Ancient human extinction risk: Implications from high-precision computation and fossil evidence

Sumei Zhou[1,2]†, Yiwen Zhou[1]†, Fabio Di Vincenzo[3], Giorgio Manzi[3], Wangjie Hu[4], Ziqian Hao[5], Yi-Hsuan Pan[2]*, Haipeng Li[1]*

[1]CAS Key Laboratory of Computational Biology, Shanghai Institute of Nutrition and Health, University of Chinese Academy of Sciences, Chinese Academy of Sciences; Shanghai, China.

[2]Key Laboratory of Brain Functional Genomics of Ministry of Education, School of Life Science, East China Normal University; Shanghai, China.

[3]Department of Environmental Biology, Sapienza University of Rome; Rome, Italy.

[4]Department of Genetics and Genomic Sciences, Icahn School of Medicine at Mount Sinai; New York, USA.

[5]College of Medical Information and Artificial Intelligence, Shandong First Medical University & Shandong Academy of Medical Sciences; Jinan, China.

†These authors contributed equally to this work.

*Corresponding authors: Yi-Hsuan Pan, and Haipeng Li

Email: yxpan@sat.ecnu.edu.cn, lihaipeng@sinh.ac.cn

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Abstract

Reconstructing ancient population size dynamics is essential for understanding human evolution. Using the fast infinitesimal time coalescent process (FitCoal), we identified a severe population bottleneck approximately 930,000 years ago, which pushed human ancestors to near extinction but left only subtle genomic traces in present-day humans. Detecting this signal requires precise computational methods. Compared with *mushi* and ten billion simulations performed using *msprime*, FitCoal provides the fastest and most accurate inference of expected branch lengths across site frequency spectrum categories. Independent fossil and paleoclimate records corroborate the timing and evolutionary impact of this bottleneck, highlighting the need to integrate genetic, paleontological, and environmental evidence. These findings refine our understanding of hominin evolution and the demographic events that shaped modern human ancestry.

Introduction

Over the past four million years, at least 22 hominin taxa have emerged, yet only modern humans, *Homo sapiens*, have survived to the present day. It is estimated that modern humans, Neanderthals, and Denisovans diverged from a common ancestor approximately 600 thousand years ago (Ka) (1). This ancestor likely arose as a derived species in Africa during the Middle Pleistocene transition, a period marked by the decline of African *H. erectus* (2). To reconstruct the evolutionary trajectory leading to modern humans, it is therefore essential to investigate their population size history from approximately 1,000 to 100 Ka, a timeframe coinciding with significant adaptive phenotypic changes.

Results and Discussion

We developed the fast infinitesimal time coalescent process (FitCoal) to infer both recent and ancient population size histories (3). FitCoal enables high-precision computation of the expected site frequency spectrum (SFS) and its associated likelihood under arbitrary demographic models. While a given SFS can theoretically be explained by different synthetic demographic models (4), FitCoal overcomes this challenge by prioritizing biologically realistic scenarios and gradually increasing model complexity until the optimal model is identified (3, 5). Applying FitCoal to present-day human genomic sequences, we identified a severe population bottleneck that occurred around 930 Ka in 12 African and 19 non-African populations (3). Notably, the timing and the severity of this bottleneck are nearly identical in both African and non-African populations (Figure 1A), challenging conclusions from two recent papers (6, 7). Furthermore, we observed greater variance in bottleneck estimates among non-African populations compared with African populations (Figure 1B), likely due to the dilution of genetic signals caused by the out-of-Africa dispersal.

To trace the human evolutionary trajectory, it is crucial to minimize confounding factors. High-frequency mutations are particularly susceptible to positive selection, introgression, population structure, and misclassification of derived and ancestral variants. A recent study introduced a non-demographic correction parameter to mimic the misclassification process, thereby complicating its model (6). In contrast, FitCoal adopts a different approach, mitigating these effects by using a subset of the SFS that is less impacted by these confounding factors or a collapsed SFS (3, 5), while maintaining high efficiency in inferring population size history. A key strength of FitCoal lies in its ability to extract population size history information not only from individual SFS categories but also from their relative ratios (3). To demonstrate this, we compared FitCoal-inferred histories using both the full SFS and a subset of the SFS. Remarkably, a bottleneck model was accurately inferred even when only 10% of SFS categories were analyzed (Figure 1C). These findings highlight the multidimensional richness of demographic information embedded within the SFS, allowing FitCoal to remain robust despite the complexities of evolutionary history.

High-precision computation is crucial for reconstructing ancient population size history. To evaluate FitCoal's accuracy, we tested a synthetic model where it might misidentify a bottleneck (6, 7). Comparing the expected branch lengths for each SFS category, FitCoal and *mushi* (8) showed a maximum difference of

6.21%, with a total discrepancy of 9,981 generations (Figure 1D, Table 1). To determine which method aligns better with true values, we conducted 1×10^{10} *msprime* simulations to generate benchmark branch lengths. The results showed that FitCoal's estimates were nearly identical to those from *msprime*, reducing the total discrepancy to just 21 generations, whereas *mushi* exhibited much larger deviations (Figure 2). This confirms the superior accuracy of FitCoal. Additionally, FitCoal completed the computation in 0.00013 seconds, while *msprime* required 4.90 years, highlighting FitCoal's computational efficiency. Furthermore, simulations of 1,000 polymorphic datasets using *msprime* (9) under the synthetic model consistently confirmed FitCoal's inference (Figure 1E). These findings emphasize the importance of simulated datasets in validating ancient severe bottlenecks and underscore the necessity of high-precision computation for accurately estimating the expected SFS and SFS-related likelihood.

The presence of this severe bottleneck is further supported by an African hominin fossil gap, the timing of ancestral chromosome fusion, significant cultural and behavioral shifts (10), climatic changes during the Early-to-Middle Pleistocene transition (11), and fluctuations in mammalian speciation and extinction rates (12). Additionally, this severe bottleneck may have contributed to a major human diaspora from Africa to Eurasia (13). A comprehensive understanding of hominin evolution thus requires integrating genetic, fossil, and paleoclimate records.

Between 1,000 and 100 Ka, at least two major macroevolutionary events occurred (Figure 1F), coinciding with the so-called 'muddle in the middle'— a period of hominin coexistence and morphological diversity. Given that small population size can drive speciation (14), our findings suggest that the severe bottleneck played a pivotal role in shaping phenotypic and behavioral evolution in human ancestors. In particular, its impact on adaptation and speciation warrants further investigation. The fixation of fused chromosome 2 and its potential role in reproductive isolation remain key questions in human evolution. To explore these issues, we analyzed endocranial volume and the encephalization quotient in African fossil specimens. Brain size increased significantly following the severe bottleneck (Figure 1G, Table 2), suggesting a possible link between population contraction and accelerated cognitive and social evolution. Additionally, recent evidence indicates that the last populations of African *H. erectus* experienced extreme arid conditions at the onset of the bottleneck and, in order to survive, diversified their behaviors to maximize resource exploitation (15).

Together, these cross-disciplinary findings provide new insights into hominin speciation, the genetic consequences of severe population contraction, and the evolutionary forces shaping modern human ancestry. These refine our understanding of key events preceding the out-of-Africa dispersal and highlight the importance of integrating multiple lines of evidence in evolutionary studies.

Materials and Methods

To rigorously assess the accuracy of FitCoal in demographic inference, we tested it against a synthetic model from Deng et al. (7), used here as the true model. This model was derived by inferring demographic parameters while restricting the occurrence of a severe bottleneck, using an expected SFS generated by *mushi* from a severe bottleneck model (7). The synthetic model is also similar to two previously investigated models (see Figure 4B and 4F in Hu et al. 2023). We obtained the synthetic model using the authors' scripts. The expected SFS was calculated by multiplying the branch lengths by the total mutation rate of the considered sequence fragments.

We compared expected branch length across SFS category under the synthetic model using three independent methods. First, the expected branch lengths were obtained using *mushi*, as suggested by two recent studies (6, 7). Second, FitCoal's expected branch lengths were calculated using FitCoal version 1.3, which can be freely downloaded (https://doi.org/10.5281/zenodo.4765446). This version is released alongside this manuscript. Third, we used *msprime* (9) to simulate 1×10^{10} coalescent trees of a single locus based on the synthetic model. The mean branch length for each SFS category was then obtained. The number of simulations was determined by examining the accuracy of the expected branch lengths (Figure

2). Given the rounding of decimal values, 1×10^{10} coalescent simulations were determined as the minimum required to achieve sufficient accuracy in inferring ancient population size history.

To examine the robustness of FitCoal in inferring population demography, we obtained 1,000 simulated SFSs under the synthetic model using *msprime* (9). The parameters of the simulation were aligned with the previous study (7), in which mutation and recombination rates were both set as 1.2×10^{-8} per base per generation with 216 sequences, each 100 Mb in length. Since the simulated data were generated under the single-population neutral model, there was no need to exclude high-frequency mutations. We used FitCoal with default parameters and inferred 1,000 population size histories.

The endocranial volume of Buia was obtained from Bruner et al. (16), KNM-ER 42700 from Neubauer et al. (17), and others from Holloway, Broadfield and Yuan (18). The encephalization quotient for each specimen was calculated following a previous study (19). Body mass (in kilograms) was obtained from three studies (20-22) to derive the quotient.

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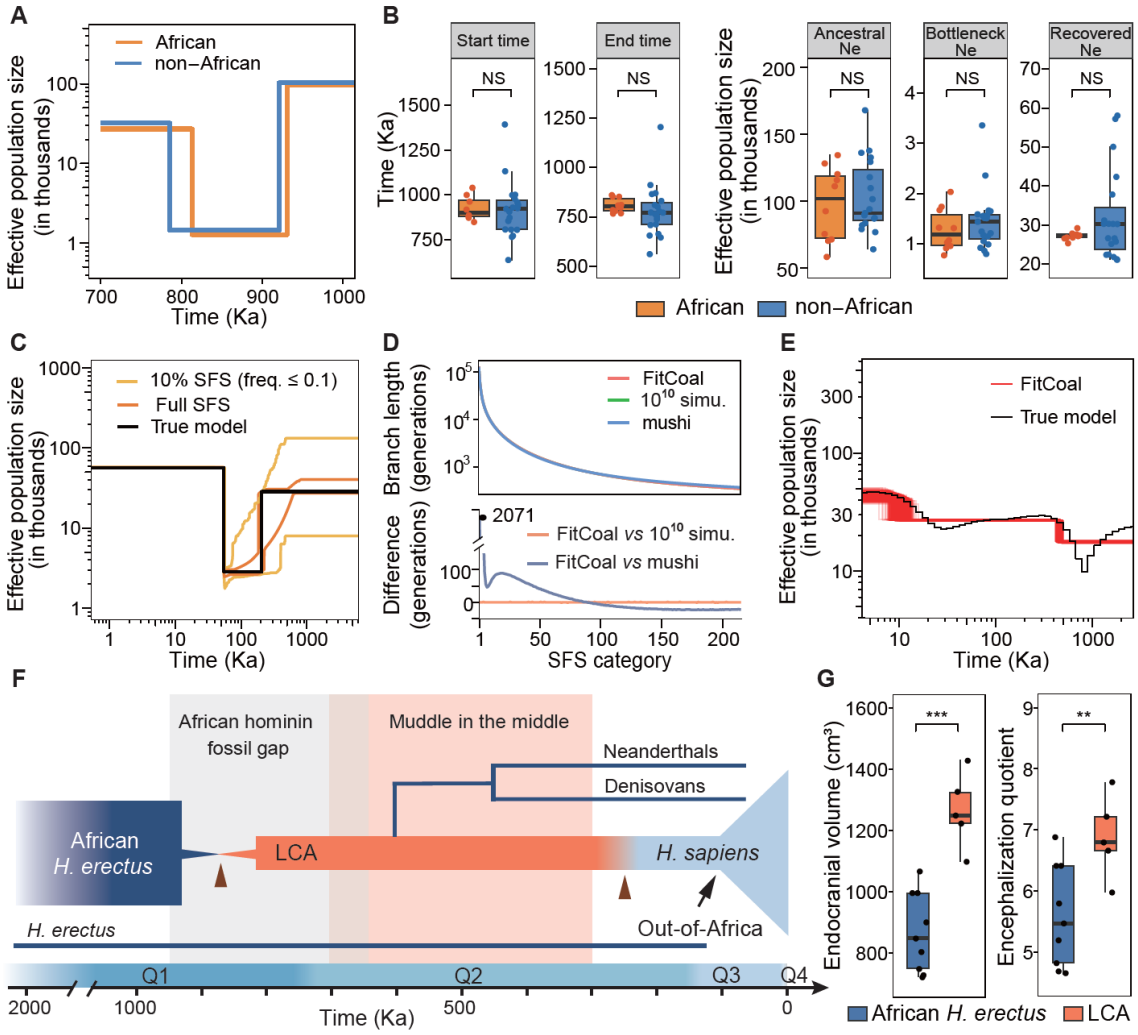

Figure 1. Implications of ancient human extinction risk, high-precision computation, and fossil evidence. (**A**) The severe bottleneck in African and non-African populations. (**B**) Estimated bottleneck parameters in 10 African and 19 non-African populations. Two South African populations (San and Bantu) were excluded due to their small sample sizes. (**C**) The 2.5th and 97.5th percentiles of FitCoal-inferred population size histories using full-SFS and minor alleles ($freq \leq 0.1$). (**D**) The upper panel shows the expected branch length for each SFS category calculated by FitCoal, *mushi*, and 1×10^{10} *msprime* simulations. The lower panel displays their differences from FitCoal estimates. (**E**) FitCoal-inferred population size histories based on different SFSs under the synthetic model proposed by Deng et al. Red lines represent FitCoal-inferred histories based on 1,000 simulated datasets (n=216, L=100 Mb). (**F**) Evolutionary history of hominins over the past one million years. The LCA refers to the last common ancestor shared by Denisovans, Neanderthals, and modern humans. The two triangles indicate the speciation events. Q1 – Q4 indicate the Early Pleistocene, Middle Pleistocene, Late Pleistocene, and Holocene, respectively. (**G**) Endocranial volume and the encephalization quotient of African fossil specimens before and after the severe bottleneck. Two-tailed Student's t-test, ***P < 0.001, **P < 0.01 and NS = not significant. (**A – C**) Data were obtained from the previous results (3).

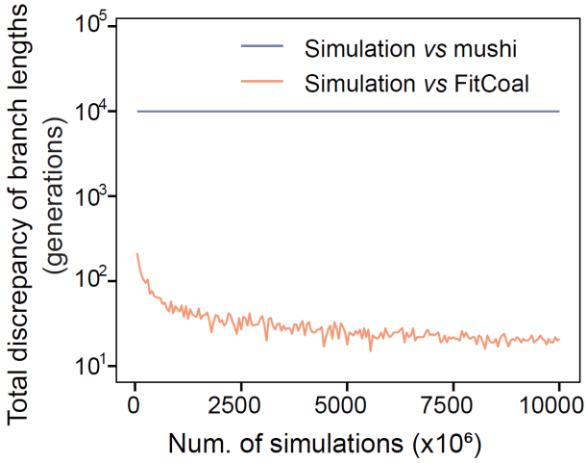

Figure 2. Influence of the number of simulations on the accuracy of averaged branch lengths compared with FitCoal and *mushi*. The synthetic model (Figure 1E) was used.

Table 1. Expected branch lengths (in generations) for each SFS category.

SFS category[a]	FitCoal (Generations)	1×10^{10} simulations (Generations)	mushi (Generations)	Diff. FitCoal *vs.* simulations	Diff. FitCoal *vs.* mushi
1	129,059	129,059	126,988	0 (0.00%)	2,071 (1.60%)
20	4,778	4,778	4,689	0 (0.00%)	89 (1.86%)
40	2,124	2,124	2,066	0 (0.00%)	58 (2.73%)
60	1,293	1,293	1,265	0 (0.00%)	28 (2.17%)
80	914	914	908	0 (0.00%)	6 (0.66%)
100	709	709	716	0 (0.00%)	7 (0.99%)
140	504	504	523	0 (0.00%)	19 (3.77%)
180	406	406	428	0 (0.00%)	22 (5.42%)
200	374	374	396	0 (0.00%)	22 (5.88%)
215	354	354	376	0 (0.00%)	22 (6.21%)
Total diff.[b]	–	–	–	21	9,981
Computing time	0.00013 sec	4.90 years	1.29 sec	–	–

[a]The number of sampled sequences is 216, following Deng et al. (7).

[b]The summation of differences over all categories, including ones not shown in the table.

Table 2. Endocranial volume and the encephalization quotient of African *Homo erectus* and the LCA.

Taxon	Specimen	Endocranial volume (cm^3)	Encephalization quotient
H. erectus (Africa)	KNM-ER 3732	750	4.83
	KNM-ER 3733	848	5.46
	KNM-ER 3883	804	5.18
	Daka	995	6.41
	Buia	995	6.41
	KNM-ER 42700	721	4.64
	KNM-WT 15000	900	5.79
	OH 9	1,067	6.87
	OH 12	727	4.68
LCA	Bodo	1,250	6.80
	Broken Hill 1	1,325	7.21
	Saldanha	1,225	6.66
	Omo-Kibish 2	1,430	7.77
	Ndutu	1,100	5.98