

README file

This file follows the structure of the code checklist.

Source codes: Figs1-3-4-5-inland.F90, Figs1-3-sea.F90, Fig_S1a-inland.F90, Fig_S1a-sea.F90. These 4 codes are available at <https://doi.org/10.5281/zenodo.11099073>

Small (simulated or real) dataset to demo the software/code: Not needed because these codes do not use any dataset.

1. System requirements

Operating Systems: We run these codes using Fortran 90 (Fortran PowerStation 4.0) and Windows 10.

Versions the software has been tested on: please see the previous line.

Any required non-standard software: not required.

2. Installation guide

Instructions: (1) Open one of the 4 source codes above (file *.F90); (2) Build Compile *.F90; (3) Build Build *.exe; (4) Build Execute *.exe.

Typical install time on a "normal" desktop computer: less than 10 seconds.

3. Demo

Instructions to run on data: Not needed because these codes do not use any data.

Expected output: For codes Figs1-3-4-5-inland.F90 and Fig_S1a-inland.F90, files Archaeological_Time_Land_Model.dat and Fraction_Land_Model.dat. For codes Figs1-3-sea.F90 and Fig_S1a-sea.F90, files Archaeological_Time_Sea_Model.dat and Fraction_Sea_Model.dat. These files can be opened with WordPad. They can be also imported with any graphics program to prepare the corresponding figures (we used Origin 2023).

Expected run time for demo on a "normal" desktop computer: 15 seconds.

4. Instructions for use

How to run the software on your data: (1) Open one of the 4 source codes above (file *.F90); (2) Build Compile *.F90; (3) Build Build *.exe; (4) Build Execute *.exe.

Reproduction instructions: Two runs of the same code will not yield exactly the same results for the genetic output because the program is stochastic (see Supp. Methods, Sec. S2-D) but the differences are negligible (below 0.1% frequency of haplogroup K).