The CKMR data improved the accuracy and precision of *M* estimates apparently more so than those of *R0*. This was perhaps a function of CKMR informing estimates in the terminal end of the time series much more so than at the beginning, and *R0* is primarily used to obtain initial scale of the population and recruitment in each year.

This is actually because CKMR directly looks at SSBy and survival. R0 is just a parameter that eventually makes up SSBy.

Although I have presented simple cases where assessment models are correctly specified, it may be that a more important true value of CKMR integration is in righting the model when some other model aspect is mis specified, such as an index of abundance not being proportional to the stock abundance or a gross underestimation of catch ().

CKMR is a retrospective inference, backdated to the year of birth of the younger individual for POPs and the years of birth for each sibling in HSPs, hence the maximum improvements in the performance metrics on *SSBy* were observed some years before the terminal year of the time series. Although the metrics were still improved for the terminal year of *SSBy* compared to the assessments without CKMR data, it was less so than the minimum.

Although when HSPs are added to the analyses and the data integrated into a stock assessment, a full simulation-estimation approach such as presented here is likely a more informative approach. Even better would be to use a pedigree simulator such as CKMRpop (Anderson, 2022) as an operating model.

Note that CKMR requires that samples are random with respect to kin, conditional on covariates like age. Theoretically this needn’t be violated with clustered composition sampling. Thus the composition data could be less informative than simulated herein and the CKMR data of more relative value than my results show.