

Supplementary Material

Table S1. List of computer software referred to in Table 2 of the main text. This is intended only as an example of some of the analytical methods that can be used in a complementary manner for phylogeographic inference. All of the software listed here is freely-available.

Software	Website	Reference(s)
ARLEQUIN	http://cmpg.unibe.ch/software/arlequin3/	[1]
AUGIST	http://www.lycaenid.org/augist/	[2]
BAYESASS	http://sites.google.com/site/rannalaorg/software	[3]
BARRIER	http://www.mnhn.fr/mnhn/ecoanthropologie/software/barrier.html	[4]
BEAST	http://beast.bio.ed.ac.uk/	[5]
BEST	http://www.stat.osu.edu/~dkp/BEST/	[6,7]
BOTTLENECK	http://www1.montpellier.inra.fr/URLB/bottleneck/bottleneck.html	[8]
DNASP	http://www.ub.es/dnasp/	[9]
FLUCTUATE	http://evolution.gs.washington.edu/lamarc/lamarc_prog.html	[10,11]
FSTAT	http://www2.unil.ch/popgen/softwares/fstat.htm	[12]
GARLI	https://www.nescent.org/wg_garli/	[13]
GENALEX	http://www.anu.edu.au/BoZo/GenALEX/	[14]
GENECLASS	http://www1.montpellier.inra.fr/URLB/index.html	[15]
GENELAND	http://www2.imm.dtu.dk/~gigu/Geneland/	[16,17]
GENEPOP	http://genepop.curtin.edu.au/	[18]
GENETICSTUDIO	http://dyerlab.bio.vcu.edu/software/geneticstudio.html	[19]
GEODIS	http://darwin.uvigo.es/software/geodis.html	[20]
IBDWS	http://ibdws.sdsu.edu/~ibdws/	[21]
IM	http://genfaculty.rutgers.edu/hey/software	[22,23]
KINGROUP	http://code.google.com/p/kingroup/	[24]
LDNE	http://fish.washington.edu/xfer/LDNE/	[25]
MIGRATE	http://popgen.sc.fsu.edu/Migrate-n.html	[26,27]
MR BAYES	http://mrbayes.csit.fsu.edu/	[28]
MSVAR	http://www.rubic.rdg.ac.uk/~mab/software.html	[29]
ONESAMP	http://genomics.jun.alaska.edu/asp/Default.aspx	[30]
PHYLIP	http://evolution.genetics.washington.edu/phylip/software.html	[31]
R8S	http://loco.biosci.arizona.edu/r8s/	[32]
SAMOVA	http://cmpg.unibe.ch/software/samova/	[33]
STRUCTURE	http://pritch.bsd.uchicago.edu/structure.html	[34]
TCS	http://darwin.uvigo.es/software/tcs.html	[35]

Supplementary References

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