

Supplementary Material of "Deep divergences of human gene trees and models of human origins"

- Supplementary figure 1: Relative probabilities of the scenarios of human evolution based on the divergence of gene trees.
- Supplementary table 1: Prior distribution for the models of human origins.
- Supplementary table 2: Posterior distribution of the ancestral effective population size N_A .
- Supplementary table 3: Posterior distribution of the TMRCA.

Figure 1: **Relative probabilities of the scenarios of human evolution based on the divergence of gene trees.** The x axis is the percentage of accepted simulations in ABC. We estimate model probabilities using local multinomial logistic regression.

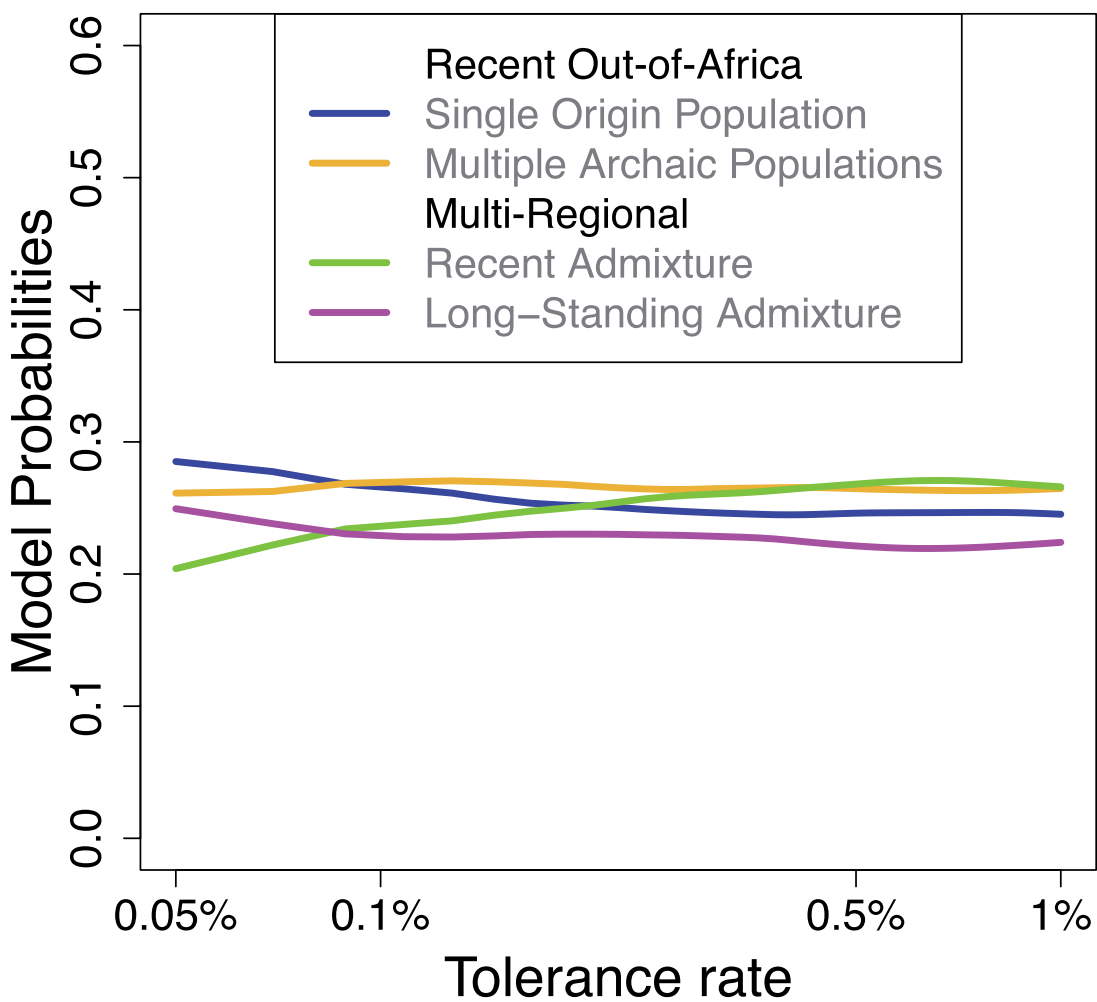


Table 1: **Prior distribution for the models of human origins.** Scenario 1-4 correspond to 1) Recent Out-of-Africa, 2) Out-of-Africa with African archaic admixture, 3) Multi-Regional with recent admixture, and 4) Multi-Regional with long-standing admixture.

Parameter	Scenario				Values		Distribution
	1	2	3	4	Min.	Max.	
Effective population sizes							
Ancestral size in Africa	•		•		5,000	50,000	Log-uniform
Ancestral size in Africa		•		•	500	50,000	Log-uniform
Size of archaic humans			•		5,000	50,000	Log-uniform
Timing (Years)							
Out-of-Africa T	•	•	•		40,000	100,000	Uniform
Duration of the Out-of-Africa bottleneck	•	•	•	•	0	20,000	Uniform
Time T_s during which there is a single ancestral African population		•			50,000	200,000	Uniform
Ancestral Split between African populations $T + T_s + T_M$		•			800,000	2,000,000	Uniform
Time of admixture T_{admix}			•		30,000	70,000	Uniform
Split between archaic and pre-modern T_O			•	•	350,000	700,000	Uniform
Time of the ancient non-African expansion				•	300,000	650,000	Uniform
Time of the recent non-African expansion				•	40,000	100,000	Uniform
Intensity of expansion and contraction $N_{\text{after}}/N_{\text{before}}$							
African expansion	•	•	•	•	1	100	Log-uniform
Out-of-Africa bottleneck	•	•	•	•	0.5	10^{-3}	Log-uniform
Non-African expansion	•	•	•		1	1000	Log-uniform
Non-African 1 st expansion				•	1	100	Log-uniform
Non-African 2 nd expansion				•	1	100	Log-uniform
Migration-Admixture (Years)							
Number of effective migrants M		•		•	0	20	Uniform
Proportion of archaic humans contributing to the modern gene pool			•		10^{-5}	1	Log-uniform
Potential bottleneck 150,000 years ago							
Reduction of population size b	•				10^{-3}	1	Log-uniform
Inbreeding coefficient F during the bottleneck	•				0	1	Uniform

Table 2: **Posterior distribution of the ancestral effective population size.**

Quantiles-summary statistics	2.5%	25%	Mode	Mean	50%	75%	97.5%	s.d.
Model								
Out-of-Africa, Single Origin	12,200	13,600	14,300	14,400	14,300	15,200	16,800	1,200
Out-of-Africa, Ancestral Bottleneck	11,500	13,000	14,100	15,500	14,600	17,300	23,500	3,100
Out-of-Africa, Multiple Archaic Pops.	5,130	7,100	8,100	9,400	9,100	11,200	15,500	2,800
Multi-regional, Recent Admixture	9,600	12,900	14,000	13,900	13,900	15,000	17,600	1,900
Multi-regional, Long-Standing Admixture	7,300	10,800	12,900	12,100	12,400	13,600	16,000	2,300

Table 3: **Posterior distributions of the TMRCAs.** All the dates are in thousand of years. The distribution of the TMRCA estimates is also given in the table. Due to recombination, each 20kb sequence may have multiple ancestors so that each-autosomal and X-linked-TMRCA measures an average of the different ages for the ancestors. The notation s.d. stands for standard deviation.

Quantiles-summary statistics	2.5%	25%	Mode	Mean	50%	75%	97.5%	s.d.
Autosomal markers								
Out-of-Africa, Single Origin	730	1,130	1,350	1,400	1,380	1,620	2,260	390
Out-of-Africa, Ancestral Bottleneck	330	1,140	1,400	1,400	1,410	1,700	2,310	470
Out-of-Africa, Multiple Archaic Pops.	530	1,080	1,320	1430	1,370	1,700	2,600	570
Multi-Regional, Recent Admixture	730	1,100	1,370	1,370	1360	1,590	2,150	380
Multi-Regional, Long-Standing Admixture	620	1,020	1,270	1,290	1,280	1,530	2,110	380
Data	-	960	1,430	1,390	1,470	1,700	-	560
X-linked markers								
Model	2.5%	25%	Mode	Mean	50%	75%	97.5%	s.d.
Out-of-Africa, Single Origin	460	830	990	1,050	1,020	1,250	1,780	340
Out-of-Africa, Ancestral Bottleneck	280	744	1,090	990	1,000	1,250	1,750	380
Out-of-Africa, Multiple Archaic Pops.	300	830	1,030	1,160	1,010	1,410	2,210	640
Multi-regional, Recent Admixture	520	860	1,000	1,080	1,050	1,270	1,830	330
Multi-regional, Long-Standing Admixture	470	780	960	1,000	980	1,190	1,670	311
Data	-	710	1,020	1,060	1,020	1,240	-	450
mtDNA and Y chromosome								
Model	2.5%	25%	Mode	Mean	50%	75%	97.5%	s.d.
Out-of-Africa, Single Origin	150	250	270	390	350	480	920	200
Out-of-Africa, Ancestral Bottleneck	150	150	170	280	220	340	690	160
Out-of-Africa, Multiple Archaic Pops.	110	180	210	430	280	550	1430	400
Multi-Regional, Recent Admixture	160	270	290	420	370	530	960	210
Multi-Regional, Long-Standing Admixture	210	330	370	460	420	540	930	180