

cross-country variation in development, inequality, or institutions, pointing towards an important direction for future research.

While various preferences exhibit economic and geographic patterns, preferences may also be correlated amongst each other, giving rise to country-level preference profiles. To investigate the relationship among different preferences, Table 3 shows Pearson correlations of preferences together with levels of significance.¹⁴ The significant correlations indicate that preferences are not distributed independently of one another. One set of traits that goes together is risk tolerance and patience, as shown by the positive and statistically significant correlation at the country level. This is in spite of the special case of Sub-Saharan African countries, which tend to be risk seeking and impatient, as discussed above.¹⁵ Another grouping of positively correlated traits involves prosociality, i.e., the traits of positive reciprocity, altruism and trust. While trust constitutes a belief rather than a preference, all of these traits share in common that they describe positive behavioral dispositions towards others. The correlation between altruism and positive reciprocity is particularly high, and trust also tends to be higher where people are positively reciprocal. This is intuitive as it is hard to imagine stable and high levels of trust in environments absent positive reciprocity, i.e., trust rewarding behaviors.¹⁶ Despite being related to the social domain, negative reciprocity is not at all correlated with prosociality. We report the correlation structure among preferences at the individual level in Appendix B.

Evidence that preference dispositions vary substantially across countries does not imply that cross-country or cultural differences are the primary source of preference

Table 3: Pairwise correlations between preferences at country level

	Patience	Risk taking	Pos. reciprocity	Neg. reciprocity	Altruism	Trust
Patience	1					
Risk taking	0.231**	1				
Positive reciprocity	0.0202	-0.256**	1			
Negative reciprocity	0.262**	0.193*	-0.154	1		
Altruism	-0.00691	-0.0155	0.711***	-0.132	1	
Trust	0.186	-0.0613	0.363***	0.160	0.272**	1

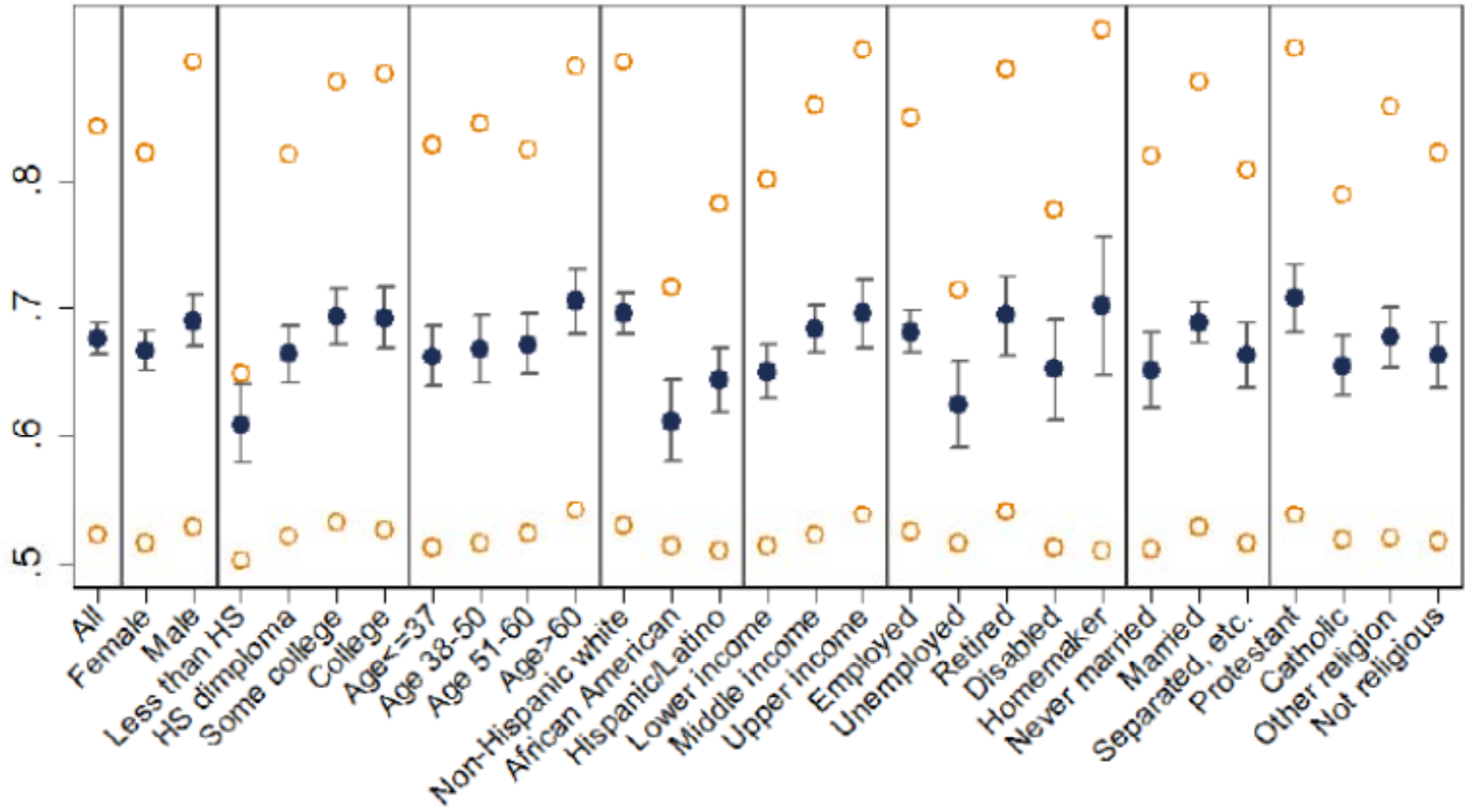
Notes. Pairwise Pearson correlations between average preferences at country level. * $p < 0.10$, ** $p < 0.05$, *** $p < 0.01$.

¹⁴The results are similar when computing Spearman correlations.

¹⁵Excluding African countries, the positive correlation between risk taking and patience increases to 0.30, while other correlations remain largely the same. The correlation between the staircase risk and patience items is 0.19, while that between the two qualitative risk and patience items is 0.55.

¹⁶Given that our survey item for trust measures only the belief-component of trust (as opposed to first-mover behavior in trust games, which is also affected by risk preferences), the low correlation between trust and risk taking is consistent with previous within-country findings.

The mean estimated fair-mindedness by sub-group



The median estimated equality-efficiency tradeoff by sub-group

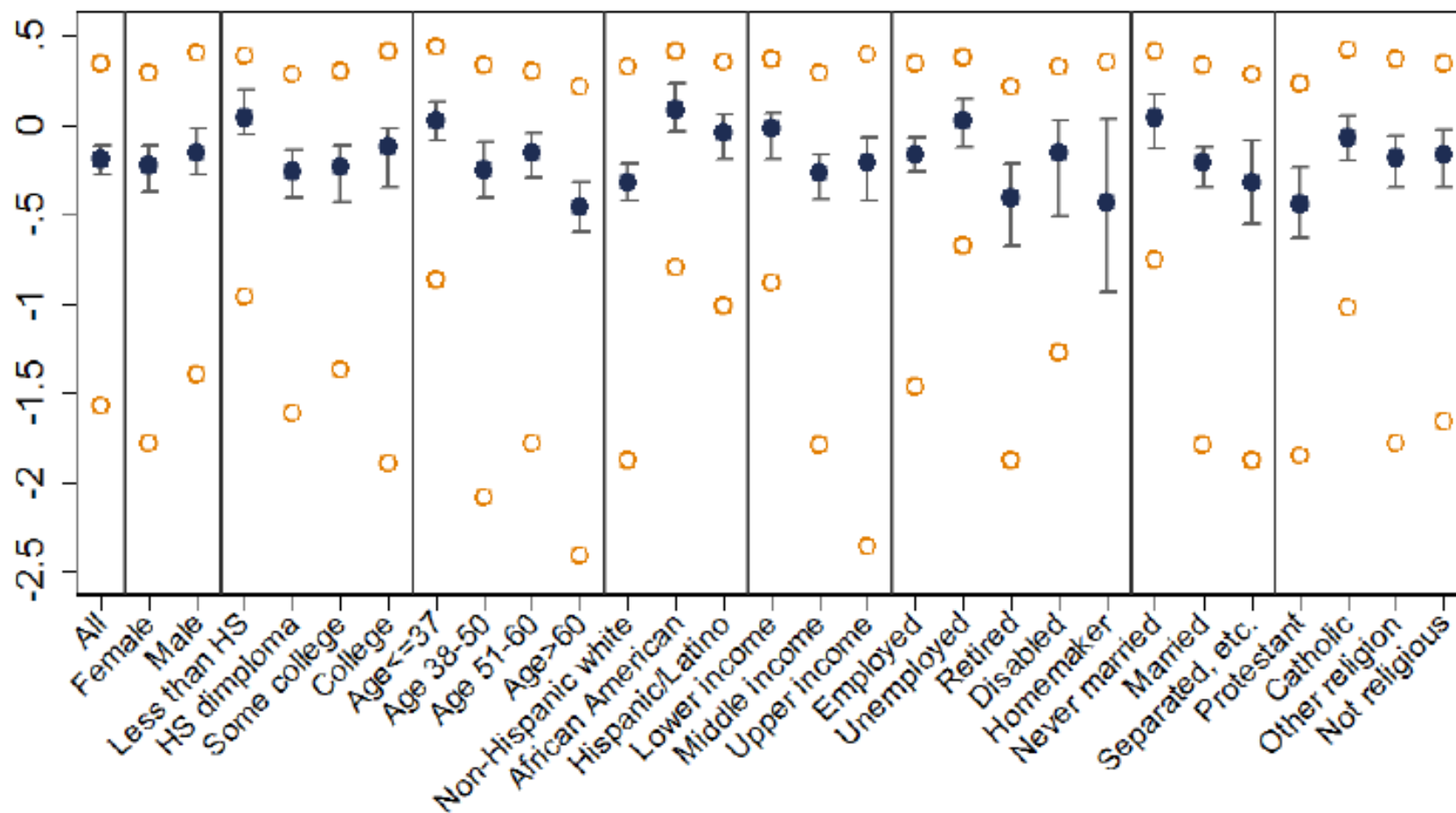


Table 1 – Joint Significance of Ethnolinguistic Dummies in Questions from the World Values / European Values Integrated Surveys, by Region

	# of regressions	Share of regressions w/ jointly significant ethnic dummies	R ² without ethnic dummies	R ² with ethnic dummies	ΔR ²
Whole Sample	21,469	0.430	2.688	4.074	1.386
Africa	3,623	0.548	2.468	4.064	1.597
<i>Of which: Sub-Saharan Africa</i>	2,724	0.616	2.369	4.274	1.905
<i>Of which: North Africa</i>	899	0.344	2.766	3.430	0.663
Europe	7,769	0.373	3.045	4.144	1.099
<i>Of which: Western and Southern Europe</i>	2,369	0.313	3.567	4.399	0.832
<i>Of which: Eastern and Central Europe</i>	5,400	0.399	2.816	4.032	1.215
Asia	5,656	0.571	2.360	4.519	2.159
<i>Of which: East and Southeast Asia</i>	2,090	0.626	2.161	4.614	2.452
<i>Of which: South Asia</i>	852	0.667	2.899	6.363	3.463
<i>Of which: Southwestern and Central Asia</i>	1,511	0.479	2.223	3.391	1.168
<i>Of which: Middle East</i>	1,203	0.525	2.494	4.464	1.971
America	3,749	0.235	2.480	3.188	0.708
<i>Of which: North America</i>	741	0.513	3.157	4.075	0.918
<i>Of which: Latin America and Caribbean</i>	3,008	0.166	2.313	2.970	0.656
Oceania	672	0.342	3.669	4.509	0.840

Note: North America is defined here as Canada and the US. Mexico is included with Latin America and the Caribbean. R² is expressed in % terms.

Table 2 - Joint Significance of Ethnolinguistic Dummies in Questions from the World Values / European Values Integrated Surveys, by Question Category and Question Type

	# of regressions	Share of regressions with jointly significant ethnic dummies	R ² without ethnic dummies	R ² with ethnic dummies	ΔR ²
Breakdown by Question Category					
A: Perceptions of Life	4,382	0.425	3.270	4.618	1.347
B: Environment	971	0.427	2.185	3.640	1.454
C: Work	2,409	0.398	2.404	3.546	1.143
D: Family	1,319	0.445	3.240	4.599	1.359
E: Politics and Society	9,046	0.409	2.407	3.717	1.310
F: Religion and Morals	2,316	0.516	3.268	5.043	1.775
G: National Identity	1,026	0.495	1.801	3.682	1.881
Breakdown by Question Type					
Binary questions	4,551	0.426	2.854	4.248	1.394
Binary from unordered response questions	7,029	0.362	1.616	2.707	1.091
Scale questions	9,889	0.479	3.373	4.965	1.592

Note: This result does not change if you break it down by continent: there is little difference in shares of questions with significant ethnolinguistic dummies when the breakdown by category is done continent by continent. R² is expressed in % terms.



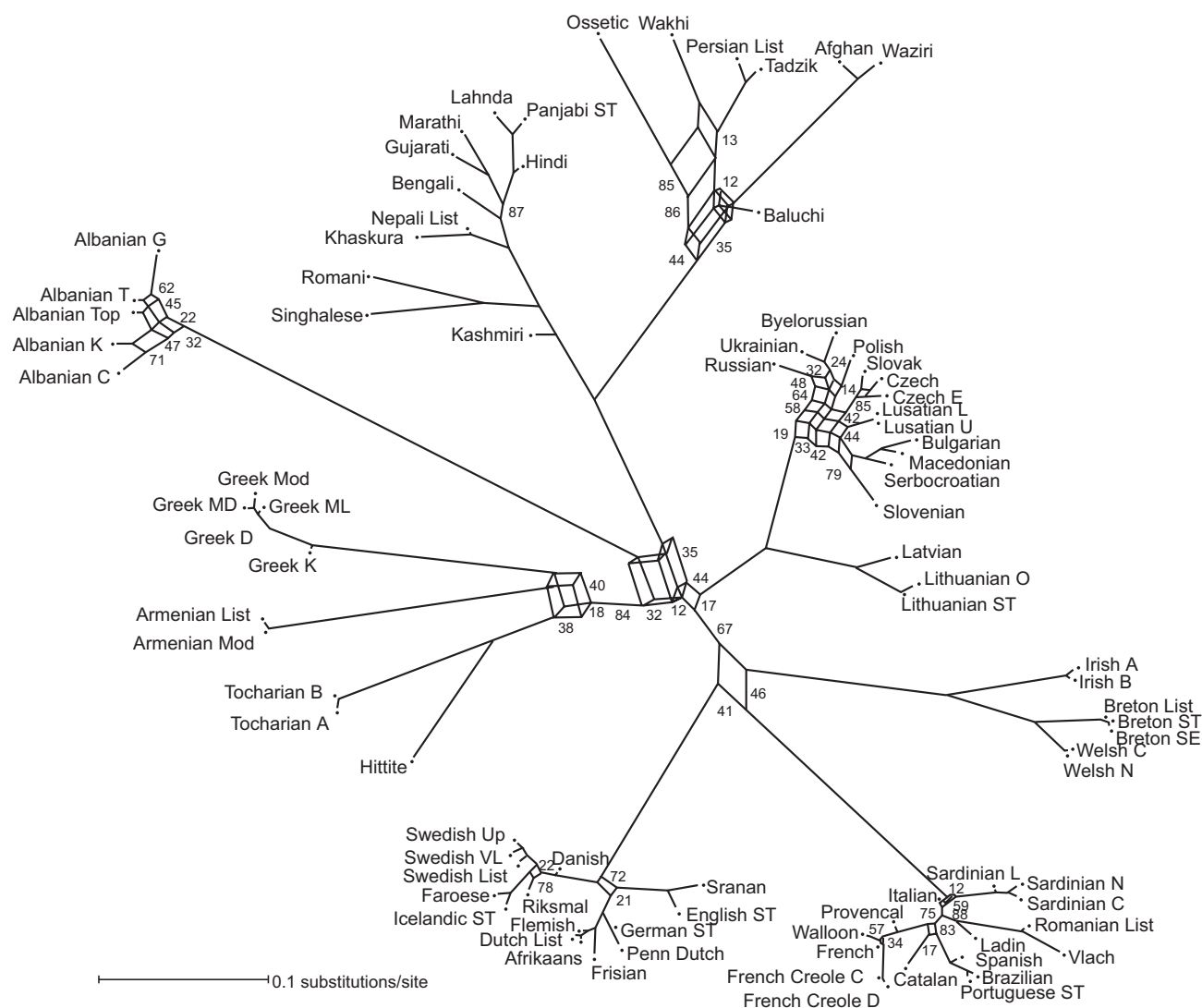


Figure 8.6. Consensus network from the Bayesian MCMC sample of trees. Values express the posterior probability of each split (values above 90 per cent are not indicated). A threshold of 10 per cent was used to draw this splits graph — i.e. only those splits occurring in at least 10 per cent of the observed trees are shown in the graph. Branch lengths represent the median number of reconstructed substitutions per site across the sample distribution.

depicting uncertainty in the reconstructed relationships. These graphs are, however, just useful pictorial summaries of the analysis. The fundamental output of the analysis is the distribution of trees.

The consensus network from a Bayesian sample distribution of 100 trees is shown in Figure 8.6. The values next to splits give an indication of the uncertainty associated with each split (the posterior probability, derived from the percentage of trees in the Bayesian distribution that contain the split). For example, the value 41 next to the parallel lines separating Italic and Celtic from the of the Indo-European sub-families indicates that that split was present in 41 per cent of

the trees in the sample distribution. Similarly, the split grouping Italic and Germanic languages was present in 46 per cent of the sample distribution.

7. Rate variation and estimating dates

There are at least two types of rate variation in lexical evolution. First, rate variation can occur between cognates. For example, even in the Swadesh word list, the Indo-European word for *five* is highly conserved (1 cognate set) whilst the word for *dirty* is highly variable (27 cognate sets). This is akin to site-specific rate variation in biology. Biologists can account for

How Old is the Indo-European Language Family?

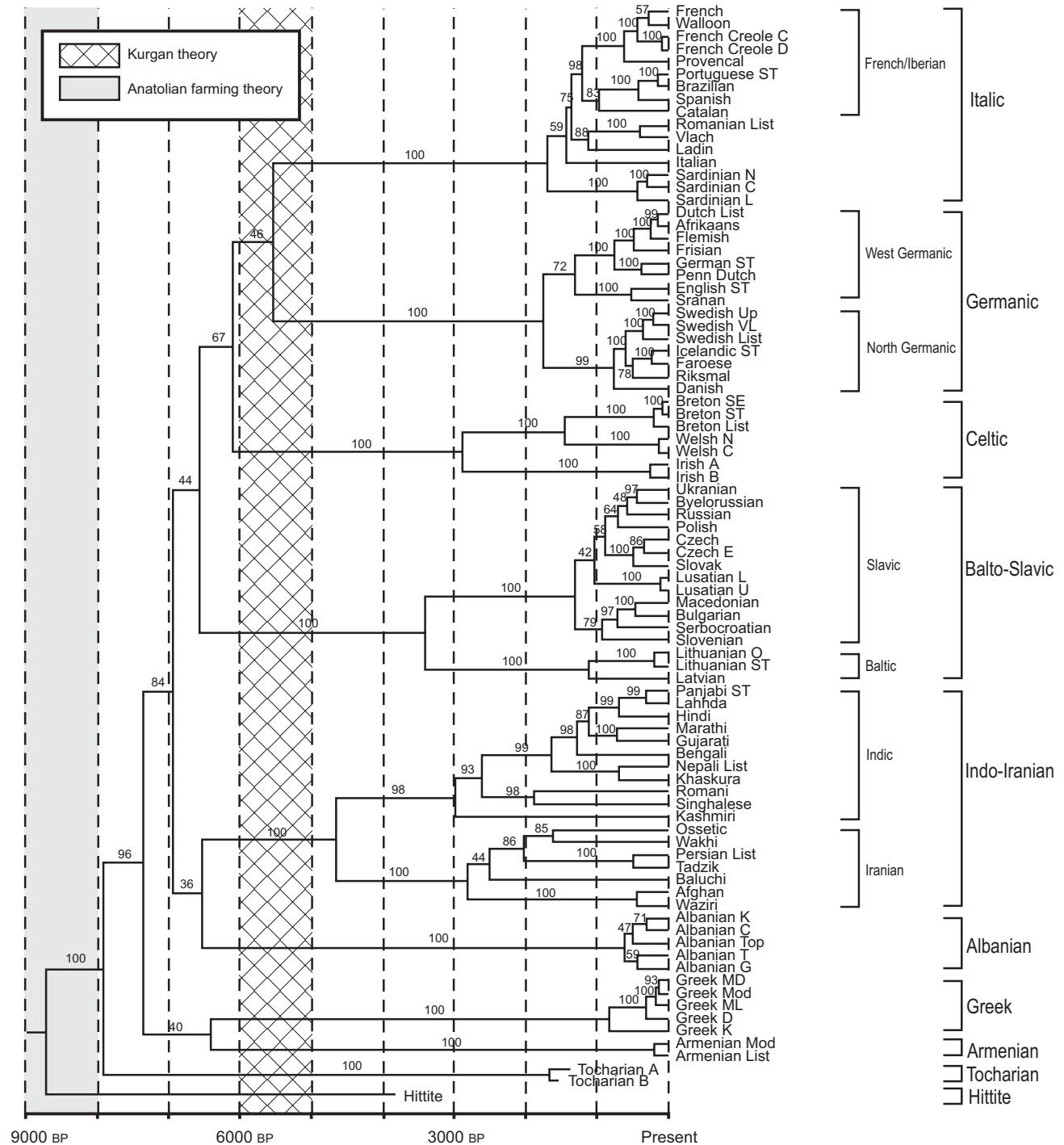


Figure 8.8. Majority-rule consensus tree from the initial Bayesian MCMC sample of 1000 trees (Gray & Atkinson 2003). Values above each branch indicate uncertainty (posterior probability) in the tree as a percentage. Branch-lengths are proportional to time. Shaded bars represent the age range proposed by the two main theories — the Anatolian theory (grey bar) and the Kurgan theory (hatched bar). The basal age (8700 BP) supports the Anatolian theory.

methodology is to produce divergence time distributions for nodes that were not constrained in the analysis and compare this to the historically attested

time of divergence. For example, Figure 8.10 shows the inferred divergence time distributions for the North and West Germanic subgroups. The grey band in

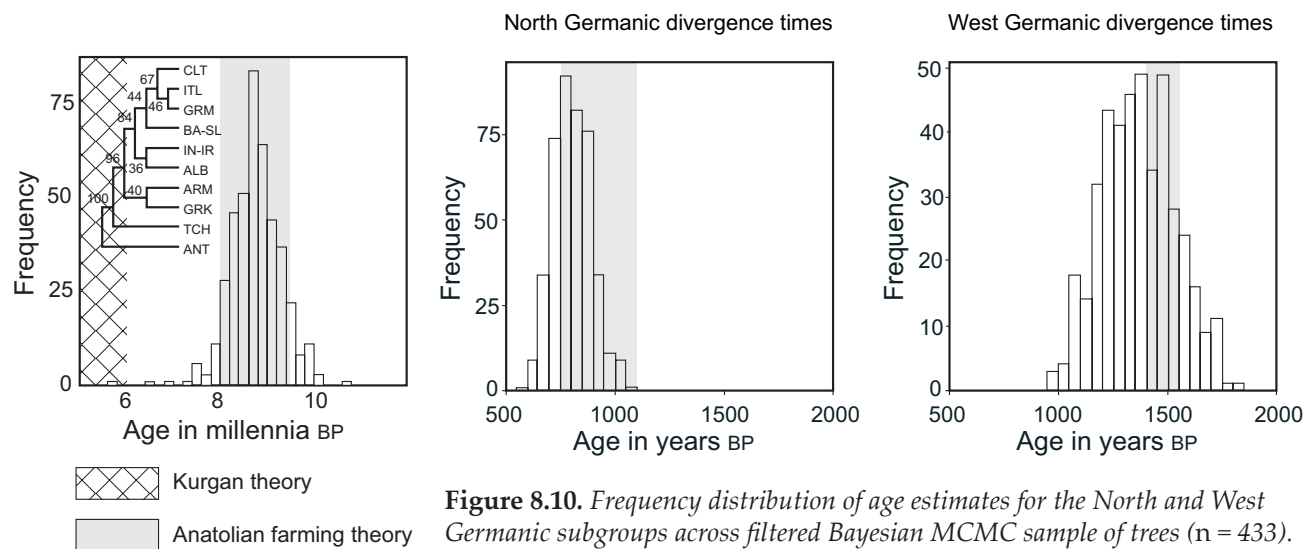


Figure 8.9. Frequency distribution of basal age estimates from filtered Bayesian MCMC sample of trees for the initial assumption set ($n = 435$). The majority-rule consensus tree for the entire (unfiltered) sample is shown in the upper left.

these figures indicates the likely age of each subgroup based on the historical record. The age estimates for the North Germanic clade correspond with written evidence for the break up of these languages between AD 900 and AD 1250. Similarly, estimated ages of the West Germanic clade are consistent with historical evidence dating the Anglo-Saxon migration to the British Isles about 1500 years ago.

8. Testing robustness

A key part of any Bayesian phylogenetic analysis is an assessment of the robustness of the inferences. To do this we tested the effect of altering a number of different parameters and assumptions of the method.

8.1. Bayesian 'priors'

Initializing each Bayesian MCMC chain required the specification of a starting tree and prior parameters ('priors') for the analysis. The sample Bayesian distribution was the product of ten separate runs from different random starting trees. Divergence time and topology results for each of the separate runs were consistent. Other test analyses were run using a range of priors for parameters controlling the rate matrix, branch-lengths, gamma distribution and character state frequencies. The inferred tree phylogeny and branch-lengths did not noticeably change when priors were altered.

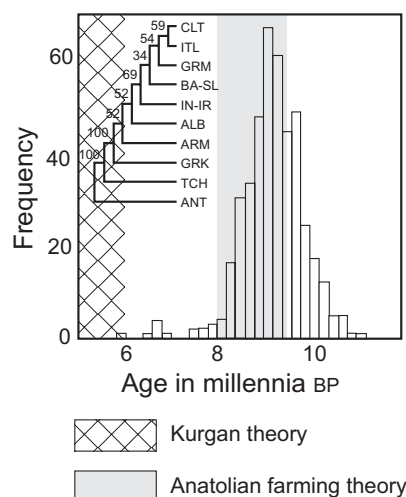


Figure 8.11. Frequency distribution of basal age estimates from filtered Bayesian MCMC sample of trees for analysis with doubtful cognates excluded ($n = 433$). The majority-rule consensus tree for the entire sample is shown in the upper left.

8.2. Cognacy judgements

The Dyen *et al.* (1992) data base contained information about the certainty of cognacy judgements. Words were coded as 'cognate' or 'doubtful cognates'. In the initial analysis we included all cognate information in an effort to maximize any phylogenetic signal. However, we wanted to test the robustness of our results to changes in the stringency of cognacy decisions. For this reason, the analysis was repeated with doubtful cognates excluded. This produced a similar age range to the initial analysis, indicating that our results were robust to errors in cognacy judgements (see Fig. 8.11).

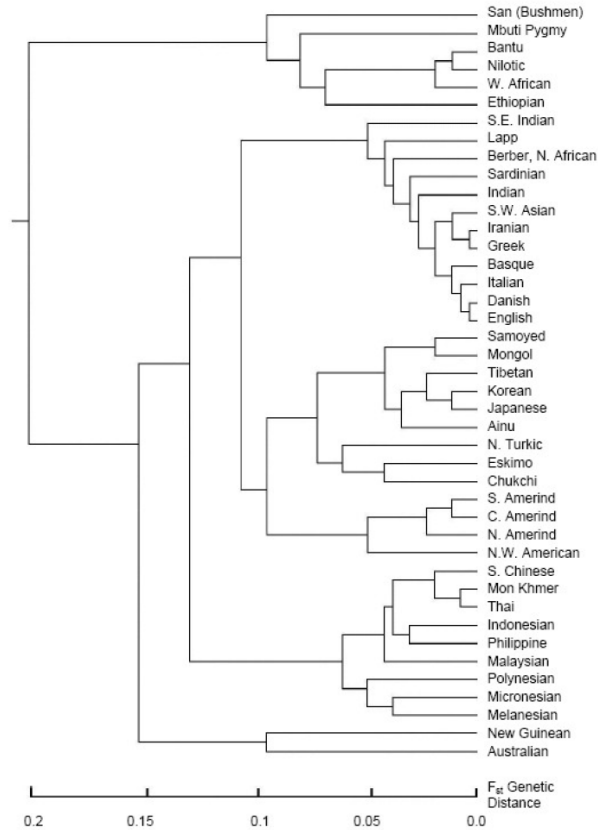


Figure 13: Genetic Distance Between 42 Populations. Source: Cavalli Sforza, Menozzi, and Piazza (1994).

across populations is an effect of heterogamous marriages and diffusion, as in the analyses of the Neolithic transition discussed in Section 3.3, genetic distance is appropriately interpreted as a proxy for cultural distance. This literature exploits data collected by Cavalli Sforza, Menozzi, and Piazza (1994; see pp. 75-76 and Figure 13 below) on allele frequencies in different populations. Genetic distance between two populations is measured as the probability that two alleles at a given genetic locus selected at random from the two populations will be different.⁴⁷

In this literature, notably, Guiso, Sapienza and Zingales (2004) use genetic distance between European populations as an instrument for trust in trade gravity regressions.⁴⁸

⁴⁷The genetic loci sampled are chosen to be relatively neutral with respect to evolutionary selection. This measure of genetic distance can then also be interpreted as a measure of distance from the most recent common ancestors of the two populations.

⁴⁸Giuliano, Spilimbergo, and Tonon (2006) however dispute the effect of genetic distance on trade

