1. The code ‘A\_PARAMETERS’ should be run first.
   1. Chose in the code the parameters for Survival and Fertility
   2. Chose the ‘vec.sigma’ table code corresponding to all the sigma(y1,y2,y3) for the chosen sociocultural scenario. Because it is a little time consuming to build, it is advised to store them.
2. Run the codes ‘B\_Fn\_AgeFather’, B\_Fn\_AgeMother’, ‘B\_Fn\_Salpha’ and ‘C\_Fn\_Unions’.
   1. These includes all the functions corresponding to equations in supplementary text, part I and III.
3. Run the code ‘D\_Population\_Dynamics\_Solver’
   1. It solves the corresponding Euler-Lotka equation and return population dynamics characteristics.
4. Function ‘E\_Fn\_W’ allow to calculate the selective values of carriers according to:
   1. A *Ld* vector of survival to the disease
   2. Whether the Mother, the Grandmother and the Father also carry the allele (TRUE or FALSE)
5. Code ‘F\_Calculations\_SelectionGradients\_FigMaintexte’ allows to calculate the selection coefficient presented in the figure 2A and 2B of the main texte.
6. Code ‘F\_Calculations\_BigGraph’ allows to reproduce supplementary figure 1
7. Code ‘F\_Calculations\_AdditionalRes’ allows to reproduce supplementary figures 2 and 3
8. Code ‘F\_Calculations\_DemoRegime’ allows to reproduce supplementary figure 4 (do not forget to chose parameters for Sweden into the ‘A\_parameters’ file.)

Code for calculating specific disease selection coefficients (figure 2C) is available on request.