

Eats, moults & leaves: estimating grey seal pup production from serial counts at breeding colonies

Estimating pinniped abundance is difficult due to their complex life histories. In the UK, robust estimates of grey seal population size and trends depend on reliable estimates of pup production (i.e., the number of pups born in any one year). Grey seals give birth at breeding colonies over an approximately two-month period. Pups are born white and moult to a greyish brown colour before leaving the colony. This staggered birth, moult, and leaving process means that not all pups are present at the colony at any one time.

At most UK breeding colonies, a series of digital photographic aerial surveys are conducted between September and January. During each survey, photographs are taken encompassing the entire breeding colony. In postprocessing, experienced analysts count the numbers of white and moulted seal pups. Pups are not individually identifiable from these photographs. Counts are combined with information on life history parameters to derive a birth curve and estimate pup production.

Unfortunately, the model previously used to estimate pup production from these data has fundamental structural limitations that prevent it being adapted for future use. Therefore, we developed a more flexible state-space pup production model that can incorporate age-dependent misclassification errors and be structured hierarchically so that that information from data-rich colonies and years is shared with data-poor colonies and years. We implemented this model in TMB and fit it using maximum likelihood. We show that our model performs well on simulated and real datasets.

While this model was developed to estimate grey seal pup production, it could be applied to other taxa for which successive counts of different life stages are collected, and could be used to investigate key ecological questions, including, for example, the impact of climate change on phenology. This could be particularly valuable in situations where not all individuals are present in the same place and time and are not individually identifiable. In future, we would like to explore fitting the model in a Bayesian framework so that prior information on life-history parameters can be included.