To the Editor,

I am writing on behalf of myself and my coauthors regarding our manuscript “*Effective number of white shark (Carcharodon carcharias, Linnaeus) breeders is stable over four successive years in the population adjacent to eastern Australia and New Zealand*” which was published in Ecology and Evolution (Volume 11, Issue 1, pp 186-198) on 7 October 2020. We have been made aware of an error in the processing of our data which impacted the published results and because of this we wish to submit a correction for our manuscript.

In our study, we made estimates for the effective number of breeders (Nb), an analogue of effective population size (Ne), using a population of white sharks as a case study. Many populations of this species have suffered recent significant recent declines, and bather protection programs used globally offer an opportunity to develop long-term genetic monitoring programs. We used two independent methods (linkage-disequilibrium and sibship assignment) and two independent marker types (single-nucleotide polymorphism and microsatellite loci) to estimate Nb. We show how Nb has remained stable over the years measured and discuss how this relates to the life-history, conservation and recovery of the study species.

The error identified appears isolated to an intermediate data file used to make the estimates of Nb using SNPs; checks have shown the original data remains unaffected and are suitable to use for re-analysis. We have since used the original data and a corrected data processing pipeline to recalculate our estimates of Nb and associated quantities. Importantly, the corrected estimates do not change the conclusions of the original work. We have made a table comparing the old with the new estimates, and plotted them for visualisation (see below).

Included with this letter is:

* An analysis of the differences between the original and published data (Report.html).
* A re-analysis of the data from the beginning of the pipeline with an updated result (Report.html).
* A corrected version of our manuscript and supplementary materials; all changes between the original and the updated manuscript are highlighted (CorrectManuscript\_Davenport2020.doc, ece37007-sup-0001-supinfo-updated.doc).

A document detailing the changes (Correction\_documentation.doc). We apologise for any inconvenience this has caused for you, the journal and your readers. We hope we have provided you with a comprehensive explanation of the situation regarding the data and updated results. We look forward to answering any questions or addressing next steps in this process.

Regards,

Danielle Davenport (Lead Author)

Table comparing the original published estimates for Nb using SNPs with the updated (reanalysis) estimates.

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Year | S | Nb\_LD\_est | Nb\_LD\_lower | Nb\_LD\_upper | Nb\_SA\_est | Nb\_SA\_lower | Nb\_SA\_upper | Nb\_COM\_est | Nb\_COM\_SD | Na\_Nb\_ratio |
| Original |  |  |  |  |  |  |  |  |  |  |
| 2010 | 29 | 193.2 | 91.1 | NA | 271 | 136 | 1430 | NA | NA | NA |
| 2011 | 42 | 195.1 | 104.2 | 952.9 | 344 | 204 | 923 | 233.2 | 69.5 | 0.31 |
| 2012 | 52 | 165.6 | 104.2 | 359.6 | 341 | 157 | 399 | 206.1 | 45.9 | 0.27 |
| 2013 | 63 | 208.5 | 116.4 | 712.7 | 289 | 200 | 461 | 252 | 46.7 | 0.34 |
| Reanalysis (updated) |  |  |  |  |  |  |  |  |  |  |
| 2010 | 29 | 62.1 | 32.7 | 249.5 | 96 | 56 | 198 | 74.56624 | 20.56712 | 0.099422 |
| 2011 | 39 | 208.1 | 110.1 | 1135.9 | 247 | 148 | 567 | 228.6637 | 57.75423 | 0.304885 |
| 2012 | 52 | 201.9 | 126.7 | 449 | 196 | 132 | 332 | 197.2146 | 39.0757 | 0.262953 |
| 2013 | 63 | 179.8 | 121.9 | 320.8 | 174 | 123 | 252 | 174.8467 | 29.34475 | 0.233129 |

A graph with lines and numbers

Description automatically generated

Figure above shows original published estimates (red) and updated (new) estimates (blue).