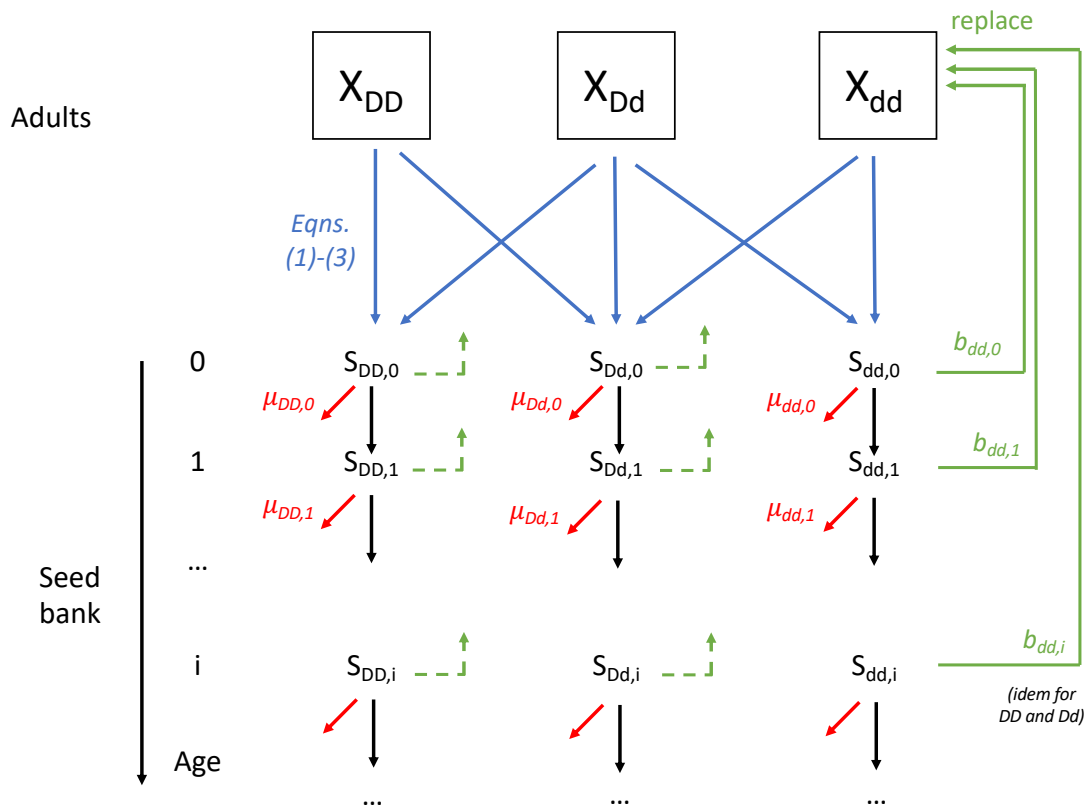# Text S1. Model of gene drive dynamics in seed banks.

This document presents a brief description of the model used in Box 1.

Model description

This model simulates the dynamics of an idealised annual plant population with a seed bank. The above-ground plant population is considered to be well-mixed, strictly outcrossing, is not age-structured, and is reconstituted every year from the germination of underground seeds. The seed population is tracked within the seed bank, and is therefore age-structured. Seeds of each age can germinate at a given rate b (and therefore be moved to the above-ground population), be removed at a given rate μ (representing dead or unviable seeds), and otherwise

are moved to the next age category every year. All associated parameters are described below.

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. Each age and stage compartment is therefore split in 3 genotypes: DD, Dd and dd. The model operates on discrete time t with annual time steps, tracking the age a of each seed cohort. Finally the above-ground population size is kept to a constant size, and therefore normalised at each time step.

The drive is defined here as a simple meiotic distorter, where heterozygotes Dd produce D gametes with a frequency of $\frac{1}{2}(1 + \epsilon)$ and d gametes with a frequency of $\frac{1}{2}(1 - \epsilon)$ (with $\epsilon \in [0, 1]$). Finally, each genotype g is associated with a fitness c_g expressed as the relative fecundity of adults of genotype g.

Model variables and parameters

$S_{g,a}$	Number of seeds of genotype g and age a
X_g	Number of above-ground plants of genotype g
N	Number of generations to run
μ	Mortality rate of non-germinated seeds per generation (genotype-specific)
c	Plant fecundity (genotype-specific)
ϵ	Drive conversion rate (sex-specific, ϵ_M and ϵ_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:

ν	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):

$$\mu = 0.1$$
$$c = 1$$
$$\epsilon = 0.9$$
$$\nu = 0.5$$
$$m = 0$$

Model equations

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

$$S_{DD,0}(t+1) = c_{DD}X_{DD}\left(X_{DD} + \frac{1}{2}\left(1 + \epsilon_M\right)X_{Dd}\right)$$
$$+ \frac{1}{2}\left(1 + \epsilon_F\right)c_{Dd}X_{Dd}\left(X_{DD} + \frac{1}{2}\left(1 + \epsilon_M\right)X_{Dd}\right)$$

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

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

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

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

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

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