

**Bruce E. Kendall, Gordon A. Fox, Masami Fujiwara, and Theresa M. Nogeire. 2011. Demographic heterogeneity, cohort selection and population growth. *Ecology* 92:1985-1993.**

## Appendix E. The loop analysis of the two-type model

Loop analysis (van Groenendaal et al., 1994; Wardle, 1998) identifies the unique closed pathways in a matrix population model and allocates the matrix elasticities to the pathways; the resulting “loop elasticity” is often interpreted as the relative contribution of the corresponding life-history pathway. It is often used, for example, to compare the importance of early vs. late reproduction. When a given matrix element is shared by multiple loops, there are subtleties with allocating the elasticities among loops, but that does not apply in our models.

The various matrix models in the main text can each be decomposed into three loops: two self-loops (type 1 to itself and type 2 to itself, each incorporating adult survival and same-type reproduction) and the cross-type reproduction loop (type 1 to type 2 and back). Note that the latter involves two reproduction events,

so cannot be readily interpreted as a life history pathway as is usually done in loop analysis.

Since the loops do not share any links, their elasticities are easy to calculate: they are  $E_{11}$ ,  $E_{22}$ , and  $E_{12} + E_{21}$ , respectively, where  $E_{ij}$  is the elasticity of  $\lambda$  to matrix element  $A_{ij}$ . Various views of these elasticities are shown in Figs. E.1–E.3. In all cases, the cross-type reproduction loop elasticity is lowest, while the high survival/reproduction self-loop elasticity is highest; the latter increases (at the expense of both other loop elasticities) with increases in either type of heterogeneity or in the parent-offspring correlation.

## References

- van Groenendaal, J., H. de Kroon, S. Kalisz, and S. Tuljapurkar. 1994. Loop analysis: evaluating life history pathways in population projection matrices. *Ecology* **75**:2410–2415.
- Wardle, G. M. 1998. A graph theory approach to demographic loop analysis. *Ecology* **79**:2539–2549.

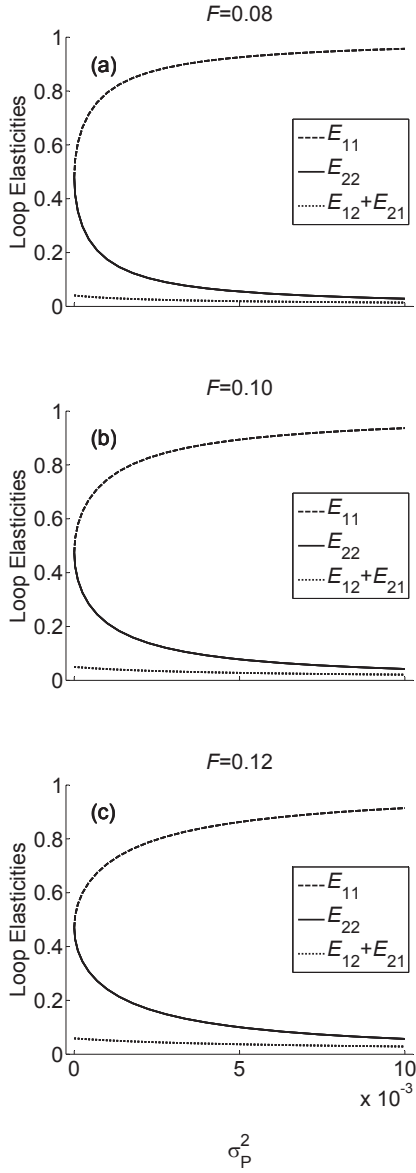


Figure E.1: Loop elasticities of the survival heterogeneity model as a function of the survival variance ( $\sigma_P^2$ ), for several values of  $F$ .  $E_{11}$  and  $E_{22}$  are the self-loop elasticities, while the curve labeled “ $E_{12} + E_{21}$ ” is the cross-type reproduction loop elasticity. In all panels,  $\bar{P} = 0.9$  and  $h = 0$ .

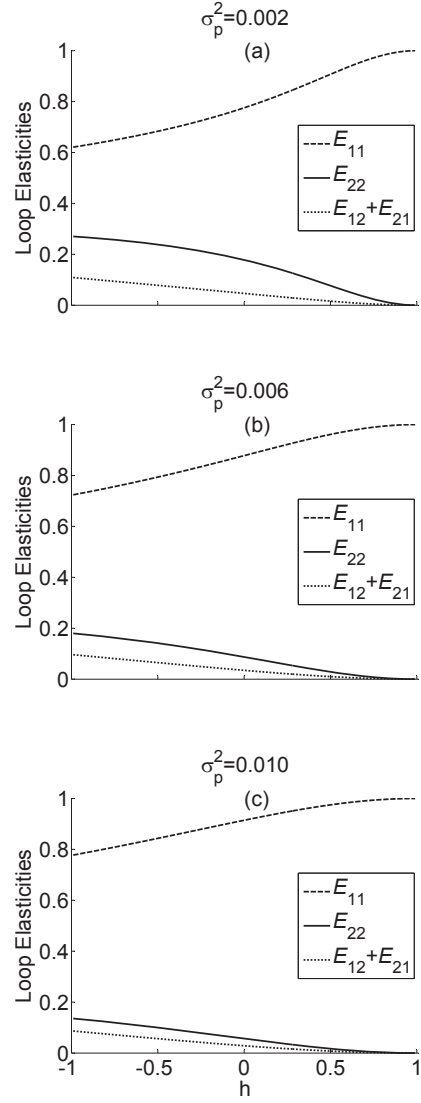


Figure E.2: Loop elasticities of the survival heterogeneity model as a function of the parent-offspring correlation ( $h$ ), for several values of  $\sigma_P^2$ .  $E_{11}$  and  $E_{22}$  are the self-loop elasticities, while the curve labeled “ $E_{12} + E_{21}$ ” is the cross-type reproduction loop elasticity. In all panels,  $\bar{P} = 0.9$  and  $F = 0.101$ .

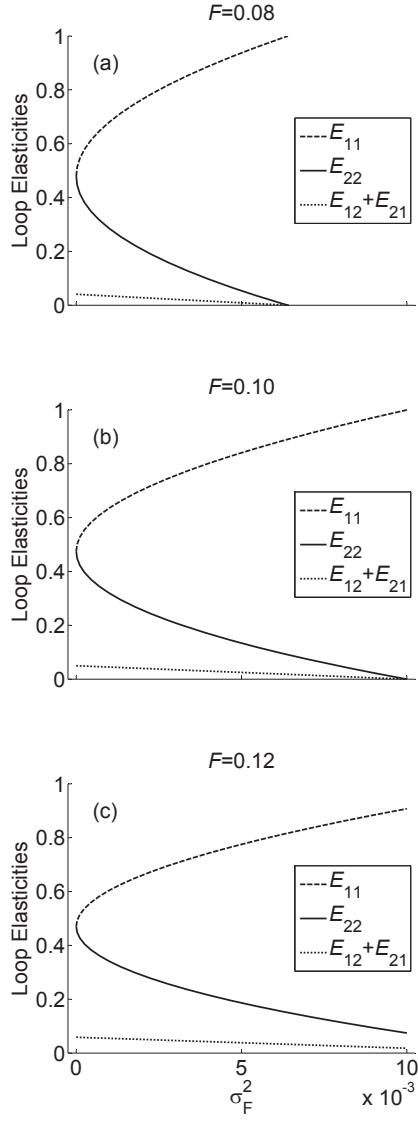


Figure E.3: Loop elasticities of the reproductive heterogeneity model as a function of the reproductive variance ( $\sigma_F^2$ ), for several values of  $\bar{F}$ .  $E_{11}$  and  $E_{22}$  are the self-loop elasticities, while the curve labeled “ $E_{12} + E_{21}$ ” is the cross-type reproduction loop elasticity. In all panels,  $P = 0.9$  and  $h = 0$ .