

Notes on **DriftAgeStruct**: An R Script to perform drift simulations in age-structured populations.

Andrew D.J. Overall

School of Pharmacy & Biomolecular Sciences, University of Brighton, BN2 4GJ, UK

1 Instructions

DriftAgeStruct is an R script that performs drift simulations for age-structured populations following the method outlined in Overall & Faragher (2019). Example input files are provided (e.g., **US_females.txt**). To run this script, copy into the working directory containing your input files and type

```
> source("DriftAgeStruct.r")
```

Once the script has been copied into the working directory of R the **leslie.drift** function can be called:

```
leslie.drift = function(infile,B,N,T,iteration,initial,s)
```

Arguments:

infile is the input file consisting of three columns of data: Age, l_x and m_x .

B is the starting frequency of the mutation.

N is the population size.

T is the number of generations the simulation runs for.

iteration is the number of simulation repeats.

initial is the number of iterations of the leslie matrix run to stabilise.

s is the selection coefficient.

Example of use:

```
> leslie.drift(infile="datafile.txt",B=0.5,N=1000,T=1000,iteration=1000,initial=100,s=0.005)
```

A line plot is generated (an example output file is provided (`Output of DriftAgeStruct Figure 4.txt`, which is that presented in Overall & Faragher, (2019)) and the allele B frequencies at each time point are printed (`mean.HET`). The allele B frequencies at the final time point are also printed (`het.DIST`), which can be used to create boxplots as in the manuscript (Overall & Faragher, 2019).

2 References

Overall ADJ and Faragher RGA. Population type influences the rate of ageing. Heredity (in press).