

## Text S1. Model of gene drive dynamics in seed banks.

This document presents a brief description of the model used in Box 1, simulating the dynamics of a gene drive in an annual plant population with a seed bank.

The model is restricted to a single locus with two alleles, a drive allele  $D$  and a wild-type allele  $d$ , and therefore ignores issues associated with resistant alleles. The model operates on discrete time  $t$  with annual time steps, tracking the age  $a$  of each seed cohort. The above ground population is reconstituted from the seed bank at each time step. The population size is fixed to a constant size.

### Model description

For each generation, new seeds  $S_{g,0}$  (genotype  $g$ , age 0) are produced from the previous generation's adult population  $X_g$ :

$$\begin{aligned} S_{DD,0}(t+1) &= c_{DD}X_{DD} \left( X_{DD} + \frac{1}{2} (1 + \epsilon_M) X_{Dd} \right) \\ &\quad + \frac{1}{2} (1 + \epsilon_F) c_{Dd}X_{Dd} \left( X_{DD} + \frac{1}{2} (1 + \epsilon_M) X_{Dd} \right) \\ S_{Dd,0}(t+1) &= c_{DD}X_{DD} \left( \frac{1}{2} (1 - \epsilon_M) X_{Dd} + X_{dd} \right) \\ &\quad + \frac{1}{2} (1 + \epsilon_F) c_{Dd}X_{Dd} \left( \frac{1}{2} (1 - \epsilon_M) X_{Dd} + X_{dd} \right) \\ &\quad + \frac{1}{2} (1 - \epsilon_F) c_{Dd}X_{Dd} \left( \frac{1}{2} (1 + \epsilon_M) X_{Dd} + X_{DD} \right) \\ &\quad + c_{dd}X_{dd} \left( X_{DD} + \frac{1}{2} (1 + \epsilon_M) X_{Dd} \right) \\ S_{dd,0}(t+1) &= \frac{1}{2} (1 - \epsilon_F) c_{Dd}X_{Dd} \left( \frac{1}{2} (1 - \epsilon_M) X_{Dd} + X_{dd} \right) \\ &\quad + c_{dd}X_{dd} \left( \frac{1}{2} (1 - \epsilon_M) X_{Dd} + X_{dd} \right) \end{aligned}$$

Older seeds (age  $a$ ) are calculated for each genotype  $g$  :

$$S_{g,a+1}(t+1) = (1 - \mu_{g,a}) (1 - b_{g,a}) S_{g,a}(t)$$

Finally the adult population is constituted from the germination of previous generation seeds (and normalised to a constant size):

$$X_g(t+1) = \sum_{a=0}^t b_{g,a} S_{g,a}(t)$$

## Parameters

$N$	Number of generations to run
$\mu$	Mortality rate of non-germinated seeds per generation (genotype-specific)
$c$	Plant fecundity (genotype-specific)
$\epsilon$	Drive conversion rate (sex-specific, $\epsilon_M$ and $\epsilon_F$ resp.)
$b$	Germination rate (genoytpe- and age-specific)

For genotype  $g$  and age  $a$ ,  $b$  is calculated as:

$$b_{g,a} = \frac{\nu_g}{a^{m_g}}$$

with:

$\nu$	Baseline germination rate (genotype-specific)
$m$	Steepness of the seed bank germination profile (genotype-specific)

## Default values

Unless otherwise specified, the following default values are used (for all genotypes):

$$\mu = 0.1$$

$$c = 1$$

$$\epsilon = 0.9$$

$$\nu = 0.5$$

$$m = 0$$