

AGENE – a program to calculate N_e and N_b in age-structured populations

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AGENE is a Fortran95 program for PC platforms written by Chi Do and Robin Waples; it implements the analyses described in the following paper:

Waples, R.S., C. Do, and J. Chopelet. Calculating N_e and N_e/N in age-structured populations: a hybrid Felsenstein-Hill approach. Ecology (in press).

The notes below should allow you to run the program and generally understand the results.

To run, simply copy the .exe file to a suitable folder on your computer. It is not necessary to formally install it. The current version runs only on the PC platform. A command-line window will open when you double click the program and will prompt you for the name of an input file. This should be a simple text file and it is easiest if you put it in the same directory; otherwise, you need to specify a path. The program will also ask you for the name of an output file, which will show up in the same directory as the program.

That's it. The program will consider 3 separate scenarios: haploid, separate sexes, separate sexes with sex change. Sample input files are presented for each, and the program will automatically detect to which scenario the input file applies.

Input file specifications (use tabs or spaces to separate fields):

Line 1: The first line is free, so include comments or useful information here. This information will appear in the output.

Line 2:

Haploid model (see file 'haploid.txt' for example)

Requires 2 positive integers: MaxAge (age in years of oldest individuals), and N_I (number of newborns each year).

Two sexes, no sex change (see 'TwoSex.txt')

Requires 3 values: MaxAge, N_I , and the fraction of newborns that are male.

Two sexes with sex change (see 'SexChangeText')

Requires 3 entries: MaxAge, N_I , and designation of initial sex [either 'female' or 'male', without quotes!]. If the last entry is 'female', then sex change is from female to male; if the entry is 'male', sex change is male to female.

Lines 3 and beyond: each line is data for one age, up to MaxAge years. So, the total number of input lines for each population is 2+MaxAge.

Haploid model

The first column for each of these lines is the age, followed by age-specific survival rate (s_x), birth rate (b_x), and Poisson factor.

A sample line (for age 3) looks like this: 3 0.5 2 1

Two sexes, no sex change

As in haploid model, but vital rates for females are in columns 2-4 and for males in columns 5-7

A sample line (for age 2) looks like this: 2 0.6 2 1 0.5 2 1

Two sexes with sex change

As in standard two-sex model, but an additional column 8 specifies that desired fraction of the population at the specified age that is MALE.

A sample line (for age 2) looks like this: 2 0.6 2 1 0.5 2 1 0.55

Note: multiple files as described above can be stacked together into a single input file (see sample input file, "multi.txt")

Output

- $\sum xB_x/N_I$ for each sex is the sex-specific generation length
- Eq 2 refers to the Waples et al. in press paper and is the same as Equation 16 in Hill 1972
- Eq A1 refers to the Appendix of the Waples et al. in press paper and is the same as Equation 17 in Hill 1972

Caveats and constraints:

- 1) MaxAge should be a positive integer. It can be arbitrarily large, although realistic scenarios where MaxAge $> 10^2$ will be rare.
- 2) Age-specific survival rate (s_x) takes values in the range 0-1 and should be 0 for age = MaxAge (all individuals are expected to die after reaching MaxAge).
- 3) Age-specific birth rates (b_x) are automatically scaled to produce a constant population size. Therefore, it is only necessary to input relative fecundities for each age. The scaled fecundities (b'_x) are shown in the output file.
- 4) In theory, the size of the newborn cohort (N_I) can be arbitrarily large. However, since the output file is formatted to fit within a page width of 78 characters, using $N_I \geq 10^7$ will cause formatting problems with the output. Since N_e/N and N_b/N do not depend on N_I (because N_e and N_b are simple linear functions of N_I), very large populations could be modeled by using a smaller N_I and scaling the results up linearly.
- 5) The Poisson factor should be non-negative (it can be 0, in which case there is no variance in the number of newborns produced by same-age individuals). The program has the capability to allow the Poisson factor to vary by age (within each sex independently). However, the expressions for the variance and covariance terms for different gametic pathways in the Appendix of Waples et al. (in press) assume a constant Poisson factor. Therefore, if the Poisson factor varies among ages within a sex or between sexes, N_e is calculated only for Equation 2 in the main text.
- 6) In the change-sex option, it is assumed that sex change can only occur in one direction (as stipulated by the last entry on line 2). The program will terminate and return an error message if either of two conditions arises:
 - a. If specified values for the age-specific sex ratio (column 8 of the input file) are impossible to achieve (for example, if achieving the specified sex ratio would require sex change in the opposite direction to that allowed).

- b. If achieving the specified sex ratio requires zero individuals to change sex at any age. In this case, some of the potential sex-change pathways have zero individuals, which causes division by zero.

Hill, W.G., 1972. Effective size of population with overlapping generations. *Theoretical Population Biology* **3**:278–289.

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