

Supporting Information

File S5. Analysis of Human data

We use *ARGweaver* (Rasmussen et al., 2014) with the following code lines:

European population:

```
arg-sample -s data1000/CEU_10.sites
-N 11534 -r 1.6e-8 -m 1.26e-8
--ntimes 200 --maxtime 200e3 -c 1 -n 10
-o data1000/CEU.sample/out
```

Yoruban population:

```
arg-sample -s data1000/YRI_10.sites
-N 11534 -r 1.6e-8 -m 1.26e-8
--ntimes 200 --maxtime 200e3 -c 1 -n 10
-o data1000/YRI.sample/out
```

ARGweaver time is measured in units of generations, so in order to generate Figure 8, we multiplied time by $1/(2 \times 11,534)$. To obtain $\log N(t)$ displayed in Figure S4, we multiplied our estimates by $1/(8 \times 11,532)$ and converted them in logarithmic scale.

We note that *ARGweaver* assumes the SMC and not the SMC' model so our estimates of $N(t)$ are biased. One source of such a bias is that the $A^i(t)$ functions that indicate the number of lineages present at time t in the SMC' are replaced by $A^i(t) - 1$ if the pruning branch is present at time t in the SMC. Another source of bias is the lack of invisible recombination events in *ARGweaver* realizations. To approximate the effect of this difference we re-run our algorithm replacing $A^i(t)$ by $A^i(t) - 1$. Figure S4 shows that the main conclusions about inferred recent past population sizes remain valid; in our analysis of human data (Figure 8) we only focus on the recent past.

References

Rasmussen, M. D., Hubisz, M. J., Gronau, I., and Siepel, A. (2014). Genome-wide inference of ancestral recombination graphs. *PLoS Genet*, 10(5):e1004342.

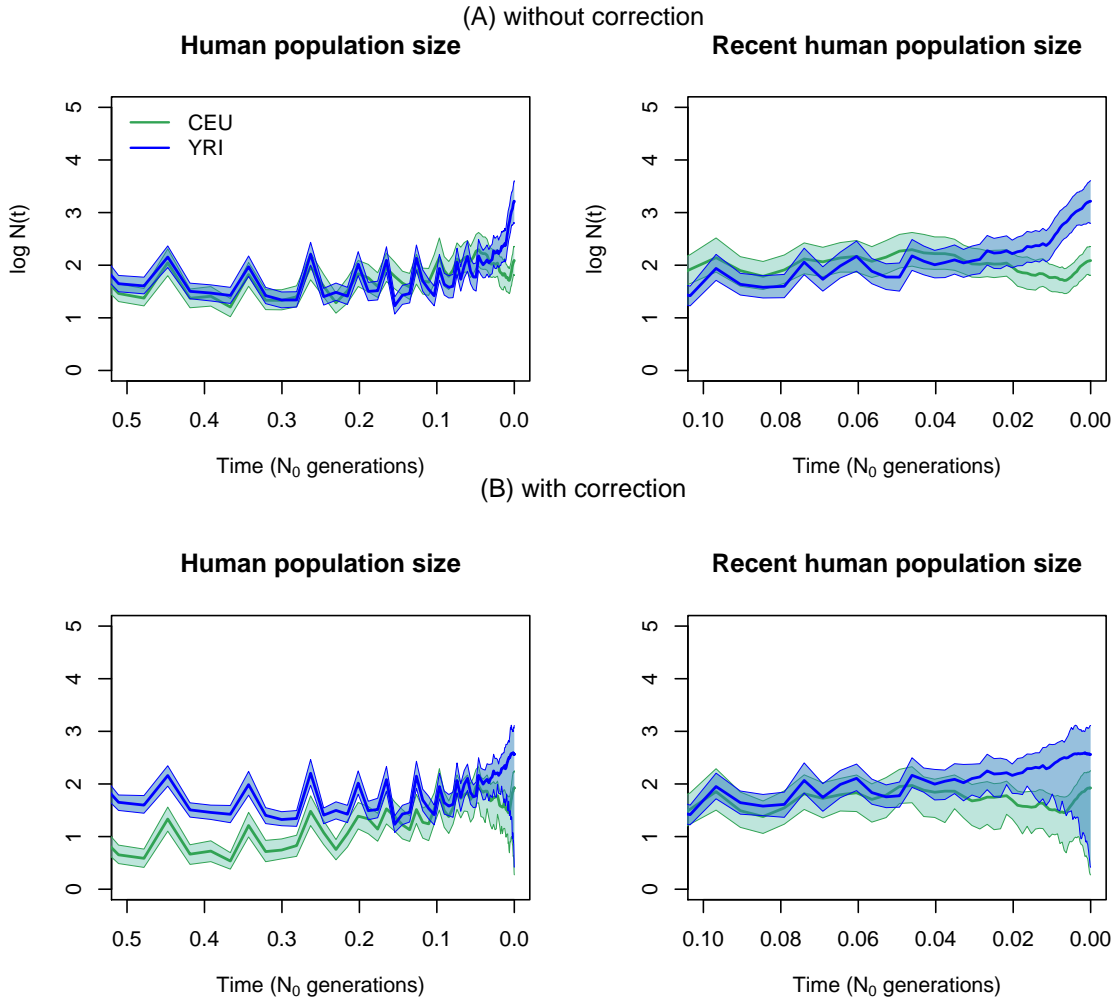


Figure S4: **Inference of human population size trajectories $N(t)$ for $n = 10$.** Green solid line and green shaded areas represent the posterior median and 95% BCI for European population (CEU) and blue solid line and blue shaded areas represent the posterior median and 95% BCI for Yoruban population. **(A) Without correction.** We ignore the fact that our genealogies were generated assuming the SMC process instead of SMC'. **(B) With correction.** We corrected the function of the number of lineages to approximate the SMC likelihood. Figures on the right show the same results as in the left side for the recent past $(0, 0.1N_0)$.