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Appendix A from W. F. Morris et al., "Low Demographic Variability in Wild Primate Populations: Fitness Impacts of Variation, Covariation, and Serial Correlation in Vital Rates"

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Parameter Estimation and Generation of Random Vital Rates

This appendix provides additional details about the database, procedures we used to estimate vital rates, and methods we used to generate random vital rates with the estimated means, variances, covariances, and serial correlations.

The Primate Life History Database

As described in more detail by Strier et al. (2010), life-history data for individual animals in the Primate Life History Database (PLHD) are stored in two data tables (illustrated at http://demo.plhdb.org/). In the "Biography" table, each individual has a single row. Relevant columns of the table are as follows: the observed (or estimated) birth date, type of entry into the study population (birth, present at onset of the study, or immigration into the study population, the latter two requiring estimation of birth date), date of departure from the study, type of departure (death, emigration, present at the last field census, or permanent disappearance), sex, mother's identity, and whether the individual was its mother's first live-born offspring. Entry type and depart type columns provide information about which individual life histories are left and right censored, respectively. A second table, the "Fertility" table, contains data for females only; each row represents a time period during which a female's reproduction was closely monitored, such that she could not have given birth to a live offspring without that birth being observed. Each row has start and end dates, as well as start and end types corresponding to the start and end types in the "Biography" table (thus containing information about left and right censoring of reproduction). A given female may have more than one row in the "Fertility" table if her reproduction was not observed continuously, with the interval between successive rows thus representing a gap in observation.

Accounting for Left and Right Censoring in Estimating Vital Rates

If an individual entered the study after the original census and in a manner other than by birth, that individual contributed only that fraction of its first intercensus interval in the study to the number of survivors and the sample size for estimating survival for that interval. Similarly, if an individual left the study in a manner other than death between the current census and the subsequent one, it contributed only the portion of the intercensus interval that it was still in the study population to the survivors and sample size for that interval. For estimating fertilities in a given intercensus interval, a female in a given stage (juvenile or adult) that entered or left the set of intensively monitored females other than by birth or death, respectively, contributed to the sample size in proportion to the fraction of the interval her fertility was observed (using information from the "Fertility" table). Any live-born offspring she produced during the interval contributed to the stage-specific number of births in proportion to the fraction of the interval her fertility was observed. Because sex was not determined for all newborns before they died, we computed the number of daughters per female per year by multiplying the (weighted) number of births (of known and unknown sex) by the sex ratio (table 3) and dividing by the (weighted) number of females during that year.

These procedures for accounting for left and right censoring resulted in noninteger numbers of "successes" (e.g., number of survivors) and "trials" (e.g., sample size for estimating survival), but the generalized linear random effects model we used to correct for sampling variation (with binomial errors) assumes that the numbers of successes and trials are integers. Therefore, we rounded the numbers of successes and trials to the nearest integers before applying the generalized linear model.

Generation of Stochastic Vital Rates with Specified Means, Variances, Covariances, and Serial Correlations

The method we used to generate vital rates with specified variances, covariances, and serial correlations largely followed the approach described in chapter 8 of Morris and Doak (2002), as modified from the procedure of Gross et al. (1998). Specifically, we first used a matrix of correlations between vital rates in adjacent years that were estimated from the demographic data to produce a large, multiyear correlation matrix, assuming that all of the correlations between vital rate values separated by more than 1 year are produced by the 1-year correlations. We included enough years in this large correlation matrix that any correlations greater in magnitude than 0.00001 between a rate in the current year and that or any other rate in any previous year was retained. Using the square root of this large correlation matrix, we then generated a series of standard normal random variables with the specified correlations and with 50,000 values for each vital rate. As this procedure produces normal random variables and our desired vital rates are bounded by 0 and 1 (unlike the standard normal distribution), we converted the normal random variables into beta random variables by substituting the cumulative distribution function value of each normal variable into the inverse cumulative distribution function for the beta distribution with the desired mean and variance. This conversion tends to produce series of beta random variables with standard deviations that are biased (usually downward) relative to the standard deviations of the original vital rates. However, by first generating the normal random variables with a standard deviation equal to the inverse of the bias, we could virtually eliminate the bias in the resulting beta random variables, so that all of our simulated vital rates had standard deviations within $\pm 0.5\%$ of the values estimated from the data.

To simulate long-term fitness in the absence of serial correlation, we simply followed the above procedure using only the within-year correlation matrix, and to simulate the IID case (variation but no covariation or serial correlation), we generated each vital rate starting with independent normal random variables.