Notes on Hake.

Analyses are complicated.

From Malick et al. 2020

Acoustic backscatter measurements at 38 kHz were collected using a calibrated Simrad EK60 echosounder. Acoustic backscatter data analysis pro- ceeded in 5 steps (see Fleischer et al. 2008 for details). First, backscatter attributable to Pacific hake was manually identified by an acoustician. To in crease consistency, all acoustic assignments were cross-checked, validated, and documented by at least 2 scientists. This initial processing of the acoustic backscatter was conducted as a joint effort between scientists in the USA and Canada. Second, each Pacific hake region identified in the acoustic back- scatter was assigned a validation trawl based on the depth, acoustic backscatter patterns, and proximity to trawl sampling locations. Trawls/aggregations were then assigned to biological strata based on a hake length frequency distribution using a Kolmogorov- Smirnov goodness of fit test. Third, a target strength to length relationship was used to convert the com- posite length-frequency distribution to the expected backscattering cross-section (σbs) for a biological stratum (Traynor 1996). Fourth, the nautical area scattering coefficient (s*A*) was calculated for cells defined by 10 m vertical depth strata and 0.926 km (0.5 n miles) horizontal intervals along a transect by integrating the mean volume backscattering coeffi- cient (s*V*) vertically across depth strata for the interval (MacLennan et al. 2002). Finally, length-specific biomass estimates of Pacific hake were derived by calculating numbers of hake for each interval and length class based on the values of s*A* and σbs and then con- verting numbers of hake to hake biomass using an empirical length−weight relationship. Biomass by length was converted to biomass by age via a stratum-based length-at-age key, which was calculated using ages derived from otolith analysis.

Age-specific hake biomass was estimated for hake age 2 and older. Although information on age-1 hake was collected during the survey, this age class was excluded from the biomass estimates because of concerns about different catchability in trawl gear and differences in migration patterns compared to older hake (Stewart et al. 2011, Edwards et al. 2018). Evidence also suggests that cohort-specific ageing error may exist where uncertain age determinations tend to be assigned to the dominant age class in a particular year, which was not included as part of our analysis (Edwards et al. 2018).

This procedure resulted in age-specific hake bio- mass estimates for 0.926 km (0.5 n miles) bins along each transect. We further aggregated the biomass data into 20 km bins along transects to reduce cross- shelf (i.e. east−west) variance in the biomass data because our primary focus was investigating latitudinal gradients (i.e. north−south) in hake biomass dis- tribution. Further, to ensure the northern and south- ern extremes of hake distribution were not unduly influenced by one or a few years, we limited the analysis to only transects that fell within the common latitudinal range of the survey across all years (36.6°−54.7° N; Table 1). In subsequent analyses and data summaries, only bins where biomass was greater than 0 were used because exploratory analyses indicated that temperature did not constrain the distribution of Pacific hake (see Fig. S1 in the Supplement at www.int-res.com/articles/suppl/m639p185\_ supp.pdf).

Qs for Mike.

Why is there no third dimension in your model. Why sum to surface?

Covariates – distance to the 200m isobath.