run-file notes

1.VitiLevuEBSP\_popMCMC.xml

Heated BEAST2 run-file for Viti Levu population EBSP (Fig. 3a).

2.KadavuEBSP\_pop.xml

Not heated BEAST2 run-file for Kadavu population EBSP (Fig. 3a).

3.fjLD2\_SNP\_EBSP.xml

Not heated BEAST2 run-file for the Viti Levu population single nucleotide polymorphism data with a linkage filtering value of 0.2 (Fig. 4a-c).

4.fjLD7\_SNP\_EBSP.xml

Not heated BEAST2 run-file for the Viti Levu population single nucleotide polymorphism data with a linkage filtering value of 0.7 (Fig. 4d-f).

5.fjLD9\_SNP\_EBSP.xml

Not heated BEAST2 run-file for the Viti Levu population single nucleotide polymorphism data with a linkage filtering value of 0.9 (Fig. 4g-i).

7.fjRm\_Secondaries\_SNP\_EBSP.xml

Not heated BEAST2 run-file for the Viti Levu population single nucleotide polymorphism data with no linkage filtering and with secondaries removed from the dataset (Fig. 4j-l).

6.fjW\_secondaries\_SNP\_EBSP.xml

Heated BEAST2 run-file for the Viti Levu population single nucleotide polymorphism data with no linkage filtering and with secondaries still in the dataset (Fig. 4m-n).

8.1.fjLD7\_ExpConst.xml, 8.2.fjLD7\_ExpNeg.xml, and 8.3.fjLD7\_ExpPos.xml

Viti Levu nested sampling BEAST run-files using SNP data for constant, exponential negative, and exponential positive, respectively (Appendix).

9.1.Kadavu\_constant.xml, 9.2.Kadavu\_ExpNeg.xml, and 9.2.Kadavu\_Exp.xml

Kadavu nested sampling BEAST run-files using COI data for constant, exponential negative, and exponential positive, respectively (Appendix).

10.1.Viti\_Levu\_Constant.xml, 10.2.Viti\_Levu\_ExpNeg.xml, and 10.3Viti\_Levu\_Exp\_growthChanged.xml

Viti Levu nested sampling BEAST run-files using COI data for constant, exponential negative, and exponential positive, respectively (Appendix).

11.Hfijiensis\_DIYABC-RF\_files.zip

The files associated with the DIYABC-RF run, including outputs and figures (Appendix).

12.AI\_infer\_outgrou\_heated.xml

Heated EBSP run using all islands to reconstruct ancestral geographic states with COI data (Fig. S4).

13.BEAST2\_outputs.zip

Output files from BEAST2 runs.

Tweet:

Past population sizes, inferred using molecular data, of a native Fijian bee finds positive impacts of early human habitation on the lowland species, *Homalictus fijiensis*.