

Original Research

On the Demographic History of Chimpanzees and Some Consequences of Integrating Population Structure in Chimpanzees and Other Great Apes

Camille Steux^{1,2,3,*}, Clément Couloigner^{3,4}, Armando Arredondo^{5,6}, Willy Rodríguez^{5,6}, Olivier Mazet^{5,6}, Rémi Tournebize^{1,3,7} and Lounès Chikhi^{1,2,3*}

1. Centre de Recherche sur la Biodiversité et l'Environnement (CRBE), Université de Toulouse, CNRS, IRD, Toulouse INP, Université Toulouse 3 – Paul Sabatier (UT3), 31062 Toulouse, France; Email: remi.tournebize@ird.fr
2. Centre for Ecology, Evolution and Environmental Changes (cE3c), Faculdade de Ciências da Universidade de Lisboa, Campo Grande, 1749-016 Lisboa, Portugal
3. Instituto Gulbenkian de Ciência, 780-156 Oeiras, Portugal; Email: clement.couloigner.1@ulaval.ca
4. ACentre d'Etude de la Forêt, Département de Biologie, Université Laval, G1V 0A6 Québec, Canada
5. Université de Toulouse, Institut National des Sciences Appliquées, Institut de Mathématiques de Toulouse, 31077 Toulouse, France; Emails: arm.plus@gmail.com (A.A.); willyrv@gmail.com (W.R.); omazet@insa-toulouse.fr (O.M.)
6. Institut de Mathématiques de Toulouse; UMR5219. Université de Toulouse, 31062 Toulouse, France
7. UMR DIADE - Diversité, adaptation, développement des plantes, CIRAD, CNRS, IRD, Université de Montpellier, 34394 Montpellier, France

* **Correspondence:** Camille Steux; Email: camille.steux@univ-tlse3.fr; Lounès Chikhi; Email: lounes.chikhi@univ-tlse3.fr

Supplementary Materials

1. Supplementary Information S1: On the Validation Process

The validation process that we applied in this study is similar to that used in ABC studies. We started with a PSMC curve for which we inferred ten scenarios corresponding to ten runs of SNIF, as explained in the Materials and Methods section. When these ten scenarios were similar we chose one of them, say scenario S^* , and generated a new IICR curve using the corresponding *ms* command. This IICR curve served as input to a new SNIF inference and we obtained ten newly inferred scenarios, $S_1^{**}, S_2^{**}, \dots, S_{10}^{**}$ from the ten independent runs. If these scenarios are different from each other, this may suggest that the optimization has not reached equilibrium and the number of iterations should be increased. Assuming now that the $S_1^{**}, S_2^{**}, \dots, S_{10}^{**}$ do not differ significantly from each other but differ from S^* , this suggests that the inferred scenario S^* should not be trusted at this stage since SNIF was not able to infer it despite using ten independent runs and reaching equilibrium. This was never the case with the chimpanzee data and we come back to this below.

In such a case where S^* should not be trusted, we suggest several solutions. One could explore more simple n-island models (with smaller c values for instance) to determine if S^* is too parameter-rich to be inferred by SNIF. If this fails too, it could also indicate that the real evolutionary history may be too complex to be approximated by a piecewise stationary n-island model such as S^* or simpler versions of S^* . In such a case, other demographic models should be explored, perhaps involving population size changes or spatial structure (stepping stone models for instance), or tree models.

If, on the contrary, S^* can be inferred reasonably well (*i.e.*, the S_i^{**} scenarios are similar to S^*) as we observe with the chimpanzees, this could suggest that the scenario S^* is not only able to explain the original observed

data but it can be inferred by SNIF if it were true. In other words, if the real species had evolved under S^* we would be able to infer S^* with SNIF. This does not prove that the species evolved under S^* but that S^* might be a reasonable approximation of reality to explain the PSMC computed for that species, at least until we find better alternatives.

These (or other) validation steps are fundamental and we suggest that they should be applied more often in demographic inference studies. It is more commonly applied in ABC studies, but there are still studies which infer a scenario without demonstrating that if real data had been generated under the inferred scenario, the authors would indeed be able to infer it back again, even approximately. While this validation process may be difficult to apply to some methods using genomic data, the current study shows that it is possible.

2. Supplementary Information S2: Adding Between Sub-species Migration Rates in the General Tree Model

As mentioned in the main text, several studies have pointed out the existence of gene flow between subspecies of common chimpanzees [1–5], and two of them have found patterns of IBD across the whole species and within Eastern and Central chimpanzees [6,7]. Furthermore, our general tree model, where no gene flow is allowed between the different subspecies, does not correctly predict between-species genetic differentiation. Therefore, a way to improve our general tree model to make it more realistic would be to add migration between the four subspecies. The short work presented here is a first attempt at doing so, in order to determine if it is indeed doable to find a better general tree model while still matching the PSMC curves and improving the fit to empirical statistics.

2.1. Methods

The general tree model displayed in **Figure 7** in the main text of the paper was modified to add gene flow between subspecies, as shown in **Figure S1**. Precisely, the between-subspecies migration rate M_b corresponds to the total number of new migrants in a deme coming from the demes of the other three subspecies each generation, and is constant through time. This implies that when two subspecies join backward in time, the local migration rates are increased so that the global between-subspecies migration rate stays the same. For instance, given that $n_W=25$, $n_{NC}=12$, $n_C=17$ and $n_E=13$ ($n_{total}=67$), the coefficient in the migration matrix for a deme of Western chimpanzees is equal to $M_b / (n_{total} - n_W)$ from the present until T_{CE} . After the Eastern and Central chimpanzees have joined (backward in time), the same coefficient in the migration matrix becomes $M_b / (n_{total} - n_E - n_W)$. M_b is identical across all pairs of subspecies.

Adding migration rates between subspecies decreased the fit of the simulated IICR to the empirical PSMC (see **Figure S2**). Therefore, we then tried to adjust the within-subspecies migration rates (inferred by SNIF) to improve the fit. We manually fitted the simulated IICR to the empirical PSMC by increasing the within-species migrations rates that were inferred by SNIF, for $M_b=0.1$. Supplementary **Table S1** shows the new migration rates and the ones inferred by SNIF for comparison. The increase ratio varied between two and around 100.

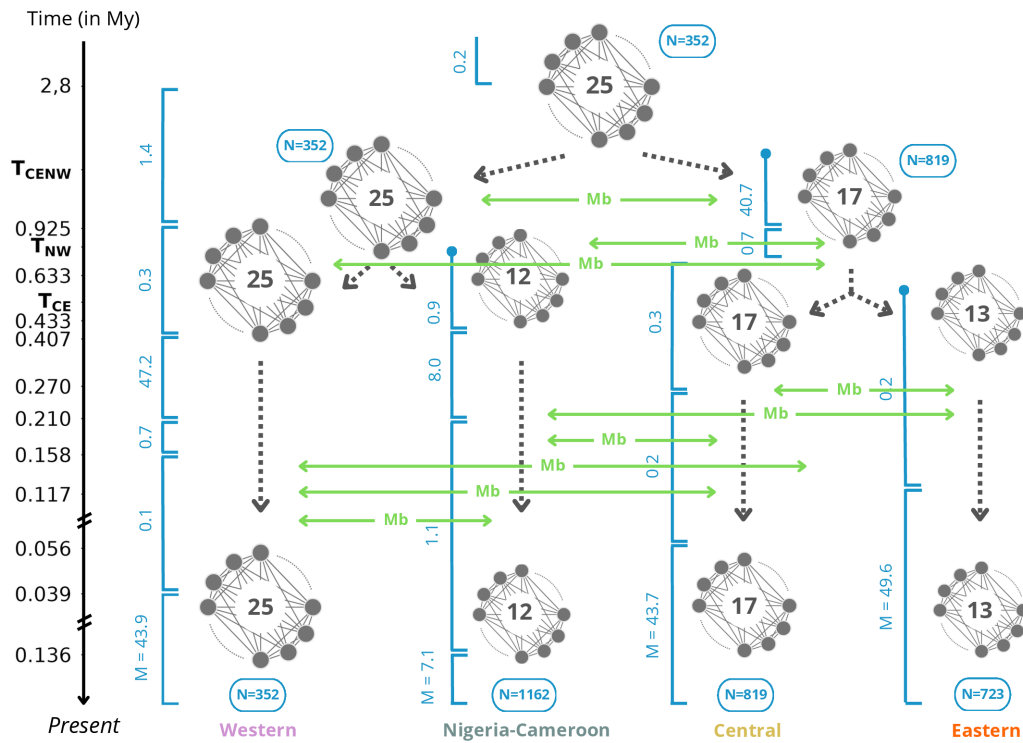


Figure S1 Proposed general n -island model for the history of the four subspecies of common chimpanzee with migration rates between subspecies. Dark full circles symbolize subpopulations structured in n -island models, and the number in the middle center corresponds to the number of demes n . Deme size N is given in number of diploid individuals. T_{CE} , T_{NW} and T_{CENW} correspond to the times at which two meta-populations join each other (backward in time), for Central/Eastern Chimpanzees, Nigeria-Cameroon/Western chimpanzees, and the two ancestral meta-populations respectively. In blue, along the vertical intervals, are the within-subspecies migration rates $M_i = 4Nm_i$, and the horizontal green arrows represent the between-subspecies migration rates M_b .

Table S1 Inferred and adjusted within-species migration rates specified in the general tree model with $M_b=0.1$. Inferred M_i values correspond to the M_i inferred by SNIF, Adjusted M_i values corresponds to the modified Inferred M_i to improve the fit of the model to the empirical PSMC, and Ratio values correspond to the ratio Adjusted M_i /Inferred M_i . Elements highlighted in blue correspond to the cases where the Inferred M_i were adjusted.

Subspecies	Migration rate	M0	M1	M2	M3	M4	M5	M6	M7
Western	Inferred M_i	43.94	0.13	0.66	47.16	0.35	1.37	0.16	
	Adjusted M_i	80.00	0.23	40.00	50.00	20.00	1.37	0.16	
	Ratio	1.82	1.77	60.65	1.06	57.14	1.00	1.00	
Nigeria Cam.	Inferred M_i	7.10	1.11	8.04	0.92	43.22	1.29	0.23	
	Adjusted M_i	7.10	2.00	43.00	2.00	43.22	1.29	0.23	
	Ratio	1.00	1.00	5.34	2.17	1.00	1.00	1.00	
Central	Inferred M_i	43.71	0.21	0.27	0.73	40.48	0.68	0.23	1.44
	Adjusted M_i	43.71	0.40	1.00	3.75	40.48	0.68	0.23	1.44
	Ratio	1.00	1.94	3.71	5.13	1.00	1.00	1.00	1.00
Eastern	Inferred M_i	49.64	0.21	0.65	2.85	0.73	0.15	0.40	
	Adjusted M_i	49.64	0.90	1.20	2.85	0.73	0.15	0.40	
	Ratio	1.00	4.29	1.86	1.00	1.00	1.00	1.00	

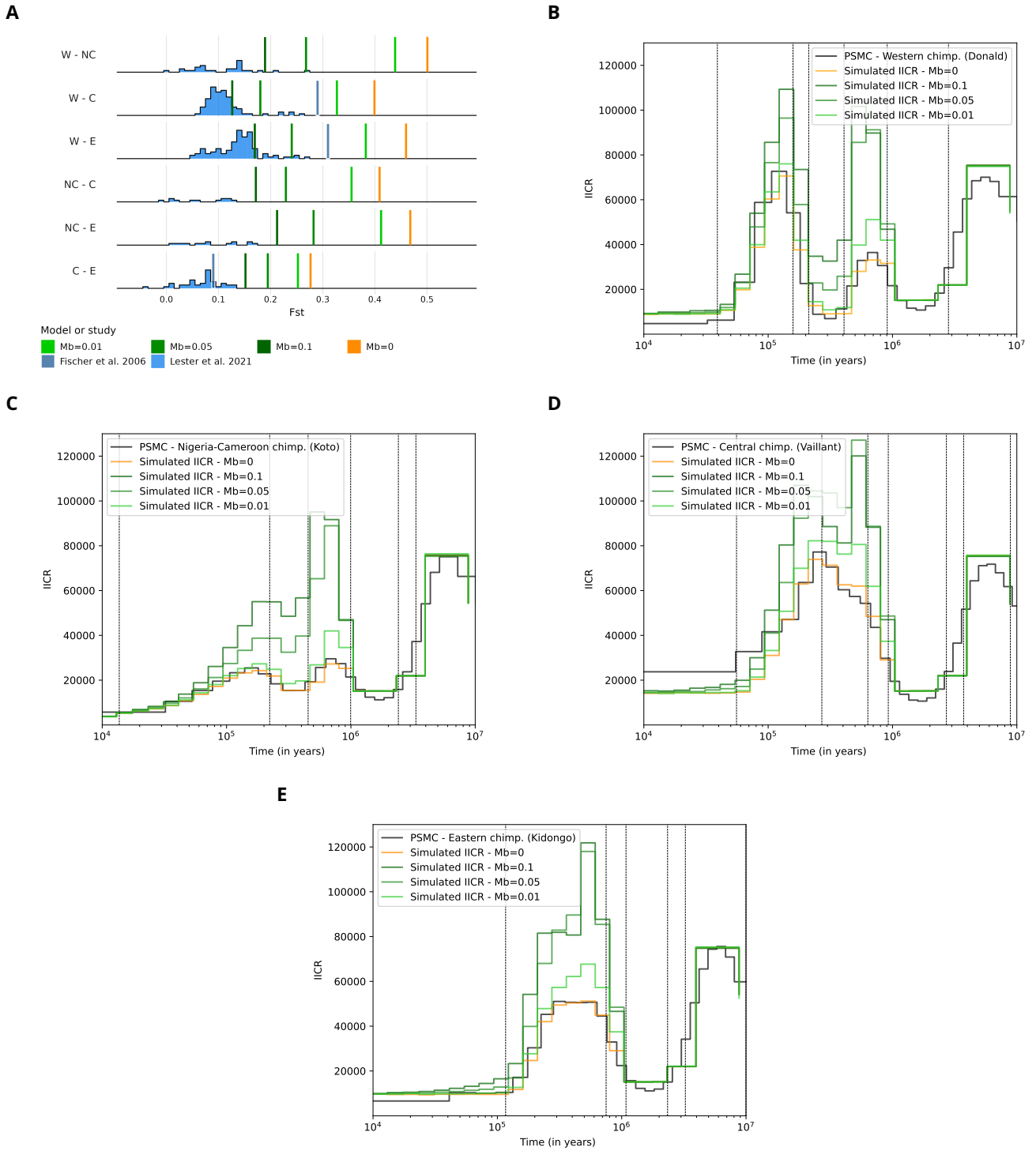


Figure S2 Simulated F_{ST} and IICR for the general tree model when adding a migration rate M_b between subspecies for $M_b = 0.1, 0.05$ and 0.01 . A. Simulated F_{ST} and empirical F_{ST} retrieved from Lester *et al.* 2021 [7] and Fischer *et al.* 2006 [8]. B-E. Simulated IICR and empirical PSMC for Western (B), Nigeria-Cameroon (C), Central (D) and Eastern (E) chimpanzees.

As we did for the main analysis, we simulated 10^6 T_2 values with *ms* to produce the corresponding IICR, sampling one diploid individual in a deme for each subspecies. We also simulated 100 sequences of 10^6 bp, again with *ms*, sampling 10 individuals in one deme of each subspecies and computed the F_{ST} using scripts from Tournébois and Chikhi (2024) [9]. Empirical values are retrieved from Lester *et al.* 2021 and Fischer *et al.* 2006. More information regarding these studies is available in Supplementary Table S2.

Table S2 Information about the studies where empirical statistics were retrieved from: Prado-Martinez *et al.* 2013 [10] and de Manuel *et al.* 2016 [1] for estimates of genetic diversity, Lester *et al.* 2021 [7] and Fischer *et al.* 2006 [8] for estimates of genetic differentiation.

Study	Statistic	Type of data	Samples
Prado-Martinez <i>et al.</i> 2013 [10]	Individual observed heterozygosity	Whole genomes (mean coverage 22.5X)	25 individuals across the 4 subspecies. - W: 3 wild-born individuals and 2 captive-born individuals - NC: 10 wild-born individuals (from Cameroon) - C: 4 wild-born individuals (from Gabon) - E: 6 wild-born individuals (from DRC, Tanzania and Uganda)
Note that the individual Donald, supposedly a Central-Western hybrid chimpanzee, was included in our analysis as a Western chimpanzee, as his PSMC is very close to other Western chimpanzees.			
de Manuel <i>et al.</i> 2016 [1]	Individual observed heterozygosity	Whole genomes (mean coverage 24.4X)	65 individuals in total across the 4 subspecies (25 individuals from Prado-Martinez <i>et al.</i> 2013 and 40 novel genomes). - W: 10 wild-born individuals (from Ivory Coast, Liberia and Guinea when origin known) and 2 captive-born individuals - NC: 10 wild-born individuals (from Cameroon) - C: 20 wild-born individuals (from Gabon and Equatorial Guinea when origin known) - E: 23 wild-born individuals (from DRC, Tanzania, Uganda, Zambia and Rwanda)
Lester <i>et al.</i> 2021 [7]	F_{ST} computed with Arlequin 3.5.2.2	Microsatellites	939 wild individuals in total across 44 locations and across the 4 subspecies. - W: 523 individuals from 21 locations (in Guinea Bissau, Guinea, Senegal, Mali, Sierra-Leone, Liberia, Côte d'Ivoire) - NC: 46 individuals from 2 locations (in Nigeria and Cameroon) - C: 133 individuals across 9 locations (in Gabon, Cameroon and Congo) - E: 237 individuals across 12 locations (in Uganda, Rwanda, DRC and CAR)
Fischer <i>et al.</i> 2006 [8]	Hudson's F_{ST}	Autosomal regions (22,400 bp in total)	30 wild-born individuals in total across the Western, Central and Eastern subspecies. - W: 10 individuals from Sierra-Leone - C: 10 individuals from Gabon - E: 10 individuals from Kenya

2.2. Results

We see in **Figure S2B-E** that for $M_b=0.01$ and for the four subspecies, the simulated IICR is very close to the empirical PSMC and the IICR without between-subspecies migration rates. Furthermore, adding gene flow between subspecies decreased the F_{ST} values (**Figure S2A**), though they are still higher than empirical F_{ST} . For $M_b=0.05$ and $M_b=0.1$, the IICR curves are shifted towards higher values, especially during periods where the

IICR is already high. Interestingly though, the shape of the curves are maintained, particularly for W and NC chimpanzees. For C and E chimpanzees, there is an increase in the IICR between 500 and 600 kya which is not present in the model without gene flow between subspecies. Regarding F_{ST} values, they are on average 2 and 2.5 times smaller for $M_b=0.05$ and $M_b=0.1$ than for $M_b=0$, respectively. Compared to empirical values, the simulated F_{ST} fall within the distribution of F_{ST} retrieved from Lester *et al.* 2021 for the following pairs of subspecies W-NC, W-C, W-E and C-E, and are smaller than the values from Fischer *et al.* 2006 except for C-E F_{ST} for which the simulated F_{ST} are still 1.5 to 2 times higher.

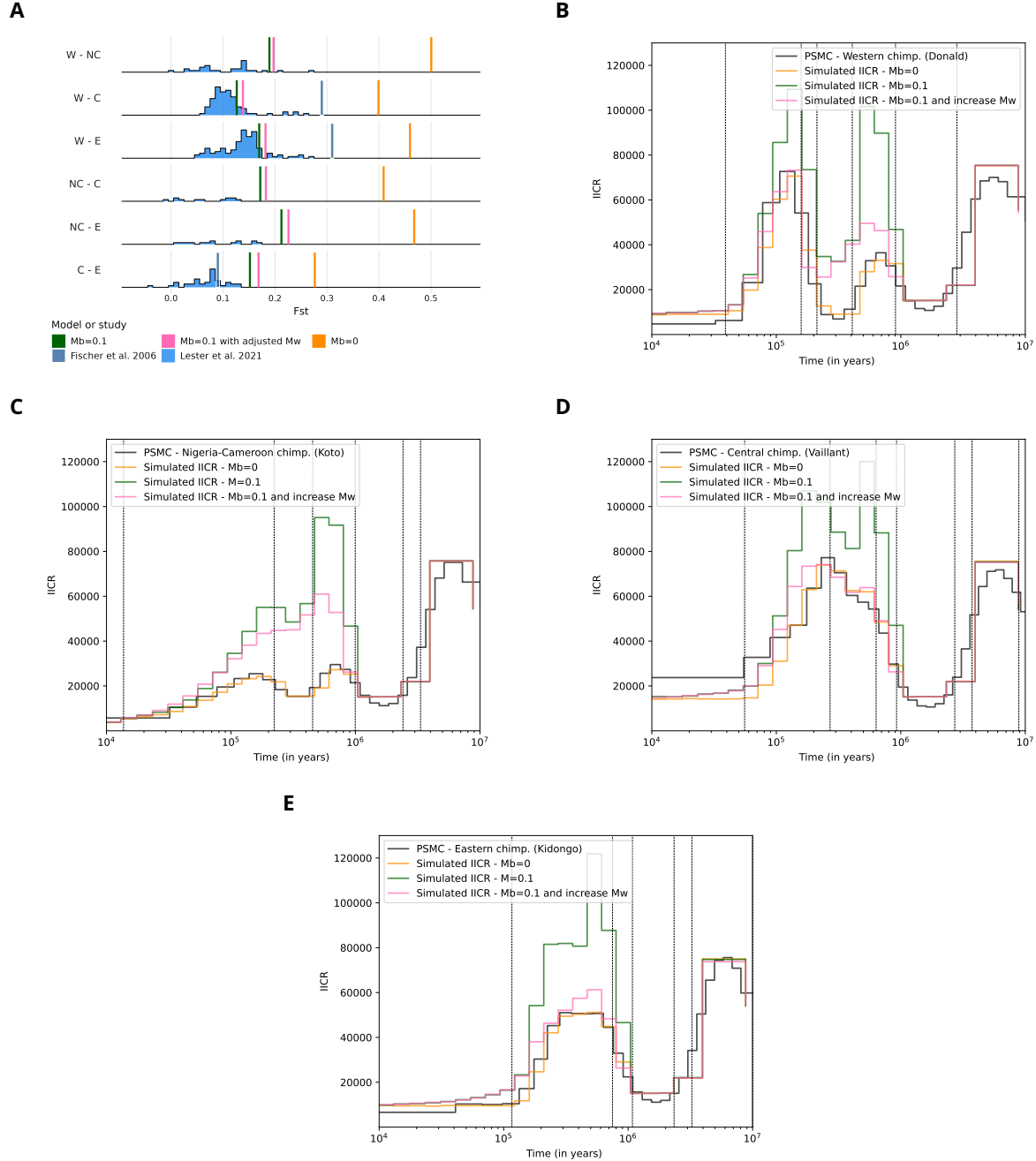


Figure S3 Simulated F_{ST} and IICR for the general tree model when adding a migration rate M_b between subspecies for $M_b = 0.1$, and adjusting the within-subspecies (M_w) migration rates inferred by SNIF to fit the empirical PSMC. A. Simulated F_{ST} and empirical F_{ST} retrieved from Lester *et al.* 2021 [7] and Fischer *et al.* 2006 [8] 2006. B-E. Simulated IICR and empirical PSMC for Western (B), Nigeria-Cameroon (C), Central (D) and Eastern (E) chimpanzees.

Since the shape of the IICR curves were maintained despite the addition of between subspecies migration rates, and since the fit of the F_{ST} was improved in these new models, we increased the within-species migration rates that were inferred by SNIF. The reason for this is that theoretical studies show that this leads to a decrease in the IICR and thus a better fit of the empirical PSMC. Results for $M_b=0.1$ are shown **Figure S3**. For C and E chimpanzees, we recovered the empirical PSMC. For W chimpanzees, the most recent increase and decrease (forward in time) in the PSMC is well fitted, while the second more ancient one is still higher than the empirical curve. Finally, for NC chimpanzees, we did not manage to fit the empirical PSMC when adjusting the within-species migration rates. Increasing the within-species migration rates leads to removing the period of low IICR between 300 and 500 kya, whichever the combination of within-subspecies migration rates we used. Regarding the F_{ST} values, they are almost identical to the model where we did not adjust the within-species migration rates.

2.3. Discussion

This supplementary analysis was a first attempt at adding gene flow between subspecies to improve the fit of the model to the observed levels of between subspecies genetic differentiation and to account for patterns of isolation by distance that have been identified by some studies [6,7]. By adding migration rates between subspecies in our general tree model, we expected the IICR to differ significantly and thus not fit the empirical PSMC. Surprisingly though, by adjusting the within-species migration rates originally inferred by SNIF, we managed to keep the fit of the simulated IICR for Western, Central and Eastern chimpanzees. We did not succeed in doing so for Nigeria-Cameroon chimpanzees, which is difficult to explain. Furthermore, as we expected, adding gene flow between subspecies reduced their genetic differentiation and better match empirical values of F_{ST} , though we are aware that direct comparison might be tricky as the other studies had a different sampling scheme, different types of genetic data, and/or estimated genetic differentiation with different estimators than ours.

These results show that it is therefore feasible to find a demographic model with structured populations and between-subspecies gene flow that would fit both the PSMC curves and genetic differentiation for at least three of the four chimpanzee subspecies. As we mention in the main text, the next step would be to add different between-subspecies migration rates depending on the spatial distribution of the subspecies. For instance, adding a higher migration rate between Central and Eastern chimpanzees than between Western and Eastern chimpanzees would probably be more realistic. Increasing M_b between Central and Eastern chimpanzees would also be more consistent with the patterns of IBD found in these two subspecies [6], and reduce genetic differentiation that would better match the empirical F_{ST} computed by Fischer *et al.* 2006 [8]. Finally, it is possible that decreasing the global migration of Nigeria-Cameroon chimpanzees would help recover the fit to the empirical PSMC. Altogether, these results are very promising and suggest that adding spatial and population structure is not only feasible but likely important.

3. Supplementary Information S3: Spatial Structure Confounds Ancient Admixture Estimates

Several studies have inferred ancient admixture events between lineages of the *Pan* genus [1–4] (cf. Brand *et al.* [5] for a review). The mode and tempo of these putative events vary greatly with little consistency across studies (see the Discussion section in the main manuscript). This could suggest a complex admixture history involving the different subspecies and the bonobos, of which previous research works identified only some elements. Alternatively, the inferred admixture events might also be caused by the confounding effect of population structure (or other departures from model assumptions) which could generate different results across studies, depending on the models, statistics, samples, *etc.* used by the authors.

For instance, de Manuel *et al.* [1] inferred introgression between chimpanzees and bonobos using different approaches including the D -statistic [11], TreeMix method, and SFS -based demographic inference (Site Frequency Spectrum). However, like most previous studies, they assumed panmixia within each subspecies, and thus did not test for ancient population structure, which is an increasingly recognised confounder for the detection of admixture [9,11–13].

Here, we implemented a simple linear stepping-stone model to test the hypothesis that population structure alone, without any gene flow between bonobos and chimpanzees, could replicate the observed D -statistics. We found that non-zero D -statistics could indeed be generated, following a gradient similar to what is observed on the empirical data. Noteworthy, our model not only predicted the empirical levels of D but it also predicted realistic values of the nucleotide diversity and the F_{ST} among chimpanzee subspecies. Altogether, this suggests that population structure can reproduce several signals of present-day genetic diversity, including purported admixture ones. It thus calls for more caution regarding the strength of the evidence favoring ancient admixture over population structure in the extant *Pan* genus, in a way that is similar to that suggested in recent research on the genus *Homo* [9,12,13].

3.1. Methods

3.1.1 Demographic Model

We implemented a simple linear (one-dimensional) stepping-stone model (**Figure S4A**), where each subspecies of chimpanzee is treated as a "metapopulation" of five connected demes of respective size N_i diploids. Bonobos are modelled in a similar way, except that no bonobo subspecies is currently recognised. We will abbreviate henceforth: Western chimpanzees as "W", Nigeria-Cameroon as "NC", Central as "C", Eastern as "E", and Bonobos as "P" (for *paniscus*). Thus, the full model is composed of five metapopulations of five demes each.

For simplicity, we set the deme size in each metapopulation using the θ_W estimate produced by de Manuel *et al.* [1] (**Table S2** in the original article), with $N = \theta_W / (4n\mu)$, where n is the number of demes we consider in this study for each metapopulation ($n = 5$). We used the same mutation rate as de Manuel *et al.*, *i.e.*, $\mu = 1.2 \times 10^{-8}$ per bp per generation. This led us to set $N_{NC} = 5,559$ diploids, $N_E = 6,498$, $N_C = 9,462$. For Western chimpanzees, we found that the original θ (leading to $N_W = 3,475$) produced an excess of nucleotide diversity compared to empirical values and we thus set it to a lower value ($N_W = 600$). We fixed the deme size in bonobos to $N_P = 4,000$ (about half N_C [14]), in the absence of the θ_W estimate in de Manuel *et al.* [1].

Within all metapopulations, demes are connected to their neighbours with a per-generation symmetric migration rate of $m_w = 10^{-2}$ (*i.e.*, $M_{i,j} = m_w N_i$ diploid individuals migrating from deme i to deme j at each generation, backward). The different chimpanzee metapopulations are connected to the neighbouring metapopulation by a low-level (symmetric) gene flow of $m_b = 8 \times 10^{-4}$. The migration rate within the bonobo metapopulation was fixed at $m_{w,P} = 1.1 \times 10^{-4}$.

We acknowledge that several of these parameter values were fixed arbitrarily, since our purpose was not to infer parameters. We intended to showcase how a simple model can explain empirical data (when accounting for known population structure, without requiring unknown ancient admixture events), especially in producing apparent signatures of putative ancient admixture events.

Metapopulations split times were implemented in the model using the average of the divergence times reported in de Manuel *et al.* [1] (Figure 3 in the original article). Specifically, NC started to expand from W at 250 kya, E from C at 160.5 kya, the two ancestral chimpanzee lineages at 588.5 kya, bonobos from chimpanzees at 1.88 Mya. Each expansion is modelled, forward in time, by successive founding of each within-metapopulation deme, every 200 years. We note that these founding events correspond exclusively to the instantaneous creation of a deme of size N_i (*i.e.*, no bottlenecks).

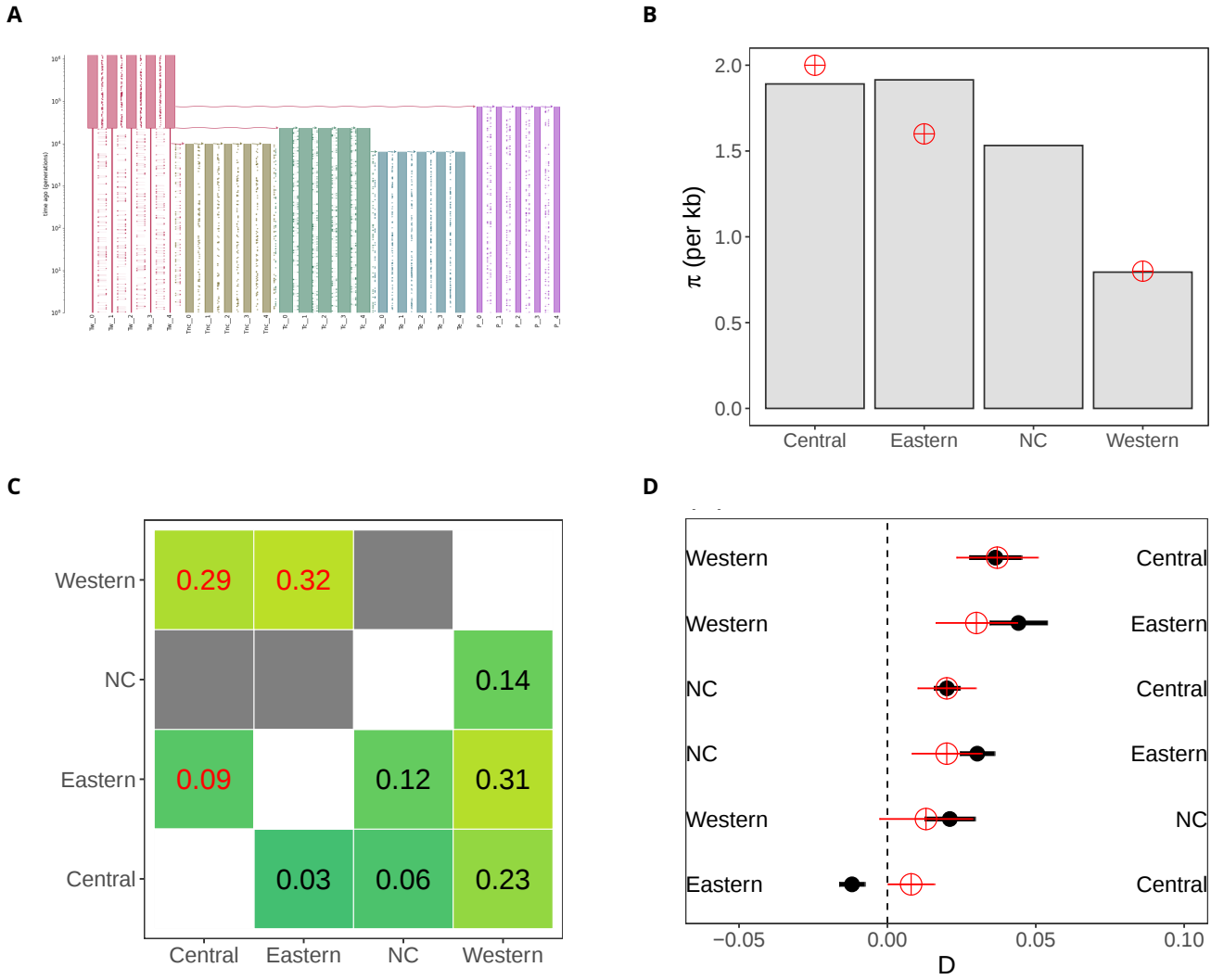


Figure S4 Model and statistics calculated under a no-admixture structured population model. A. Representation of the simulated demographic model. Each color corresponds to a chimpanzee subspecies or to the bonobos. Red: W, olive: NC, green: C, blue: E, purple: bonobos. B. Nucleotide diversity per kbp estimated for each population, for the data simulated under the structured population model (gray bars), and on the empirical data (red points). No NC samples were available in the [8] study. C. Pairwise F_{ST} obtained on the simulated data (lower-right triangle, black text) and on the empirical data (upper-left triangle, red text). We note that in the original article, the NC population was not studied [8], thus appearing here as empty gray cells. D. D -statistics from the simulated data (black points with 95% confidence interval) and empirical data (red points). The D -statistic values were calculated as $D(X, Y, P, O)$ with "P" the bonobos and "O" the outgroup (see further Section 3.1.3 for the simulated data and Section 3.1.4 for the empirical data). On the plot, X populations are labeled on the right and Y on the left.

For the time period prior to the first split between chimpanzee metapopulations (588.5 kya), the deme sizes in the ancestral chimpanzees were set to $N_{anc} = 7,000$ and the migration rate between the demes of this ancestral metapopulation was set to the same value as the present-day bonobo migration rate (*i.e.*, $m_{anc} = m_{w,P} = 1.1 \times 10^{-4}$). All parameters for the remaining bonobo metapopulation were kept the same.

It should be clear that this model assumes that bonobos and chimpanzees never exchange gene flow at any time of their history after they separated 1.88 Mya.

The total number of non-redundant parameters in our model is 15, making it less parameter-rich than the panmictic model of de Manuel *et al.* [1]:

- 1 parameter for the number of demes per metapopulation (set to 5),

- 2 parameters for within-metapopulation migration rate in chimpanzees and bonobos (set to $m_w = 10^{-2}$ and 1.1×10^{-4} , respectively),
- 1 parameter for between-metapopulation migration rate in chimpanzees (set to $m_b = 8 \times 10^{-4}$),
- 5 parameters for deme sizes (N_i),
- 1 parameter for ancestral deme size (N_{anc}),
- 4 expansion times (*i.e.*, the founding of the different metapopulations),
- 1 parameter for the delay between successive founding of demes (set to 200 years).

3.1.2 Simulations

Using msprime v1.1 with Hudson's coalescent algorithm [15,16], we simulated genetic data for 20 chromosomes of 20 Mbp each ($G = 400$ Mbp), sampling 15 diploid individuals in the central deme of each metapopulation. This resulted in a total of 75 diploid genotypes per segregating site. Mutations were generated using a binary model, with two flipping alleles, at a rate of 1.2×10^{-8} per bp per generation. Recombination was assumed uniform, with rate 0.7×10^{-8} per bp per generation. We used a generation time of 25 years for both chimpanzees and bonobos [1].

3.1.3 Statistics

Based on the simulated biallelic genetic data, we calculated, using the `scikit-allel` v1.3.5 package:

- The nucleotide diversity π for each population sample (average number of pairwise differences).
- The differentiation index F_{ST} (Hudson's formula based on expected heterozygosities) between all pairs of chimpanzee populations.
- The D -statistic, as $D(X, Y; bonobo, outgroup)$ with X and Y being any chimpanzee population sample, and *outgroup* being a virtual diploid genotype homozygous for the ancestral allele. To calculate the standard error (SE), we used a block-weighted jackknife with a typical block size of around 5 Mbp [17]. Confidence intervals at 95% were calculated as $D \pm 1.96 \times SE$.

3.1.4 Observed data

We retrieved the empirical statistical values from previously published papers:

- π (average pairwise differences): from Fischer *et al.* [8], calculated on 26 intergenic sequences totalling 22.4 kbp for around 10 diploids in each sampled population.
- F_{ST} (Hudson's formula): from Fischer *et al.* [8], calculated on the same dataset as π .
- D -statistic: from de Manuel *et al.* [1], calculated as $D(X, Y, bonobo, humans)$ using whole-genome sequences on a set of 68 *Pan* samples. We used the D values estimated by the authors when aligning the *Pan* sequences on the human *hg19* assembly.

3.2. Results

Our 1D stepping-stone structured population model replicated the observed gradient of D -statistics across focal chimpanzee subspecies (**Figure S4D**). It further predicted the empirical values of between-chimpanzee F_{ST} (with the Central-Eastern being slightly underestimated in our simulations) (**Figure S4C**), as well as the nucleotide diversity, with a slight excess of diversity for Eastern chimpanzees (**Figure S4A**) (which likely results from the N_E value that we extracted from [1]).

In conclusion, these results show that the ancient admixture inferred in the *Pan* genus might not be robust to ancestral population structure.

We further investigated the variation of the D -statistic as a function of the ancestral connectivity, *i.e.*, the connectivity within the metapopulation ancestral to extant chimpanzees (and further, extant *Pan* species) from 588.5 kya towards the past. To this end, we sampled $N_{anc}m_{anc}$ values from 10^{-3} to 10, every 0.2 on a $\log_{10}$ -scale. Keeping N_{anc} fixed at 7,000 (cf. previous model), we derived m_{anc} according to the composite parameter $N_{anc}m_{anc}$. All other demographic and simulation parameters were kept the same as in the previous model, except for genome size, restricted to 10×10 Mbp chromosomes for computational reasons. We estimated D between present-day Central and Western chimpanzees: $D(C, W, bonobo, outgroup)$.

Our results (**Figure S5**) show that the D -statistic values follow a sigmoid curve, "saturating" at zero for the highest $N_{anc}m_{anc}$ values (towards the right). This is expected, since with such high connectivity, the population model becomes nearly panmictic, and it does not incorporate admixture from bonobos into C lineages. The curve also plateaus around 0.6 for the lowest $N_{anc}m_{anc}$ range. Interestingly, we note that the D -statistic values start to become significant, in our model, around $N_{anc}m_{anc} = 1$ migrant per generation. A steep variation in D is observed for connectivity values ranging between around 0.06 and 0.6 migrants per generation. These results confirm that very significant values of the D -statistic can be produced under a structured population model in the absence of admixture, and that they depend mostly on the level of the ancestral connectivity within the metapopulation ancestral to the tested samples. We show that D can reach very high values (0.6) compared to the empirical values reported here, confirming that the level and significance of the D statistic cannot be used as indisputable evidence for admixture.

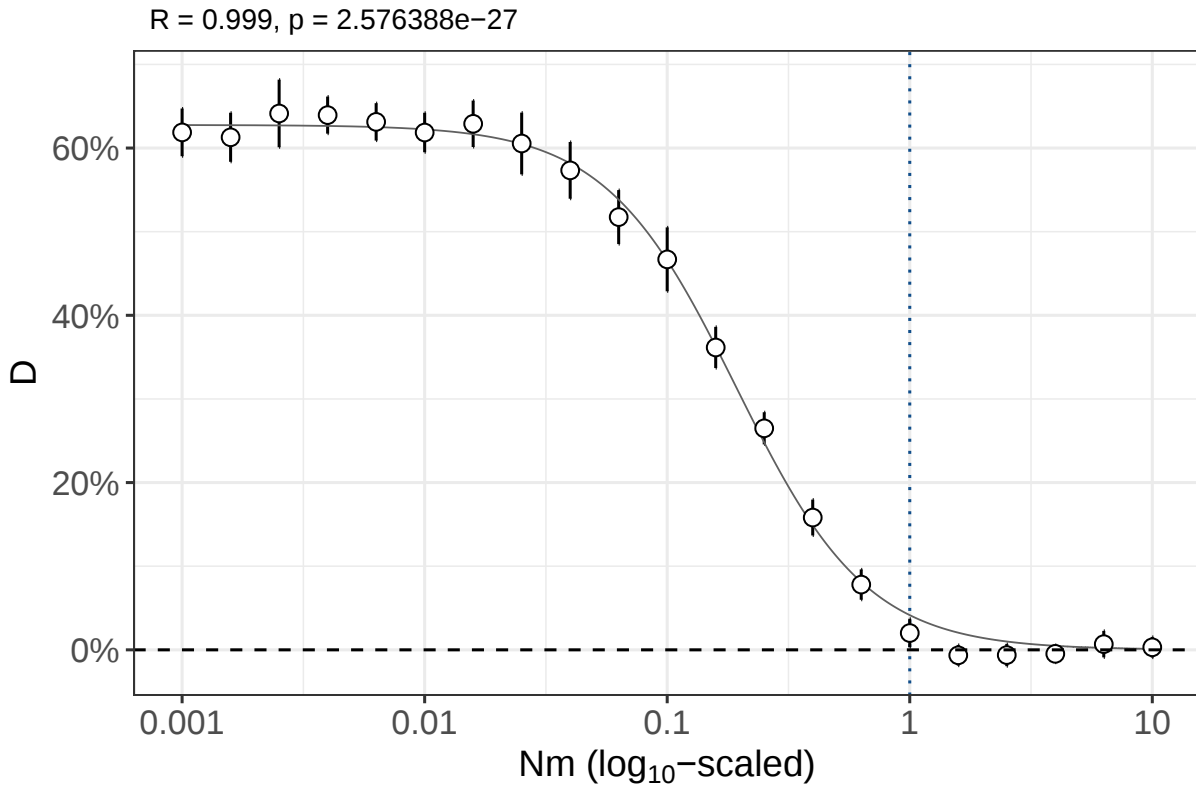


Figure S5 Distribution of the D -statistic as a function of ancestral migration rates. The D -statistic was computed as $D(C, W, P, O)$ for our no-admixture structured model, where we allowed the migration rate in the ancestral metapopulation to vary. This ancestral metapopulation corresponds to the period prior to 1.88 Mya, *i.e.*, before the foundation of the bonobos (cf. model description). We allowed $N_{anc} \times m_{anc}$ to vary from 10^{-3} to 10. The error bars represent the confidence intervals at 95%. The x -axis is $\log_{10}$ -scaled. The vertical blue dotted line represents the first tested $N_{anc}m_{anc}$ value from decreasing order with significant D -statistics. The gray curve is a logistic fit to the empirical scatter plot. The Pearson's correlation coefficient representing the fit of the curve to the empirical data is reported in the title.

Table S3 Prior ranges of the t_i (times at which migrations rates are allowed to change, delimiting the components) given to SNIF for the final analysis. Note that here the times are given in years, but they have to be divided by the generation time when given to SNIF.

Subspecies	c	Priors of t_i (in years)
Western	7	(2e4, 1e5), (1e5, 3e5), (1e5, 3e5), (3e5, 7e5), (7e5, 1.5e6), (1.5e6, 5e6)
Nigeria-Cam.	7	(1e4, 1e5), (1.5e5, 3e5), (3.5e5, 5e5), (8e5, 1.1e6), (2e6, 3e6), (4e6, 7e6)
Central	8	(5e4, 2e5), (2e5, 4e5), (5e5, 2e6), (5e5, 2e6), (2e6, 5e6), (2e6, 5e6), (6e6, 1e7)
Eastern	7	(5e4, 2e5), (4e5, 1.5e6), (4e5, 1.5e6), (2e6, 6e6), (2e6, 6e6), (7e6, 1e7)

Table S4 Distribution of inferred n , the number of demes of the n -island models.

Subspecies	Min	25% quantile	Median	Mean	75% quantile	Max
Western	12	17	21	23	31	48
Nigeria-Cameroon	6	10	11	11	13	20
Central	13	16	18	21	20	55
Eastern	8	11	13	13	15	23

Table S5 Distribution of inferred N , the deme size of the n -island models (in number of diploids).

Subspecies	Min	25% quantile	Median	Mean	75% quantile	Max
Western	112	239	305	285	335	437
Nigeria-Cameroon	616	1009	1154	1174	1311	1980
Central	227	589	737	694	834	1101
Eastern	561	728	801	863	975	1306

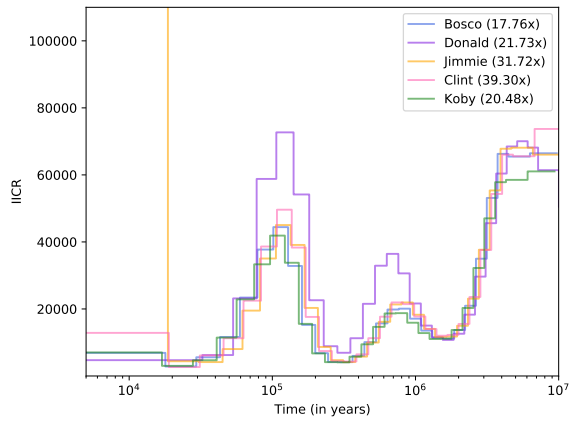
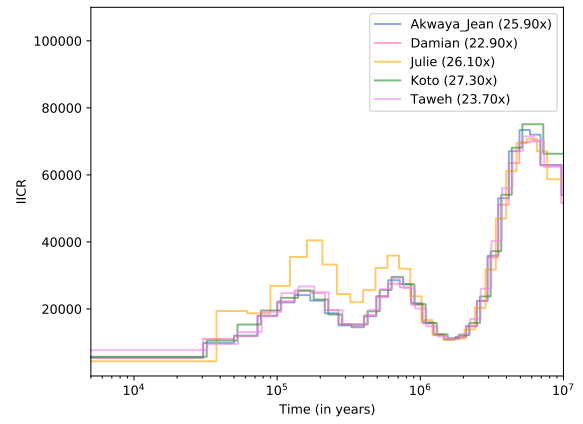
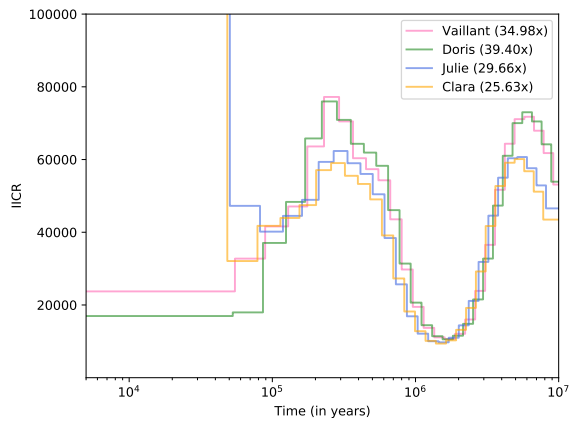
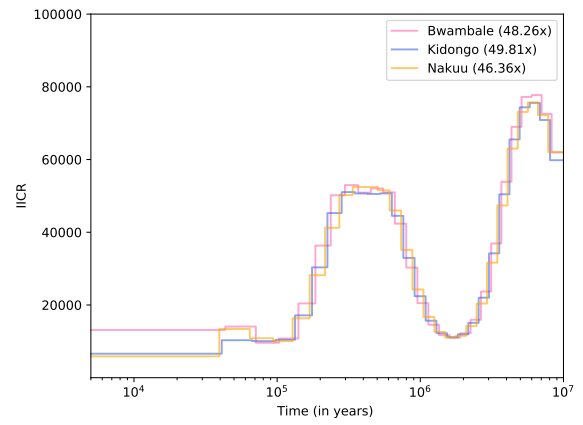
A**B****C****D**

Figure S6 Empirical PSMC curves of chimpanzees used as input data for the inferential process. A. Western chimpanzees, B. Nigeria-Cameroon chimpanzees, C. Central chimpanzees and D. Eastern chimpanzees, computed using PSMC files provided to us by Prado-Martinez *et al.* [10].

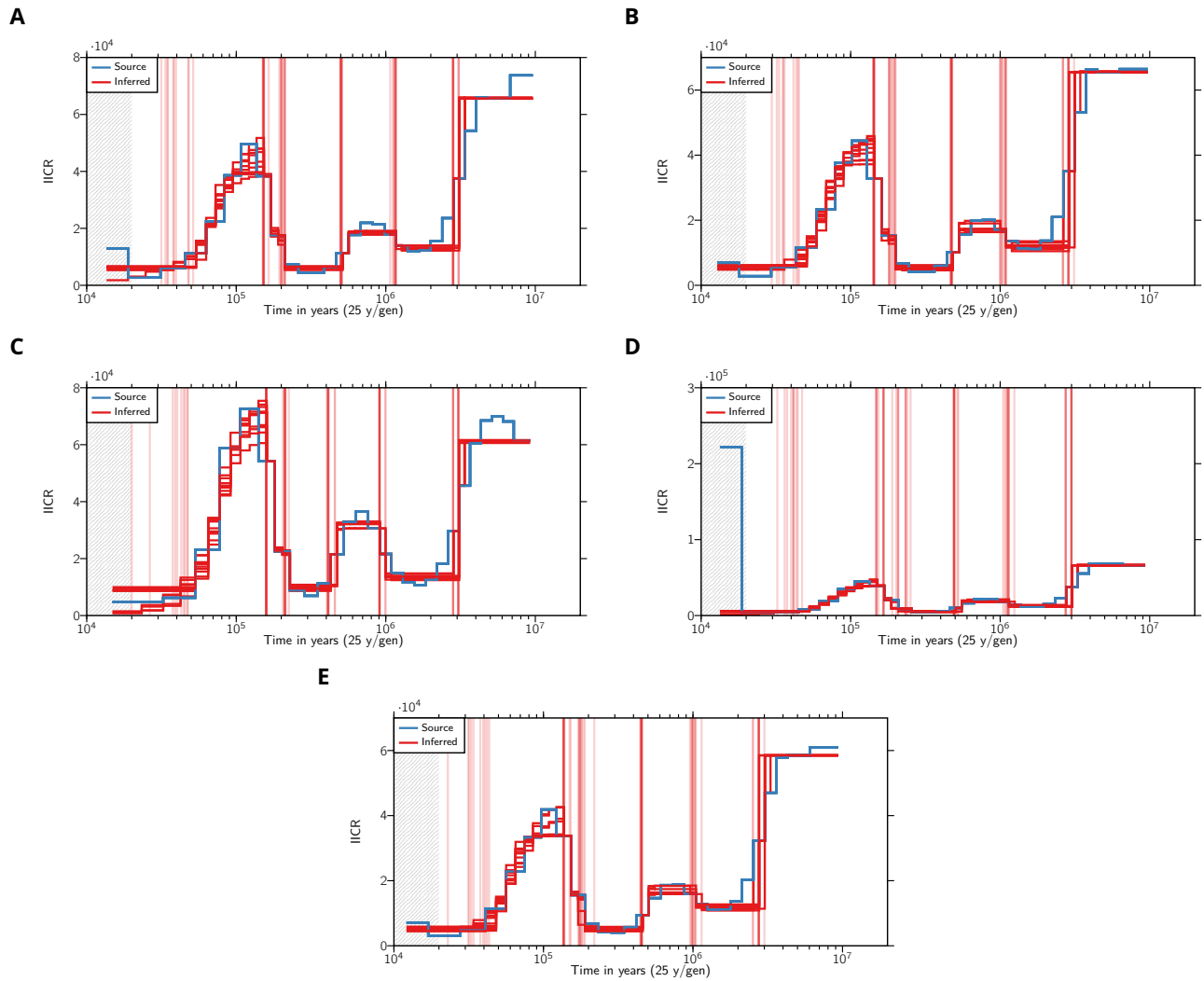


Figure S7 Inferred IICR curves (in red) and empirical PSMC (in blue) for the five Western common chimpanzees. Each curve is a repetition of SNIF. The vertical red lines highlight the times at which there is an inferred change in migration rate and therefore delimit the components. A. Clint, B. Bosco, C. Donald, D. Jimmie and E. Koby. The grey zone corresponds to a part of the source PSMC which was not taken into account for the fitting of the curve by SNIF (see Material and Methods).

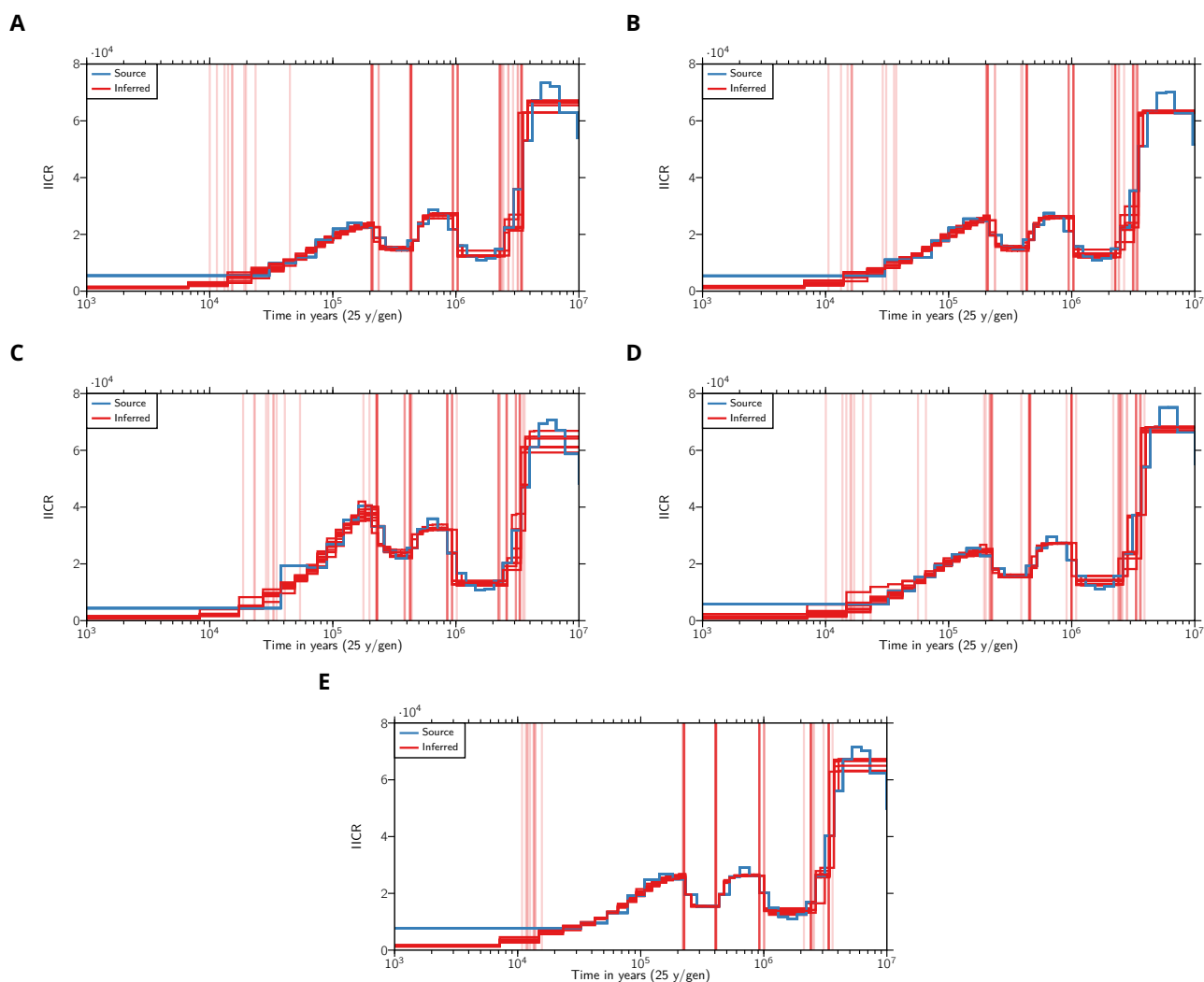


Figure S8 Inferred ICR curves (in red) and empirical PSMC (in blue) for the five Nigeria-Cameroon common chimpanzees. Each red curve is a repetition of SNIF. The vertical red lines highlight the times at which there is an inferred change in migration rate and therefore delimit the components. A. Akwaya-Jean, B. Damian, C. Julie, D. Koto and E. Taweh.

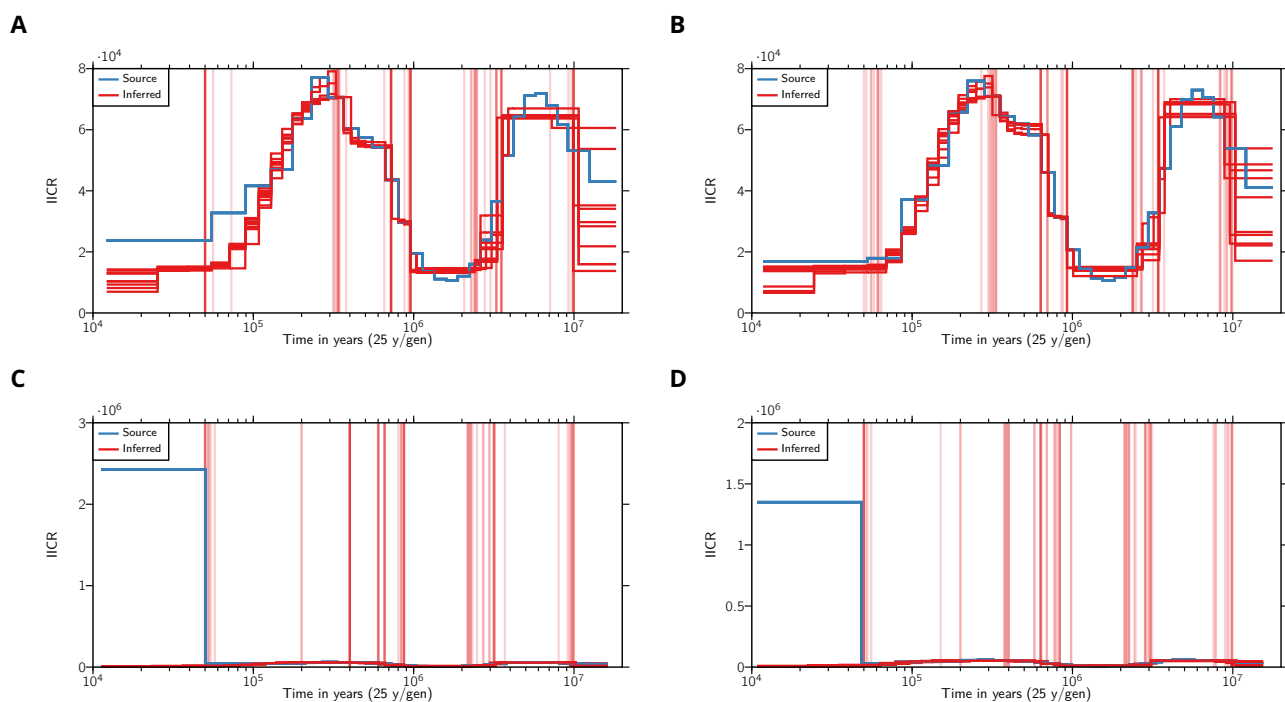


Figure S9 Inferred IICR curves (in red) and empirical PSMC (in blue) for the four Central common chimpanzees. Each red curve is a repetition of SNIF. The vertical red lines highlight the times at which there is an inferred change in migration rate and therefore delimit the components. A. Vaillant, B. Doris, C. Julie and D. Clara.

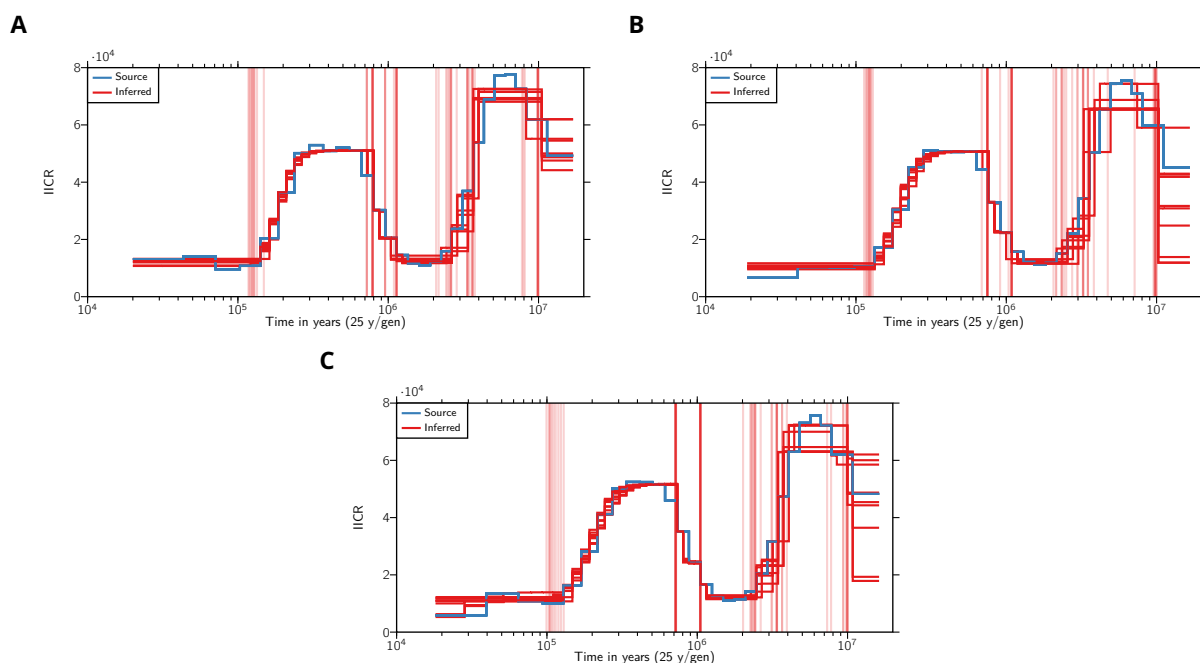


Figure S10 Inferred IICR curves (in red) and empirical PSMC (in blue) for the three Eastern common chimpanzees. Each red curve is a repetition of SNIF. The vertical red lines highlight the times at which there is an inferred change in migration rate and therefore delimit the components. A. Bwambale, B. Kidongo and C. Nakuu.

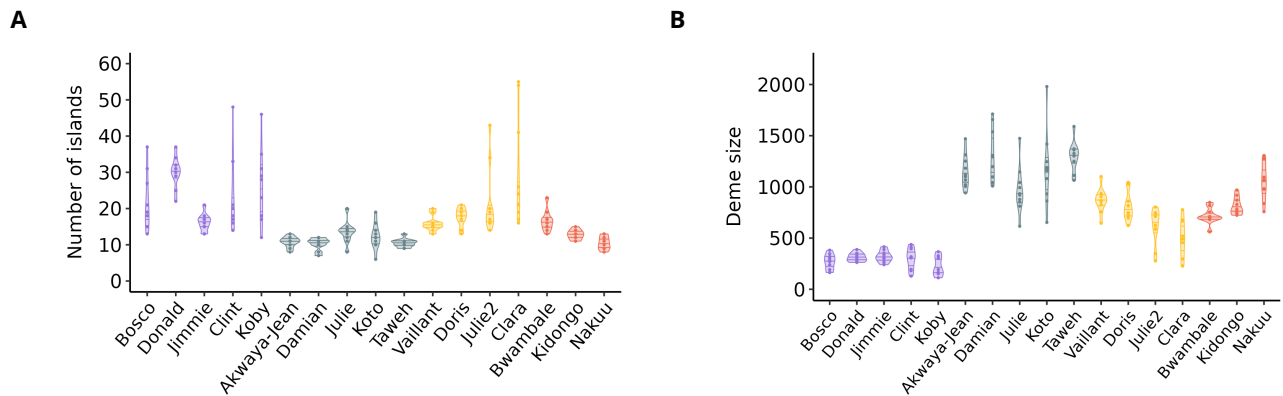


Figure S11 Distribution of the inferred number and size of the demes for each chimpanzee individual. A. Number of islands. B. Deme size (given in number of diploid individuals). Results are given across the 10 repetitions for each individual, using the parameter space shown **Table 1** in the main text of the paper. Horizontal lines in the violins represent the 25%, 50% (median) and 75% quantiles.

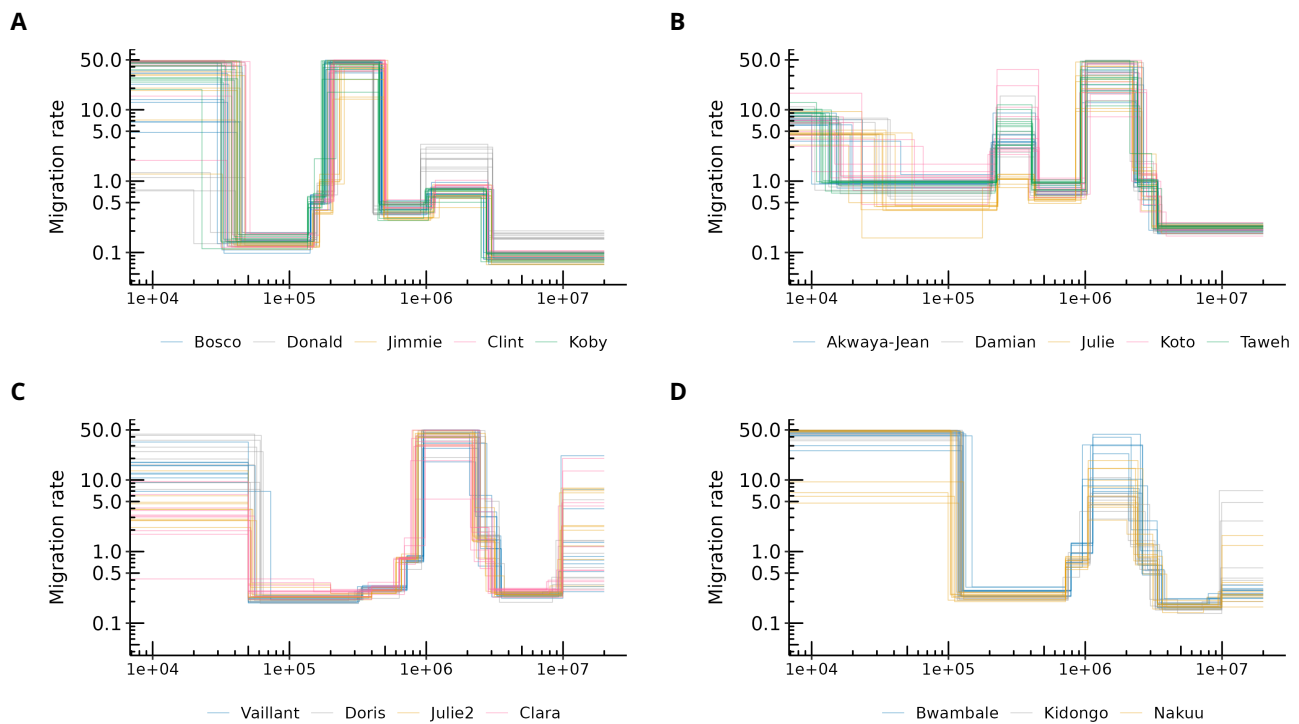


Figure S12 Connectivity graph (migration rates along successive time components) inferred by SNIF coloured by chimpanzee individuals. A. Western chimpanzees, B. Nigeria-Cameroon chimpanzees, C. Central chimpanzees and D. Eastern chimpanzees. Each line corresponds to one inference (one repetition of SNIF) using one PSMC curve (or individual) as observed data.

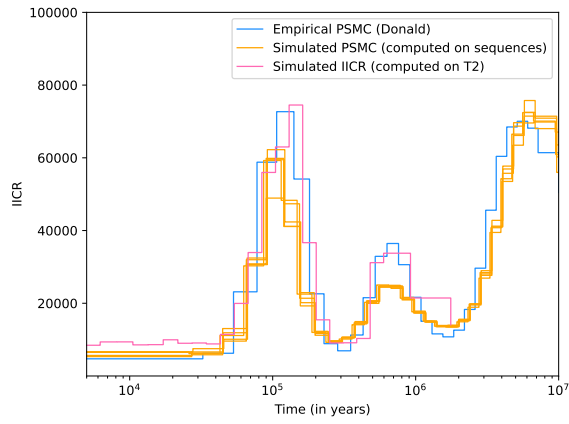
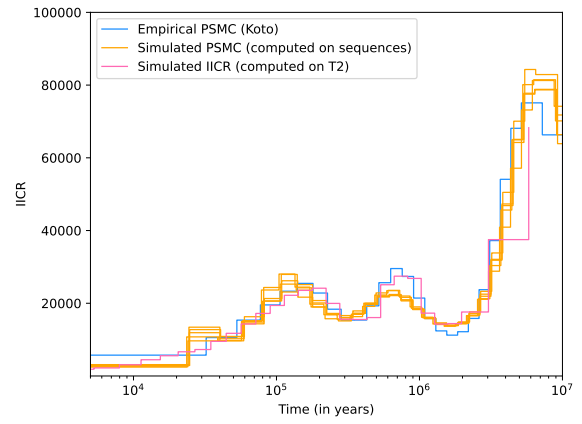
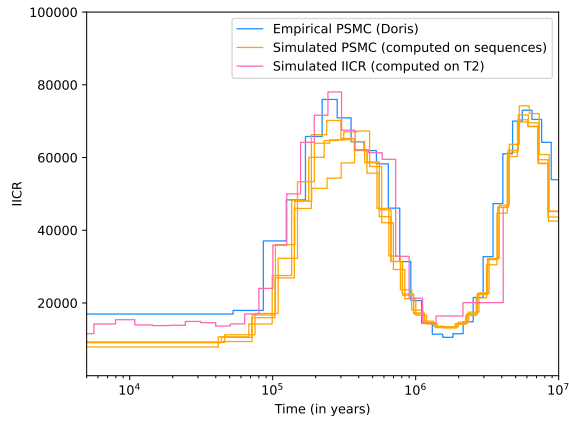
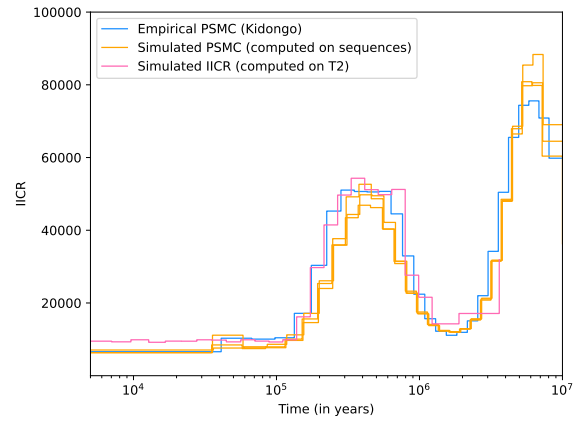
A**B****C****D**

Figure S13 Empirical PSMC (in blue), simulated PSMC computed on simulated sequences (10x100Mb) (in orange) and simulated IICR computed on simulated coalescent times (T_2) (in red), given to SNIF as pseudo-observed data for the validation procedure. A. Western chimpanzees, B. Nigeria-Cameroon chimpanzees, C. Central chimpanzees and D. Eastern chimpanzees.

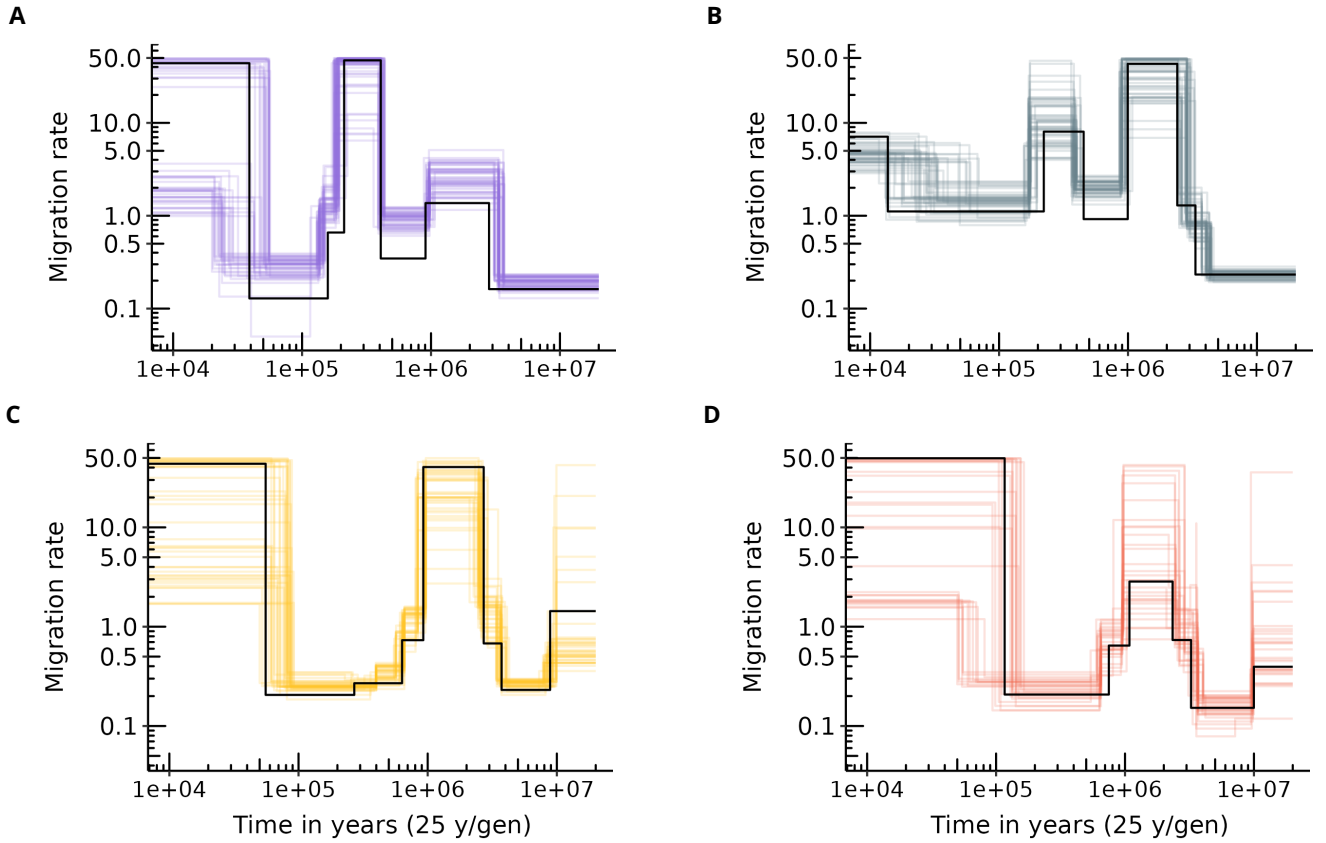


Figure S14 Inferred connectivity graph for PSMC curves computed on simulated genomic data. A. Western, B. Nigeria-Cameroon, C. Central and D. Eastern chimpanzees (see the orange curves in **Figure S13**). Each coloured line corresponds to a repetition of the inference on one simulated PSMC and the black lines correspond to the simulated values.

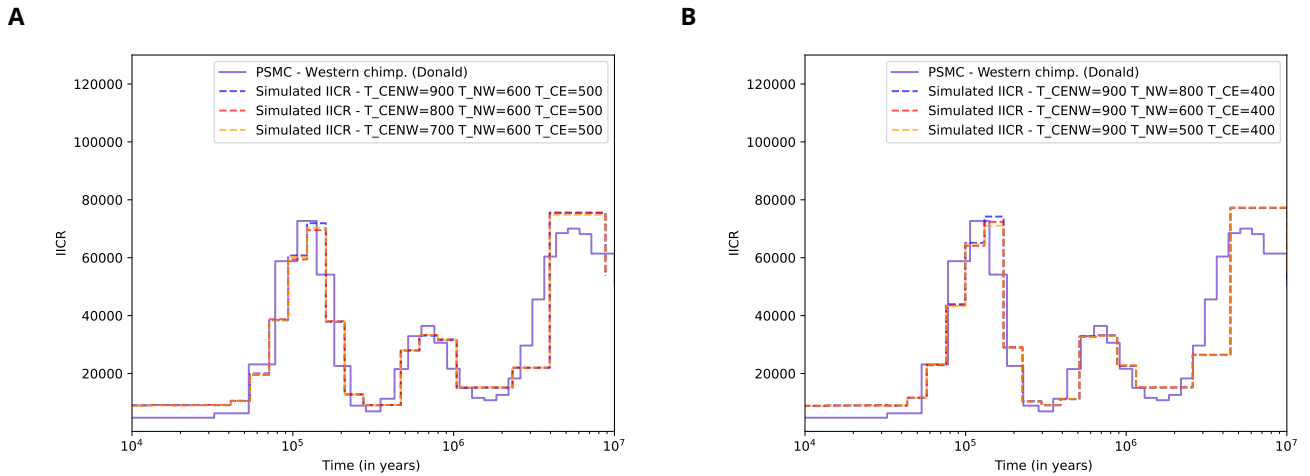


Figure S15 Empirical PSMC (solid line) and simulated IICR (dotted lines) for Western common chimpanzees under the general n-island model Figure 7 in the main text of the paper for different values of splitting times. (A) $T_{CENW} \in \{700, 800, 900\}$, $T_{NW} = 600$ and $T_{CE} = 500$ and (B) $T_{CENW} = 900$, $T_{NW} \in \{500, 600, 800\}$ and $T_{CE} = 400$ (in kya).

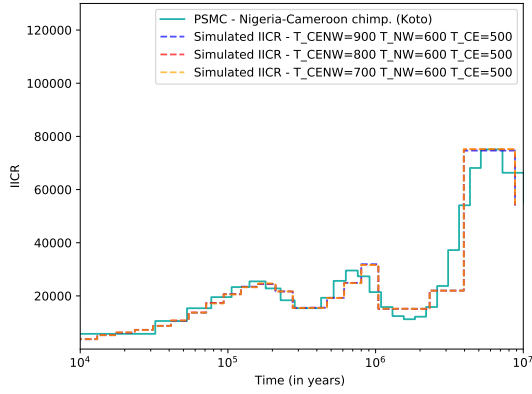
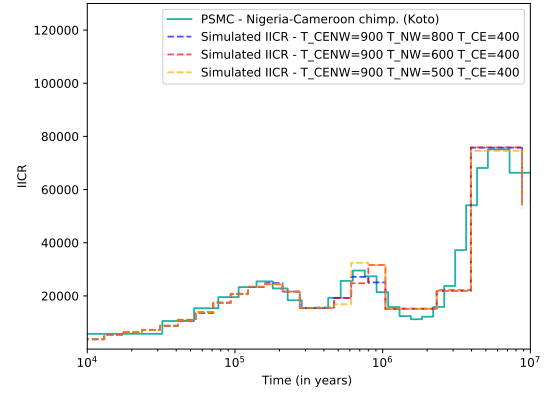
A**B**

Figure S16 Empirical PSMC (solid line) and simulated IICR (dotted lines) for Nigeria-Cameroon common chimpanzees under the general n-island model Figure 7 in the main text of the paper for different values of splitting times. (A) $T_{CENW} \in \{700, 800, 900\}$, $T_{NW} = 600$ and $T_{CE} = 500$ and (B) $T_{CENW} = 900$, $T_{NW} \in \{500, 600, 800\}$ and $T_{CE} = 400$ (in kya).

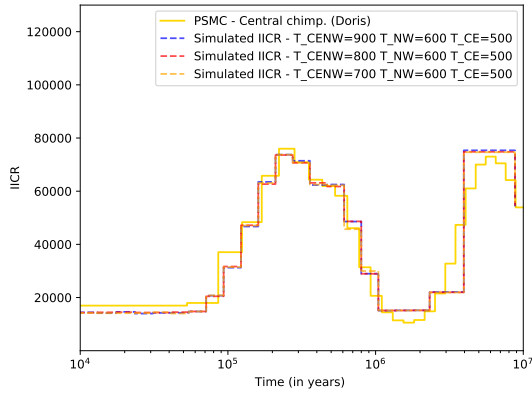
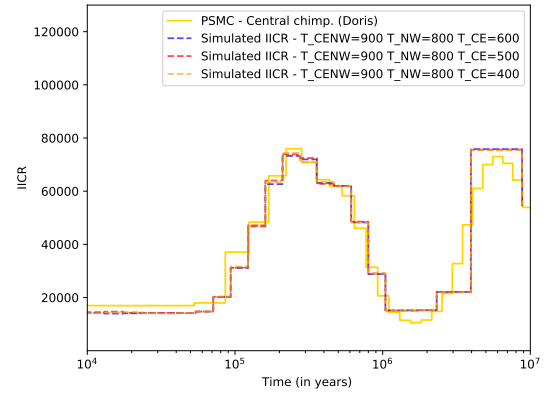
A**B**

Figure S17 Empirical PSMC (solid line) and simulated IICR (dotted lines) for Central common chimpanzees under the general n-island model Figure 7 in the main text of the paper for different values of splitting times. (A) $T_{CENW} \in \{700, 800, 900\}$, $T_{NW} = 600$ and $T_{CE} = 500$ and (B) $T_{CENW} = 900$, $T_{NW} = 800$ and $T_{CE} \in \{400, 500, 600\}$ (in kya).

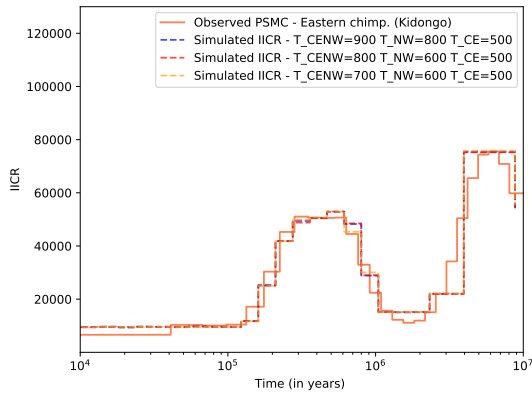
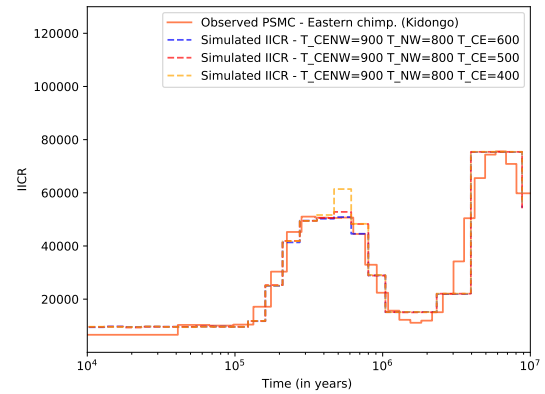
A**B**

Figure S18 Empirical PSMC (solid line) and simulated IICR (dotted lines) for Eastern common chimpanzees under the general n-island model Figure 7 in the main text of the paper for different values of splitting times. (A) $T_{CENW} \in \{700, 800, 900\}$, $T_{NW} = 600$ and $T_{CE} = 500$ and (B) $T_{CENW} = 900$, $T_{NW} = 800$ and $T_{CE} \in \{400, 500, 600\}$ (in kya).

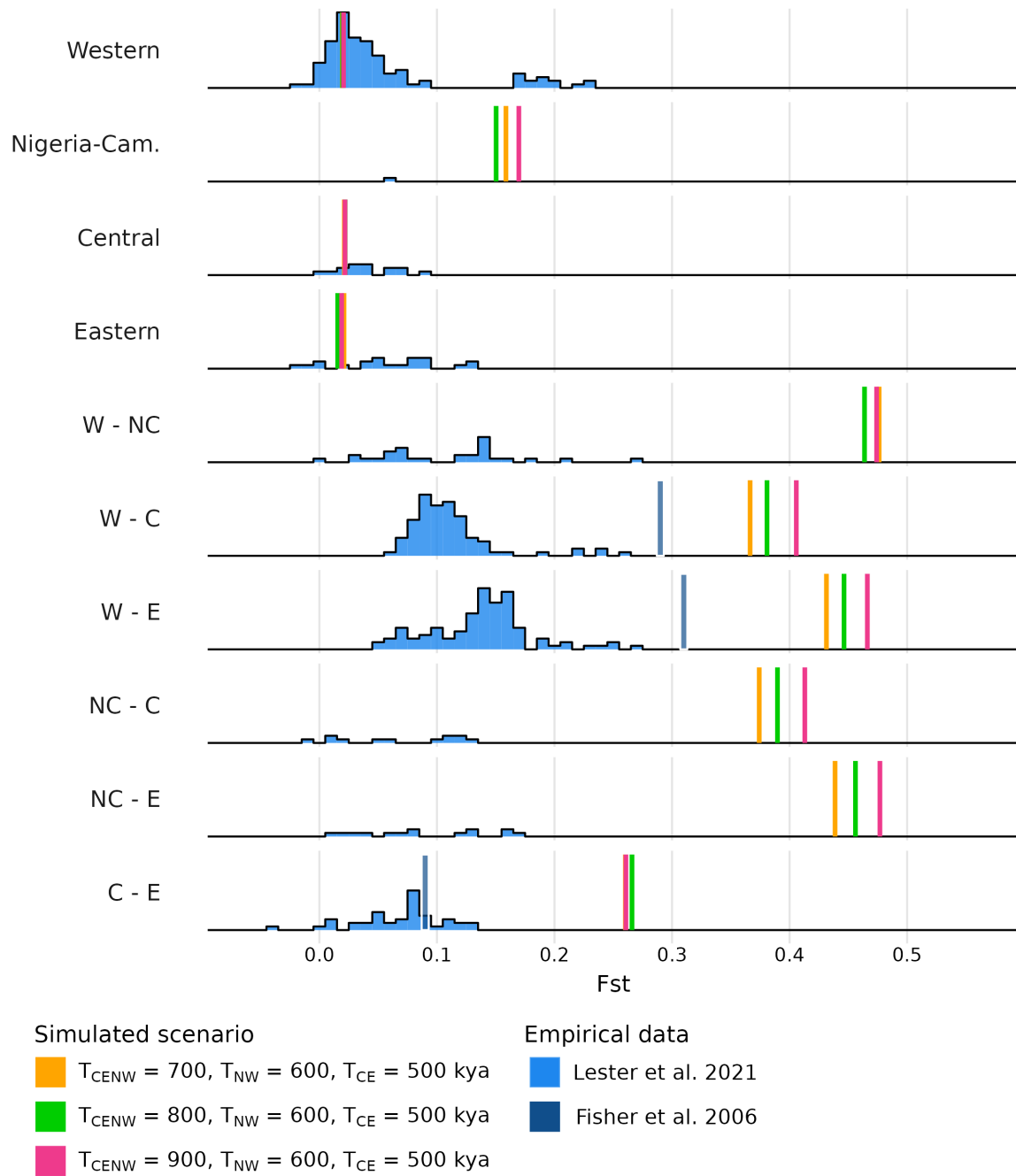


Figure S19 Genetic distance (F_{ST}) between demes of the same subspecies or between demes from different subspecies computed on genomic data simulated under the model Figure 7 in the main text of the paper with $T_{CE} = 500$ kya, $T_{NW} = 600$ kya and $T_{CENW} \in \{700, 800, 900\}$ kya. In blue are the empirical values: histograms were retrieved from Lester *et al.* [7] and the darker blue vertical lines were retrieved from Fischer *et al.* [8].

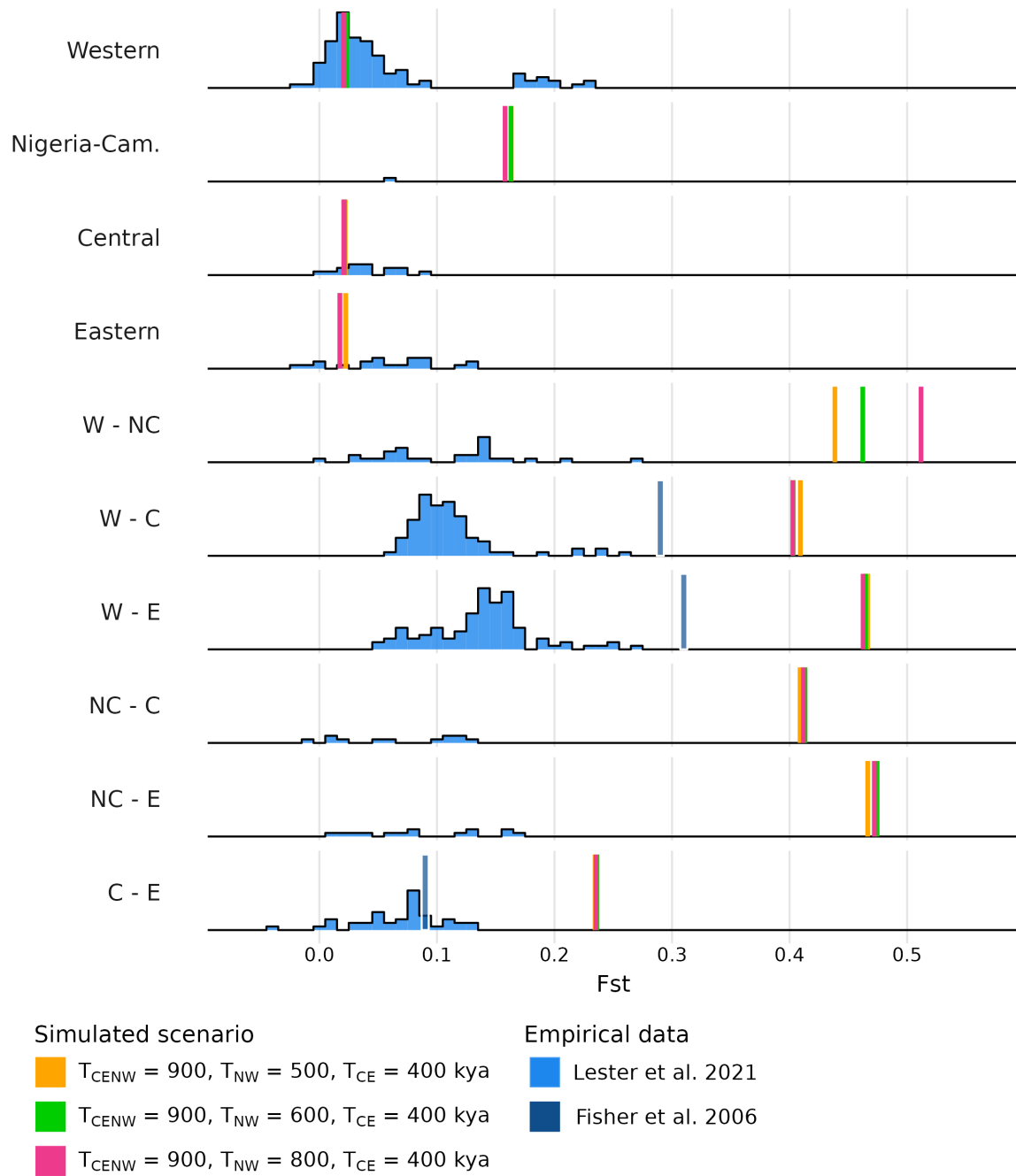


Figure S20 Genetic distance (F_{ST}) between demes of the same subspecies or between demes from different subspecies computed on genomic data simulated under the model Figure 7 in the main text of the paper with $T_{CE} = 400$ kya, $T_{CENW} = 900$ kya and $T_{NW} \in \{500, 600, 800\}$ kya. In blue are the empirical values: histograms were retrieved from Lester *et al.* [7] and the blue vertical lines were retrieved from Fischer *et al.* [8].

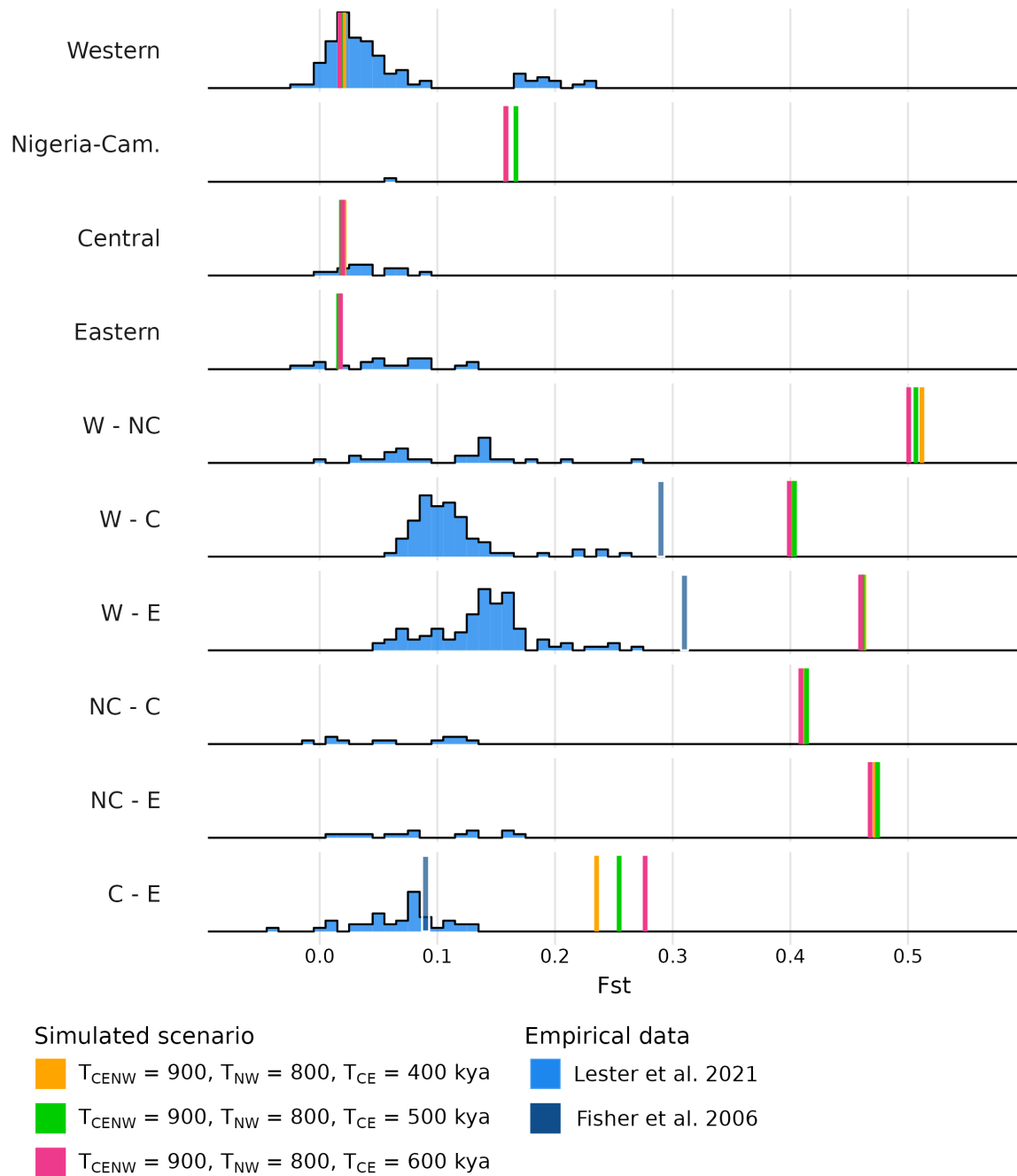


Figure S21 Genetic distance (F_{ST}) within and between subspecies computed on genomic data simulated under the model Figure 7 in the main text of the paper with $T_{CENW} = 900$ kya, $T_{NW} = 800$ kya and $T_{CE} \in \{400, 500, 600\}$ kya. In blue are the empirical values: histograms were retrieved from Lester *et al.* [7] and the blue vertical lines were retrieved from Fischer *et al.* [8].

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