

Supplementary Material

1 *Zosterops* samples

All the samples used for PSMC and their location are in the Supp files. All these samples were published in Leroy et al., 2021 under the BioProject number PRJNA661201. In the study, they differentiate the two highland forms HBHB and GRY. In our study, they will be presented For the inference with SNIF, we used the alignment with the best coverage except for *Z. olivaceus* for which we selected the second best as the best individual was sequenced at high depth.

2 Structure in *Zosteriops* species

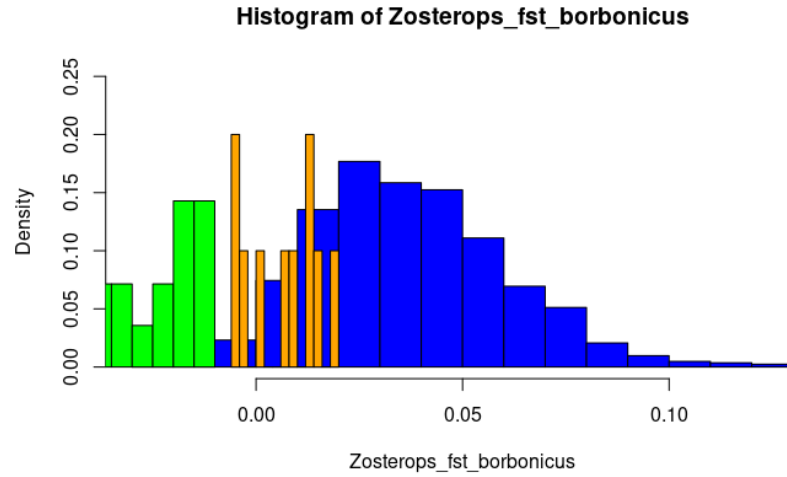


Figure S1: FST values from GBS data

The GBS data are from Gabrielli, Nabholz, et al. (2020).

From the MSMC curves, we supposed that there is structure in the three species of *Zosterops* (see Lounès Chikhi et al., 2024).

3 *Zosterops* PSMC

The PSMC curves of Figure 2 present differences between individuals. We supposed that this variance results from differences in the coverage. For *Z. borbonicus* and *Z. olivaceus*, it is clear that the differences between the

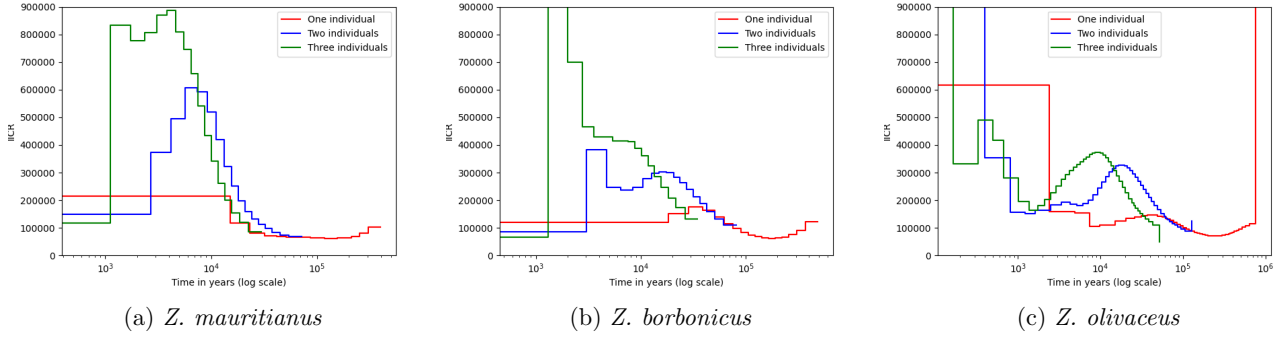


Figure S2: MSMC curves from *Zosterops* whole genomes.

772 PSMC curves are due to the quality of the coverage having an effect on the
 773 PSMC inference (Figure S3). For *Z. olivaceus* other factors like the quality of
 774 the sequences might impact the quality of the alignment. Also, we used the
 775 *Z. borbonicus* reference for the alignment. As *Z. olivaceus* is more distant
 776 than *Z. mauritanus* from the *Z. borbonicus* reference, the quality of the
 777 alignment can be inferior.

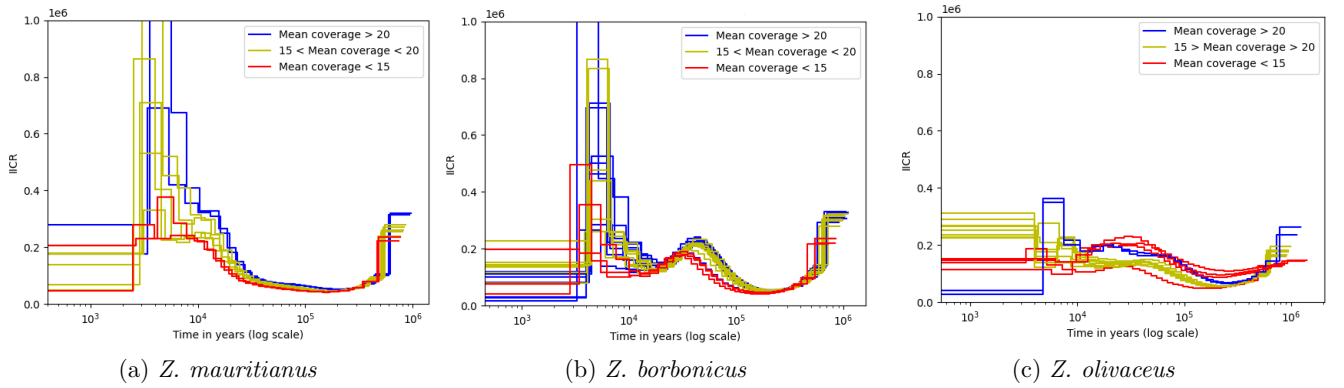


Figure S3: Effect of the coverage on the PSMC. We plotted the PSMC curves for each individual and differentiated them based on mean coverage: higher than 20 in blue, lower than 15 in red, and in between in yellow.

778 We performed 100 bootstrap repetitions on the PSMC of the best in-
 779 dividuals (in grey in Table Supp). The aim is to assess which part of the
 780 curve was robust. Figure S4 shows that the most variable part of the curve is
 781 around 10^4 years. More globally, the robustness has decreased in the recent
 782 past.

783 For all three species, there was a peak around 10^4 years ago. We tried
 784 to remove this peak by testing different atomic time patterns for the PSMC

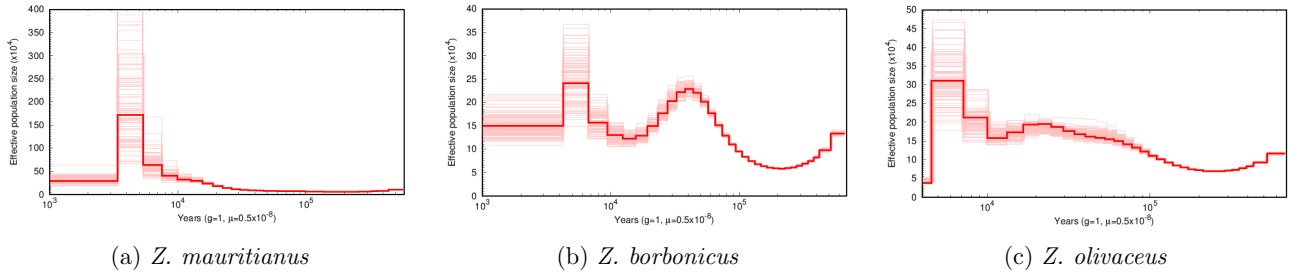


Figure S4: 100 bootstrap repetitions for *Z. mauritanus*, *Z. borbonicus* and *Z. olivaceus*. The initial PSMC curve is thick and the bootstrap repetitions are represented as thinner red curves.

analyses. We could not obtain reliable curves lacking this peak. It seems that all the curves start with the bar more or less high.

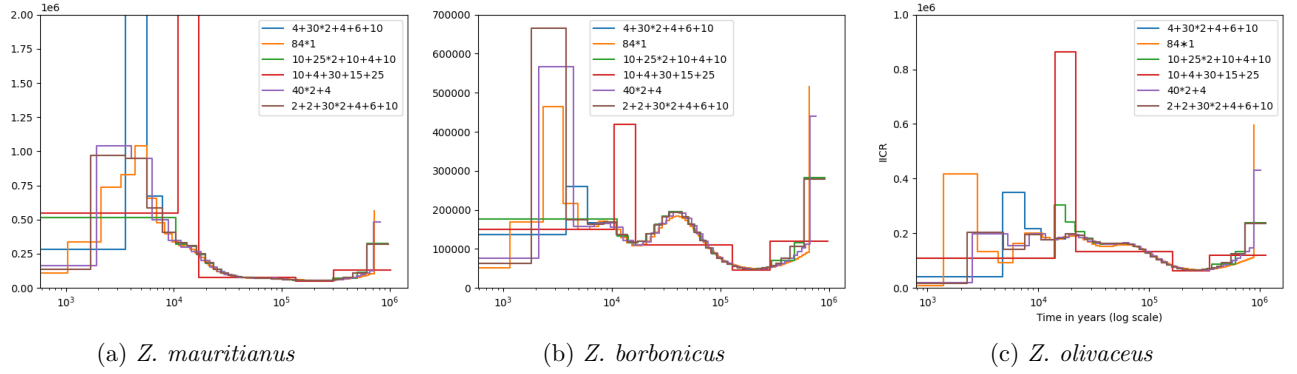


Figure S5: Effect of the atomic patter on PSMC curves of *Z. mauritanus*, *Z. borbonicus* and *Z. olivaceus*. We used different patterns.

4 The ms models

We simulated 1e6 independent coalescent times using ms. For all the models (except when specified), we took an initial population of size $N_0 = 1000$. For each model cited in the Material and Methods, we will provide the ms command, a representation of the model with demes (Gower et al., 2022) and the IICR curves with one inference. For some models, the scale migration rate takes the value 0.5 or 1. Here, we will write the commands using a migration rate of 0.5. In some models also, we create a new population or change the population size at varying times. In the commands, the time of these events will be 0.25 but could be replaced by 2.5 or 25.

Model A2RPan

Command : ms 2 100000 -I 3 0 2 0 -m 1 2 0.5 -m 2 1 0.5 -ej 0.25 3 2

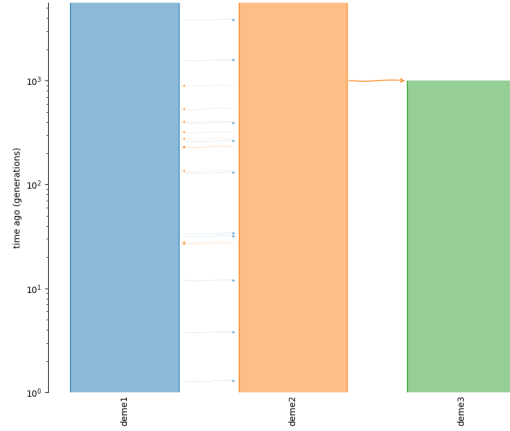


Figure S6: Representation of the model A2RPan with demes

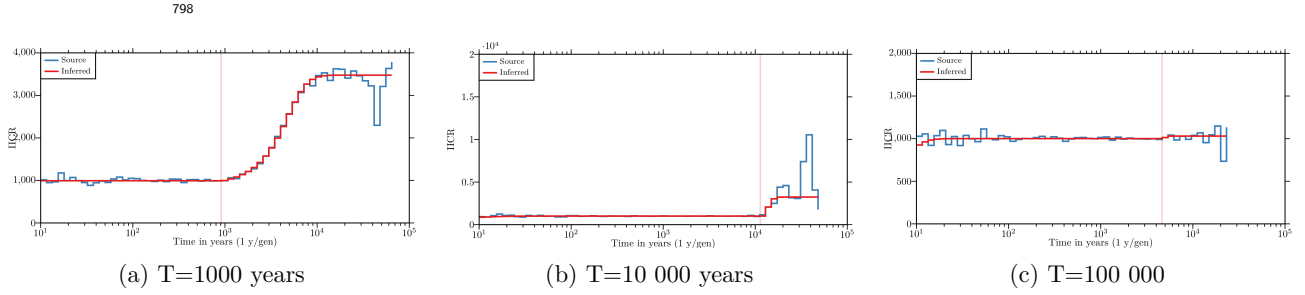


Figure S7: Inference given by SNIF (in red) and IICR curve (in blue) for the model A2RPan. The colonisation event happens at time T.

Model A10RPan

Command : ms 2 100000 -I 11 0 0 0 0 0 0 0 0 0 2 -ma 0 0.5 0.5 0.5 0.5
0.5 0.5 0.5 0.5 0.5 0 0.5 0 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0 0.5 0.5 0.5 0.5
0.5 0.5 0.5 0.5 0 0.5 0.5 0.5 0 0.5 0.5 0.5 0.5 0.5 0.5 0 0.5 0.5 0.5 0.5
0.5 0.5 0.5 0 0.5 0.5 0.5 0.5 0 0.5 0.5 0.5 0.5 0.5 0.5 0 0.5 0.5 0.5 0.5
0.5 0.5 0 0.5 0.5 0.5 0.5 0.5 0.5 0 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0
0.5 0 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0 0 0 0 0 0 0 0 0 0 -ej 0.25 11 10

Model A10R5

Command : ms 2 100000 -I 15 0 0 0 0 0 0 0 0 0 0 0 2 -ma 0 0.5 0.5
0.5 0.5 0.5 0.5 0.5 0.5 0.5 0 0 0 0 0.5 0 0.5 0.5 0.5 0.5 0.5 0.5 0 0
0 0 0.5 0.5 0 0.5 0.5 0.5 0.5 0.5 0.5 0 0 0 0 0.5 0.5 0.5 0 0.5 0.5 0.5
0.5 0.5 0 0 0 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0 0 0 0.5 0.5 0.5 0.5

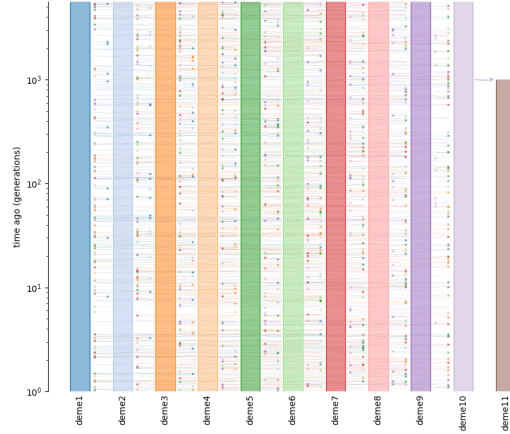


Figure S8: Representation of the model A10RPan with demes

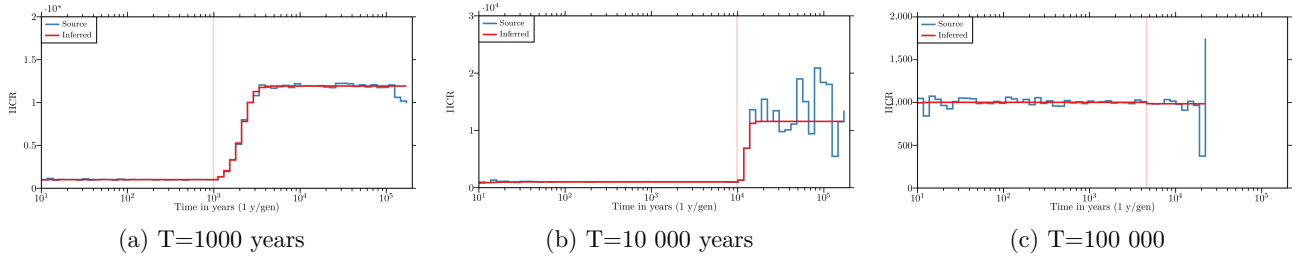


Figure S9: Inference given by SNIF (in red) and IICR curve (in blue) for the model A10RPan. The colonisation event happens at time T.

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811 0.5 0 0.5 0.5 0.5 0.5 0 0 0 0 0.5 0.5 0.5 0.5 0.5 0 0.5 0.5 0.5 0 0 0 0 0.5
812 0.5 0.5 0.5 0.5 0.5 0.5 0 0.5 0.5 0 0 0 0 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0 0.5
813 0 0 0 0 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0 0 0 0 0 0 0 0 0 0 0 0 0 0
814 0.5 0.5 0.5 0.5 0 0 0 0 0 0 0 0 0.5 0 0.5 0.5 0.5 0 0 0 0 0 0 0 0.5 0.5
815 0 0.5 0.5 0 0 0 0 0 0 0 0 0.5 0.5 0.5 0 0.5 0 0 0 0 0 0 0 0 0.5 0.5 0.5
816 0.5 0 -ej 0.25 11 10 -ej 0.25 12 10 -ej 0.25 13 10 -ej 0.25 14 10 -ej 0.25 15 10

```

817 **Model Pan**

818 Command : ms 2 100000

819 **Model PanPopSizeChange**

820 Command : ms 2 100000 -eN 0.25 2

821 **MZB**

822 Command : ms 2 100000 -I 15 0 0 0 0 0 0 0 0 0 0 0 0 2 -ma 0 0.5 0.5

823 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0 0 0 0 0.5 0 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0 0

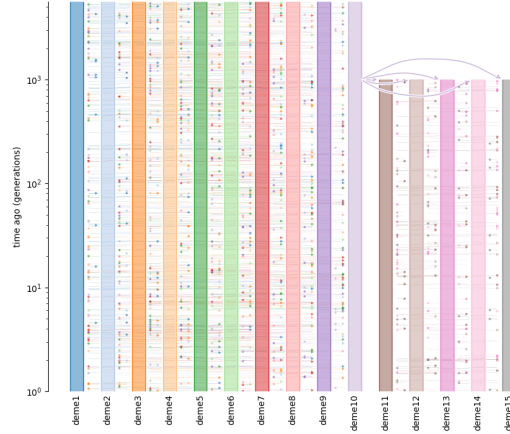


Figure S10: Representation of the model A10R5 with demes

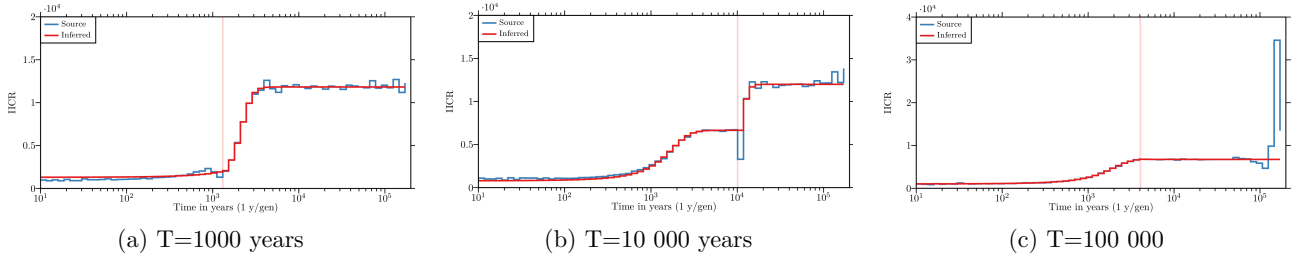


Figure S11: Inference given by SNIF (in red) and IICR curve (in blue) for the model A10R5. The colonisation event happens at time T.

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824 0 0 0.5 0.5 0 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0 0 0 0 0.5 0.5 0.5 0 0.5 0.5 0.5 0.5
825 0.5 0.5 0 0 0 0 0.5 0.5 0.5 0.5 0 0.5 0.5 0.5 0.5 0.5 0 0 0 0 0.5 0.5 0.5 0.5
826 0.5 0 0.5 0.5 0.5 0.5 0 0 0 0 0.5 0.5 0.5 0.5 0.5 0.5 0 0.5 0.5 0.5 0 0 0 0 0.5
827 0.5 0.5 0.5 0.5 0.5 0.5 0 0.5 0.5 0 0 0 0 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0 0.5
828 0 0 0 0 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0 0 0 0 0 0 0 0 0 0 0 0 0
829 0.5 0.5 0.5 0.5 0 0 0 0 0 0 0 0 0.5 0 0.5 0.5 0.5 0 0 0 0 0 0 0 0.5 0.5
830 0 0.5 0.5 0 0 0 0 0 0 0 0 0.5 0.5 0.5 0 0.5 0 0 0 0 0 0 0 0 0.5 0.5 0.5
831 0.5 0 -ej 100 11 10 -en 0.25 11 1 -ej 0.25 12 11 -ej 0.25 13 11 -ej 0.25 14 11
832 -ej 0.25 15 11 -en 0 11 0.2 -en 0 12 0.2 -en 0 13 0.2 -en 0 14 0.2 -en 0 15 0.2

```

833 **Model PanManyPopSizeChange**

```

834 Command : ms 2 1000000 -eN 0.0075 1.75 -eN 0.02 0.9 -eN 0.06 1.5 -eN
835 0.4 0.75 -eN 0.5 0.9 -T -L

```

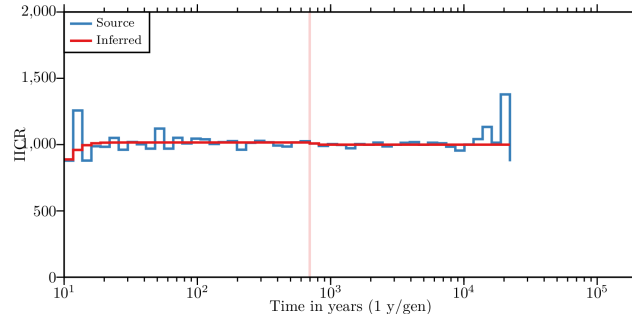


Figure S12: Inference given by SNIF (in red) and IICR curve (in blue) for the model Pan.

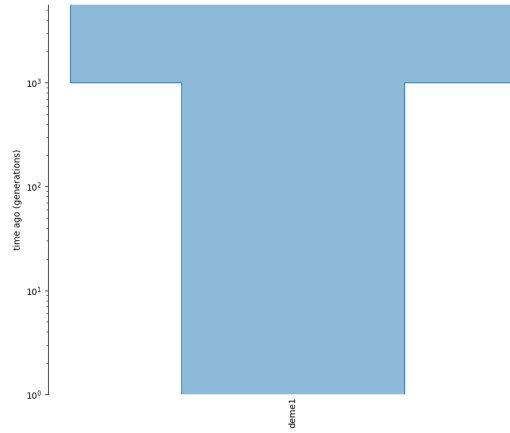


Figure S13: Representation of the model PanPopSizeChange with demes

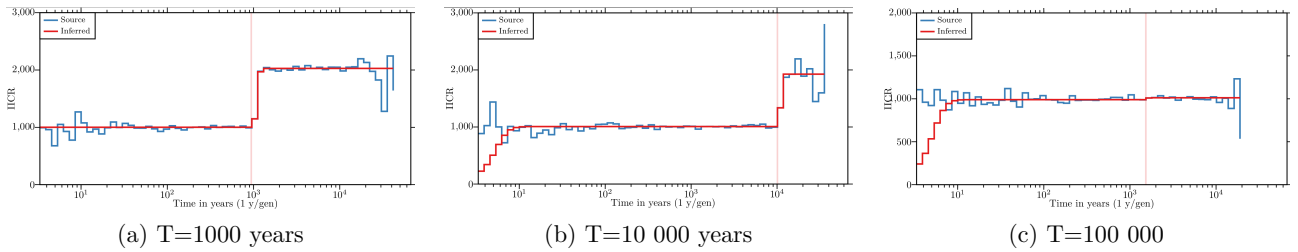


Figure S14: Inference given by SNIF (in red) and IICR curve (in blue) for the model PanPopSizeChange. The population size change happens at time T.

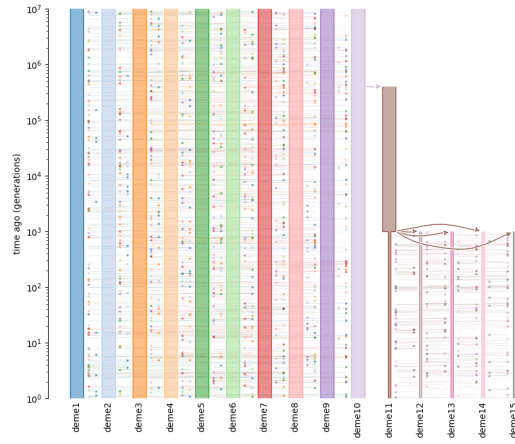


Figure S15: Representation of the model MZB with demes

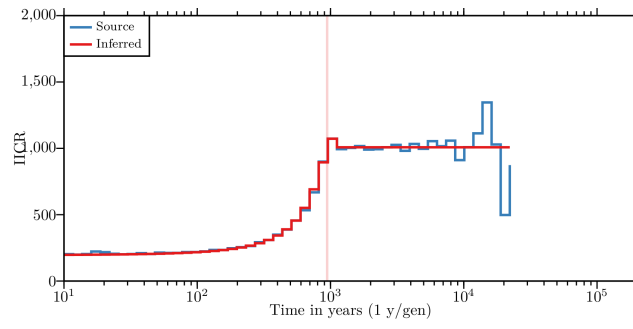


Figure S16: Inference given by SNIF (in red) and IICR curve (in blue) for the model MZB.

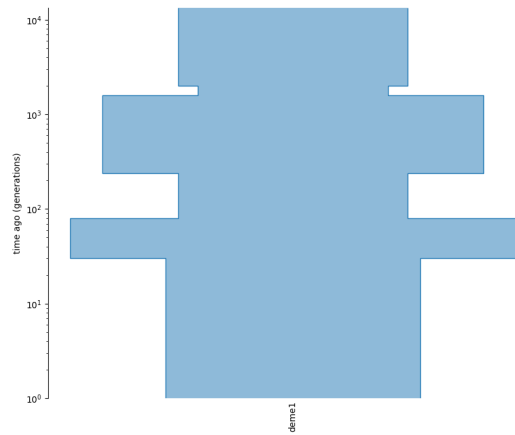


Figure S17: Representation of the model PanManyPopSizeChange with demes

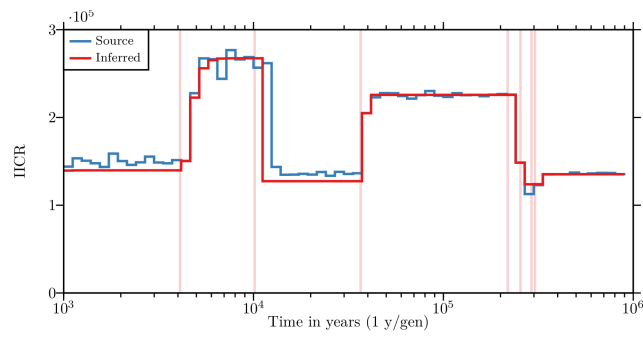


Figure S18: Inference given by SNIF (in red) and IICR curve (in blue) for the model PanManyPopSizeChange.