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Estimating the variation and autocorrelation of phenotypic selection on great tit

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Temporal variation in phenotypic selection in the wild has traditionally been estimated through the Lande & Arnold approach without properly accounting for sampling error and without any underlying biological model for temporal auto-correlated fluctuations in the fitness function. Here we introduce state-space models (SSMs) to analyse the phenotypic selection process and recommend using Template Model builder (TMB), an R package for fast fitting statistical latent variable models (including state-space and mixed models) by maximising the Laplace approximation of the marginal likelihood computed using automatic differentiation. With a long-term great tit data set, we fit several SSMs with TMB and conduct model selection based on Akaike information criterion (AIC) to assess the support for stabilizing selection on breeding time of the great tit population. Using TMB to fit SSMs allows us to estimate additional parameters, the variation, correlation and autocorrelation of the fitness parameters without substantial increase in computational costs.

Specifically, the maximum fitness, the optimal phenotype and the width of fitness function are estimated with order-1 vector autoregressive model (VAR1), and the count of failed broods (zero inflation) is modelled as a separate episode of selection. Our results agree with the change patterns of the mean number of fledgling of each brood and the mean probability of failed brooding from the previous studies of this species. We conclude that our method can be directly applied to exploring phenotypic selection induced by environmental change for other species.