

Read me file for supplementary materials to paper “A matrix model for density-dependent selection in stage-classified populations, with application to pesticide resistance in *Tribolium*”

C. de Vries, R.A. Desharnais, H. Caswell

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1 Matlab files

1.1 Matlab_code_Figure1.m

Figure 1 in the main paper is created in this Matlab file by projecting the population vector using the *Tribolium* model described in section 3 of the main paper with the parameters listed in the caption of Figure 1. The code calls on a few functions, which are described below.

1.2 Matlab_code_Figure3.m

Figure 3 in the main paper is created in this Matlab file by projecting the population vector using the *Tribolium* model described in section 5 (and 3) of the main paper with the parameters listed in the caption of Figure 3. The code calls on a few functions, which are described below.

1.3 matrix_create_tribo.m

This MATLAB function creates the nonlinear genotype-specific matrices $\mathbf{U}_i(\tilde{\mathbf{n}})$, $\mathbf{F}_i(\tilde{\mathbf{n}})$. The function takes four arguments as input: the number of stages, ω , the number of genotypes, $g = 3$,

a vector of parameters, p , and the current population vector, $\tilde{\mathbf{n}}$. The function produces two cell arrays, F and U , as output such that $F\{1,i\} = \mathbf{F}_i$ and $U\{1,i\} = \mathbf{U}_i$.

1.4 `app_tribo_3.m` and `app_tribo_additive_alleles.m`

These two functions do not take any input variables. Instead they read the parameter values from the `tribo_xxx.m` files described below. They create a structure array with the initial conditions, and a vector of parameters:

- Figure 1 is created using `app_tribo_additive_alleles.m`, which sets each parameter for all 3 genotypes equal to the parameters reported in Table 1 in Dennis et al. (1995), except for the fecundity β , which is assigned as follows, $\beta_{AA} = 5.68$, $\beta_{Aa} = 8.68$, $\beta_{aa} = 11.68$.
- Figure 3 is created using `app_tribo_3.m`, which creates the vector of parameters measured in a laboratory experiment by Cheung (2002).

1.5 `tribo_chaosbook.m`, `tribo_RR_pooled.m`, `tribo_SS_3.m`

These three matlab files contain a list of parameter values and are used by the previous functions to assign parameter values to the genotypes.

- `tribo_chaosbook.m` contains the parameters used in Figure 1, from Table 1 in Dennis et al. (1995).
- `tribo_RR_pooled.m` contains demographic parameters for the resistant homozygote (rr) genotype and the heterozygote (due to complete dominance), used to create Figure 3.
- `tribo_SS_3.m` contains demographic parameters for the susceptible homozygote (ss) genotype, used to create Figure 3.

1.6 `vec.m`

MATLAB function which stacks the columns of an $m \times n$ matrix to create an $mn \times 1$ vector.

1.7 `vecperm.m`

MATLAB function that takes two arguments, (m, n) , and creates a vec-permutation matrix \mathbf{K}_{mn} of size $m \times n$.

References

- Cheung, W. (2002). The effects of natural selection on nonlinear population dynamics. Master's thesis, California State University.
- Dennis, B., Desharnais, R. A., Cushing, J., and Costantino, R. (1995). Nonlinear demographic dynamics: mathematical models, statistical methods, and biological experiments. *Ecological Monographs*, 65(3):261–282.