

The population history of Central Europe in the Early Bronze Age (2200/2100–1600/1500 BC) - A craniometric approach

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Figure S1. Model 1 –Only geographic distance was considered in this model, and distance was represented as distance-based MEMs (db-MEMs) without consideration for spatial topography.

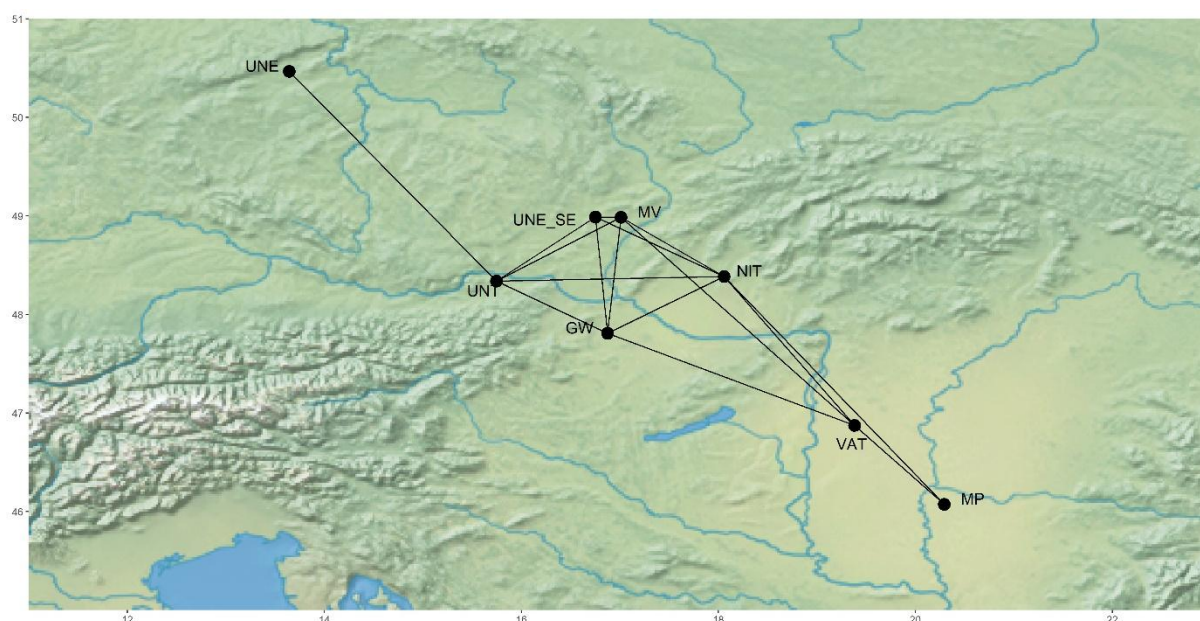


Figure S2. Model 2 – The Danube hinders the geneflow of the adjacent regions thus, only groups located on the same side of the Danube were considered neighbours.

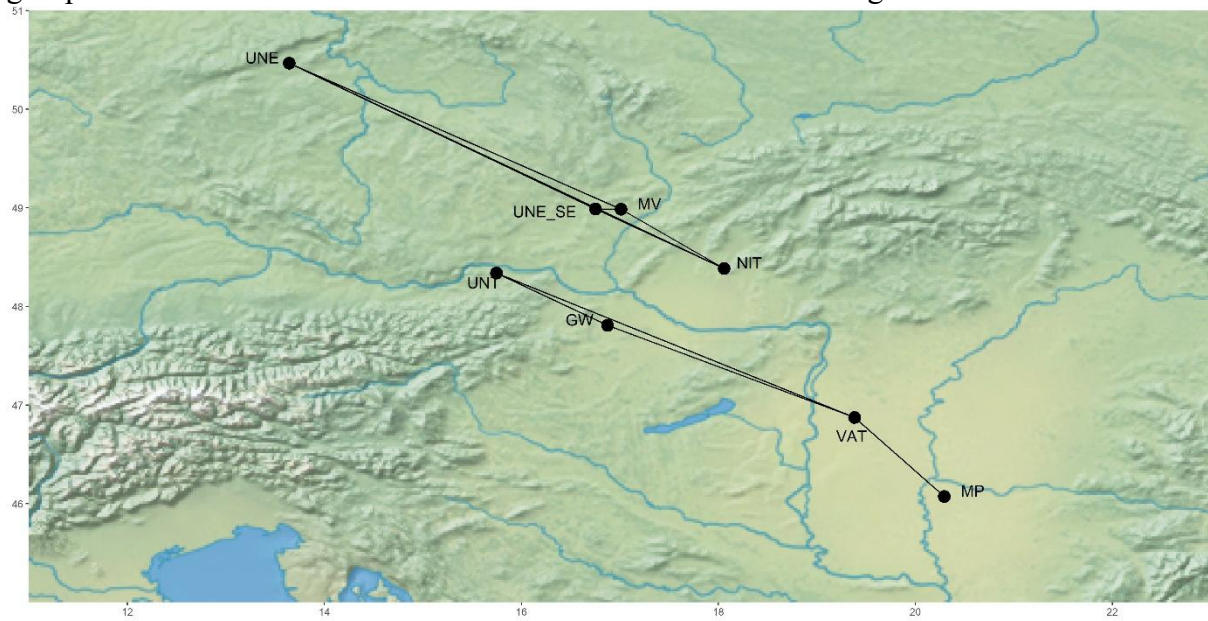


Figure S3. Model 3 – The NW Section of the Danube facilitates gene flow, while the M and SE sections operate as a boundary.

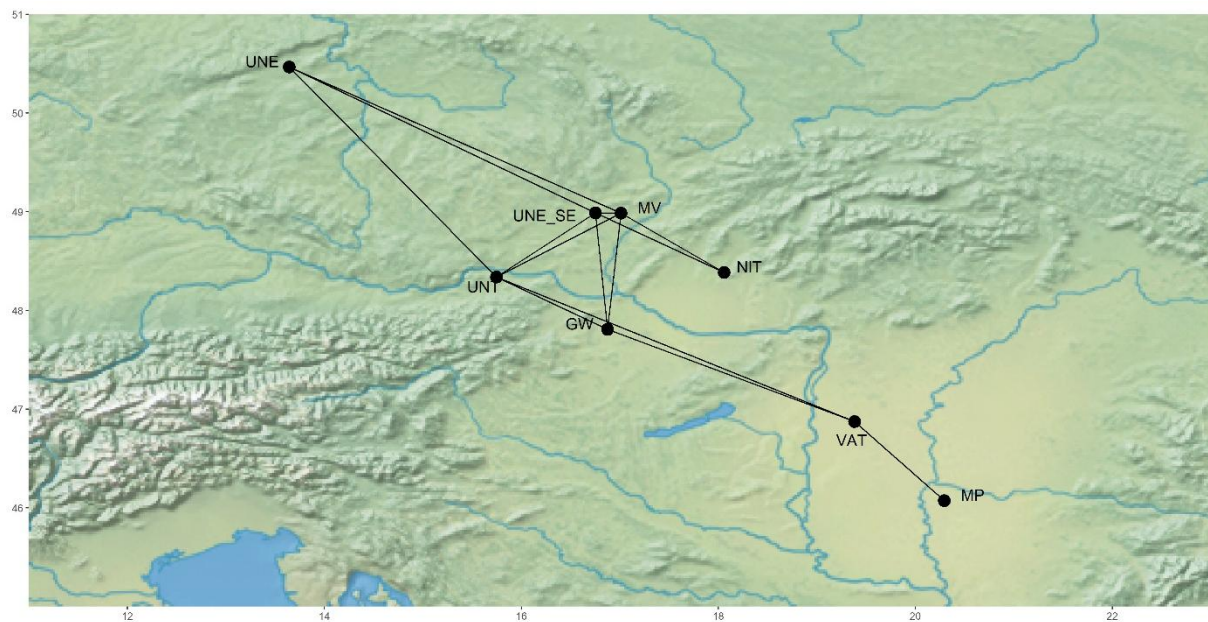


Figure S4. Model 4 – The M section of the Danube promotes the gene flow while the NW and SE sections act as a boundary.

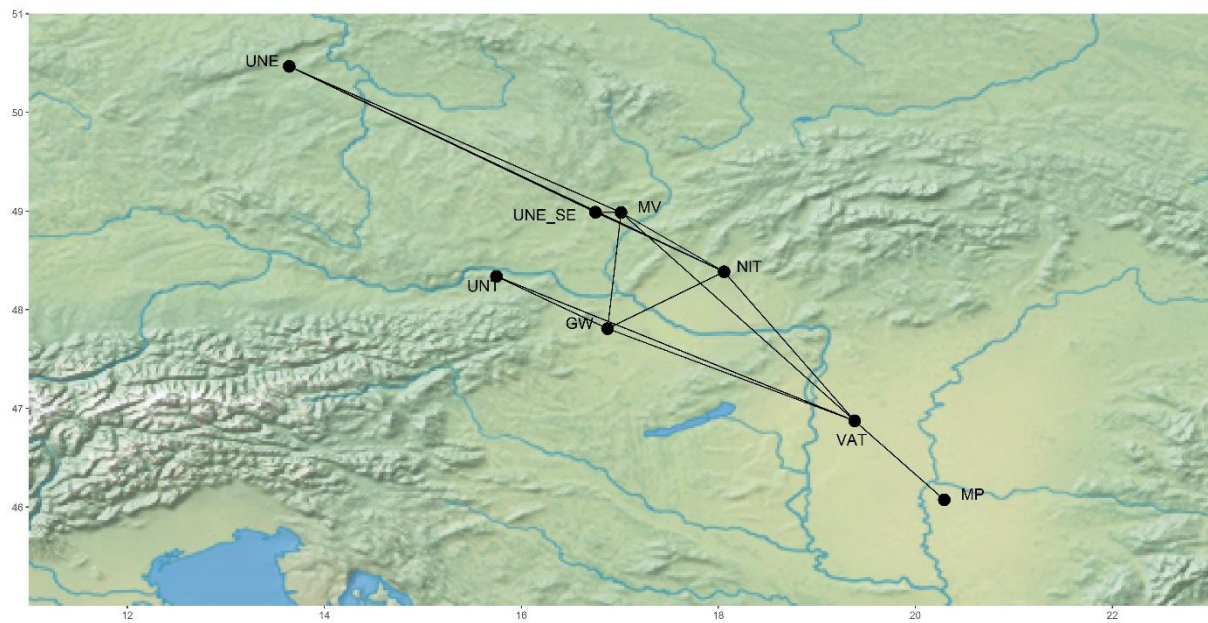


Figure S5. Model 5 – The SE Section of the Danube promotes gene flow, while the NW and M restrict it.

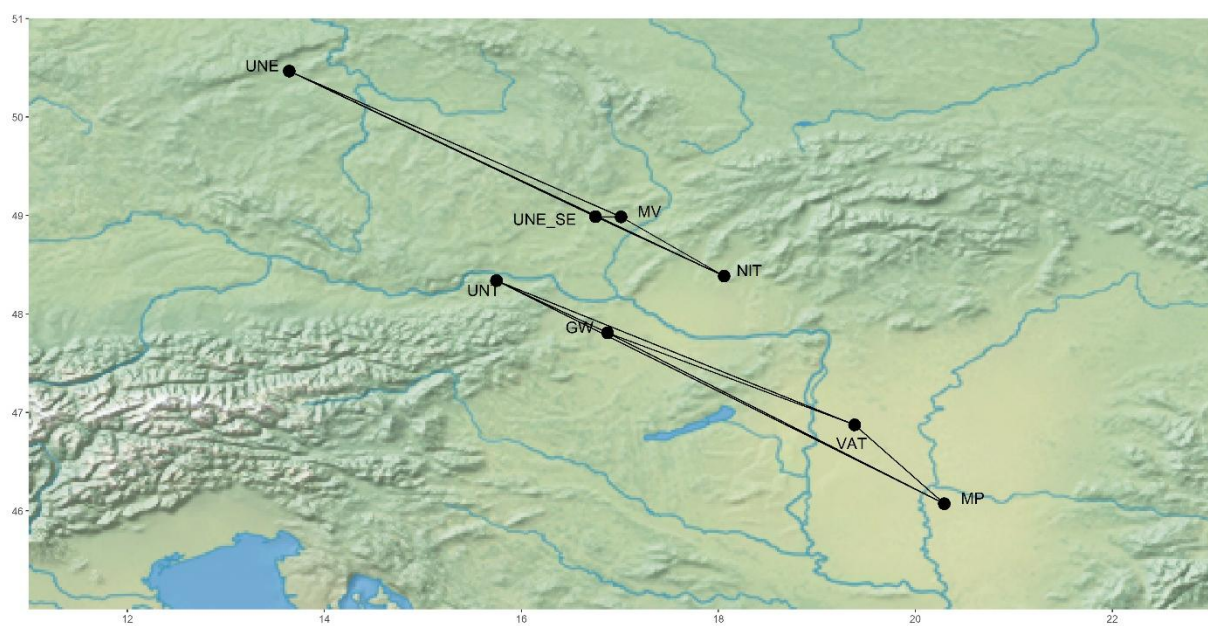


Figure S6. Model 6 – The NW and M sections of the Danube facilitate geneflow between the adjacent territories, while the SE parts operate as a barrier.

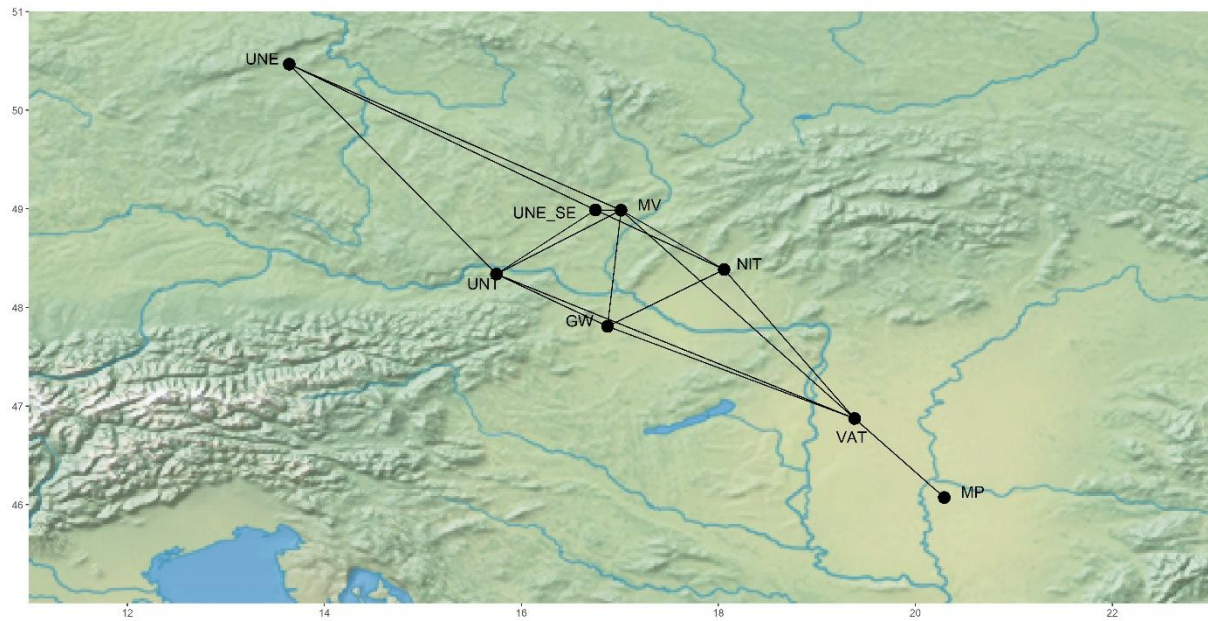


Figure S7. Model 7 – Along the NW and SE sections of the Danube geneflow is promoted, while the M section acts as a barrier.

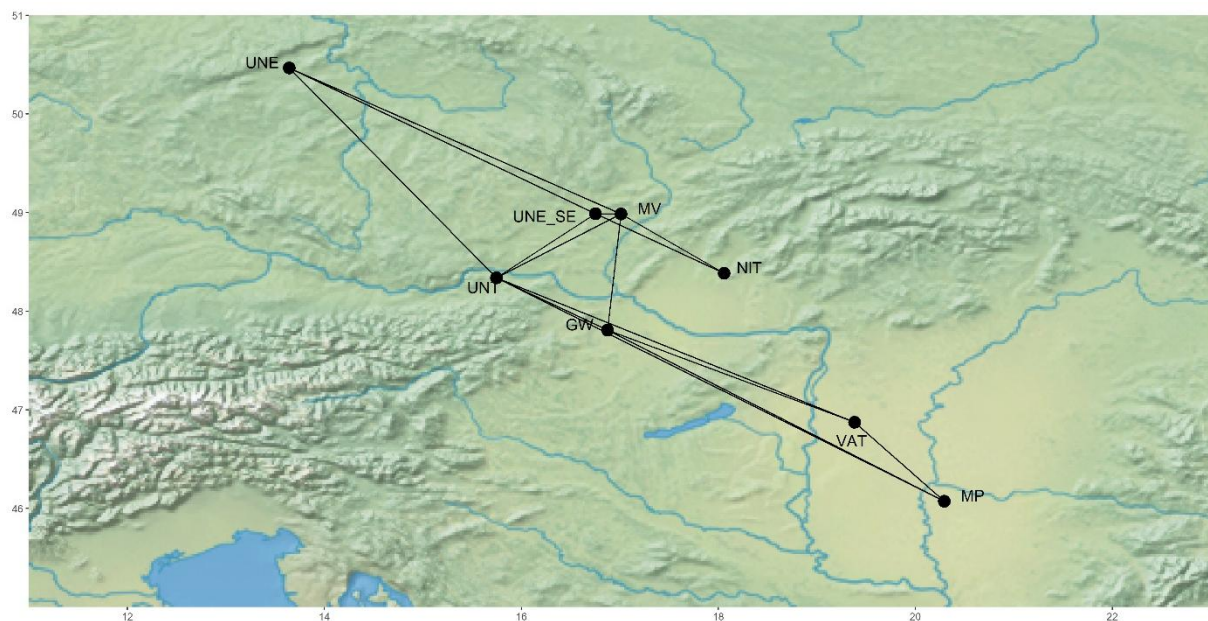


Figure S8. Model 8 – Geneflow is promoted along the M and SE sections of the Danube, while the NW sections function as a barrier

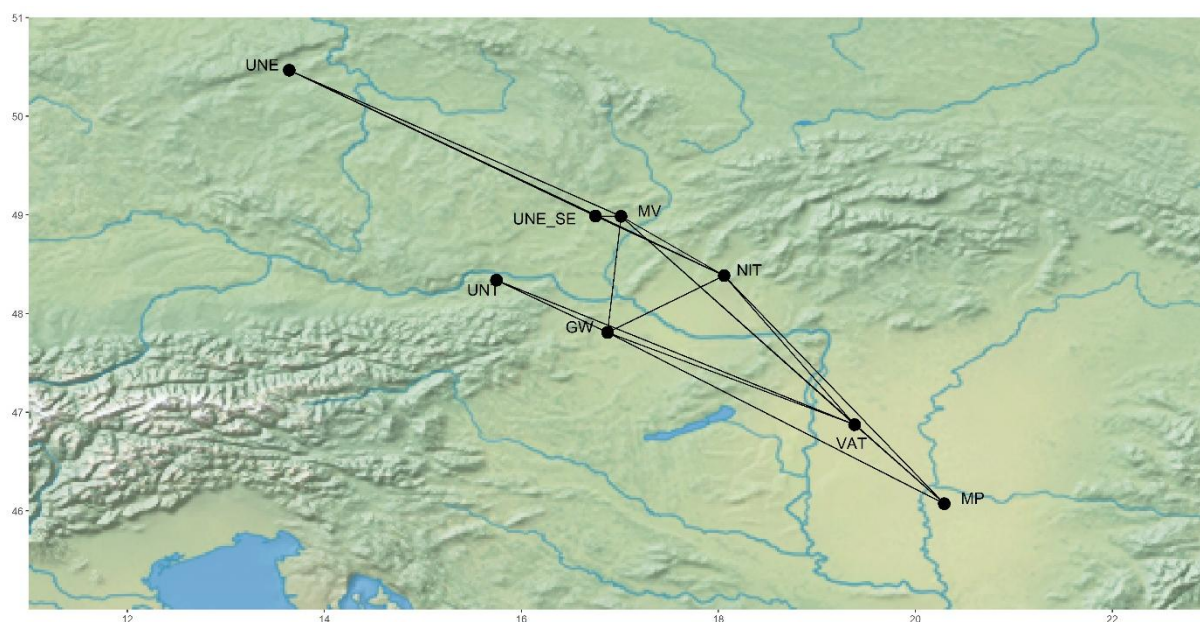


Figure S9. Boxplots for the pairwise biological distances between EBA groups and BBE based on the bootstrapped samples. D2: phenotypic distance. Culture: population sample associated to archaeological culture; see Table 1 of main text for abbreviations.

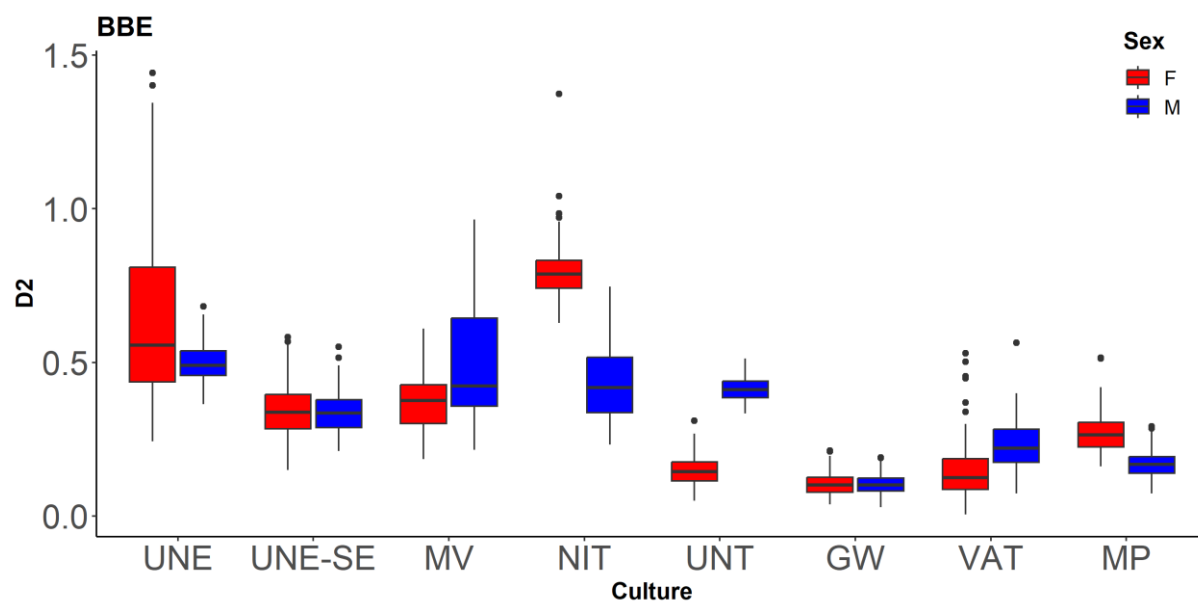


Figure S10. Boxplots for the pairwise biological distances between EBA groups and BBM based on the bootstrapped samples. D2: phenotypic distance. Culture: population sample associated to archaeological culture; see Table 1 of main text for abbreviations.

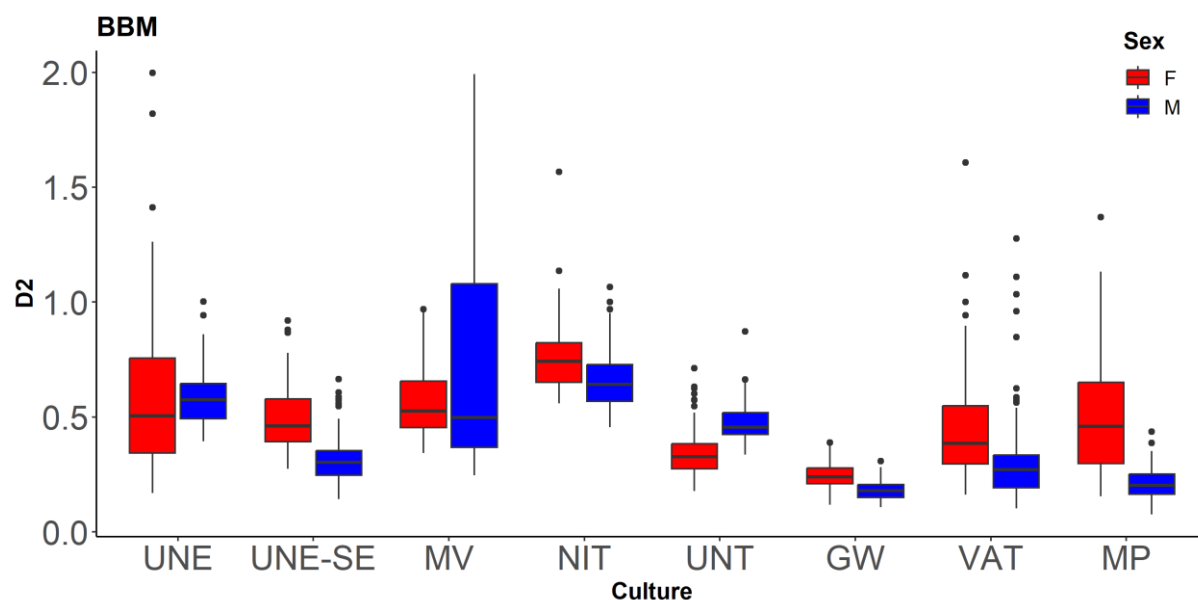


Figure S11. Boxplots for the pairwise biological distances between EBA groups and CW based on the bootstrapped samples. D2: phenotypic distance. Culture: population sample associated to archaeological culture; see Table 1 of main text for abbreviations.

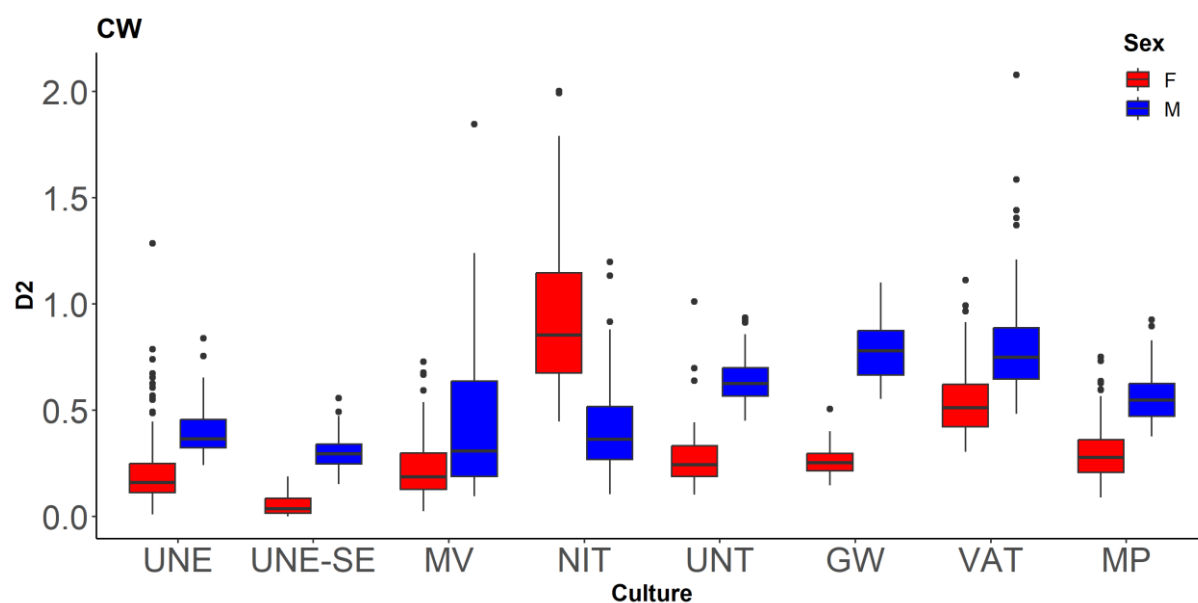


Figure S12. Boxplots for the pairwise biological distances between EBA groups and EM based on the bootstrapped samples. D2: phenotypic distance. Culture: population sample associated to archaeological culture; see Table 1 of main text for abbreviations.

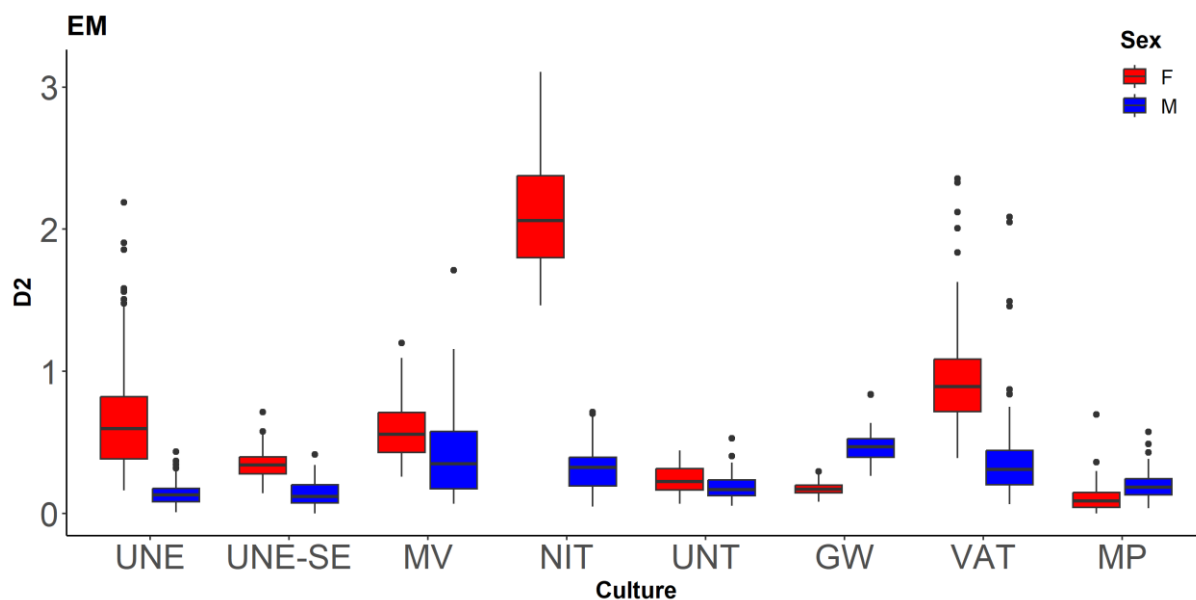


Figure S13. The mean and 95% CI of the degree centrality values of the EBA cultures separately for females (F) and males (M) based on the bootstrapped samples. X axis: mean degree centrality, which is the number of edges that connect to a population node; Y axis: population sample associated to archaeological culture; see Table 1 of main text for abbreviations.

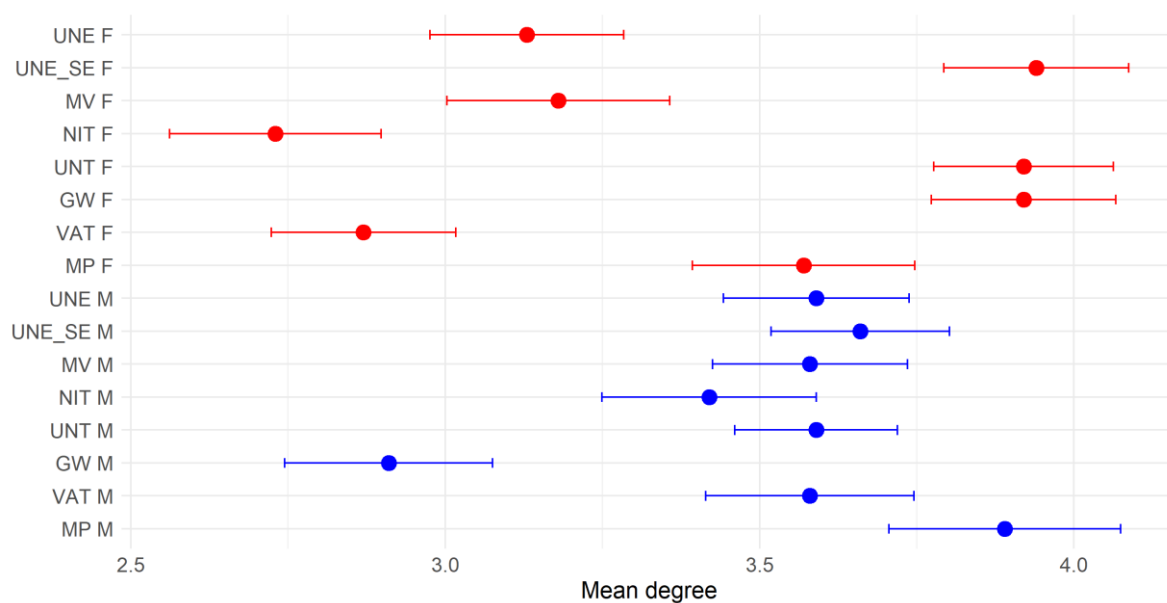


Figure S14. The mean and 95% CI of the closeness centrality values of the EBA cultures separately for females (F) and males (M) based on the bootstrapped samples. X axis: mean closeness, which is calculated as the inverse of the average shortest distance from a given node to all other reachable nodes in a network; Y axis: population sample associated to archaeological culture; see Table 1 of main text for abbreviations.

