trap survey south of the St. Lucy area and North of Cape Hatteras, even if the used methodology results in video data only (no trapped fish).

2.4 ADDENDA

Addendum A

Supplemental information requested by the Review Panel and provided by D. Nathan Hostetter during the Review Workshop.



Bayesian Hierarchical Integrated Modeling – Reponses to review questions

Contributors: Christopher A. Custer, Krishna Pacifici, Jeffrey A. Buckel, Brian J. Reich, Erin M. Schliep, Nathan M. Bacheler, Kyle W. Shertzer, Benjamin R. Goldstein, Viviane Zulian, J. Christopher Taylor, Walter J. Bubley, Joseph H. Tarnecki, William F. Patterson III, Nathan J. Hostetter

These slides are in response to a request for additional information on the Bayesian Hierarchical Integrated Model presentation on 13-Jan-2026

Specific topics:

1. Posterior correlations and identifiability of specific parameters in the hierarchical model. Specifically:
    - $\gamma_{rov}, \mathrm{ESA_j}$ correlations
    - $\mathrm{ESA_j}$ correlations
    - $\gamma_{rov}, \mathrm{ESA_j}$, and global intercept ($\beta_0$)
    - $\gamma_{paired}, \gamma_{rov}$ correlation
2. Plot detection probability to help interpret hyperparameters (z_1, z_2). Specifically,
    - mean detection and uncertainty in the mean
    - Density function of detection given median estimates of z_1, z_2

Bayesian Hierarchical Integrated Modeling – Statistical model

Abundance process at the 90x90 meter grid cell level:

$\log(\lambda_g) = \beta_0 + \boldsymbol{\beta} \boldsymbol{x}_g^{'} + \alpha_{r[\mathrm{cell}\,[g]]}$ # $\boldsymbol{x}_g^{'}$ are covariates for grid cell g (90x90m)

$\boldsymbol{\alpha}_{1:R} \sim \mathrm{CAR}(0, \tau)$ # spatial autocorrelation at 5.5x5.5km level

ROV counts at site *i*:

$Y_i \sim \mathrm{Poisson}(\mu_i)$

$\mu_i = \lambda_{g_i} \times \mathrm{area}_i \times \exp(\gamma_{\mathrm{paired}} \times E_i) \times \gamma_{\mathrm{rov}}$

SERFS Camera counts at site *j*:

$N_j \sim \mathrm{Poisson}(\lambda_{g_j} ESA_j)$

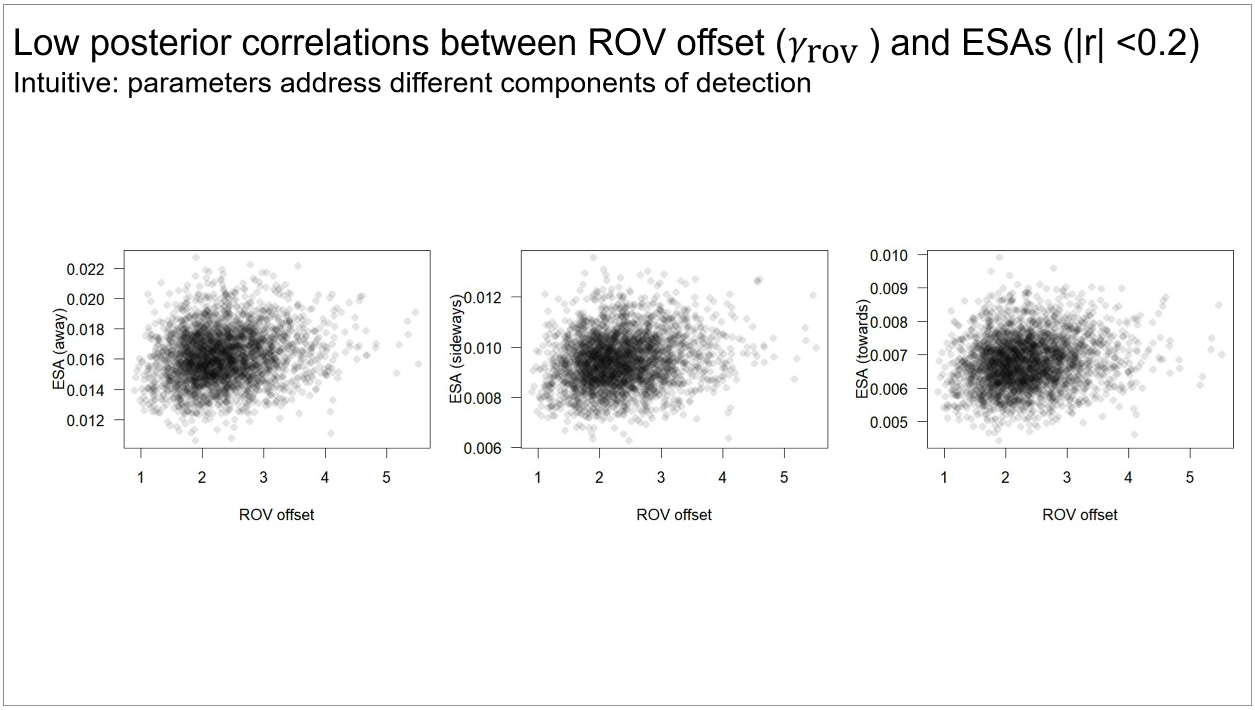
$W_{jf} \sim \mathrm{Binomial}(p_{jf}, N_j)$

$p_{jf} \sim \mathrm{Beta}(z_1 z_2, (1 - z_1) z_2)$

Data

Parameters – Vague priors

Parameters – Informative priors



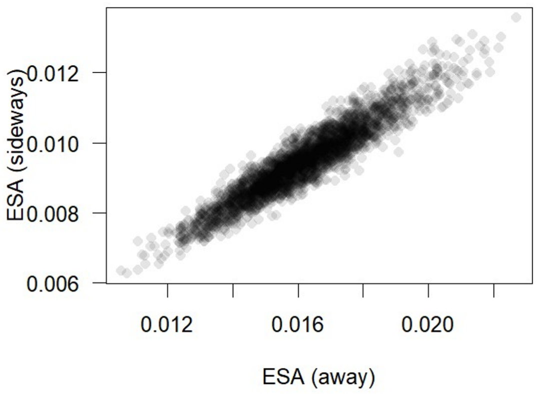
Low posterior correlations between ROV offset (γ_{rov}) and ESAs (|r| <0.2)

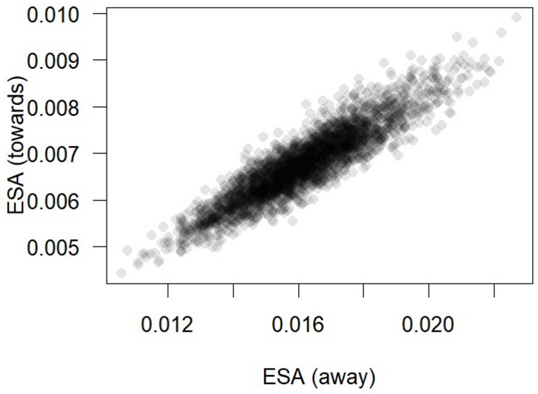
Intuitive: parameters address different components of detection

High posterior correlations among ESAs (|r|>0.9)

Correlations may be affected through detection probability ($z_1 z_2$) and/or abundance parameters

i.e., when lower detection probabilities are proposed, something has to change with either ESAs (all larger), density (lower), or both

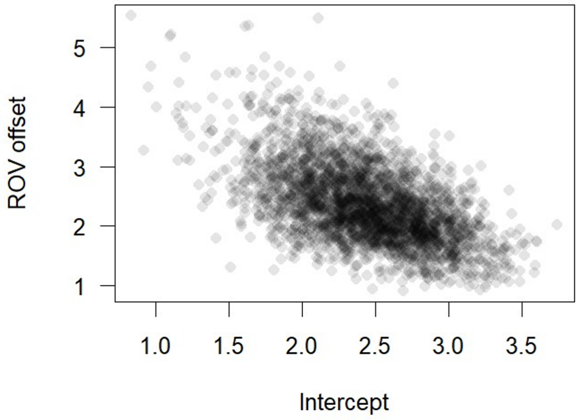


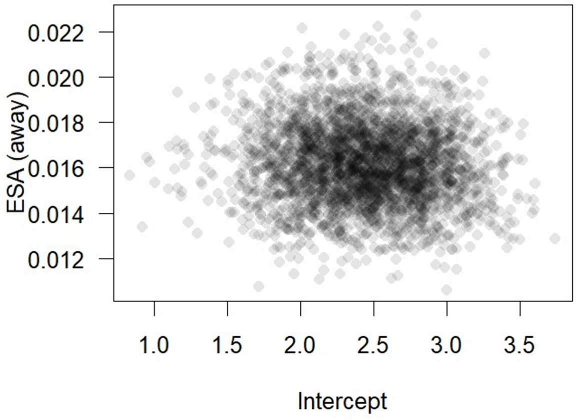


ROV offset moderately correlated with intercept (-0.55)

- Intuitive: as offset approaches 1.0 (ROV perfectly observes density), average density increases (Intercept)

ESA has low correlation with intercept.





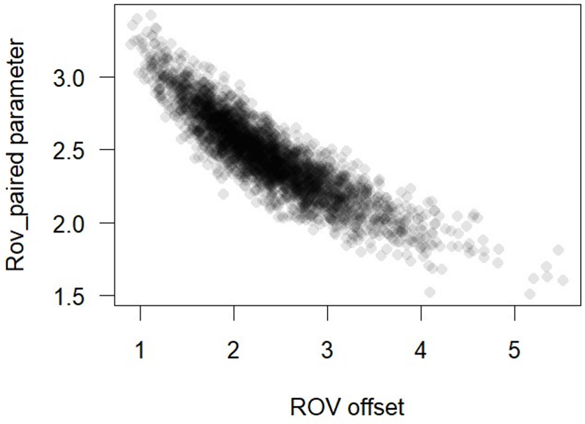
Correlation between ROV offset (γ_{rov}) and ROV Paired (γ_{paired})

Fairly intuitive:

- Paired sites observed higher than expected abundances.
- If ROVs observed actual density (ROV offset approaches 1), then the higher counts at paired sites are increasingly assigned to the paired effect (negative covariance).

Covariance may be artifact of unbalanced design with respect to habitat

- Increased balanced sampling designs may reduce covariance

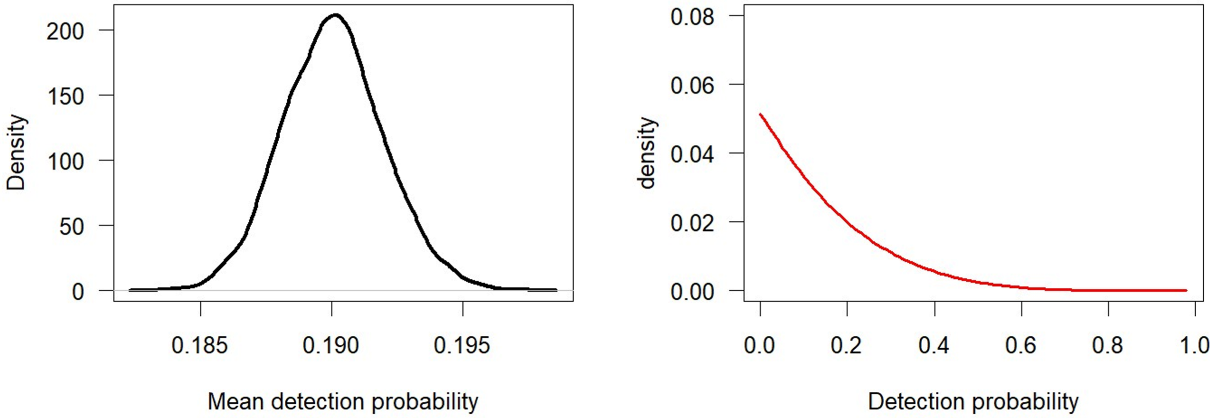


N-mixture model (SERFS sub-model) detection probability

(left) Posterior distribution of mean detection probability

(right) Density plot of $p_{jf} \sim \text{Beta}(z_1 z_2, (1 - z_1) z_2)$ at median z's (0.19, 5.55)

Fairly intuitive: During the 20-minute survey (41 frames), numerous fish are exposed to sampling (N_j), but in any given frame, most counts are often low or 0.



ADDENDUM B

Supplemental information requested by the Review Panel and provided by Dr. David Portnoy during the Review Workshop.

This report documents the Program Team's responses for additional information from the Review Panel.

Additional Requested Information: CKMR:

A central element of the pseudolikelihood is the half-sibling kinship probability, which is formulated in terms of the ERRO and $N_{i,t}$, the abundance of age-i individuals at time t. ERRO for age i at time t is proportional to the product of percent maturity (*P*), fecundity (*Fec*) and the relative proportion of individuals of age i at time t which can be calculated from estimates of mortality or input directly as age composition data.

$$\mathrm{ERRO}_{\mathrm{i,t}} = \frac{P_i \mathrm{Fec}_i R_{i,t}}{\sum_i P_i \,\mathrm{Fec}_i R_{i,t}}.$$

This quantity is the same for male and female adults, given the assumption of balanced sex ratios and reproductive output.

Given a pair of samples with birth years b_1 and b_2, respectively, such that b_1 is the first born (i.e., $b_1 < b_2$) the probability that b_1 and b_2 are half siblings can be calculated by:

$$P(\mathrm{HS}|b_1 b_2, \mathrm{N}, \Theta) = \sum_{a*=1}^{a*=20-d} \left(\mathrm{ERRO}_{a,b_1} \times \mathrm{ERRO}_{a+d,b_2} \left[\prod_{a=i-d}^{a+d} S_a \right] \frac{4}{N_{i,2}} \right)$$

This occurs because the pair will only be half siblings if:

1. b_1 and b_2 were born d years apart, i.e., b_1 was born to an a year old at time 1 and b_2 was born to an $a+d$ year old at time 2. This is reflected in the product $\mathrm{ERRO}_{\mathrm{a,b1}} \times \mathrm{ERRO}_{\mathrm{a+d,b2}}$
2. the mother of $b_{\&}$ survived for the d years until the time of b's birth, reflected in the product

$$\prod_{a=i-d}^{a+d} S_a$$

3. The factor of 4 accounts for maternal and paternal half-siblings with an even sex ratio and similar survival and reproductive success between sexes for N reproductive adults of age i at time 2.

CIE Independent Report

South Atlantic Red Snapper Research Program *(SARSRP)* Review

January 13 – 15, 2026

Charleston, SC

Dr. Noel Cadigan

Centre for Fisheries Ecosystems Research
Marine Institute of Memorial University of Newfoundland
St. John's, NL. Canada

Executive Summary

An independent peer review of the South Atlantic Red Snapper Research Program (SARSRP) was conducted during January 13-15, 2026 in Charleston, SC. The objective of the SARSRP review was to: 1) evaluate two study designs used for developing estimates of absolute abundance of age-2+ red snapper in the U.S. South Atlantic region, 2) evaluate the statistical/modeling methods used to analyze the data, and to construct the absolute abundances estimates and their variances, and 3) assess if estimates of absolute abundance (age-2+ red snapper) and their variances are reliable. The two methods were:

1) A Bayesian Hierarchical Integrated Model (BHIM), which utilized data from the Southeast Reef Fish Survey (SERFS) video trap and remotely operated vehicle (ROV) video samples. BHIM predicted absolute abundance throughout the stock area by utilizing an estimate of effective area sampled (ESA) of the video traps and modelled relationships with hardbottom habitat and depth data.
2) A close-kin mark-recapture (CKMR) estimate based on red snapper fin clips sampled from fisheries-independent and dependent sources along the U.S. Atlantic Coast during 2021-2023.

The CKMR sampling design and the realized sampling effort were sufficient for estimation of total population size. The SERFS sampling design and sampled locations were sufficient to estimate average camera counts of red snapper for the entire SERFS sampling frame. The ROV sampling design and sampled locations were sufficient for estimating red Snapper abundance over unconsolidated bottom habitat and for calibrating the ROV counts with video trap counts in hardbottom areas.

The CKMR statistical and modeling methods were overall applied appropriately. The uncertainty in ages obtained from the SARSRP imputation procedure is an important source of variability. CKMR abundance estimates are weakly dependent on demographic parameters and uncertainty in these parameters was not accounted for in the CKMR abundance estimate; hence, the variances of the estimates are likely too low.

The BHIM methods were applied appropriately overall. However, bottom habitat information used by BHIM was too uncertain to provide a sufficiently reliable estimate of absolute abundance (age 2+). This was the main source of uncertainty in the application of the BHIM. In addition, the estimate of the ESA by the video traps obtained from a study in a small area may not reflect red snapper ESA throughout the SEUSA Atlantic stock area. An unknown number of age 1 (and possibly age 0) may have been included in the absolute 2+ abundance estimate. These uncertainties were not included in variance estimates; hence, those variances will be too low.

There was no evidence of bias in the CKMR or the BHIM abundance estimates. The problem with the BHIM estimate was high uncertainty. Both the CKMR or the BHIM abundance estimates are not independent of red snapper assessment results.

Sampling and genotyping should continue with the goal of providing a time series of CKMR estimates. The BHIM can be improved with better information about bottom type/habitat classification by mapping or other methodologies and additional telemetry project/analyses in other areas to assess spatial variation in ESA.

Background

NOAA Fisheries science products, including scientific advice, are often controversial and may require timely scientific peer reviews that are strictly independent of all outside influences. A formal external process for independent expert reviews of the agency's scientific products and programs ensures their credibility. Therefore, external scientific peer reviews are essential to strengthening scientific quality assurance for fishery conservation and management actions. Scientific peer review is defined as the organized review process where one or more qualified experts review scientific information to ensure quality and credibility. These expert(s) must conduct their peer review impartially, objectively, and without conflicts of interest.

The South Atlantic red snapper fishery is economically and recreationally important but has faced challenges due to overfishing and restrictive management. The red snapper population has grown in the last 15 years. However, harvest opportunities for red snapper remain limited because of the large quantity of discarded fish and uncertainty in the exact number of fish in the population. The goal of the *South Atlantic Red Snapper Research Program (SARSRP*) was to generate an absolute estimate of abundance with an accompanying measure of uncertainty for the entire South Atlantic red snapper stock. This estimate will serve as an independent benchmark on which to inform a currently ongoing stock assessment. The SARSRP included the following three approaches: (1) Close-kin and meta-population genetics analyses; (2) Existing and possibly supplemental new South Atlantic trap-video survey data to scale-up density estimates to total abundance; and (3) a research technique similar to that pursued in the Gulf Red Snapper abundance assessment, focusing predominantly on use of active acoustics and visual ground-truthing. Research began in the Fall of 2020 and finished in August of 2025, hence the request for CIE review at this time.

The objective of the *SARSRP* peer review was to 1) evaluate the study designs used for developing estimates of absolute abundance of age-2+ red snapper in the U.S. South Atlantic region, 2) evaluate the statistical/modeling methods used to analyze the data, and to construct the absolute abundances estimates and their variances, and 3) assess if estimates of absolute abundance (age-2+ red snapper) and their variances are reliable.

Reviewers were required to have expertise in quantitative methods applied to fisheries. It was desirable to have at least one reviewer with expertise in capture-recapture methodology, especially Bayesian hierarchical modeling, and at least one reviewer with expertise in genetic close-kin mark-recapture applications.

I have worked in fisheries science for 35 years. I have a PhD in Statistics (Survey methods) and my research and publications deal with statistical methods for fish stock assessment and sustainable fisheries management. I have experience and publications using hierarchical modeling. I have extensive experience in the assessment of North Atlantic stocks, primarily commercially important groundfish species. Recently my research has focused on spatiotemporal models for complex fisheries data and integrated state-space stock assessment models, including using conventional tagging data to improve model estimation.

The Review Panel consisted of Drs. Marcel Reichert (Chair), Luiz Barbieri (South Atlantic Fisheries Management Council's Scientific and Statistical Committee), Daniel Ruzzante (Center for Independent Experts, CIE), Noel Cadigan (CIE), and Joe Powers (CIE). The Review Panel was assisted by Southeast

Data, Assessment, and Review (SEDAR) staff Julie Neer and Emily Ott and various South Atlantic Fisheries Management Council (SAFMC) staff.

Each reviewer was required to write an individual review report in accordance with the Performance Work Statement (PWS), Office of Management and Budget (OMB) Guidelines, and the Terms of Reference (ToRs) below. All TORs must be addressed in each reviewer's report. Review documents are listed in Appendix 1. TORs for this peer review are provided in Annex 1 of Appendix 2. The draft meeting agenda is provided in Annex 2. Annex 3 describes the Individual Independent Review Report Requirements.

Role of reviewer in the review activities

The main report for the review (WP #1 in Appendix 1) was provided on December 22, 2025, via a South Carolina SeaGrant website, along with several appendices. All additional Appendices were provided early in January. This provided me with ample time to carefully read the main report and the appendices. In addition, I reviewed substantial recent literature on genetic close-kin mark-recapture (see Appendix 1). Presentations for the peer review were made available shortly before the peer review meeting via the South Carolina SeaGrant website. One supporting information document was also provided during the review meeting.

I reviewed the background documents I was provided with and compiled a list of issues for clarification during the Review Panel meeting. I attended the entire Review Panel meeting. I reviewed presentations and reports and participated in the discussion of these documents, in accordance with the SoW and ToRs (see Annex 2). During and after the meeting, I contributed to drafting the panel summary report.

This CIE report is structured according to the required format and content described in Annex 3 of Appendix 2. I provide a summary of findings for each TOR in which the weaknesses and strengths are described, and conclusions and recommendations in accordance with the TORs. My report will provide greater detail than the Peer Reviewer Summary Report on some ToRs. Note that only a rough draft of the final Panel Summary Report was available when I wrote this CIE report.

Summary of findings

The Review Panel (i.e., the Panel) much appreciated the very collegial nature of the review deliberations. The Panel thanked the SARSRP team for the incredible amount of work and the streamlined report, and the presentations during the review. I fully support these statements.

I particularly appreciated the effective documentation of the Bayesian hierarchical integrative model (BHIM). This consisted of several model components that were clearly described, which greatly facilitated the Panel's findings on the strengths and weaknesses of the approach. I had little research experience with close-kin mark-recapture (CKMR) methods, apart from conducting a focused literature review prior to the Panel meeting. However, the SARSRP team's presentations were also effective, and I gained a good understanding of the strengths and weaknesses of that methodology.

My criticism of the review process is that presentations were not provided on two important aspects of both the BHIM and CKMR for red snapper. In hindsight, I feel Appendices 2 and 5 (2 appendices out of a total of 10) should have been presented and reviewed in plenary. The Appendices were considered by the Panel as background documents and were not reviewed in detail during the Panel meeting. I appreciate that it is not possible to review all aspects of sampling design and estimation procedures and the SARSRP team made judicious choices about what to review within the time frame of the meeting. Providing too much material would reduce time for critical discussion with the SARSRP team and reduce time for the Panel to deliberate and write their report. I largely agree with the SARSRP team's choices about what to present, except for Appendices 2 and 5. However, this did not impact on the Panel's ability to draw conclusions relative to the ToRs.

ToR 1. Evaluate the study designs used for developing estimates of absolute abundance of age-2+ red snapper in the U.S. South Atlantic region (Florida, Georgia, South Carolina, North Carolina).

a. Assess the study design and sampling sufficiency as they pertain to the application of genetic close-kin mark-recapture methodology.

A design was implemented in which red snapper fin clips were sampled from fisheries-independent and -dependent sources along the U.S. Atlantic Coast between Port St. Lucie, Florida and Cape Hatteras, North Carolina during 2021-2023. I agree with the Panel's conclusions that the sampling design and the realized sampling effort exceeded the recommendations implied by the sampling simulations conducted prior to field work. The design was conditioned on the most recent assessment and Data Workshop demographic parameters (age composition (ages 1-20+), survival rates and fecundity) are sufficiently adequate for estimation. The study design appears robust and the sampling effort seems to have been sufficient for an initial estimate of population abundance with a reasonable 95% credible interval, although that may be too narrow because of unaccounted sources of uncertainty, which are described for ToRs 2 and 3 below.

There was a missing figure in Appendix 5, which described the simulations to support the sampling design, and some other figures were mis-ordered. This was corrected during the meeting.

b. Assess the study design and sampling sufficiency as they pertain to the application of hierarchical Bayesian abundance modeling.

The Bayesian Hierarchical Integrated Model (BHIM) utilized data from the Southeast Reef Fish Survey (SERFS) video trap as well as from fish count estimates produced with remotely operated vehicle (ROV) video samples. BHIM predicted abundance throughout the stock area by utilizing modelled relationships with hardbottom (reefs, rocks, and areas of high relief) habitat and depth data. Two additional, complimentary studies were conducted to estimate the effective sample area (ESA) of camera-trap gear so that red snapper count data could be expressed as density, which was critical for estimating total abundance, or population size.

I agree with the Panel conclusion that the SERFS sampling design and sampled locations were sufficient to estimate average camera counts of red snapper for the entire sampling frame. Approximately 25% of the 4,300 potential sites were sampled in 2021 and 2022, which is high survey coverage.

During the SERFS camera-trap surveys red snappers were counted in each of 41 snapshots spaced 30 seconds apart, beginning 10 minutes after the video trap reached the seafloor and spanning a total of 20 minutes. I conclude this aspect of the sampling design was good. A shorter sampling period would reduce the sample size and decrease the reliability of fish density estimates and the ability to differentiate this with detection probabilities (see below). A longer sampling period at each sampling station would increase the chance of violating the closed population assumption of the N-mixture model (see below).

The primary purpose of the ROV survey was to estimate red snapper density over a variety of habitats, assuming that “area swept” could be estimated accurately. Importantly, ROV data were used to test whether red snapper occurs on unconsolidated habitats not targeted by the SERFS survey. There was uncertainty about whether there was a significant Red Snapper abundance/biomass on unconsolidated habitat not sampled by SERFS, and thus not accounted for in (stock assessment based) abundance estimates. I agree with the Panel and the ROV study conclusions that Red Snapper abundance over unconsolidated bottom was very low in Atlantic SEUSA. The ROV sampling design and sampled locations were entirely adequate for this purpose. I also agree with the Panel’s conclusion that the additional paired ROV-SERFS sampling design and sampled locations were sufficient for the purpose of calibrating the ROV counts with video trap counts.

Two additional, complementary studies were conducted to estimate the effective sample area (ESA) of video trap gear such that red snapper count data could be expressed as density (number per unit area), which was critical for estimating total abundance, or population size. These complementary studies involved telemetry experiments at two sites: Chicken Rock, North Carolina and Turtle Mound, Florida. The Panel did not review these studies in detail, but it seems that the sampling was insufficient to reliably estimate ESA at Turtle Mound but was sufficient at Chicken Rock. ESA estimated at Chicken Rock agreed with an earlier study in that area, which provides evidence of the reliability of the estimate.

However, I agree with the Panel’s conclusion that the study on Chicken Rock was insufficient to estimate video trap ESA for red snapper, and the factors that influence ESA, throughout the SEUSA Atlantic stock area. The discussion section in Appendix 2 of the SARSRP WP recognized this limitation and described that the next step is to assess variation in ESA across habitats, and better characterization of drivers of variation in ESA.

ToR 2. Evaluate the statistical/modeling methods used to analyze the data, and to construct the absolute abundances estimates and their variances.

a. Are the close-kin mark-recapture methods applied appropriately?

The CKMR population size estimator was based on a pseudolikelihood using an annual (2014-2023) age-structured demographic model (ages 1-10) to predict half-sibling (HS) pairs identified from genetic analyses of Red Snapper tissue samples. I agree with the Panel conclusions that the CKMR statistical and modeling methods were overall applied appropriately, but some details were difficult to evaluate.

Some fish did not have age measurements (~18%), which are required for CKMR estimation of population size. The SARSRP team addressed this by imputing ages using a month-specific age-length key derived from von Bertalanffy growth model with parameters. This was a feasible approach; however, the distribution of age at length will change over time even when growth rates are constant, because of variation in cohort strength. I do not think using the ALK approach for red snapper was a serious source of bias or uncertainty because it only affects 18% of the sampled fish and cohort sizes do not seem to have varied dramatically during 2014-2023; however, it is an issue to be aware of, especially in potential applications of CKMR in the future. The uncertainty in ages obtained from the SARSRP imputation procedure resulted in a considerable range of HS pairs identified (39 to 56 cross-cohort HS pairs), which directly affect the estimation of population size, so treatment of uncertain ages is an important issue.

I conclude that the SARSRP team made reasonable decisions about the choice of demographic parameters to include in the CKMR estimation procedure. Some sensitivity analyses were provided about the impact of the population age-composition on the CKMR abundance estimate. These sensitivities were not large. However, they suggested that uncertainty in demographic parameters will impact the uncertainty in the CKMR abundance estimate. This source of uncertainty was not accounted for in the CKMR abundance estimate; hence, I conclude that the variances of the estimates are likely too low.

b. Are the hierarchical Bayesian modeling methods applied appropriately?

I agree with the Panel conclusion that the BHIM methods were applied appropriately. This model integrated Red Snapper density information from two surveys (video trap and ROV) using well-reasoned observation models. This included an N-mixture model component that the Review Panel concluded was a strength of the BHIM. N-mixture models are used for estimating the size N of a population given imperfect detection of individuals at multiple sampling sites and sampling occasions (e.g., video frames) within sites. The Bayesian approach requires parameter priors and the SARSRP team's choices for priors were objective, which the Panel concluded was a strength of the approach.

One concern I had with the application of the N-mixture model was the assumption that the numbers of Red Snapper observed in each of the frames of the camera-trap at a site were independent. The frames are a time-series separated by 30 second intervals. I would expect serial correlation in the fish counts, possibly through time-series correlation in the latent number of red snapper available to be sampled. This may be accounted for using time-series correlation in the detection probabilities. After the panel meeting I did some literature review of the N-mixture model and found two papers that concluded that un-modelled heterogeneity was a serious source of bias. Duarte et al. (2018) found that the magnitude of bias in estimated mean abundance with even slight amounts of unmodeled heterogeneity was substantial. Link et. al. (2018) found that small unmodeled variation in population size over time and unmodeled variation in detection probability over time can lead to large biases in estimation. I recommend that this issue requires further research for the BHIM, especially since the BetaBinomial (see below) N-mixture model seems novel and not studied by others. Apart from bias, I expect that un-modelled heterogeneity and correlation in the latent number of red snapper available to be sampled will result in under-estimates of variances.

The SEUSA red snapper N-mixture model assumed that the number of red snapper observed in a frame was a Binomial random variable that depended on 1) the latent number of red snapper available to be sampled during the 20-minute camera trap deployment, and 2) the detection probability, which was assumed to be independent and identically distributed (iid) Beta random variables for different camera frames and sampling sites. Bayesian posterior distributions were obtained using MCMC sampling procedures provided by the NIMBLE R package. I suggest that the posterior sampling may be improved by simply assuming that the camera trap counts are iid BetaBinomial random variables that involve the latent number of red snapper available to be sampled and the Beta distribution parameters for the detection probabilities.

If there is only one sampling occasion (i.e., frame) then, conditional on the site detection probability, the marginal (wrt to the latent number of red snapper available) distribution of the camera trap counts is still Poisson (e.g., see Section 2.5 in Madsen and Royle, 2023). In that case the detection probability and the fish density parameter will not be identifiable. When there are only a few sampling occasions these parameters may be poorly identified. Hence, having 41 camera trap catches is a strength; however, sampling for longer periods increases the risk that the latent number of fish available may change.

Madsen and Royle (2023) described some dynamic models for the latent number of fish available to be detected.

Note that even if there was only one sampling occasion then the Poisson-Beta distribution involved in the red snapper N-mixture model does not have a marginal closed form (e.g., Herschtal, 2025).

The assumption that detection probabilities come from the same Beta distribution at all sampling sites requires further verification. I expect that between-site variation in these probabilities will be greater than within-site variation because of greater between-site variation in water turbidity and possibly other factors.

The BHIM N-mixture model detection probabilities were assumed to be independent Beta random variables, $p_f \sim \text{Beta}(z_1 z_2, z_2 - z_1 z_2)$, with mean z_1 and $Var(p_f) = z_1(1 - z_1)/(z_2 + 1)$. The posterior estimates were z_1=0.19 and z_2=5.55. Hence, the expected probability of detection of a fish is 0.19. The expected total counts from all 41 frames is roughly 41x0.19 = 7.8 times the latent number of red snapper available. Hence, this suggests that red snapper are detected about 8 times on average at a camera trap station. This could be checked in cases where tagged red snapper can be uniquely identified. The lower and upper quartiles of this Beta distribution are 0.068 and 0.276, which suggests there is considerable variation in detection probabilities between frames and sites.

The Chicken Rock study was provided in Appendix II and was not reviewed in detail by the Panel. Some Panel members noted that it was difficult to fully understand how the results were produced. Some parts of the Appendix 2 paper I found unclear, and other comments, are:

2.1. Top pg 4. I wondered if nearby predators like sharks affect camera catches, which might reduce the ESA to 0.

2.2. Bottom pg. 8. Were excluded fish with fewer than 1,000 total geoposition estimates because they left the study area, or would these be fish with low mobility (possibly dead?). I would have liked more context described about the excluded fish. Also, directly describe how many were excluded.

2.3. Pg. 14. Is M unknown, or assumed to be some value? A little more guidance will help the reader. The authors should “walk” the reader through the analysis more. It is an Appendix and there are no space limitations. I feel these papers should be written such that a graduate student in the general area can follow the paper.

2.4. Pg 15. Describe how the heat map values h_c are calculated. Also, it would be useful to illustrate (text or figure) how β affects the strength of the relationship between the telemetry heatmap and the relative distribution of latent activity centroids. Consider β = 0, 1, and 2.

2.5. Bottom Pg. 15. It is useful to remind the reader what z_i is and why it is in the equation. I could not find a description of x_{jt}. I assume it is the location of the camera trap, but I did not understand why the location was time-varying (i.e., subscript t). I prefer quantities to be defined close to an equation, which was not the case for w_{crt}. Otherwise, it makes the paper more difficult to read.

2.6. Pg. 16 ROV submodel equation. What is the script M? Is the sum in the denominator also c=1,…,scriptM? Just above, is sum for n from i=1,…,M? At this stage I do not understand the purpose of the data augmentation on Pg 14? Some help on this in the text will benefit the reader.

2.7. Pg. 17. I think a figure should be given to illustrate how w_{crt} is calculated. The clues in the appendix paper are minimal on this.

2.8. Pg. 18 near first p_q. Useful to remind the reader about the levels of q.
2.9. Because of time constraints I did not review the section: Alternate approaches to calculating ESA.
2.10. Pg. 20. Add 'each' before yielded.

Additional Literature Cited

Duarte, A., Adams, M.J. and Peterson, J.T., 2018. Fitting N-mixture models to count data with unmodeled heterogeneity: Bias, diagnostics, and alternative approaches. *Ecological modelling*, *374*, pp.51-59.

Herschtal, A., 2025. Poisson Beta Regression for Count Data With an Application to Hospital Length of Stay Data. Statistics in Medicine, 44(18-19), p.e70217.

Link, W.A., Schofield, M.R., Barker, R.J. and Sauer, J.R., 2018. On the robustness of N-mixture models. *Ecology*, *99*(7), pp.1547-1551.

Madsen, L. and Royle, J.A., 2023. A review of N-mixture models. Wiley Interdisciplinary Reviews: Computational Statistics, 15(6), p.e1625.

ToR 3. Are the estimates of absolute abundance (age-2+ red snapper) and their variances reliable?

Close-Kin Mark-Recapture

I conclude the CKMR estimate is reliable overall, but it is weakly dependent on age-structure and demographics parameters (survival rates and fecundity) obtained from the most recent assessment and Data Workshop for red snapper. Uncertainty in demographic parameters will impact the uncertainty in the CKMR abundance estimate. This source of uncertainty was not accounted for in the CKMR abundance estimate; hence, I conclude that the variance is likely too low.

Hierarchical Bayesian modeling

I agree with the Panel conclusion that the bottom habitat information was too uncertain to provide a sufficiently reliable population estimate of absolute abundance (age 2+) using BHIM for red snapper in the SEUSA Atlantic stock area. This was the main source of uncertainty in the application of the BHIM. In addition, it is uncertain whether the effective sampling area (ESA) for the Chicken Rock area reliably reflects ESA throughout the stock area. Also, The Panel noted that an unknown number of age 1 (and possibly age 0) may have been included in the BHIM estimate of absolute 2+ abundance, which should be considered when this estimate is compared with the assessment outcomes. These uncertainties were not included in variance estimates; hence, those variances will be too low.

a. For each of the two estimation approaches, are assumptions appropriate, given study design considerations?

Close-kin mark-recapture methods

I agree with the Panel conclusion that the current assumptions are appropriate given study design considerations. The estimation of absolute abundance requires demographic parameters (age composition (ages 1-20+), survival rates and fecundity) and the SARSRP team took these values from recent assessment or data input meetings. The Panel did not identify better values to use.

Hierarchical Bayesian modeling

I agree with the Panel conclusions that the assumptions for the BHIM were generally appropriate but there are some concerns. I provided some text about assumptions for the N-mixture model part of the BHIM under ToR 2b. In hindsight the assumption that bottom type could be classified as hardbottom or unconsolidated and used as a covariate in BHIM was not reliable. The SARSRP team demonstrated that changes in the hardbottom classification could have a large impact on abundance estimates. I appreciate that understanding hardbottom classification was not directly part of the SARSRP. In hindsight it seems it should have been. Better analysis of hardbottom uncertainty and how this could be reflected in the BHIM are necessary. Also, the assumed prior for ESA seems too informative (see Research Recommendations). It seems unlikely to me that the estimate of ESA, and its uncertainty, from the study on Chicken Rock is sufficient to reflect red snapper ESA throughout the SEUSA Atlantic stock area.

b. Are there potential sources of uncertainty that were not considered when developing the estimates of abundance?

Close-kin mark-recapture methods

The Panel noted that the CKMR variance of the abundance estimate is conditional on values of the age-length key, stock age composition, and demographic parameters. Uncertainty in stock age composition and demographic parameters was not directly included in the variance of the abundance estimate. The uncertainty in age compositions was partially evaluated using some sensitivity analyses. The Panel noted that a potential source of uncertainty in the analysis is the lack of consideration of sex differences in age at 50% maturity, in the fecundity at age or fecundity at size relationship. I am not sure how important these issues may be for this red snapper stock.

Hierarchical Bayesian modeling

I agree with the Panel conclusion that uncertainty in the area and location of hard-bottom habitat was not (fully) accounted for in the population estimate (see above).

The Panel also discussed current velocity as a potential source of unaccounted uncertainty.

Within-site changes in the latent number of red snapper available to be detected by the camera-traps (within the 20-minute sampling time-frame) was not included in the model; however, this may not be an important source of uncertainty. The BHIM model included between-frame and between-site variation in detection probabilities and this variation is considerable (see ToR 2b); however, I suggest that between-site variation in detection probabilities (e.g., because of different turbidity) will usually be larger than within-site but between-frame variation in detection probabilities. I recommend that future model refinements consider these issues. A hierarchical approach to modelling variability in detection probabilities could be used.

c. For each of the two estimation approaches, describe the magnitude and direction of any potential biases?

The Panel did not identify evidence of potential sources of bias in the CKMR methods. I also agree with the Panel that (significant) biases for the BHIM total abundance estimate were not apparent. There was just a high uncertainty.

ToR 4. Provide future research recommendations.

a. How could each of the methods used in this study be improved for more accurate estimates?

Panel Research Recommendations

Genetic close-kin mark-recapture methodology

1. Continue sampling and genotyping with the goal of providing a time series of CKMR estimates.
2. Revise and expand the simulations and sensitivity analyses conducted in Appendix V as follows:
    a. Conduct the simulation in CKMRpop using adult fish mass (mean weights-at-age) instead of just using fecundity-at-age.
    b. Evaluate the sensitivity of CKMR abundance estimates over a range of overdispersion (i.e., reproductive skew) values; perhaps low, medium and high.
3. Collection of additional data to inform the fecundity-age (or size) relationships for males and females, and spawning season duration for individual fish can considerably improve the population size estimate.
4. Use the epigenomic aging clock to estimate the age of as many individuals as feasible, including all those identified as members of HSPs and a subset of the unrelated individuals; rerun the CKMR model.
5. Provide the chromosome level genome sequence to assess the degree of linkage among the ~ 1755 multiallelic haplotypic loci used to obtain the current estimate.
6. A recommendation regarding the population structure analysis upon which the CKMR work relies: Instead of running hierarchical AMOVAs grouping samples by state (a political boundary), the Panel suggested that samples be grouped by hardbottom aggregations. Samples from hardbottom locations within a 5-10 km radius should be grouped together and separate from samples collected from hardbottom locations located 50s or 100s km apart from each other. The Panel found it somewhat surprising for a fish species that uses natural reefs or is associated with hardbottom substrate and is not otherwise a long-distance migratory species not to show any sign of meta-population structure over a few thousand kilometers.

Bayesian Hierarchical Integrative Modeling

1. There is substantial uncertainty about the bottom classification in some areas of the Atlantic SEUS. This uncertainty may have substantial impacts on the BHIM estimates of red snapper total abundance, and the uncertainty of the estimates. The Panel recommends increasing the accuracy of bottom type/habitat classification by mapping or other methodologies. This will provide a more reliable habitat covariate for use in the BHIM to estimate red snapper total abundance.
2. In addition to #1 above, investigate assigning a probability of hard bottom based on other sources of information (modeling) and include this major uncertainty in the BHIM abundance estimation.
3. The BHIM estimate of red snapper total abundance used information from SERFS and ROV surveys. The BHIM also required information on the effective sampling area for the SERFS camera counts. This was derived from a telemetry/camera/ROV study in a small region (Chicken Rock). The Panel recommends repeating the “Chicken Rock” telemetry project/analyses in other areas to assess spatial variation in effective sampling area and to gain more understanding about the factors that affect ESA.
4. Explore integrating trap catches into the BHIM. This involves determining the effective sampling area of trap catches (versus video).
5. Measure water current velocity at video trap locations to improve estimation of ESA.

6. Analyze recordings from both trap video cameras for fish abundance. Currently only the recordings from one of the cameras are used for BHIM (and other) analyses.
7. Expand video trap survey south of the St. Lucy area and North of Cape Hatteras, even if the used methodology results in video data only (no trapped fish).

My additional Research Recommendations for BHIM

A1. Simulation test the BHIM. This could include consideration of un-modelled heterogeneity and correlation in the latent number of red snapper available to be sampled

A2. Provide residual diagnostics to check the BHIM assumptions. This includes diagnostics for possible temporal autocorrelation in the fish counts from video frames, and whether between-site variation in detection probabilities is larger than within-site variation.

A3. If diagnostics in A2 indicate model misspecification, revise the model to account for this.

A4. Investigate factors that may contribute to variation in detection probabilities, particularly between-sites.

A5. Explore if multiple detections of individual tagged fish could be used to check if BHIM estimates of repeat counts are plausible.

b. Are there other sampling or survey methods that could be used to improve the accuracy of estimates of absolute abundance?

The Panel noted that conventional tagging is another sampling method that could be used to estimate estimates of absolute abundance of the exploited population. Tagging experiments should include double tagging to estimate tag shedding rates.

Conclusions and Recommendations

Conclusions

ToR 1. Evaluate the study designs used for developing estimates of absolute abundance of age-2+ red snapper in the U.S. South Atlantic region (Florida, Georgia, South Carolina, North Carolina).

a. Assess the study design and sampling sufficiency as they pertain to the application of genetic close-kin mark-recapture methodology.

The sampling design and the realized sampling effort exceeded the recommendations implied by the sampling simulations conducted prior to field work. The design was conditioned on the most recent assessment and Data Workshop demographic parameters (age composition (ages 1-20+), survival rates and fecundity) are sufficiently adequate for estimation.

b. Assess the study design and sampling sufficiency as they pertain to the application of hierarchical Bayesian abundance modeling.

The SERFS sampling design and sampled locations were sufficient to estimate average camera counts of red snapper for the entire sampling frame. Approximately 25% of the 4,300 potential sites were sampled in 2021 and 2022, which is high survey coverage. For the Bayesian Hierarchical Integrated Model (BHIM) estimation, red snappers were counted in each of 41 snapshots spaced 30 seconds apart, beginning 10 minutes after the video trap reached the seafloor and spanning a total of 20 minutes. I conclude this aspect of the sampling design was sufficient and appropriate.

ROV sampling found that red Snapper abundance over unconsolidated bottom was very low in the Atlantic SEUSA. The ROV sampling design and sampled locations were sufficiently adequate for this purpose. The additional paired ROV-SERFS sampling design and sampled locations were sufficient for the purpose of calibrating the ROV counts with video trap counts.

Two additional and complementary studies were conducted to estimate the effective sample area (ESA) of video trap gear such that red snapper count data could be expressed as density (number per unit area), which was critical for estimating total abundance, or population size. The sampling was insufficient to reliably estimate ESA at Turtle Mound but was sufficient at Chicken Rock. However, the study on Chicken Rock seems insufficient to estimate video trap ESA for red snapper throughout the SEUSA Atlantic stock area.

ToR 2. Evaluate the statistical/modeling methods used to analyze the data, and to construct the absolute abundances estimates and their variances.

a. Are the close-kin mark-recapture methods applied appropriately?

The close-kin mark-recapture (CKMR) statistical and modeling methods were overall applied appropriately. The uncertainty in ages obtained from the SARSRP imputation procedure is an important source of variability. CKMR abundance estimates are weakly dependent on demographic parameters and uncertainty in these parameters was not accounted for in the CKMR abundance estimate; hence, the variances of the estimates are likely too low.

b. Are the hierarchical Bayesian modeling methods applied appropriately?

The BHIM methods were applied appropriately overall. Bayesian priors were objective, which is a strength of the approach. The choice of video frames to count red snapper and use when estimating the BHIM was appropriate.

The assumption that camera-trap detection probabilities come from the same Beta distribution at all sampling sites requires further verification. I expect that between-site variation in these probabilities will be greater than within-site variation because of greater between-site variation in water turbidity and possibly other factors.

ToR 3. Are the estimates of absolute abundance (age-2+ red snapper) and their variances reliable?

The CKMR estimate is reliable overall, but it is weakly dependent on age-structure and demographics parameters (survival rates and fecundity) obtained from the most recent assessment and Data Workshop. Uncertainty in demographic parameters was not accounted for in the CKMR abundance estimate; hence, the variance is likely too low.

Bottom habitat information was too uncertain to provide a sufficiently reliable population estimate of absolute abundance (age 2+) using BHIM. This was the main source of uncertainty in the application of the BHIM. In addition, it is uncertain whether the ESA for the Chicken Rock area reliably reflects ESA throughout the stock area. Also, an unknown number of age 1 (and possibly age 0) may have been included in the absolute 2+ abundance estimate. These uncertainties were not included in variance estimates; hence, those variances will be too low.

a. *For each of the two estimation approaches, are assumptions appropriate, given study design considerations?*

Close-kin mark-recapture methods

Assumptions are appropriate given study design considerations. The estimation of absolute abundance requires demographic parameters (age composition (ages 1-20+), survival rates and fecundity) and the SARSRP team took these values from recent assessment or data input meetings. The Panel did not identify better values to use.

Hierarchical Bayesian modeling

The BHIM assumptions were generally appropriate; however, assumptions about how detection probabilities vary within- and between-sites may be improved. The assumption that bottom type could be classified as hardbottom or unconsolidated and used as a covariate in BHIM was found by the SARSRP team to be not reliable. The prior used for ESA seemed too informative to reflect ESA throughout the SEUSA Atlantic stock area.

b. *Are there potential sources of uncertainty that were not considered when developing the estimates of abundance?*

Close-kin mark-recapture methods

The variance of the abundance estimate is conditional on values of the age-length key, stock age composition, and demographic parameters. Hence, uncertainty in these values were not directly included in the variance of the abundance estimate. The uncertainty in age compositions was partially evaluated using some sensitivity analyses.

Hierarchical Bayesian modeling

Uncertainty in the area and location of hard-bottom habitat was not (fully) accounted for in the population estimate. Between-frame serial correlation in camera-trap counts should be investigated. If this correlation is substantial then this is an additional source of uncertainty.

c. *For each of the two estimation approaches, describe the magnitude and direction of any potential biases.*

There was no evidence of bias in CKMR or the BHIM abundance estimates.

ToR 4. Provide future research recommendations.

These are listed in *Summary of findings* for ToR 4.

Appendix 1: Bibliography of materials provided for review

Working papers for the South Atlantic Red Snapper Research Program (SARSRP) Review

Patterson III, W.F., D.S. Portnoy, and J.A. Buckel, editors. 2025. Population Estimation of U.S. Atlantic Red Snapper, Final Report to the South Atlantic Red Snapper Research Program. South Carolina Sea Grant, NOAA Sea Grant. 95 pp. plus appendices.

Appendix documents

1. Zulian, V., Pacifici, K., Bacheler, N.M., Buckel, J.A., Patterson Iii, W.F., Reich, B.J., Shertzer, K.W. and Hostetter, N.J., 2024. Applying mark-resight, count, and telemetry data to estimate effective sampling area and fish density with stationary underwater cameras. *Canadian Journal of Fisheries and Aquatic Sciences*, *82*, pp.1-11.
2. Goldstein, B.R., K. Pacifici, J.A. Buckel, N.M. Bacheler, E.M. Schliep, B. Reich, K.W. Shertzer, J.H. Tarnecki, W.F. Patterson III, and N.J. Hostetter. 2025. An integrated approach to estimating the effective sampling area of baited underwater cameras. Appendix II.
3. Bacheler, N.M., Patterson III, W.F., Tarnecki, J.H., Shertzer, K.W., Buckel, J.A., Hostetter, N.J., Pacifici, K., Zulian, V. and Bubley, W.J., 2025. Spatiotemporal dynamics and habitat use of Red Snapper (Lutjanus campechanus) on the southeastern United States Atlantic continental shelf. *Fisheries Research*, *281*, p.107200.
4. Monroe, A., C.M. Hollenbeck, C.L. Lanoue, W.F. Patterson III, and D.S. Portnoy. 2025. Genetic population structure of red snapper, Lutjanus campechanus, in the U.S. Atlantic and eastern Gulf of America. Appendix IV.
5. Kehoe, L., E.C. Anderson, P.B. Conn, C.M. Hollenbeck, D.D. Chagaris, K.W. Shertzer, W.F. Patterson III, and D.S. Portnoy. 2025a. Evaluating the effect of uncertainty in life history parameters on close-kin mark-recapture estimates of fish population size through simulation. Appendix V.
6. McLaughlin, P.S, E.C. Anderson, P.B. Conn, M.D. Damiano, C.M. Hollenbeck, A.A. Monroe, W.F. Patterson III, D.S. Portnoy, K.W. Shertzer, and M.T. Vincent. 2025. Incorporating close-kin mark-recapture data into an integrated stock assessment model for southeast United States Atlantic red snapper (Lutjanus campechanus). Appendix VI.
7. Kehoe, L., K.W. Shertzer, M.V. Lauretta, J.A. Buckel, D.S. Portnoy, W.F. Patterson III, and D.D. Chagaris. 2025b. Estimating reef fish discard exploitation rates in catch and release fisheries with conventional or genetic tags. Appendix VII.
8. Rudershausen, P.J., B.J. Runde, R.M. Tharp, J.H. Merrell, N.M. Bacheler, W.F. Patterson III, and J.A. Buckel. 2025b. Discard mortality rates of Red Snapper after barotrauma and hook trauma: insights from using acoustic telemetry in the U.S. Atlantic. North American Journal of Fisheries Management 45:270–282.
9. Rudershausen, P.J., Runde, B.J., Tharp, R.M., Merrell, J.H., Bacheler, N.M., Patterson III, W.F. and Buckel, J.A., 2025. Discard mortality rates of Red Snapper after barotrauma and hook trauma: Insights from using acoustic telemetry in the US South Atlantic. North American Journal of Fisheries Management, 45(2), pp.270-282.
10. Zimmermann, S., L. Kehoe, M.A. Taylor, J.H. Tarnecki, N.M. Bacheler, Z.A. Siders, and W.F. Patterson III. 2025. Post-release mortality of red snapper, Lutjanus campechanus, in Atlantic waters off northeast Florida estimated with three-dimensional acoustic telemetry. Appendix X.

Background documents provided during the peer review

Additional Papers I Reviewed

Babyn, J., Ruzzante, D., Bravington, M. and Mills Flemming, J., 2024. Estimating effective population size using close-kin mark–recapture. Methods in Ecology and Evolution, 15(11), pp.2059-2073.

Mark V. Bravington. Hans J. Skaug. Eric C. Anderson. "Close-Kin Mark-Recapture." Statist. Sci. 31 (2) 259 - 274, May 2016. https://doi.org/10.1214/16-STS552

Bravington, M.V., Grewe, P.M. and Davies, C.R., 2016. Absolute abundance of southern bluefin tuna estimated by close-kin mark-recapture. Nat Commun 7: 13162 [online]

Casas, L. and Saborido-Rey, F., 2023. A review of an emerging tool to estimate population parameters: the close-kin mark-recapture method. Frontiers in Marine Science, 10, p.1087027.

Conn, P.B., Bravington, M.V., Baylis, S. and Ver Hoef, J.M., 2020. Robustness of close-kin mark–recapture estimators to dispersal limitation and spatially varying sampling probabilities. *Ecology and Evolution*, *10*(12), pp.5558-5569.

Conn, P.B., 2025. Simulation-Based Inference for Close-Kin Mark-Recapture: Implications for Small Populations and Nonrandom Mating. Environmetrics, 36(8), p.e70049.

Delaval, A., Bendall, V., Hetherington, S.J., Skaug, H.J., Frost, M., Jones, C.S. and Noble, L.R., 2023. Evaluating the suitability of close-kin mark-recapture as a demographic modelling tool for a critically endangered elasmobranch population. Evolutionary Applications, 16(2), pp.461-473.

Peterman, F.T., Thomas, L., Harris, D., Bradley, D. and Papastamatiou, Y.P., 2024. Age is not just a number: How incorrect ageing impacts close-kin mark-recapture estimates of population size. Ecology and Evolution, 14(6), p.e11352.

Punt, A.E., Thomson, R., Little, L.R., Bessell-Browne, P., Burch, P. and Bravington, M., 2024. Including close-kin mark-recapture data in statistical catch-at-age stock assessments and management strategies. *Fisheries Research*, *276*, p.107057.

Ruzzante, D.E., McCracken, G.R., Førland, B., MacMillan, J., Notte, D., Buhariwalla, C., Mills Flemming, J. and Skaug, H., 2019. Validation of close-kin mark–recapture (CKMR) methods for estimating population abundance. Methods in Ecology and Evolution, 10(9), pp.1445-1453.

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Appendix 2: CIE Statement of Work

Performance Work Statement (PWS)

National Oceanic and Atmospheric Administration (NOAA)
NOAA Fisheries
Center for Independent Experts (CIE) Program
External Independent Peer Review

South Atlantic Red Snapper Research Program *(SARSRP)* Review
January 13 – 15, 2026

Background

The NOAA Fisheries is mandated by the Magnuson-Stevens Fishery Conservation and Management Act, Endangered Species Act, and Marine Mammal Protection Act to conserve, protect, and manage our nation's marine living resources based upon the best scientific information available (BSIA). NOAA Fisheries science products, including scientific advice, are often controversial and may require timely scientific peer reviews that are strictly independent of all outside influences. A formal external process for independent expert reviews of the agency's scientific products and programs ensures their credibility. Therefore, external scientific peer reviews have been and continue to be essential to strengthening scientific quality assurance for fishery conservation and management actions.

Scientific peer review is defined as the organized review process where one or more qualified experts review scientific information to ensure quality and credibility. These expert(s) must conduct their peer review impartially, objectively, and without conflicts of interest. Each reviewer must also be independent from the development of the science, without influence from any position that the agency or constituent groups may have. Furthermore, the Office of Management and Budget (OMB), authorized by the Information Quality Act, requires all federal agencies to conduct peer reviews of highly influential and controversial science before dissemination, and that peer reviewers must be deemed qualified based on the OMB Peer Review Bulletin standards[1]. Independent scientific peer review is a hallmark of gold standard science[2].

Scope

The South Atlantic red snapper fishery is economically and recreationally important, but has faced challenges due to overfishing and restrictive management. The red snapper population has shown a remarkable rebound in the last 15 years. Fishermen and scientists agree that red snapper are far more abundant and larger than they used to be. Harvest opportunities for red snapper remain limited because of the large amount of discarded fish and uncertainty in the exact number of fish in the

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[1] https://www.whitehouse.gov/wp-content/uploads/legacy_drupal_files/omb/memoranda/2005/m05-03.pdf

[2] https://www.whitehouse.gov/presidential-actions/2025/05/restoring-gold-standard-science/

[3] https://www.fisheries.noaa.gov/southeast/recreational-fishing/working-toward-increasing-fishing-opportunities-red-snapper-south-atlantic

[4] https://www.scseagrant.org/south-atlantic-red-snapper-research-program/

population. The South Atlantic Council, in recent years, has struggled with how to reduce the high amounts of red snapper discards and end overfishing, as required by the law[3].

The *South Atlantic Red Snapper Research Program (SARSRP*) was administered through the South Carolina Sea Grant Consortium[4]. A Request for Proposals (RFP) was issued with a full proposal deadline of February 1, 2021. The goal of the SARSP is to generate an absolute estimate of abundance with an accompanying measure of uncertainty for the entire South Atlantic red snapper stock. Preference was given to proposals that seek to produce a single absolute estimate of abundance for the entire geographic region. This estimate will serve as an independent benchmark on which to inform a currently ongoing stock assessment. It will provide a metric of abundance of what the size (number of individual fish) of the stock is in the South Atlantic for the period of the survey. The SARSP awarded project is led by a team of researchers spanning the following research institutions: University of Florida, Texas A&M Corpus Christi, N.C. State University, NOAA Fisheries, S.C. Department of Natural Resources, NOAA NOS Center for Coastal Fisheries Habitat Research, Florida Fish & Wildlife Conservation Commission, and GA Department of Natural Resources.

The awarded research proposal included the following three approaches: (1) Close-kin and meta-population genetics analyses; (2) Existing and possibly supplemental new South Atlantic trap-video survey data to scale-up density estimates to total abundance; and (3) a research technique similar to that pursued in the Gulf Red Snapper abundance assessment, focusing predominantly on use of active acoustics and visual ground-truthing. Research began in the Fall of 2020 and will finish in August of 2025, hence the request for CIE review at this time.

Fisheries management depends on science based advice for setting accurate quotas. Scientific peer-review serves as the cornerstone and gold standard of best science. This peer review will further the NOAA mission to conserve and manage coastal and marine ecosystems and resources by providing science based advice. This advice is consistent with National Standard 2 (NS2), which is a statutory (Magnuson Stevens Act) requirement at 16 U.S.C. 1851(a)(2) and states that "conservation and management measures shall be based upon the best scientific information available (BSIA). This review aligns this statute because this CIE peer review is an essential part of determining whether the assessment used meets the criteria for BSIA under NS2. It will also further the NOAA Fisheries mission of productive and sustainable fisheries and healthy ecosystems.

The specified format and contents of the individual peer review reports are found in **Annex 1**. The Terms of Reference (ToRs) of the peer review are listed in **Annex 2**. The tentative agenda of the panel review meeting is attached in **Annex 3.**

Requirements

NOAA Fisheries requires three **(3)** reviewers to conduct an impartial and independent peer review in accordance with the Performance Work Statement (PWS), OMB guidelines, and the ToRs below. The reviewers shall have expertise in quantitative methods applied to fisheries. It is desirable to have at least one reviewer with expertise in capture-recapture methodology, especially Bayesian hierarchical modeling, and at least one reviewer with expertise in genetic close-kin mark-recapture applications.

The review panel chair, who is in addition to the three reviewers, will not be provided by the CIE. Although the chair will be participating in this review, the chair's participation (e.g., labor and travel) is not covered by this contract.

Each reviewer will write an individual review report in accordance with the PWS, OMB Guidelines, and the ToRs below. Modifications to the PWS and TORs cannot be made during the peer review, and any PWS or ToRs modifications prior to the peer review shall be approved by the Contracting Officer's Representative (COR) and the CIE contractor. All ToRs must be addressed in each reviewer's individual report.

Tasks for Reviewers

1) Pre-review Background Documents: Review the following background materials and reports prior to the review:
   Two weeks before the peer review, the NOAA Fisheries Project Contact will send by electronic mail or make available at an FTP site to the CIE reviewer all necessary background information and reports for the peer review. In the case where the documents need to be mailed, the Project Contact will consult with the CIE on where to send documents. The CIE reviewer shall read all documents in preparation for the peer review.
2) Attend and participate in an in-person review meeting. The meeting will consist of presentations by NOAA and other scientists, stock assessment authors and others to facilitate the review, to answer any questions from the reviewers, and to provide any additional information required by the reviewers.
3) After the review meeting, reviewers shall conduct an independent peer review report in accordance with the requirements specified in this PWS, OMB guidelines, and ToRs, in adherence with the required formatting and content guidelines. Reviewers are not required to reach a consensus.
4) Each reviewer shall assist the Chair of the meeting with contributions to the summary report based on the ToRs. Reviewers are not required to reach consensus.
5) Deliver their reports to the Government according to the specified milestones dates.

Foreign National Security Clearance

When reviewers participate during a panel review meeting at a government facility, the NOAA Fisheries Project Contact is responsible for obtaining the Foreign National Security Clearance approval for reviewers who are non-US citizens. For this reason, the reviewers shall provide requested information (e.g., first and last name, contact information, gender, birth date, passport number, country of passport, travel dates, country of citizenship, country of current residence, and home country) to the Project Contact for the purpose of their security clearance, and this information shall be submitted at least two weeks in advance. For additional information, please see the following link: https://www.commerce.gov/osy/programs/foreign-access-management. The contractor is required to use all appropriate methods to safeguard Personally Identifiable Information (PII).

Place of Performance

The place of performance shall be in Charleston, SC.

Period of Performance

Each reviewer's duties shall not exceed **14** days to complete all required tasks.

Schedule of Milestones and Deliverables: The contractor shall complete the tasks and deliverables in accordance with the following schedule.

Within 2 weeks of award	Contractor selects and confirms reviewers
Approximately 2 weeks prior to the review	Contractor provides the pre-review documents to the reviewers
January 13 – 15, 2026	Panel review meeting
Approximately 2 weeks later	Contractor receives draft reports
Within 3 weeks of receiving draft reports	Contractor submits final reports to the Government

* The Peer Review Summary Report will not be submitted to, reviewed, or approved by the Contractor.

Applicable Performance Standards

The acceptance of the contract deliverables shall be based on three performance standards:
(1) The reports shall be completed in accordance with the required formatting and content (2) The reports shall address each ToR as specified (3) The reports shall be delivered as specified in the schedule of milestones and deliverables.

Confidentiality and Data Privacy

This contract may require that services contractors have access to Privacy Information. Services contractors are responsible for maintaining the confidentiality of all subjects and materials and may be required to sign and adhere to a Non-disclosure Agreement (NDA).

Travel

All travel expenses shall be reimbursable in accordance with Federal Travel Regulations (Travel resources | GSA), and all contractor travel must be approved by the COR prior to the actual travel. Any travel conducted prior to the receipt of proper written authorization from the COR will be done at the Contractor's own risk and expense. International travel is authorized for this contract. Travel is not to exceed the contracted amount.

NOAA Fisheries Project Contact

Erik H. Williams, Ph.D., Director of the Atlantic Fisheries Branch
Sustainable Fisheries Division
Southeast Fisheries Science Center
erik.williams@noaa.gov

Office Tel: 252-666-7428

Annex 1. Terms of Reference for the Peer Review

South Atlantic Red Snapper Research Program Review

January 13 - 15, 2026

CIE reviewers are contracted to complete their independent peer review based on the ToRs. Therefore, the CIE-NOAA Fisheries review and approval process is based on whether the CIE independent reports addressed each ToRs.

1. Evaluate the study designs used for developing estimates of absolute abundance of age-2+ red snapper in the U.S. South Atlantic region (Florida, Georgia, South Carolina, North Carolina).
    a. Assess the study design and sampling sufficiency as they pertain to the application of genetic close-kin mark-recapture methodology.
    b. Assess the study design and sampling sufficiency as they pertain to the application of hierarchical Bayesian abundance modeling.

2. Evaluate the statistical/modeling methods used to analyze the data, and to construct the absolute abundances estimates and their variances.
    a. Are the close-kin mark-recapture methods applied appropriately?
    b. Are the hierarchical Bayesian modeling methods applied appropriately?

3. Are the estimates of absolute abundance (age-2+ red snapper) and their variances reliable?
    a. For each of the two estimation approaches, are assumptions appropriate, given study design considerations?
    b. Are there potential sources of uncertainty that were not considered when developing the estimates of abundance?
    c. For each of the two estimation approaches, describe the magnitude and direction of any potential biases.

4.Provide future research recommendations.
    a. How could each of the methods used in this study be improved for more accurate estimates?
    b. Are there other sampling or survey methods that could be used to improve the accuracy of estimates of absolute abundance?

Annex 2. Tentative Agenda

South Atlantic Red Snapper Research Program Review

January 13 – 15, 2026
Location: Charleston, SC

Dates: January 13 -15, 2026
Times each day: 0830-1700 hrs

January 13, 2026
0830 to 0850
    Introductions and review of agenda
0850 to Morning Break (10 min, TBD by Chair)
    Presentations by SARSP team with clarifying questions from panel after each presentation
End of Morning Break to Lunch Break
    Presentations by SARSP team with clarifying questions from panel after each presentation
Lunch Break to last 1.5 hrs
End of Lunch Break to Afternoon Break (10 min, TBD by Chair)
    Presentations by SARSP team with clarifying questions from panel after each presentation
End of Afternoon Break to 1700
    Presentations by SARSP team with clarifying questions from panel after each presentation

January 14, 2026
0830 to Morning Break (10 min, TBD by Chair)
    Presentations by SARSP team with clarifying questions from panel after each presentation
End of Morning Break to Lunch Break
    Presentations by SARSP team with clarifying questions from panel after each presentation
Lunch Break to last 1.5 hrs
End of Lunch Break to Afternoon Break (10 min, TBD by Chair)
    Questions and discussions between review panel and SARSP team
End of Afternoon Break to 1700
    Questions and discussions between review panel and SARSP team

January 15, 2026
0830 to Morning Break (10 min, TBD by Chair)
    Questions and discussions between review panel and SARSP team
End of Morning Break to Lunch Break
    Questions and discussions between review panel and SARSP team
Lunch Break to last 1.5 hrs
End of Lunch Break to Afternoon Break (10 min, TBD by Chair)
    Deliberations and report writing by review panel
End of Afternoon Break to 1700
    Deliberations and report writing by review panel

Annex 3. Individual Independent Peer Reviewer Report Requirements

1. The independent Peer Reviewer report shall be prefaced with an Executive Summary providing a concise summary of whether they accept or reject the work that they reviewed, with an explanation of their decision (strengths, weaknesses of the analyses, etc.).

2. The report must contain a background section, description of the individual reviewers' roles in the review activities, summary of findings for each ToR, in which the weaknesses and strengths are described, and conclusions and recommendations in accordance with the ToRs.

   a. Reviewers must describe in their own words the review activities completed during the panel review meeting, including a brief summary of findings, of the science, conclusions, and recommendations.

   b. Reviewers should discuss their independent views on each ToR even if these were consistent with those of other panelists, but especially where there were divergent views.

   c. Reviewers should elaborate on any points raised in the summary report that they believe might require further clarification.

   d. Reviewers shall provide a critique of the agency review process, including suggestions for improvements of both process and products.

   e. The report shall be a stand-alone document for others to understand the weaknesses and strengths of the science reviewed, regardless of whether or not they read the summary report. The report shall represent the peer review of each ToR, and shall not simply repeat the contents of the summary report.

3. The report shall include the following appendices:

   Appendix 1: Bibliography of materials provided for review
   Appendix 2: A copy of this Performance Work Statement
   Appendix 3: Panel membership or other pertinent information from the panel review meeting.

Appendix 3: Panel membership or other pertinent information from the panel review meeting.

The Panel included a chairperson and three independent scientists selected by the Center for Independent Experts (CIE):

1. Dr. Paul Rago (chair; United States)
2. Dr. Joe Powers (CIE; United States),
3. Dr. Noel Cadigan (CIE; Canada), and
4. Dr. Daniel Ruzzante (CIE; Canada).

Dr. Rago is a member of the Mid-Atlantic Fishery Management Council's Scientific and Statistical Committee (SSC). All four Panel members have extensive experience fisheries surveys.

Many participants from NOAA MRIP and two consultants attended the review panel and made presentations (see Appendix 1) or provided responses to panel questions. The panel focused their questions and discussions by following the ToRs listed in Annex 1 of Appendix 2 of this report.

Other information from the panel review meeting is described under ToR 7 above.

Independent Peer Review of the South Atlantic Red Snapper Research Program

Feb 2026
Submitted to the
Center of Independent Experts
by

Joseph Powers

Executive Summary

The purpose of the review was to evaluate work conducted by the South Atlantic Red Snapper Research Project (SARSRP) in their implementation of Close-Kin Mark-Recapture Methodology (CKMR) and Hierarchical Bayesian Model (HBM) to provide estimates of abundance of age 2+ red snapper off the southeast US Atlantic coast.

Close-Kin Mark-Recapture Methodology (CKMR) The CKMR methodology and study design appears robust and the sampling effort sufficient for an estimate of population abundance. The CKMR methods and analyses developed were consistent with theory and modeling experience and were applied appropriately, and the resulting CKMR population estimate is reliable given the identified assumptions and uncertainties. An important note is that CKMR methods are conditioned on life-history parameters and demographic data that under current estimation approaches can only be derived from stock assessment analyses. Thus, the abundance estimate based on the CKMR is not independent from the SEDAR 73U stock assessment information nor will it be independent from the upcoming assessment. Thus, the appropriate approach is to integrate the CKMR data and models into the stock assessment likelihood in future assessments.

The basic CKMR estimation model uses life history and demographic data (i.e., age-distributions, natural and fishing mortality rates and fecundity and other life history data), to provide the reproductive (genetic) output of males and females. This is used to determine the expected number of half-sibling pairs in a population. Then the detection of the probability of observing half-siblings comes from the genetic analyses of sampled fish. Combing the two through binomial pdfs provides the basis for estimation of abundance.

Considerable planning, exploratory research and simulation work was done prior to sampling to ensure that sampling would be sufficient and that genetic marks could be determined at an adequate frequency.

Because these CKMR estimates will always be depend on life history/demographic parameters and because currently those parameters are defined from the most recent stock assessment, a number of sensitivity analyses were conducted assuming alternative parameter sets. Generally, the results of the demographic sensitivities were robust with the exception of the determination of reproductive output when it is skewed to older ages. However, the sensitivities were not examined using the exact estimation model of the final report. Thus, it is recommended that the sensitivities be repeated to be consistent with the final estimation model.
The SARSRP reported estimate for 2020 (for example) was mean abundance of age 2+ fish =1,444,565; median=1,414,694 and the CV=0.172. It is likely that the CV is underestimated (the sources of the additional variance discussed in the body of the report herein). Nevertheless, the central tendency estimates are somewhat lower than the SEDAR 73U stock assessment, but well within confidence intervals.

However, both the theory of half-sibling CKMR estimates and the applications explicitly indicate that the estimate is conditional on demographic parameters. And the source of those parameter estimates is through a stock assessment. Thus, the abundance estimates using the CKMR data are not final. They will evolve as they are integrated into the assessment.

Hierarchical Bayesian Model (HBM) The sampling design and sampled locations were sufficient to estimate average camera counts of red snapper for the entire sampling frame of the Southeast Reef Fish Survey (SERFS). Paired sampling with SERFS video trap and remotely operated vehicle (ROV) to calibrate red snapper counts occurred in three areas. This was sufficient for the purpose of calibration with video trap counts. Based on the ROV data, red snapper abundance over unconsolidated bottom was very low in the Atlantic SE. The two complementary studies conducted at Chicken Rock (North Carolina) and Turtle Mound (Florida) to estimate the effective sample area (ESA) of video trap gear were critical for estimating total red snapper abundance. However, the Turtle Mound estimates were considered unrealistic by the SARSRP team and not put forward. The Chicken Rock study was conducted in only one area over a limited time. Thus, it is unlikely that the resulting ESA represents the overall ESA for the entire stock area. Another area of concern was that the SERFS video data and ROV density estimates were expanded to the entire study area using uncertain information of hard bottom habitat. The HBM red snapper population estimate was sensitive to how bottom type was identified and classified, and this habitat uncertainty was not included in the overall CV of the HBM red snapper population estimate. As with the CKMR methods, the population estimate coming from the HBM is not entirely independent from stock assessment data. Video trap data from the trap cameras have been used in previous assessments as a measure of relative abundance, and were also used in the HBM analysis. Because size and age information was not included in the HBM analysis, the estimate of total abundance for age 2+ has some uncertainty as an unknown number of age 1 (and possibly age 0) may have been included in the estimate. As with the CKMR work, this is explored in the SARSRP report, but should be taken into account when this estimate is included in, or compared with the assessment outcome. There is little confidence in the HBM population estimate because the estimate of ESA is based on data from one study in one area, and more importantly because of the uncertainty in the hard bottom habitat characterization. This conclusion is demonstrated by the resulting HBM estimate of 5.31 million red snapper with a CV of 0.39 which is, itself, likely to be underestimated.

Table of Contents

1. Background

The NOAA Fisheries is mandated by the Magnuson-Stevens Fishery Conservation and Management Act, Endangered Species Act, and Marine Mammal Protection Act to conserve, protect, and manage our nation's marine living resources based upon the best scientific information available (BSIA). NOAA Fisheries science products, including scientific advice, are often controversial and may require timely scientific peer reviews that are strictly independent of all outside influences. A formal external process for independent expert reviews of the agency's scientific products and programs ensures their credibility. Therefore, external scientific peer reviews have been and continue to be essential to strengthening scientific quality assurance for fishery conservation and management actions.
Scientific peer review is defined as the organized review process where one or more qualified experts review scientific information to ensure quality and credibility. These expert(s) must conduct their peer review impartially, objectively, and without conflicts of interest. Each reviewer must also be independent from the development of the science, without influence from any position that the agency or constituent groups may have. Furthermore, the Office of Management and Budget (OMB), authorized by the Information Quality Act, requires all federal agencies to conduct peer reviews of highly influential and controversial science before dissemination, and that peer reviewers must be deemed qualified based on the OMB Peer Review Bulletin standards.

In 2020, Congress allocated funding toward the South Atlantic Red Snapper Research Program (SARSRP) to be administered by South Carolina Sea Grant (SCSG) who solicited proposals to produce "an absolute estimate of abundance with an accompanying measure of uncertainty for the entire South Atlantic red snapper stock" to inform "future spawning stock assessments." Additional funding was made available in 2021 and 2022. In addition to estimating population size, SARSRP funding was utilized to calibrate sampling gear, examine spatial and temporal trends in red snapper relative abundance, estimate red snapper release mortality, quantify stakeholder perceptions of habitat and red snapper distribution and compare to empirical and model-derived estimates, conduct tagging simulations, and test key assumptions of the population estimation approaches employed in the study. However, the focus of the study (and of this review) is on the two Atlantic red snapper population estimation approaches: close-kin mark-recapture (CKMR) and hierarchical Bayesian modeling. The results of those two studies are evaluated through the direct responses to the Terms of Reference (ToRs) highlighted below.

2. Description of the Individual Reviewer's Role in the Review Activities

CIE reviewers were contracted to complete their independent peer review based on the ToRs.
The goals of this review process are to evaluate the implementation and results of the Close-kin and meta-population genetics analyses for estimating abundance; and trap-video survey data providing density estimates, scaled-up to total abundance through habitat mapping. The report herein is my CIE evaluation of these studies in the context of the specific ToRs.

3. Summary of Findings for Each Term of Reference

I begin the discussion of TORs by presenting a general discussion of the CKMR and hierarchical Bayesian modeling (HBM) approaches to red snapper population estimation. This provides a context for evaluating the estimation approaches. After that the individual TORs are addressed.

3.1 Background discussion of CKMR SARSRP methods

As noted in the reports cited below, CKMR is a variation on traditional mark-recapture with important differences. With CKMR, the marks utilized are genetic “tags” that are never lost, can be recovered from both live and dead fish and are partially shared among related individuals, or kin. When kin relationships, such as parent offspring (PO) or half-sibling (HS) relationships, are identified in a sample of individuals of a population, they constitute a form of recapture based on these natural, genetic tags. “Analyzing kin recaptures with CKMR models ***informed by life history information (my emphasis added)*** enables one to relate the number of kin observed in a sample to (absolute) population size (Skaug 2001; Bravington et al. 2016)”.

Informed by life history information refers to basic growth parameters, fecundity/reproductive success relationships and other biological/ecological characteristics, but also includes demographic data (abundance at age by year and fishing and natural mortality rates). I make the distinction between life history and demographic data for reasons I will get into below.

In the SARSRP application the genetic component of the study determines the probability of encountering HS pairs while the life history/demographic component (LH/demo) determines the expected number of HS encounters conditional on the LH/demo data. There was some criticism of the report in that it was not exactly clear in the formulation of the LH/demo data used in the final results and sensitivities. Thus, I tried to harmonize the notation used in the main report, Appendix V and the presentation and “fill out” the equations. This is shown by the following estimation:

$$P(HS|b_1,b_2,LH/demo) = \sum_{a^*=1}^{20-\mathrm{d}} \left[\frac{E_{b_1,a^*} \quad E_{b_2,a^*+\mathrm{d}}}{¼\ N_{b_2,a^*+\mathrm{d}}} \quad \prod_{a=a^*+1}^{a^*+\mathrm{d}} S_a \quad \right]$$

$$d = b_2 - b_1 \quad b_2 > b_1 \quad S_a\ is\ the\ survival\ during\ age\ a$$

$E_{\mathrm{t,i}}$ is the expected relative reproductive output of age I in year t and $N_t \equiv \sum_{\mathrm{i}=1}^{20} N_{\mathrm{t,i}}\ and\ N_{\mathrm{t,i}} = N_t\ R_{\mathrm{t,i}}$

Let

$Fec_i \equiv c\ W_i^g$

$M_{i,t} = natural\ mortality\ rate\ of\ age\ i\ during\ year\ t$

$F_{i,t} = fishing\ mortality\ rate\ of\ age\ i\ during\ year\ t$

$P_i = proportion\ mature\ at\ age\ i$

Then

$$E_{\mathrm{t,i}} \equiv \frac{N_{\mathrm{t,i}}\ P_i\ Fec_i}{\sum_{\mathrm{i}=1}^{20} N_{\mathrm{t,i}}\ P_i\ Fec_i} = \frac{R_{\mathrm{t,i}}\ P_i\ Fec_i}{\sum_{\mathrm{j}=1}^{20} R_{\mathrm{t,j}}\ P_j\ Fec_j} = \frac{R_{\mathrm{t,i}}\ P_i W_i^g}{\sum_{\mathrm{j}=1}^{20} R_{t,j}\ P_j\ W_j^g}$$

and μ_{b_1,b_2} = expected number of half-siblings pairs in year b_2 that were spawned in year b_1:

$$\mu_{b_1,b_2} = N_{b_2}\ \ x\ \ P(HS|b_1,b_2,LH/demo\,) = \sum_{a^*=1}^{20-\mathrm{d}} \left[\frac{E_{b_1,a^*} \quad E_{b_2,a^*+\mathrm{d}}}{¼\ R_{b_2,a^*+\mathrm{d}}}\ e^{-Z_{a^*,b_2}} \quad \right]$$

where $Z_{a^*,b_2} \equiv \sum_{a=a^*+1}^{a^*+\mathrm{d}} \left(M_{a-1,b_2-(a-1)} + F_{a-1,b_2-(a-1)} \right)$.

I generalized the survival estimates to include the component fishing and natural mortality rates. I, also, included the fecundity relationship Fec=c W^g. The authors specified g=1 per the guidance of the "Data Workshop" while Appendix V explored more sophisticated fecundity relationships to address batch fecundity and other issues. I used alternative g values as a simple mechanism to explore sensitivities.

The process is modeled as a binomial distribution (mean=np=mu, variance = np(1-p)). Thus, the above tells us that the expected number of HS (mu) is defined by the LH/demo data and the actual genetic data do not enter into it. The HS probability is the component that the genetic data defines. (note that the P(HS) is adjusted in the final model by the probability of false negatives). Hence, the binomial distribution is being parameterized by mu (from LH/demo) and p (from genetic data).

So, what do the basic equations tell us? The CKMR SARSRP estimate of abundance is conditional on the LH/demo data. But where do the demo (demographic) data come from? I cannot foresee obtaining estimates of fishing mortality rates and relative age distributions from anywhere else other than a stock assessment. The authors are well aware of this and the basic theory (Bravington) acknowledges this. And fishing mortality rates and relative age distributions are subject to the vicissitudes of catch, bycatch, discards, selectivities and other issues estimated/explored in a stock assessment. What the present study provides is an abundance estimate conditional on the most recent assessment and an exploration of sensitivities to those data. In my opinion, the CKMR methods were applied appropriately and the results provide a mechanism for moving forward.

Given the prior assessment history, there are two paths for moving forward. One could do the next assessment independent of the CKMR data and then re-estimate the CKMR estimates based on the fishing mortality rates and age distributions estimated in that new assessment; OR one could integrate the genetic data (probability of HS pairs) directly into the assessment through an expanded likelihood function, balancing the CKMR data with other sources of information. The choice is obvious: integrate the CKMR data into the assessment.

It seems that there was some expectation that the CKMR estimate of abundance would be somehow independent of a stock assessment. That certainly was not the expectation of the authors, nor was it my expectation, nor was it induced by the basic theory (Bravington). The SARSRP CKMR estimate is conditional on the LH/demo data. The corollaries to this are: 1) the present CKMR estimate of abundance is not "final"; the estimate will be modified based on future detections of HS pairs; and 2) the estimate will be adjusted with each subsequent stock assessment based on interpretations of catches, indices, size distributions for the foreseeable future.

There was extended discussion at the review meeting about the sensitivity analyses and the fecundity relationship in particular. The following demonstrates that many of the LH/demo sensitivities can be approximately explored without going through the entire re-estimation. Recall

$$\mu_{b_1,b_2} = N_{b_2} \ \ x \ \ P(HS|b_1,b_2,LH/demo\,) = \sum_{a^*=1}^{20-\mathrm{d}} \left[\frac{E_{b_1,a^*} \ \ E_{b_2,a^*+\mathrm{d}}}{\frac{1}{4}\, R_{b_2,a^*+\mathrm{d}}} \ e^{-Z_{a^*,b_2}} \quad \right]$$

Using the LH/demo data of Tables 3.1, 3.2 and 3.3, the mu matrix from the above equation where the fecundity exponent g=1 is (hoping I got all the subscripts right)

		μ(b1,b2)									
Expected No. half-sibling pairs in year b2 ->			5.457552	8.866026	14.40184	16.08832	24.85471	27.36668	36.40319	30.69179	23.84871
Fec= c W^g g=1			b2: 2015	2016	2017	2018	2019	2020	2021	2022	2023
		b1↓ 2014	5.457552	4.983513	5.740138	4.951837	6.19146	5.6586	6.404133	4.67048	3.175196
		2015	0	3.882513	4.733185	4.264918	5.525398	5.208426	6.041063	4.493783	3.109616
		2016	0	0	3.928521	3.701622	4.959166	4.803358	5.689933	4.304685	3.020814
		2017	0	0	0	3.169946	4.407956	4.391747	5.315644	4.090379	2.910702
		2018	0	0	0	0	3.770727	3.901005	4.853607	3.815172	2.7617
		2019	0	0	0	0	0	3.403548	4.371627	3.519151	2.595203
		2020	0	0	0	0	0	0	3.727179	3.11343	2.360457
		2021	0	0	0	0	0	0	0	2.684708	2.106442
		2022	0	0	0	0	0	0	0	0	1.808575

An alternative table was generating where g the fecundity exponent was 1.333 (approximately equivalent to Fec proportional to Length at age^4):

		μ(b1,b2)									
Expected No. half-sibing pairs in year b2:			7.4956868	12.37199	19.81643	21.88067	33.21191	36.54958	48.43459	40.8285	30.66094
Fec=c W^g g=1.33			b2: 2015	2016	2017	2018	2019	2020	2021	2022	2023
		b1↓2014	7.4956868	6.902946	7.908804	6.810028	8.419701	7.711945	8.692406	6.3288	4.147065
		2015	0	5.46904	6.54033	5.848762	7.479582	7.068585	8.173758	6.078605	4.061182
		2016	0	0	5.367299	4.99255	6.604295	6.430806	7.618078	5.77918	3.927425
		2017	0	0	0	4.229326	5.788786	5.804884	7.042772	5.447901	3.763825
		2018	0	0	0	0	4.919545	5.103347	6.365435	5.037437	3.547264
		2019	0	0	0	0	0	4.430015	5.685538	4.607837	3.309719
		2020	0	0	0	0	0	0	4.856607	4.060402	2.993877
		2021	0	0	0	0	0	0	0	3.488333	2.650728
		2022	0	0	0	0	0	0	0	0	2.259854

Assume that the base estimate of abundance was 1.5 million when g=1 for b2=2021. This implies that P(HS) from the genetic data P(HS)=mu/1.5 million= 36.40319/1,500,000. Then if g were in fact equal to 1.33, then the estimated abundance would be: 48.43459/(36.40319/1,500,000)=1,995,756, a 33% increase from the base. While I am not totally confident that I got all the subscripts right, these results are similar to some of the batch fecundity sensitivities in Appendix V. Suffice it to say, not unexpectedly, the abundance estimates are relatively sensitive to the fecundity relationship. There is much we don't know about relative male contributions to reproductive output at age, female fecundity at age, etc. Having said this, I am not overly concerned. But it is important to realize that the variance estimates do not incorporate this uncertainty. Additionally, it is important that the same assumptions about life history and fecundity be used in the assessment as with the CKMR estimates (or more importantly, integrated into the assessment!). Presumably those assumptions should be driven by subject experts in those life history characteristics. Still, I advocate for using the methods of the above exercise to evaluate sensitivities, as it is quick and simple.

As an aside, in my opinion the CKMR data opens the possibility to expand the parameter set that is being estimated in a stock assessment. For example, the ratio of reproductive output to numbers of age 1 might be determined from Parent-Offspring ratios: S/R of a Beverton-Holt stock recruitment relationship where R= S/(a+bS) and P-O ratio= a+bS. Also, CKMR data might provide information to define natural mortality rates or, perhaps, one of the parameters of a Lorenzen M relationship. Again, this exploration awaits integration of CKMR into a stock assessment.

Overall, I felt the study was appropriate in design, sample size determination and incorporating basic biological and distributional data.

3.2 Background discussion of HBM SARSRP methods

The Hierarchical Bayesian Model (HBM) utilized data from the Southeast Reef Fish Survey (SERFS) video trap as well as from fish count estimates produced with remotely operated vehicle (ROV) video samples to obtain densities of red snapper for specific habitats (hardbottom: reefs, rocks, and areas of high relief) and depth data where the relationships between densities and habitats were statistically modeled. Then the SERFS video data and ROV density estimates were expanded to the total stock area using information on the extent of hard bottom habitat to obtain total abundance estimates

The SERFS video traps sampled reef fish across the SE USA continental shelf and upper slope between Cape Hatteras, North Carolina, and St. Lucie Inlet, Florida, using baited chevron traps with two attached video cameras. SERFS video trap data were utilized to examine temporal and spatial trends in red snapper abundance and bottom habitat in areas of the southeastern U.S. Atlantic. ROV data also contributed abundance information in hard bottom regions and were also used to test whether red snapper could be found on unconsolidated habitats not targeted by the SERFS survey. For the purpose of the HBM analysis, the number of red snapper were quantified using the video analysis only.

The sampling protocol counted red snappers in each of 41 snapshots spaced 30 seconds apart, beginning 10 minutes after the video trap reached the seafloor and spanning a total of 20 minutes. Trap catches of red snapper were not used in the HBM because of uncertain effective sampling area. However, note that the SERFS trap “catches” per unit sampling effort are the basis of the SERFS index used in the current stock assessment.

SERFS sampling locations were chosen via simple random sampling from approximately 4,300 potential sites assumed to have reef structure. An important factor to affect camera counts was current direction, which was qualitatively categorized at each location as “away”, “sideways”, or “towards” based on the movement of visible particles in the water relative to the view field of the video camera over the trap mouth. Sampling occurred during April-September in 2021 (n=1,384 video trap deployments) and 2022 (n=1,050 video trap deployments).

This sampling design was sufficient to estimate average video camera counts of red snapper for the entire SERFS sampling frame (i.e., approximately 25% of the 4,300 potential sites were sampled in 2021 and 2022). However, no video trap data was available for the area south of St. Lucy, FL and North of Cape Hatteras, NC.

The primary purpose of the ROV surveys was to estimate red snapper density over a variety of habitats, assuming that “area swept” could be estimated accurately. Importantly, ROV data were used to test whether red snapper occurs on unconsolidated habitats not targeted by the SERFS survey. Sampling was conducted during June-August 2021 (n = 262 samples) and June-October 2022 (n = 174 samples). The SEUSA was divided into six regions, and within each region, sites (n = 231) were either randomly selected for sampling (in 6 strata) or paired with SERFS camera-trap locations (n = 205). The stratified-random sampling area included the Florida Keys and the area north of Cape Hatteras that were not part of the SERFS sampling area. Prior to the study, there was uncertainty about whether there was a significant Red Snapper abundance/biomass on unconsolidated habitat not sampled by SERFS, and thus not accounted for in (stock assessment based) abundance estimates. The ROV study results indicated that red snapper abundance over unconsolidated bottom was very low in the stock area.

Additional sites (n = 205) were selected to pair with SERFS video trap locations to calibrate ROV red snapper counts with video trap counts. Paired sampling occurred in three areas. The Review Panel concluded this seemed sufficient for the purpose of calibration with video trap counts. Two additional, complementary studies were conducted to estimate the effective sample area of video trap gear such that red snapper count data could be expressed as density (number per unit area), which was critical for estimating total population size. These complementary studies involved telemetry experiments at two sites (Chicken Rock, North Carolina and Turtle Mound, Florida). At Chicken Rock, 18 sites were selected for both baited underwater video and ROV surveys, while at Turtle Mound 36 sites were selected. At Chicken Rock, 21 acoustic receivers were deployed in a grid and 45 fish were tagged with acoustic transmitters and released. At Turtle Mound, 100 receivers were deployed and 65 fish were acoustically tagged. The telemetry data were used to provide information on the movement and relative distribution of fish around the video traps and the effective sampling area (ESA) of video traps. Estimates from the Turtle Mound study were considered unrealistic by the SARSRP team. Therefore, the informative prior distribution for ESA used in the HBM was based only on the Chicken Rock study. However, it is likely that this sampling was insufficient to estimate video trap ESA for red snapper throughout the southeast US Atlantic stock area.

There was important uncertainty about the locations of hard bottom habitat throughout the stock area. Analyses by the SARSRP Team demonstrated that the HBM was sensitive to how bottom type was classified throughout the stock area. This included uncertainty about whether identified locations with hard bottom habitat were accurate, and whether the larger areas characterized as unconsolidated habitat could contain some hard bottom red snapper habitat. This leads to considerable concern with the metric of total area used to multiply the densities.

The statistical modeling was very detailed (Chapter 2 of SARSRP report) in that densities derived from ROVs and SERFS were modeled separately, including spatial scales at both the grid and site levels, including random effects and both informative and uninformative priors (hence the terminology hierarchal Bayesian modeling). The authors summarize this as “We fit the abundance model in a Bayesian framework. As previously described, we assigned informative priors to the ROV offset (γ) and camera-trap effective sampling areas ($\mathbf{b}$), while the remaining parameters were given vague prior distributions.“ Clearly, this is detailed. However, the HBM methods provided several innovative approaches that are the strength of the modeling approach.

3.3 TOR: Evaluate the study designs used for developing estimates of absolute abundance of age-2+ red snapper in the U.S. South Atlantic region (Florida, Georgia, South Carolina, North Carolina).

Assess the study design and sampling sufficiency as they pertain to the application of genetic close-kin mark-recapture methodology

Preliminary simulations of population dynamics with hypothesized CKMR sampling were conducted to determine the required sampling regime prior to the implementation of the study. Results indicated a target annual sample size of 2,500 individuals per year would produce an accurate (±4.5%) red snapper population estimate with CV ≤0.3 for population sizes of 0.5-1.5 x 10^6 individuals. When the fin clip sample size was increased to 5,000 individuals per year, the accuracy of the CKMR estimate was ±4.4% with a CV ≤0.14. Based on these results, a design was implemented in which red snapper fin clips were sampled from fisheries-independent and -dependent sources along the U.S. Atlantic Coast between Port

St. Lucie, Florida and Cape Hatteras, North Carolina during 2021-2023. The sampling design and the realized sampling effort exceeded the recommendations implied by the sampling simulations.

Assess the study design and sampling sufficiency as they pertain to the application of hierarchical Bayesian abundance modeling

Posterior distribution correlations were high between camera trap ESA for the three current direction categories. Also, there was substantial correlation in estimates of the ROV offset parameter and the parameter for paired sampling design effects. However, overall, the HBM parameters were not highly confounded.

Overall, the study design and sampling were sufficient, but the Panel noted the fact that the ESA estimates were based on data from one study in one area only. And most importantly, the uncertainty in the area of hard bottom habitat significantly increased the CV around the abundance estimate. Thus, it appears that the weak point is the habitat mapping and its quantification.

3.4 TOR: Evaluate the statistical/modeling methods used to analyze the data, and to construct the absolute abundance estimates and their variances.

Are the close-kin mark-recapture methods applied appropriately?

Yes.

The assignment of HS pairs went through a rigorous process of screening for genetic marks (adjusting for false negatives). Also, importantly, ages of sampled fish were determined directly from otoliths (~80% of the samples) and from ALK's for the rest. Additionally, background investigations of stock identification were revisited to provide support for the basic structure of the estimation method.

The statistical estimation model was based upon implementation of binomial distributions conditioned on life history and demographic data. As noted above, that conditioning is an appropriate and necessary feature of the method. However, it also means (as noted above) that the abundance estimate is not independent of the existing stock assessment, nor will it be independent of the next stock assessment.

As with any statistical estimation process the means and variances of the estimates are dependent on the model chosen (in this case binomial). Thus, the variances may not include all sources of variability. However, at this stage of the research, the current implementation is appropriate.

Are the hierarchical Bayesian modeling methods applied appropriately?

Yes, the HBM methods were applied appropriately. This model integrated red snapper density information from two surveys (video trap and ROV) using well-reasoned observation models. This included a novel mixture model component that is a strength of the HBM. Parameter priors were usually uninformative, except when other data provided information. Hence, the HBM used objective priors, which is a strength of the approach. The possible exception was the priors used for ESA based on the Chicken Rock telemetry study, which represented a small fraction of the stock area. A prior variance inflation factor could have been used to account for possible differences in ESA in other regions of the stock. However, it is recognized that the choice of variance inflation will be subjective, and a better approach to deal with this uncertainty is to do additional ESA telemetry studies.

3.5 TOR: Are the estimates of absolute abundance (age-2+ red snapper) and their variances reliable?

For each of the two estimation approaches, are assumptions appropriate, given study design considerations?

Are there potential sources of uncertainty that were not considered when developing the estimates of abundance?

For each of the two estimation approaches, describe the magnitude and direction of any potential biases.

CKMR

The Review Panel in our report concluded that insufficient information was provided thus, it was difficult to fully assess the reliability of the CKMR overall abundance estimate. While I agree in principle with this statement, apparently I am less concerned about it than others. The reason is 1) I can piece together the basic equation structure that is being used; and 2) I do not believe the current estimates are an end-point in the estimation process (see CKMR Background, above, which addresses these points). Thus, the assumptions that were employed, i.e. the conditions imposed by the life history/demographic data, were consistent with current knowledge. While there is debate about several of these conditions, that debate exists outside the framework of the CKMR estimation method. Thus, I consider the assumptions appropriate for the current model. However, I do not consider this estimate to be the “final say”, as it will be re-evaluated in the context of the next stock assessment.

Not all sources of variability are included in the variance estimate (e.g., male contribution to reproduction, rates of HS detection in schooling fish, aging of age 1 fish, age-related female fecundity, etc.). Perhaps, the estimation model might be adjusted to incorporate some of these sources, but I believe it would be most appropriate to do this in the context of an integrated stock assessment. Also, see CKMR Background above.

The CKMR background above provides a summary of the component parameters of the CKMR estimate. In terms of the life history/demographic data the effects of biases are fairly obvious: if the true reproductive output is skewed more towards older fish than what is demonstrated by the fecundity and age-frequency relationships used in the current estimation, then the true abundance would be higher than the base estimate. Alternatively, if the true values are skewed to younger ages, then the true estimate would be lower than the base. I suspect that the former bias is more likely than the latter and that the fecundity/reproductive output relationships are more important (in terms of magnitude) than the age-distributions. Of course, other sources of mis-specification can be occurring (M values, F values, selectivities, catches, etc.) which can cause biases of varying degrees. But they are best evaluated in the stock assessment.

HBM

The assumptions for the HBM were generally appropriate. The HBM estimated spatial stock size at a fine mesh grid with 14,658,041 cells of approximately 90 × 90 m. Absolute abundance was estimated by summing spatial stock size across all these grid cells. The Review Panel concluded this basic approach was appropriate. Factors including depth, bottom type (hard bottom or not), and number of hard bottom neighbors were significant and produced substantially different estimates of density depending on bottom type. The analysis demonstrated that the absolute abundance estimates were highly sensitive to how the bottom type was classified. A primary measure of model uncertainty is characterized by the posterior distributions of the estimates, which provide a comprehensive quantification of uncertainty characterized by the CV. However, the posterior distribution did not include uncertainty in bottom type classification and therefore the posterior CV is an under-estimate of true uncertainty. The prior distribution for ESA was only based on one study. This informative prior distribution may also have important impacts on the posterior distribution of absolute abundance; therefore, the Review Panel also concluded for these reasons that the posterior CV is an underestimate of true uncertainty. Overall, bottom type was a major source of uncertainty, and the Panel concluded that there is enough uncertainty in bottom type classification in the SEUS Atlantic region that the absolute abundance estimate was not reliable.

The SARSRP Report and presentations provided an adequate description of the uncertainties. However, it is likely that the HBM CVs are biased low, given the uncertainty in bottom habitat information that was not propagated into the CVs for absolute abundance estimates. Because size and age information was not included in the HBM analysis, the estimate of total abundance for age 2+ has some uncertainty as an unknown number of age 1 (and possibly age 0) may have been included in the estimate. This is explored in the SARSRP report and is probably a minor bias relative to other uncertainties. But it should be taken into account when comparing assessment outcomes. Also, the ESA estimate and more importantly, the bottom habitat information, was too uncertain to provide a sufficiently reliable HBM based absolute population abundance estimate of red snapper in the stock area at this time.

3.6 TOR: Provide future research recommendations.
How could each of the methods used in this study be improved for more accurate estimates?
Are there other sampling or survey methods that could be used to improve the accuracy of estimates of absolute abundance?

CKMR

I have listed our Review Panel list of research needs below. But I wish to **reiterate, reiterate, reiterate** that CKMR estimates will always be conditional on a stock assessment. Thus, it is disingenuous to imply that CKMR abundance estimates are independent of a stock assessment. Improvement of our understanding of LH/demo relationships with regards to reproductive output could be an important contribution. But I do not see mechanisms to estimate dynamic age-distributions and mortality rates independent of an assessment. Thus, to me, that is the highest priority.

In any case I agree with the general tenor of the research list given below:

> Continue sampling and genotyping with the goal of providing a time series of CKMR estimates.
>
> Revise and expand the simulations and sensitivity analyses conducted in Appendix V.
>
> Collection of additional data to inform the fecundity-age (or size) relationships for males and females, and spawning season duration for individual fish can considerably improve the population size estimate.
>
> Conventional tagging, including double tagging to estimate tag shedding rates.

Use the epigenomic aging clock to estimate the age of as many individuals as feasible, including all those identified as members of HSPs and a subset of the U (unrelated) individuals); rerun the CKMR model.

Provide the chromosome level genome sequence to assess the degree of linkage among the ~ 1755 multiallelic haplotypic loci used to obtain the current estimate.

Instead of running hierarchical AMOVAs grouping samples by state (a political boundary) it is suggested that samples be grouped by hardbottom aggregations. Separate samples collected from hardbottom locations located 50 or 100 km apart from each other.

HBM

There is substantial uncertainty in the bottom classification in the Atlantic SEUS which has substantial impacts on the HBM estimates of red snapper total abundance, and the uncertainty of the estimates. Thus, the primary research recommendation is to increase the accuracy of bottom type/habitat classification by mapping or other methodologies. This will provide a more reliable habitat covariate for use in the BHIM to estimate red snapper total abundance.

The HBM estimate of red snapper total abundance used information from SERFS and ROV surveys. The BHIM also required information on the effective sampling area for the SERFS video camera counts. This was derived from a telemetry/camera/ROV study in a small region (Chicken Rock). It is recommended that the “Chicken Rock” telemetry project/analyses be repeated in other areas to assess spatial variation in effective sampling area and to gain more understanding about the factors that affect ESA.

Investigate assigning a probability of hard bottom based on other sources of information (modeling) and include this major uncertainty in the HBM abundance estimation.

Determine effective sampling area of trap catches (vs video).

Explore integrating trap catches into the HBM.

Measure water current velocity at video trap locations to improve estimation of ESA.

Analyze recordings from both trap video cameras for fish abundance. Currently only the recordings from one of the cameras is used for HBM (and other) analyses. Expand video trap survey south of the St. Lucy area and North of Cape Hatteras, even if the used methodology results in video data only (no trapped fish).

4. Conclusions and Recommendations

The SARSRP report provided the results of two carefully planned and implemented research programs designed to provide estimates of southeast US Atlantic red snapper abundance: CKMR and HBM. In the process, several innovative approaches were introduced and a broader understanding of the estimation methods, strengths and weaknesses were elucidated. The SARSRP team should be lauded for this work.

Additionally, the review meeting was conducive to a collegial atmosphere and, yet, vigorous debate where we all, reviewers and SARSRP team, alike, learned some things.

The CKMR approach provides an avenue to incorporate genetic marks into abundance estimation. But by design and theory the estimates are conditional on life-history parameters (particularly those that contribute to male and female reproductive output) and on the age distribution and fishing and natural mortalities that occurred during the time period that half-siblings are being sampled. The mortalities and age distributions are estimated through a stock assessment process. Thus, the CKMR estimates are not stand alone and are conditional on an assessment. There appears to be some expectation that CKMR estimates are independent of an assessment. Clearly, that is not my opinion nor is it the opinion of the authors. In the present CKMR rendition the demographic data is derived from the most recent assessment. From that basis, an estimate was made and sensitivities evaluated. As recommended, those sensitivities should be explored further. However, it must be recognized that these CKMR estimates are not final and will evolve as further information is derived. Indeed, it is recommended that the next assessment integrate the genetic mark data into the assessment through expanded likelihood functions. In such a case the genetic marks will open the possibility to estimate additional parameters in the assessment.

The HBM approach was innovative in that it applied unique spatial models at different scales and utilized relatively objective priors within the Bayesian framework. The modeling related habitat to densities with appropriate covariates to estimate effective sampling area (ESA). The estimate was based on SERFS and ROV surveys of site-specific density, expanded by total area of habitat types from habitat mapping. Despite the modeling innovation, the ESA estimates suffered from limited data and most importantly the final estimate suffered from the quality of the habitat mapping data and the variance thereof. For those reasons, it is recommended that the HBM estimate not be implemented into the next assessment. However, the research recommendations in the previous section suggest some avenues to address these weaknesses.

A final comment is to remind people that an abundance estimate is not the end-all of the assessment-management process. The current status criteria require an estimate of current spawning biomass or reproductive output relative to that which maximizes productivity, the current fishing rate relative to that at maximum productivity and the catch levels associated with that fishing rate. While knowing abundance would assist in the estimation of status criteria, the criteria still require that abundance be viewed in the context of productivity and life history.

Appendix 1: Bibliography of materials provided for review

Bibliography
Population Estimation of U.S. Atlantic Red Snapper: Final Report to the South Atlantic Red Snapper Research Program
Appendix I: Applying mark-resight, count, and telemetry data to estimate effective sampling area and fish density with stationary underwater cameras
Appendix II: An Integrated Approach to Estimating the Effective Sampling Area of Baited Underwater Camera Traps
Appendix III: Spatiotemporal dynamics and habitat use of red snapper (*Lutjanus campechanus*) on the southeastern United States Atlantic continental shelf
Appendix IV: Genetic Population Structure of Red Snapper, *Lutjanus campechanus,* in the U.S. Atlantic and Eastern Gulf of America
Appendix V: Sensitivity of CKMR population estimates to uncertainty in life-history parameters
Appendix VI: Incorporating Close-Kin Mark-Recapture Data into an Integrated Stock Assessment Model for Southeast United States Atlantic Red Snapper (*Lutjanus campechanus)*
Appendix VII: Estimating Reef Fish Exploitation Rates in Catch-and-Release Fisheries with Conventional and Genetic Tags
Appendix VIII: Stakeholder Insights Corroborate Habitat and Reef Fish Abundance on the Southeastern U.S. Atlantic Continental Shelf
Appendix IX: Discard mortality rates of Red Snapper after barotrauma and hook trauma: Insights from using acoustic telemetry in the U.S. South Atlantic
Appendix X: Post-release Mortality of Red Snapper, *Lutjanus campechanus*, in U.S. Atlantic Waters off Northeast Florida Estimated with Three-Dimensional Acoustic Telemetry

Appendix 2: Performance Work Statement (PWS)

National Oceanic and Atmospheric Administration (NOAA)

NOAA Fisheries

Center for Independent Experts (CIE) Program

External Independent Peer Review

South Atlantic Red Snapper Research Program (SARSRP) Review

January 13 – 15, 2026

Background

The NOAA Fisheries is mandated by the Magnuson-Stevens Fishery Conservation and Management Act, Endangered Species Act, and Marine Mammal Protection Act to conserve, protect, and manage our nation's marine living resources based upon the best scientific information available (BSIA). NOAA Fisheries science products, including scientific advice, are often controversial and may require timely scientific peer reviews that are strictly independent of all outside influences. A formal external process for independent expert reviews of the agency's scientific products and programs ensures their credibility. Therefore, external scientific peer reviews have been and continue to be essential to strengthening scientific quality assurance for fishery conservation and management actions.

Scientific peer review is defined as the organized review process where one or more qualified experts review scientific information to ensure quality and credibility. These expert(s) must conduct their peer review impartially, objectively, and without conflicts of interest. Each reviewer must also be independent from the development of the science, without influence from any position that the agency or constituent groups may have. Furthermore, the Office of Management and Budget (OMB), authorized by the Information Quality Act, requires all federal agencies to conduct peer reviews of highly influential and controversial science before dissemination, and that peer reviewers must be deemed qualified based on the OMB Peer Review Bulletin standards[1]. Independent scientific peer review is a hallmark of gold standard science[2].

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[1] https://www.whitehouse.gov/wp-content/uploads/legacy_drupal_files/omb/memoranda/2005/m05-03.pdf

[2] https://www.whitehouse.gov/presidential-actions/2025/05/restoring-gold-standard-science/

[3] https://www.fisheries.noaa.gov/southeast/recreational-fishing/working-toward-increasing-fishing-opportunities-red-snapper-south-atlantic

[4] https://www.scseagrant.org/south-atlantic-red-snapper-research-program/

Scope

The South Atlantic red snapper fishery is economically and recreationally important, but has faced challenges due to overfishing and restrictive management. The red snapper population has shown a remarkable rebound in the last 15 years. Fishermen and scientists agree that red snapper are far more abundant and larger than they used to be. Harvest opportunities for red snapper remain limited because of the large amount of discarded fish and uncertainty in the exact number of fish in the population. The South Atlantic Council, in recent years, has struggled with how to reduce the high amounts of red snapper discards and end overfishing, as required by the law[3].

The South Atlantic Red Snapper Research Program (SARSRP) was administered through the South Carolina Sea Grant Consortium[4]. A Request for Proposals (RFP) was issued with a full proposal deadline of February 1, 2021. The goal of the SARSP is to generate an absolute estimate of abundance with an accompanying measure of uncertainty for the entire South Atlantic red snapper stock. Preference was given to proposals that seek to produce a single absolute estimate of abundance for the entire geographic region. This estimate will serve as an independent benchmark on which to inform a currently ongoing stock assessment. It will provide a metric of abundance of what the size (number of individual fish) of the stock is in the South Atlantic for the period of the survey. The SARSP awarded project is led by a team of researchers spanning the following research institutions: University of Florida, Texas A&M Corpus Christi, N.C. State University, NOAA Fisheries, S.C. Department of Natural Resources, NOAA NOS Center for Coastal Fisheries Habitat Research, Florida Fish & Wildlife Conservation Commission, and GA Department of Natural Resources.

The awarded research proposal included the following three approaches: (1) Close-kin and meta-population genetics analyses; (2) Existing and possibly supplemental new South Atlantic trap-video survey data to scale-up density estimates to total abundance; and (3) a research technique similar to that pursued in the Gulf Red Snapper abundance assessment, focusing predominantly on use of active acoustics and visual ground-truthing. Research began in the Fall of 2020 and will finish in August of 2025, hence the request for CIE review at this time.

Fisheries management depends on science based advice for setting accurate quotas. Scientific peer-review serves as the cornerstone and gold standard of best science. This peer review will further the NOAA mission to conserve and manage coastal and marine ecosystems and resources by providing science based advice. This advice is consistent with National Standard 2 (NS2), which is a statutory (Magnuson Stevens Act) requirement at 16 U.S.C. 1851(a)(2) and states that "conservation and management measures shall be based upon the best scientific information available (BSIA). This review aligns this statute because this CIE peer review is an essential part of determining whether the assessment used meets the criteria for BSIA under NS2. It will also further the NOAA Fisheries mission of productive and sustainable fisheries and healthy ecosystems.

The specified format and contents of the individual peer review reports are found in **Annex 1**. The Terms of Reference (ToRs) of the peer review are listed in **Annex 2**. The tentative agenda of the panel review meeting is attached in **Annex 3.**

Requirements

NOAA Fisheries requires three **(3)** reviewers to conduct an impartial and independent peer review in accordance with the Performance Work Statement (PWS), OMB guidelines, and the ToRs below. The reviewers shall have expertise in quantitative methods applied to fisheries. It is desirable to have at least one reviewer with expertise in capture-recapture methodology, especially Bayesian hierarchical modeling, and at least one reviewer with expertise in genetic close-kin mark-recapture applications.

The review panel chair, who is in addition to the three reviewers, will not be provided by the CIE. Although the chair will be participating in this review, the chair's participation (e.g., labor and travel) is not covered by this contract.

Each reviewer will write an individual review report in accordance with the PWS, OMB Guidelines, and the ToRs below. Modifications to the PWS and TORs cannot be made during the peer review, and any PWS or ToRs modifications prior to the peer review shall be approved by the Contracting Officer's Representative (COR) and the CIE contractor. All ToRs must be addressed in each reviewer's individual report.

Tasks for Reviewers

1) Pre-review Background Documents: Review the following background materials and reports prior to the review:

   Two weeks before the peer review, the NOAA Fisheries Project Contact will send by electronic mail or make available at an FTP site to the CIE reviewer all necessary background information and reports for the peer review. In the case where the documents need to be mailed, the Project Contact will consult with the CIE on where to send documents. The CIE reviewer shall read all documents in preparation for the peer review.

2) Attend and participate in an in-person review meeting. The meeting will consist of presentations by NOAA and other scientists, stock assessment authors and others to facilitate the review, to answer any questions from the reviewers, and to provide any additional information required by the reviewers.

3) After the review meeting, reviewers shall conduct an independent peer review report in accordance with the requirements specified in this PWS, OMB guidelines, and ToRs, in adherence with the required formatting and content guidelines. Reviewers are not required to reach a consensus.

4) Each reviewer shall assist the Chair of the meeting with contributions to the summary report based on the ToRs. Reviewers are not required to reach consensus.

5) Deliver their reports to the Government according to the specified milestones dates.

Foreign National Security Clearance

When reviewers participate during a panel review meeting at a government facility, the NOAA Fisheries Project Contact is responsible for obtaining the Foreign National Security Clearance approval for reviewers who are non-US citizens. For this reason, the reviewers shall provide requested information (e.g., first and last name, contact information, gender, birth date, passport number, country of passport, travel dates, country of citizenship, country of current residence, and home country) to the Project Contact for the purpose of their security clearance, and this information shall be submitted at least two weeks in advance. For additional information, please see the following link: https://www.commerce.gov/osy/programs/foreign-access-management. The contractor is required to use all appropriate methods to safeguard Personally Identifiable Information (PII).

Place of Performance

The place of performance shall be in Charleston, SC.

Period of Performance

Each reviewer's duties shall not exceed **14** days to complete all required tasks.

Schedule of Milestones and Deliverables: The contractor shall complete the tasks and deliverables in accordance with the following schedule.

Schedule	Milestones and Deliverables
Within 2 weeks of award	Contractor selects and confirms reviewers
Approximately 2 weeks prior to the review	Contractor provides the pre-review documents to the reviewers

January 13 – 15, 2026	Panel review meeting
Approximately 2 weeks later	Contractor receives draft reports
Within 3 weeks of receiving draft reports	Contractor submits final reports to the Government

* The Peer Review Summary Report will not be submitted to, reviewed, or approved by the Contractor.

Applicable Performance Standards

The acceptance of the contract deliverables shall be based on three performance standards:

(1) The reports shall be completed in accordance with the required formatting and content (2) The reports shall address each ToR as specified (3) The reports shall be delivered as specified in the schedule of milestones and deliverables.

Confidentiality and Data Privacy

This contract may require that services contractors have access to Privacy Information. Services contractors are responsible for maintaining the confidentiality of all subjects and materials and may be required to sign and adhere to a Non-disclosure Agreement (NDA).

Travel

All travel expenses shall be reimbursable in accordance with Federal Travel Regulations (Travel resources | GSA), and all contractor travel must be approved by the COR prior to the actual travel. Any travel conducted prior to the receipt of proper written authorization from the COR will be done at the Contractor’s own risk and expense. International travel is authorized for this contract. Travel is not to exceed the contracted amount.

NOAA Fisheries Project Contact

Erik H. Williams, Ph.D., Director of the Atlantic Fisheries Branch

Sustainable Fisheries Division

Southeast Fisheries Science Center

erik.williams@noaa.gov

Office Tel: 252-666-7428

Annex 1: Peer Review Report Requirements

1. The independent Peer Reviewer report shall be prefaced with an Executive Summary providing a concise summary of whether they accept or reject the work that they reviewed, with an explanation of their decision (strengths, weaknesses of the analyses, etc.).

2. The report must contain a background section, description of the individual reviewers' roles in the review activities, summary of findings for each ToR, in which the weaknesses and strengths are described, and conclusions and recommendations in accordance with the ToRs.

   a. Reviewers must describe in their own words the review activities completed during the panel review meeting, including a brief summary of findings, of the science, conclusions, and recommendations.

   b. Reviewers should discuss their independent views on each ToR even if these were consistent with those of other panelists, but especially where there were divergent views.

   c. Reviewers should elaborate on any points raised in the summary report that they believe might require further clarification.

   d. Reviewers shall provide a critique of the agency review process, including suggestions for improvements of both process and products.

   e. The report shall be a stand-alone document for others to understand the weaknesses and strengths of the science reviewed, regardless of whether or not they read the summary report. The report shall represent the peer review of each ToR, and shall not simply repeat the contents of the summary report.

3. The report shall include the following appendices:

   Appendix 1: Bibliography of materials provided for review

   Appendix 2: A copy of this Performance Work Statement

Appendix 3: Panel membership or other pertinent information from the panel review meeting.

Annex 2: Terms of Reference for the Peer Review

South Atlantic Red Snapper Research Program Review

January 13 - 15, 2026

CIE reviewers are contracted to complete their independent peer review based on the ToRs. Therefore, the CIE-NOAA Fisheries review and approval process is based on whether the CIE independent reports addressed each ToRs.

- Evaluate the study designs used for developing estimates of absolute abundance of age-2+ red snapper in the U.S. South Atlantic region (Florida, Georgia, South Carolina, North Carolina).
    - Assess the study design and sampling sufficiency as they pertain to the application of genetic close-kin mark-recapture methodology.
    - Assess the study design and sampling sufficiency as they pertain to the application of hierarchical Bayesian abundance modeling.
- Evaluate the statistical/modeling methods used to analyze the data, and to construct the absolute abundances estimates and their variances.
    - Are the close-kin mark-recapture methods applied appropriately?
    - Are the hierarchical Bayesian modeling methods applied appropriately?
- Are the estimates of absolute abundance (age-2+ red snapper) and their variances reliable?
    - For each of the two estimation approaches, are assumptions appropriate, given study design considerations?
    - Are there potential sources of uncertainty that were not considered when developing the estimates of abundance?
    - For each of the two estimation approaches, describe the magnitude and direction of any potential biases.
- Provide future research recommendations.
    - How could each of the methods used in this study be improved for more accurate estimates?
    - Are there other sampling or survey methods that could be used to improve the accuracy of estimates of absolute abundance?

Annex 3: Tentative Agenda

South Atlantic Red Snapper Research Program Review

January 13 – 15, 2026

Location: Charleston, SC

Dates: January 13 -15, 2026

Times each day: 0830-1700 hrs

<u>January 13, 2026</u>

0830 to 0850

Introductions and review of agenda

0850 to Morning Break (10 min, TBD by Chair)

Presentations by SARSP team with clarifying questions from panel after each presentation

End of Morning Break to Lunch Break

Presentations by SARSP team with clarifying questions from panel after each presentation

Lunch Break to last 1.5 hrs

End of Lunch Break to Afternoon Break (10 min, TBD by Chair)

Presentations by SARSP team with clarifying questions from panel after each presentation

End of Afternoon Break to 1700

Presentations by SARSP team with clarifying questions from panel after each presentation

<u>January 14, 2026</u>

0830 to Morning Break (10 min, TBD by Chair)

Presentations by SARSP team with clarifying questions from panel after each presentation

End of Morning Break to Lunch Break

Presentations by SARSP team with clarifying questions from panel after each presentation

Lunch Break to last 1.5 hrs

End of Lunch Break to Afternoon Break (10 min, TBD by Chair)

Questions and discussions between review panel and SARSP team

End of Afternoon Break to 1700

Questions and discussions between review panel and SARSP team

<u>**January 15, 2026**</u>

0830 to Morning Break (10 min, TBD by Chair)

Questions and discussions between review panel and SARSP team

End of Morning Break to Lunch Break

Questions and discussions between review panel and SARSP team

Lunch Break to last 1.5 hrs

End of Lunch Break to Afternoon Break (10 min, TBD by Chair)

Deliberations and report writing by review panel

End of Afternoon Break to 1700

Deliberations and report writing by review panel

Appendix 3: Panel membership and attendees of the panel review meeting.

Review Panel

Marcel Renchert (Chair)	SAFMC SSC
Luiz Barbieri	SAFMC SSC
Noel Cadigan	CIE Reviewer
Joe Powers	CIE Reviewer
Daniel Ruzzante	CIE Reviewer

Program Team

Will Patterson (Lead PI)	Univ of Florida
Nathan Bacheler	SEFSC
Jeffrey Buckel	NCSU
Nathan Hostetter	NCSU
David Portnoy	TAMUCC
Matthew Vincent	SEFSC

Staff

Julie A Neer	SEDAR
Chip Collier	SAFMC Staff
Judd Curtis	SAFMC Staff
Rachael Silvas	SAFMC Staff
Emily Ott	SEDAR

Workshop Observers

Chris Bradshaw	FLFWC
Wally Bubley	SCDNR
Chris Custer	NCSU
Amy Dukes	SCDNR
Liam Kehoe	UF

Ryan McMullen	SC Sea Grant
Emily Osborne	SC Sea Grant
Tracey Smart	SCDNR
Julie Vecchio	SCDNR
Jordy Wolfe	SCDNR

Workshop Observers via Webinar

Eric Anderson	
Jordan Bajema	FWC
Sydney Bates	SCDNR
Kristan Blackhart	NOAA
Jason Boucher	NOAA
Myra Brouwer	SAFMC Staff
Julia Byrd	SAFMC Staff
Jessica Carroll	FWC
David Chagaris	UFL
Kristin Cook	FWC
Ellie Corbett	FWC
Michael Drexler	Ocean Conservancy
Ben Dyar	SCDNR
Joseph Evans	SCDNR
Alena Figueroa	FWC
Margaret Finch	SCDNR
Kristin Foss	FWC
Dawn Franco	GA DNR
Elizabeth Ford	
Keilin Gamboa-Salazar	SCDNR
Brad Gentner	

Ben Goldstein	
Elizabeth Gooding	SCDNR
Amiee Griffin	FWC
Jenny Grossmann	COFC
Martha Guyas	ASA
Homer Hiers	SCDNR
Kathleen Howington	SAMFC Staff
Jeanette Huber	FWC
Allie Iberle	SAFMC Staff
Blaik Keppler	SCDNR
Kevin Kolmos	SCDNR
Genine McClair	FWC
Maria McGirl	FWC
Paul McLaughlin	
Nikhil Mehta	NOAA
Trish Murphey	NCDEQ
Gabby Ocampo	FWC
Krishna Pacifici	NCSU
Chloe Ramsay	FWC
Brian Reich	NCSU
Scott Sandorf	NOAA
Mike Schmidtke	SAFMC Staff
Nick Smillie	SAFMC Staff
Wiley Sinkus	SCDNR
Kevin Spanik	SCDNR
Joesph Tarnecki	
Chris Taylor	NOAA
Miaya Taylor	UFL

Erik Williams	SEFSC
Olivia Wilms	FWC
Meg Withers	SAFMC Staff
Daniel Zapf	NCDEQ

Center for Independent Experts (CIE) external independent peer review of the South Atlantic Red Snapper Research Program (SARSRP)

Jan 13-15, 2026
Charleston, SC

Daniel Ruzzante
Department of Biology
Dalhousie University
Halifax, NS, CA
B3H4R2

Executive Summary

1. **The independent Peer Reviewer report shall be prefaced with an Executive Summary providing a concise summary of whether they accept or reject the work that they reviewed, with an explanation of their decision (strengths, weaknesses of the analyses, etc.).**

This program (SARSRP) was funded by the US Congress in 2020 and administered by the South Carolina Sea Grant. The main goal was to produce a credible population abundance estimate for adult (2+) red snappers for the entire area of the species distribution in the US Atlantic Ocean from North Carolina to south Florida. A large interdisciplinary team participated in the project, with scientists from the University of Florida, Texas A&M University Campus Corpus Christi and North Carolina State University as well as scientists from federal and state agencies. The project also benefited substantially through the collaboration and participation from the stakeholders in the commercial and recreational red snapper fishery.

Two approaches were used to estimate population abundance: The first approach used a Bayesian hierarchical integrated modeling approach (BHIM) to estimate fish abundance. For this approach, they used two sources of data: first, they estimated fish density data from videos obtained with baited camera traps positioned on hardbottom (natural reefs) substrate. With this method they considered current direction in relation to the camera as a covariate. Second, they extracted data from videos obtained with remotely operated vehicles (ROV). There was some uncertainty regarding the cone of visibility of this approach. Red snappers were absent or nearly so from soft bottom unstructured areas. This finding implied that the estimate of abundance has to rely heavily on an estimate of the proportion of the total shelf area between NC and south Florida (and within a depth range) that is characterized by a hardbottom substrate or natural reefs. This proportion is unknown and its uncertainty not surprisingly affects the confidence interval of the population abundance estimate.

The second approach to estimate abundance was based on the premise that every individual fish carries (i.e., captures) the genetic make-up of each of its parents. Using a large number of genomic markers, it is possible to identify related pairs of individuals (i.e., kin pairs) and distinguish them from unrelated individuals. The number of kin pairs identified can then be used in a mark recapture framework to estimate population abundance. Knowledge of the age of the individual members of any given pair is, however, needed to estimate the probability of them being an actual pair. Also needed are estimates of fecundity at age and age specific survival rates. Given the project's short-term duration when compared to the species life span, authors focused on identifying half sib pairs (HSP) rather than Parent-offspring pairs (POPs), which would require a much longer sampling period. Authors used a two-step genomic method to genotype fish. First, they used a GTseq approach with ~200 haplotypic markers to genotype all 14,085 collected individuals and identify half sib pairs in a preliminary way. They then employed a reduced representation sequencing technique (ddRAD) to sequence the subset of individuals identified as half-sib members in the first stage. This approach allowed them to save on sequencing cost, but it increased the effort and time required in the molecular laboratory and it also led them to have to include two consecutive estimates of false negative rates (FNRs). Female fecundity was assumed to increase linearly with size, an assumption that may be violated in nature with female fecundity increasing exponentially with size. An important source of uncertainty not dealt with in the current report concerns the potential sex of the unsampled parent of the identified half-sib pairs. Identifying the sex of the unsampled parent (via mtDNA of the pair members) is necessary if the fecundity at age relationship differs between the sexes.

Such differences would affect the expected relative reproductive output (ERRO). This should be a priority for further investigation. Regardless, it is this reviewer's view that the project was successful at obtaining credible estimates. Given the assumptions regarding the fecundity at age (size) relationship and the need to identify the sex of the unsampled parents of the HSPs; however, it is likely that the confidence intervals of population abundance with the CKMR method were underestimated.

Background and Role in Review Activities

Reviewer's expertise

I am an evolutionary biologist and molecular ecologist with nearly three decades of expertise in marine population genetics and genomics with particular interest in the use of genomic tools for the management of marine fisheries and conservation of biodiversity in general. I received the link to material listed in appendix 1 from the Coordinator for the South Atlantic Red Snapper Research Program (SARSRP) review process on December 22nd, 2025. I was able to read this material in advance of the meeting and participated in the meeting held in Charleston Jan 13-15, 2026. I listened to all presentations and participated in the follow up discussions with project members and the review panel. I have published about close kin mark recapture and am currently leading a project to estimate the population abundance of a commercially harvested fish, Atlantic halibut, using the close kin mark recapture method. My expertise is therefore closer to the work described in chapter 3 of this report than that in chapter 2. My role in the review activities is therefore to focus on the strengths and weaknesses of the close kin mark recapture method.

Overall Conclusion

In my view, the study design as it concerns the CKMR approach appears robust and is consistent with theory and the sampling effort was sufficient for an initial estimate of population abundance. As stated above, however, uncertainty around the estimate is likely to have been underestimated. A top priority for further research should be the identification of the sex of the unsampled parent of the half sib pairs and to link these findings with more realistic sex-dependent fecundity at age/size relationships.

SUMMARY OF FINDINGS

ToR 1: Evaluate the study designs used for developing estimates of absolute abundance of age-2+ red snapper in the U.S. South Atlantic region (Florida, Georgia, South Carolina, North Carolina).

Assess the study design and sampling sufficiency as they pertain to the application of genetic close-kin mark-recapture methodology.

Preliminary simulations using Eric Anderson's platform CKMRpop were conducted to assess the number of samples required to estimate the population abundance of red snapper with a CV <0.30. This exercise indicated that an annual sample size of 2,500 individuals per year for two consecutive years (it was first assumed the project would run for just two years) would be sufficient to obtain a red snapper population abundance estimate with a CV ≤0.3 assuming the actual population size was between 0.5 and 1.5 million individuals. In the end, the researchers managed to collect samples over three years and obtained more than twice that many individuals (> 6000 in each of 2021 and 2022, and >7000 in 2023). After filtering and quality control, genotypic data were retained from a total of 14,085 individuals. Individual ages were estimated from otoliths for some 11,000 individuals but many individuals lacked age data because they were live discards. Ages were therefore imputed from an age-length key (ALK, see below). The study design appears robust, and the sampling effort seems to have been sufficient for an initial estimate of population abundance, but with 95%CI that is likely underestimated. Beyond the sampling effort, the genotyping was conducted in two stages requiring two PCR reactions: Authors first conducted GTseq with which they examined variation at a small number of markers (i.e., 195 haplotypic loci) in all 14,085 individuals. They then used these data to preliminarily identify potential half-sib pairs based on this limited number of markers. The second stage involved a reduced representation sequencing technique (ddRAD) but only of the individuals identified in stage 1 as potential members of a kin pair. It is argued that this procedure resulted in significant cost savings in sequencing. At the same time the two-stage procedure along with the need for two PCR reactions increased the labor in the molecular lab.

Assess the study design and sampling sufficiency as they pertain to the application of hierarchical Bayesian abundance modeling.

I do not have much to say about the BHIM effort to estimate red snapper population abundance, as this is not my area of expertise, except to commend the authors for the incredible effort! At the same time, I wondered why undertake such an intense effort without *a priori* having precise knowledge of the proportion of the total shelf area (from NC to south Florida where red snapper are distributed) that consists of hard bottom substrate, the major source of uncertainty for this estimation method! It seems to me that without this prior knowledge this method was doomed to produce a very wide confidence interval as it did, unless the team expected to find red snappers in unstructured substrate areas.

ToR 2: Evaluate the statistical/modeling methods used to analyze the data, and to construct the absolute abundances estimates and their variances.

Are the close-kin mark-recapture methods applied appropriately?

Yes, the CKMR method is applied appropriately given the existing knowledge of the life history of red snapper. However, CKMR relies heavily on the proper parameterization of life history traits and any potential differences between males and females in age at 50% maturity, the relationship between fecundity and age or size, and survival rates would lead to differences in the expected relative reproductive output (ERRO) which underpins the probabilities upon which *Nc* is estimated. Proper parameterization requires knowledge not only of sex (see below) but also of the age of all individuals genotyped. Age information was obtained from an age-length relationship or key (ALK) which provides the probability of being a certain age given the length of the individual (in 10 mm bins) and month. The probability of a given half-sib pair would have to be calculated over all possible ages the members of a pair could have been as their ages will influence expected relative reproductive output (ERRO). To simplify this computation, ages of pair members were imputed based on the ALK probability. This procedure was repeated 100 times, and each realization produced a maximum likelihood population size estimate leading to 100 estimates. These data were then used to produce a posterior mean and median population size estimate. Thus, uncertainty in the age of the pair members appears to have been dealt with appropriately.

The current estimates were obtained by assuming no sex differences in age at 50% maturity nor in the fecundity at age/size relationship. Fecundity as a function of age was assumed to be linear with average weight within an age class and constant across years. Female fecundity may increase with size at a higher rate than linearly particularly in larger females. Age specific relative reproductive output of males was assumed to scale with age the same way as the fecundity of females, but this assumption is unlikely to hold in the actual population.

Should there be differences between the sexes in (a) age at 50 % maturity, and in the fecundity at size/age relationships, then this would translate into unknown biases in the estimate of population abundance. Hence, what is required to potentially increase accuracy and perhaps precision is the identification of the sex of the *UNSAMPLED* parent of the half sib pairs. A difference between the sexes in the relationship between fecundity and age would lead to differences in the ERRO estimation which would propagate to the N_c estimation.

Are the hierarchical Bayesian modeling methods applied appropriately?

In my, albeit naive, opinion, the BHIM methods were applied appropriately.

ToR 3: Are the estimates of absolute abundance (age-2+ red snapper) and their variances reliable?

For each of the two estimation approaches, are assumptions appropriate, given study design considerations?

Assumptions for the CKMR approach seemed reasonable given the lack of information about sex differences in life history traits and their relationship with age or size. As stated above, fecundity of females was assumed to exhibit a linear relationship with age-specific average weight. Age-specific relative reproductive output of males was assumed to scale with age the same as the fecundity of females. This may not necessarily be true, but represents a first approximation in the absence of a sex specific fecundity relationship. The same can be said for age at 50% maturity.

Are there potential sources of uncertainty that were not considered when developing the estimates of abundance?

Potential sex differences in life history traits and their relationship with age or size could be considered a potential source of uncertainty. The current CKMR model assumes that male contribution to the probability of successful reproduction mimics the female fecundity weight at age relationship. This has not yet been evaluated and deserves consideration in future implementations. A potential source of uncertainty in the analysis is the lack of consideration of sex differences in age at 50% maturity, in the fecundity at age or fecundity at size relationship. Significant differences between the sexes in these metrics would lead to different ERRO estimates depending on the sex of the unsampled parent of the HSP.

Uncertainty in the age of the *UNSAMPLED* common parent was accounted for in the model by inclusion in the probability calculation of the sample age composition, the annual age-, and year-specific total survival probabilities, the age specific fraction of mature fish, and the age-specific relative reproductive output. This takes into consideration the fact that the common parent will have had to have been both mature at the time of the first-born member of a given pair and alive (and of course reproductively active) at the time of the birth of the second born individual. The common parent could be of any age within these two constraints.

Other sources of uncertainty include the following: (i) Genotyping error, particularly since the molecular method required two PCR reactions, (ii) error in age estimation, (iii) potential bias arising from linkage among markers. All three potential sources of uncertainty were dealt with through simulations in the report.

(i) Genotyping error, loglikelihoods and HWE: Log likelihoods depend on allele frequencies, and it is argued that estimates of allele frequencies were very precise because they were based on 14,000 genotyped individuals (p81). However, HSPs were ultimately determined based on the ddRAD data which were extracted from only a few hundred individuals. The GTseq data, which were available for > 11,000 individuals, resulted in only a few hundred markers. The question of what data were used to estimate allele frequencies needs clarification.

(ii) Error in age estimation: The simulations in Appendix 5 demonstrated that errors in age estimation did not have a significant effect on the estimate of *Nc*. It would be important to clarify the extent to which this result is related to the fact that very few age classes dominated the collection as 91.4% of the individuals were < 7 yrs old.

(iii) Linkage: Simulations were conducted to examine the potential influence of linkage among markers, and it was concluded that linkage would have a very minimal effect on an estimate of abundance. In any case, future efforts to obtain a chromosome level genome sequence would go a long way to put the issue of linkage among markers to rest as linkage can affect FNR.

For each of the two estimation approaches, describe the magnitude and direction of any potential biases.

This reviewer did not identify any sources of potential biases. An issue to explore once the priorities identified below and in the Panel report are dealt with would be assessing the potential bias arising from the combination of overdispersion in reproductive success with the same set of individuals being overly successful in different years. In my view, this is not a priority though until the more important issues, listed below under research recommendations, are addressed.

ToR 4: Provide future research recommendations.

How could each of the methods used in this study be improved for more accurate estimates?

(i) An improvement in accuracy and perhaps precision in the estimate of population size is the identification of the sex of the UNSAMPLED parent of the half sib pairs. A difference between the sexes in the relationship between fecundity and age would lead to differences in the ERRO estimation which would propagate to the N_c estimation. The CKMR estimate of abundance is based on HSP, the parents of which remain *unsampled.* Analysis of mtDNA haplotype composition of the members of each pair is needed to assess whether the HSPs share a common father or a common mother. A difference in the mtDNA haplotype between the HSP members would indicate the common parent is a male. The same haplotype suggests the common parent is likely a female, but this depends on the frequency of the haplotype, and this has to be accounted for. If the haplotype is present in moderate or high frequency in the population, two different females with the same haplotype could have contributed to the HSP and in this case the common parent is a male even though the two individuals share the same haplotype! Population level mtDNA haplotype frequencies are therefore needed.

(ii) Collection of additional data to inform the fecundity-age (or size) relationships for males and females, and spawning season duration for individual fish can considerably improve the population size estimate. The same applies to information on age at 50% maturity, does this age differ between males and females?

(iii) Use the epigenomic aging clock to estimate the age of as many individuals as feasible, including all those identified as members of HSPs and a subset of the U (unrelated) individuals); rerun the CKMR model.

(iv) Provide the chromosome level genome sequence to assess the degree of linkage among the ~ 1755 multiallelic haplotypic loci used to obtain the current estimate.

(v) A recommendation regarding the population structure analysis upon which the CKMR work relies: Instead of running hierarchical AMOVAs grouping samples by state (a political boundary), the Review Panel suggested that samples be grouped by hardbottom aggregations. Samples from hardbottom locations within a 5-10 km radius should be grouped together and separate from samples collected from hardbottom locations that are much farther apart from each other (e.g., 50-100 km). The Review Panel found it somewhat surprising for a fish species that uses natural reefs or is associated with hardbottom substrate and is not otherwise a long-distance migratory species not to show any sign of meta-population structure over a few thousand kilometers.

(vi) Continue sampling and genotyping with the goal of eventually being able to include parent-offspring pairs (POPs) in the estimation of census size (Nc) and also provide a time series of $Nc_{(CKMR)}$ estimates to follow population trajectory.

(vii) A further refinement of the abundance estimate can be obtained by estimating the bias that could arise when the variance in reproductive success is overdispersed and individual reproductive success is correlated across years. In other words, overdispersion in reproductive success along with the same set of individuals being consistently more successful than the rest at producing offspring across different years would likely lead to bias in the estimation of N_c. The effect of overdispersion should be tested with and without this correlation.

Are there other sampling or survey methods that could be used to improve the accuracy of estimates of absolute abundance?

Close kin mark recapture is a relatively new approach, and its implementation is likely to increase globally in many commercial fisheries. The authors of this report should be commended for their effort. Refinement of their current estimate would be a more profitable avenue for further research than diverting efforts to other methods. A potential avenue for further insight would be a comprehensive effort to integrate movement analysis from acoustic telemetry initiatives with the CMKR approach.

Editorial comments on appendix IV

- Appendix IV is a draft MS on population structure, accordingly, focus the introduction on the importance of assessing population structure in marine fishes in general and in this particular sp in particular. This MS is not about CKMR or epigenomics, both of which are mentioned in the introduction.
- Define allelic imbalance.
- Define mapping quality ratios.
- Clarify which samples and which data were used to estimate pop structure.
- Be consistent in how you list the samples, I suggest from north to south.
- Eliminate mention of evidence that there are difference in *Ne between the Gulf and the Atlantic* as evidence (albeit weak) that these are two distinct pops.
- Conduct analysis with and without loci presumed to be under selection. It can provide further insight into the processes affecting the system.
- Removal of one individual of each kin pair: This needs to be better explained. What individuals and method (Gtseq vs. ddRAD) were used in the pop structure analysis?
- AMOVAs were conducted using political (i.e., state) divisions. Can AMOVAs be conducted by grouping individuals according to distance among hardbottom aggregations? In other words, samples separated by hard bottoms located within a couple of km or a small number of km separated from those located 100 km apart (or some other large distance apart) irrespective of state?
- Table 1: Groupings need to be redefined.
- I suggest using: Region (Atlantic vs. Gulf), among locations within region, and within location (define area for sampling location).
- Table 3 lists regions north to south, elsewhere in text they are listed in a different order. Be consistent.
- Table 4 has no Confidence Intervals.

Editorial comments on appendix V

Appendix V describes a series of simulations to assess the effect of bias and imprecision in three life history traits that are used within the CKMR framework to estimate the expected relative reproductive output (ERRO). In my view, there are too many comparisons which make the paper unwieldy. There is no need to include the elasmobranch scenario in the context of this red snapper report. Leaving this example out, there are four scenarios: red snapper unfished and fished, and in both cases two other scenarios were explored: with constant population size and with recruitment variation. I suggest the most important comparisons are the latter: constant population size vs. variable population size (i.e., recruitment variation. Two important assumptions are unlikely to hold in nature: reproductive success is the same across the two sexes. Age specific maturity and survival rates are also assumed to be equal across both sexes. This leads to having equal number of paternal and maternal HSPs. Embedded in the four cases described above there is also another set of acronyms ACOS and ACED!

The report shall include the following appendices:

Appendix 1: Bibliography of materials provided for review (See below)
Appendix 2: A copy of this Performance Work Statement (submitted as a separate file)
Appendix 3: Panel membership or other pertinent information from the panel review meeting. (See below)

APPENDIX 1: LIST OF MATERIALS AVAILABLE TO THE REVIEW PANEL

Bibliography
Population Estimation of U.S. Atlantic Red Snapper: Final Report to the South Atlantic Red Snapper Research Program
Appendix I: Applying mark-resight, count, and telemetry data to estimate effective sampling area and fish density with stationary underwater cameras
Appendix II: An Integrated Approach to Estimating the Effective Sampling Area of Baited Underwater Camera Traps
Appendix III: Spatiotemporal dynamics and habitat use of red snapper (*Lutjanus campechanus*) on the southeastern United States Atlantic continental shelf
Appendix IV: Genetic Population Structure of Red Snapper, *Lutjanus campechanus,* in the U.S. Atlantic and Eastern Gulf of America
Appendix V: Sensitivity of CKMR population estimates to uncertainty in life-history parameters
Appendix VI: Incorporating Close-Kin Mark-Recapture Data into an Integrated Stock Assessment Model for Southeast United States Atlantic Red Snapper (*Lutjanus campechanus)*
Appendix VII: Estimating Reef Fish Exploitation Rates in Catch-and-Release Fisheries with Conventional and Genetic Tags
Appendix VIII: Stakeholder Insights Corroborate Habitat and Reef Fish Abundance on the Southeastern U.S. Atlantic Continental Shelf
Appendix IX: Discard mortality rates of Red Snapper after barotrauma and hook trauma: Insights from using acoustic telemetry in the U.S. South Atlantic
Appendix X: Post-release Mortality of Red Snapper, *Lutjanus campechanus*, in U.S. Atlantic Waters off Northeast Florida Estimated with Three-Dimensional Acoustic Telemetry

APPENDIX 2: COPY OF PERFORMANCE WORK STATEMENT

Performance Work Statement (PWS)

National Oceanic and Atmospheric Administration (NOAA)
NOAA Fisheries
Center for Independent Experts (CIE) Program
External Independent Peer Review

South Atlantic Red Snapper Research Program (SARSRP) Review
January 13-15, 2026

Background

The NOAA Fisheries is mandated by the Magnuson-Stevens Fishery Conservation and Management Act, Endangered Species Act, and Marine Mammal Protection Act to conserve, protect, and manage our nation's marine living resources based upon the best scientific information available (BSIA). NOAA Fisheries science products, including scientific advice, are often controversial and may require timely scientific peer reviews that are strictly independent of all outside influences. A formal external process for independent expert reviews of the agency's scientific products and programs ensures their credibility. Therefore, external scientific peer reviews have been and continue to be essential to strengthening scientific quality assurance for fishery conservation and management actions.

Scientific peer review is defined as the organized review process where one or more qualified experts review scientific information to ensure quality and credibility. These expert(s) must conduct their peer review impartially, objectively, and without conflicts of interest. Each reviewer must also be independent from the development of the science, without influence from any position that the agency or constituent groups may have. Furthermore, the Office of Management and Budget (OMB), authorized by the Information Quality Act, requires all federal agencies to conduct peer reviews of highly influential and controversial science before dissemination, and that peer reviewers must be deemed qualified based on the OMB Peer Review Bulletin standards[1]. Independent scientific peer review is a hallmark of gold standard science[2].

Scope

The South Atlantic red snapper fishery is economically and recreationally important, but has faced challenges due to overfishing and restrictive management. The red snapper population has shown a remarkable rebound in the last 15 years. Fishermen and scientists agree that red snapper are far more abundant and larger than they used to be. Harvest opportunities for red snapper remain limited because of the large amount of discarded fish and uncertainty in the

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[1] https://www.whitehouse.gov/wp-content/uploads/legacy_drupal_files/omb/memoranda/2005/m05-03.pdf

[2] https://www.whitehouse.gov/presidential-actions/2025/05/restoring-gold-standard-science/

[3] https://www.fisheries.noaa.gov/southeast/recreational-fishing/working-toward-increasing-fishing-opportunities-red-snapper-south-atlantic

[4] https://www.scseagrant.org/south-atlantic-red-snapper-research-program/

exact number of fish in the population. The South Atlantic Council, in recent years, has struggled with how to reduce the high amounts of red snapper discards and end overfishing, as required by the law[3].

The South Atlantic Red Snapper Research Program (SARSRP) was administered through the South Carolina Sea Grant Consortium[4]. A Request for Proposals (RFP) was issued with a full proposal deadline of February 1, 2021. The goal of the SARSP is to generate an absolute estimate of abundance with an accompanying measure of uncertainty for the entire South Atlantic red snapper stock. Preference was given to proposals that seek to produce a single absolute estimate of abundance for the entire geographic region. This estimate will serve as an independent benchmark on which to inform a currently ongoing stock assessment. It will provide a metric of abundance of what the size (number of individual fish) of the stock is in the South Atlantic for the period of the survey. The SARSP awarded project is led by a team of researchers spanning the following research institutions: University of Florida, Texas A&M Corpus Christi, N.C. State University, NOAA Fisheries, S.C. Department of Natural Resources, NOAA NOS Center for Coastal Fisheries Habitat Research, Florida Fish & Wildlife Conservation Commission, and GA Department of Natural Resources.

The awarded research proposal included the following three approaches: (1) Close-kin and meta-population genetics analyses; (2) Existing and possibly supplemental new South Atlantic trap-video survey data to scale-up density estimates to total abundance; and (3) a research technique similar to that pursued in the Gulf Red Snapper abundance assessment, focusing predominantly on use of active acoustics and visual ground-truthing. Research began in the Fall of 2020 and will finish in August of 2025, hence the request for CIE review at this time.

Fisheries management depends on science based advice for setting accurate quotas. Scientific peer-review serves as the cornerstone and gold standard of best science. This peer review will further the NOAA mission to conserve and manage coastal and marine ecosystems and resources by providing science based advice. This advice is consistent with National Standard 2 (NS2), which is a statutory (Magnuson Stevens Act) requirement at 16 U.S.C. 1851(a)(2) and states that "conservation and management measures shall be based upon the best scientific information available (BSIA). This review aligns this statute because this CIE peer review is an essential part of determining whether the assessment used meets the criteria for BSIA under NS2. It will also further the NOAA Fisheries mission of productive and sustainable fisheries and healthy ecosystems.

The specified format and contents of the individual peer review reports are found in **Annex 1**. The Terms of Reference (ToRs) of the peer review are listed in **Annex 2**. The tentative agenda of the panel review meeting is attached in **Annex 3.**

Requirements

NOAA Fisheries requires three **(3)** reviewers to conduct an impartial and independent peer review in accordance with the Performance Work Statement (PWS), OMB guidelines, and the ToRs below. The reviewers shall have expertise in quantitative methods applied to fisheries. It is desirable to have at least one reviewer with expertise in capture-recapture methodology, especially Bayesian hierarchical modeling, and at least one reviewer with expertise in genetic close-kin mark-recapture applications.

The review panel chair, who is in addition to the three reviewers, will not be provided by the CIE. Although the chair will be participating in this review, the chair's participation (e.g., labor and travel) is not covered by this contract.

Each reviewer will write an individual review report in accordance with the PWS, OMB Guidelines, and the ToRs below. Modifications to the PWS and TORs cannot be made during the peer review, and any PWS or ToRs modifications prior to the peer review shall be approved by the Contracting Officer's Representative (COR) and the CIE contractor. All ToRs must be addressed in each reviewer's individual report.

Tasks for Reviewers

1) Pre-review Background Documents: Review the following background materials and reports prior to the review:
   Two weeks before the peer review, the NOAA Fisheries Project Contact will send by electronic mail or make available at an FTP site to the CIE reviewer all necessary background information and reports for the peer review. In the case where the documents need to be mailed, the Project Contact will consult with the CIE on where to send documents. The CIE reviewer shall read all documents in preparation for the peer review.
2) Attend and participate in an in-person review meeting. The meeting will consist of presentations by NOAA and other scientists, stock assessment authors and others to facilitate the review, to answer any questions from the reviewers, and to provide any additional information required by the reviewers.
3) After the review meeting, reviewers shall conduct an independent peer review report in accordance with the requirements specified in this PWS, OMB guidelines, and ToRs, in adherence with the required formatting and content guidelines. Reviewers are not required to reach a consensus.
4) Each reviewer shall assist the Chair of the meeting with contributions to the summary report based on the ToRs. Reviewers are not required to reach consensus.
5) Deliver their reports to the Government according to the specified milestones dates.

Foreign National Security Clearance

When reviewers participate during a panel review meeting at a government facility, the NOAA Fisheries Project Contact is responsible for obtaining the Foreign National Security Clearance approval for reviewers who are non-US citizens. For this reason, the reviewers shall provide requested information (e.g., first and last name, contact information, gender, birth date, passport number, country of passport, travel dates, country of citizenship, country of current residence, and home country) to the Project Contact for the purpose of their security clearance, and this information shall be submitted at least two weeks in advance. For additional information, please see the following link: https://www.commerce.gov/osy/programs/foreign-access-management. The contractor is required to use all appropriate methods to safeguard Personally Identifiable Information (PII).

Place of Performance
The place of performance shall be in North Carolina.

Period of Performance
Each reviewer's duties shall not exceed **14** days to complete all required tasks.

Schedule of Milestones and Deliverables: The contractor shall complete the tasks and deliverables in accordance with the following schedule.

Schedule	**Milestones and Deliverables**
Within 2 weeks of award	Contractor selects and confirms reviewers
Approximately 2 weeks prior to the review	Contractor provides the pre-review documents to the reviewers
January 13-15, 2026	Panel review meeting
Approximately 2 weeks later	Contractor receives draft reports
Within 3 weeks of receiving draft reports	Contractor submits final reports to the Government

* The Peer Review Summary Report will not be submitted to, reviewed, or approved by the Contractor.

Applicable Performance Standards
The acceptance of the contract deliverables shall be based on three performance standards: (1) The reports shall be completed in accordance with the required formatting and content (2) The reports shall address each ToR as specified (3) The reports shall be delivered as specified in the schedule of milestones and deliverables.

Confidentiality and Data Privacy
This contract may require that services contractors have access to Privacy Information. Services contractors are responsible for maintaining the confidentiality of all subjects and materials and may be required to sign and adhere to a Non-disclosure Agreement (NDA).

Travel

All travel expenses shall be reimbursable in accordance with Federal Travel Regulations (Travel resources | GSA), and all contractor travel must be approved by the COR prior to the actual travel. Any travel conducted prior to the receipt of proper written authorization from the COR will be done at the Contractor's own risk and expense. International travel is authorized for this contract. Travel is not to exceed $9,000.00.

NOAA Fisheries Project Contact

Erik H. Williams, Ph.D., Director of the Atlantic Fisheries Branch
Sustainable Fisheries Division
Southeast Fisheries Science Center
erik.williams@noaa.gov
Office Tel: 252-666-7428

Annex 1: Peer Review Report Requirements

2. The independent Peer Reviewer report shall be prefaced with an Executive Summary providing a concise summary of whether they accept or reject the work that they reviewed, with an explanation of their decision (strengths, weaknesses of the analyses, etc.).

2. The report must contain a background section, description of the individual reviewers' roles in the review activities, summary of findings for each ToR, in which the weaknesses and strengths are described, and conclusions and recommendations in accordance with the ToRs.

   a. Reviewers must describe in their own words the review activities completed during the panel review meeting, including a brief summary of findings, of the science, conclusions, and recommendations.

   b. Reviewers should discuss their independent views on each ToR even if these were consistent with those of other panelists, but especially where there were divergent views.

   c. Reviewers should elaborate on any points raised in the summary report that they believe might require further clarification.

   d. Reviewers shall provide a critique of the agency review process, including suggestions for improvements of both process and products.

   e. The report shall be a stand-alone document for others to understand the weaknesses and strengths of the science reviewed, regardless of whether or not they read the summary report. The report shall represent the peer review of each ToR, and shall not simply repeat the contents of the summary report.

3. The report shall include the following appendices:

   Appendix 1: Bibliography of materials provided for review
   Appendix 2: A copy of this Performance Work Statement
   Appendix 3: Panel membership or other pertinent information from the panel review meeting.

Annex 2: Terms of Reference for the Peer Review

South Atlantic Red Snapper Research Program Review

January 13-15, 2026

CIE reviewers are contracted to complete their independent peer review based on the ToRs. Therefore, the CIE-NOAA Fisheries review and approval process is based on whether the CIE independent reports addressed each ToRs.

1. Evaluate the study designs used for developing estimates of absolute abundance of age-2+ red snapper in the U.S. South Atlantic region (Florida, Georgia, South Carolina, North Carolina).
    a. Assess the study design and sampling sufficiency as they pertain to the application of genetic close-kin mark-recapture methodology.
    b. Assess the study design and sampling sufficiency as they pertain to the application of hierarchical Bayesian abundance modeling.
2. Evaluate the statistical/modeling methods used to analyze the data, and to construct the absolute abundances estimates and their variances.
    a. Are the close-kin mark-recapture methods applied appropriately?
    b. Are the hierarchical Bayesian modeling methods applied appropriately?
3. Are the estimates of absolute abundance (age-2+ red snapper) and their variances reliable?
    a. For each of the two estimation approaches, are assumptions appropriate, given study design considerations?
    b. Are there potential sources of uncertainty that were not considered when developing the estimates of abundance?
    c. For each of the two estimation approaches, describe the magnitude and direction of any potential biases.
4. Provide future research recommendations.
    a. How could each of the methods used in this study be improved for more accurate estimates?
    b. Are there other sampling or survey methods that could be used to improve the accuracy of estimates of absolute abundance?

Annex 3: Tentative Agenda

South Atlantic Red Snapper Research Program Review

TBD

January 13-15, 2026
Location: Charleston, South Carolina

NOAA Fisheries Project Contact:
Erik H. Williams, Ph.D., Director of the Atlantic Fisheries Branch
Sustainable Fisheries Division
Southeast Fisheries Science Center

APPENDIX 3: LIST OF PARTICIPANTS

Review Panel

Marcel Renchert (Chair)	SAFMC SSC
Luiz Barbieri	SAFMC SSC
Noel Cadigan	CIE Reviewer
Joe Powers	CIE Reviewer
Daniel Ruzzante	CIE Reviewer

Program Team

Will Patterson (Lead PI)	Univ of Florida
Nathan Bacheler	SEFSC
Jeffrey Buckel	NCSU
Nathan Hostetter	NCSU
David Portnoy	TAMUCC
Matthew Vincent	SEFSC

Staff

Julie A Neer	SEDAR
Chip Collier	SAFMC Staff
Judd Curtis	SAFMC Staff
Rachael Silvas	SAFMC Staff
Emily Ott	SEDAR

Workshop Observers

Chris Bradshaw	FLFWC
Wally Bubley	SCDNR
Chris Custer	NCSU
Amy Dukes	SCDNR

Liam Kehoe	UF
Ryan McMullen	SC Sea Grant
Emily Osborne	SC Sea Grant
Tracey Smart	SCDNR
Julie Vecchio	SCDNR
Jordy Wolfe	SCDNR

Workshop Observers via Webinar

Eric Anderson	
Jordan Bajema	FWC
Sydney Bates	SCDNR
Kristan Blackhart	NOAA
Jason Boucher	NOAA
Myra Brouwer	SAFMC Staff
Julia Byrd	SAFMC Staff
Jessica Carroll	FWC
David Chagaris	UFL
Kristin Cook	FWC
Ellie Corbett	FWC
Michael Drexler	Ocean Conservancy
Ben Dyar	SCDNR
Joseph Evans	SCDNR
Alena Figueroa	FWC
Margaret Finch	SCDNR
Kristin Foss	FWC
Dawn Franco	GA DNR
Elizabeth Ford	
Keilin Gamboa-Salazar	SCDNR
Brad Gentner	
Ben Goldstein	
Elizabeth Gooding	SCDNR
Amiee Griffin	FWC
Jenny Grossmann	COFC
Martha Guyas	ASA
Homer Hiers	SCDNR
Kathleen Howington	SAMFC Staff
Jeanette Huber	FWC
Allie Iberle	SAFMC Staff
Blaik Keppler	SCDNR
Kevin Kolmos	SCDNR
Genine McClair	FWC
Maria McGirl	FWC
Paul McLaughlin	
Nikhil Mehta	NOAA
Trish Murphey	NCDEQ
Gabby Ocampo	FWC

Krishna Pacifici .... NCSU
Chloe Ramsay .... FWC
Brian Reich .... NCSU
Scott Sandorf .... NOAA
Mike Schmidtke .... SAFMC Staff
Nick Smillie .... SAFMC Staff
Wiley Sinkus .... SCDNR
Kevin Spanik .... SCDNR
Joesph Tarnecki ....
Chris Taylor .... NOAA
Miaya Taylor .... UFL
Erik Williams .... SEFSC
Olivia Wilms .... FWC
Meg Withers .... SAFMC Staff
Daniel Zapf .... NCDEQ