

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 (N_b), an analogue of effective population size (N_e), 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 N_b . We show how N_b 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 N_b 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 N_b 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 page 2 of this letter).

Also 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 showing the correction (correction_documentaion.docx)

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

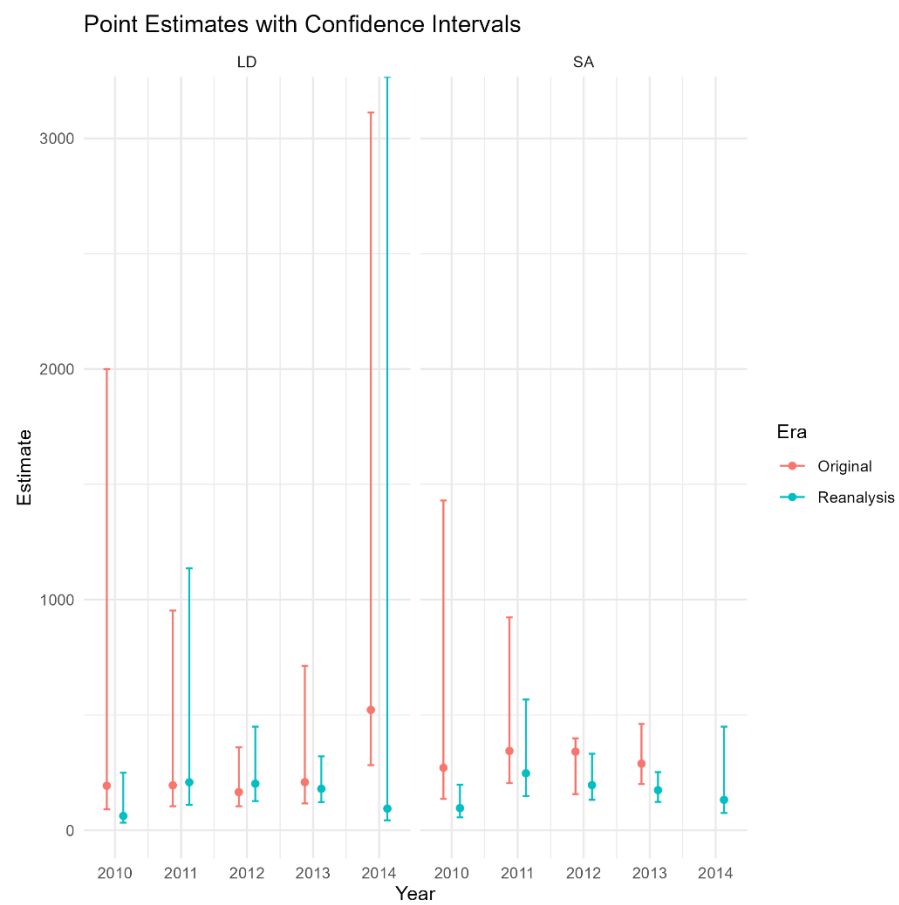


Figure above shows original published estimates (red) and updated (new) estimates (blue).