CNMI Unfished Areas LH Sampling Report

Notes

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**Simulate BMUS populations**, save as objects in a .RData (create\_simulated\_pops.R, uses functions from modify\_LH\_sample\_function.R)

Ensure values are in BMUS\_LH\_sim\_pop\_parameters.xlsx

* Enter assumed true population values in the column for each BMUS.
* Linf, K, (t0), Amax from the Life History of Bottomfish Management Unit Species of Guam. NMFS-PIFSC-170. CV assumed 2.5% for Linf, 5.7% for K, ranged 10-25% for L0 (adjusted to give reasonable L0 spread).
* M calculated from Amax following Then et al. 2015 M = 4.899\*Amax^-0.916
* F should be zero
* mincat, catsd, maxcat, maxcatsd should be reasonable values to avoid errors, but don’t matter if F = 0.
* Reminder: age\_max is not a plus group in the population dynamics, it is simply the summary age to calculate population variance at a defined “old age”.
* N can be as large as possible, but will increase run time. for Amax = 55, each 100k takes about 3 minutes to run.
* Linf\_k\_cor\_TF is a TRUE or FALSE value that determines whether Linf and k are sampled independently from each other (false), or if Linf = f(k) (true). If Linf\_k\_cor\_TF = TRUE then the Jensen 1997 Eq. 4 theoretical expected relationship between Linf and K (Linf = C1\*k^(-1/LW\_beta)) is used where LW\_beta is the theoretical allometric W-L scalar, assume = 3 here and C1 is calculated from the mean population values of Linf and k. If Linf\_k\_cor\_TF = TRUE, it may be necessary to reduce the Linf or k marginal variability (Linf\_sd and k\_sd parameters) to limit variance on the combined distribution of the two parameters. The output of the simulate\_population\_harvest $parameters$k\_Linf\_cor\_value will provide an idea of what the correlation coefficient is (I think -0.5 or so is reasonable).

**Create figures of the simulated populations** with parameters listed, consider carefully to ensure we are satisfied with our assumptions about the true growth and variability in the population.

* Run the R Markdown file Simulated\_Pops\_Summary.Rmd.

Read-in updated file of all LH samples collected, calculate expected relative error based on simulated populations and length distribution of samples

Make figures: 1) hist of samples at length (colors for existing and during survey) 2) boxplots of relative error.

3. run with every update:

Add a color code to show added samples in the hist during survey

show fig with units, provide calculated relative error as a number