

Estimating the population recombination rate in a butterfly species with chromosome fusions

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Background

- Chromosome fusions have the potential to reduce the rate of recombination.
- Recently, Barroso, Puzović and Dutheil [1] proposed a new method, the integrative sequentially Markov coalescent (iSMC), for estimating the population recombination rate (ρ) from a single diploid genome.
- Here I benchmark iSMC using a crossover map for the butterfly *Heliconius melpomene*, and then estimate the recombination landscape in another butterfly species with many recent chromosome fusions, *Brenthis ino*.

Materials and Methods

- I generated a set of high confidence variant calls for single *H. melpomene* and *B. ino* individuals.
- Using iSMC, I fit a model of coalescence with recombination that included 40 TMRCA and 10 ρ intervals, obtaining estimates of ρ and θ in 1Mb windows across the genome.
- I compared the ρ estimates for *H. melpomene* with a crossover map generated by Davey et al. [2].

Results

- ρ estimates are positively and significantly correlated with the crossover map (Spearman's $\rho = 0.53$, $p < 1e-15$, Figure 1).
- However, θ correlates just a strongly, suggesting the relationship is mainly driven by N_e .

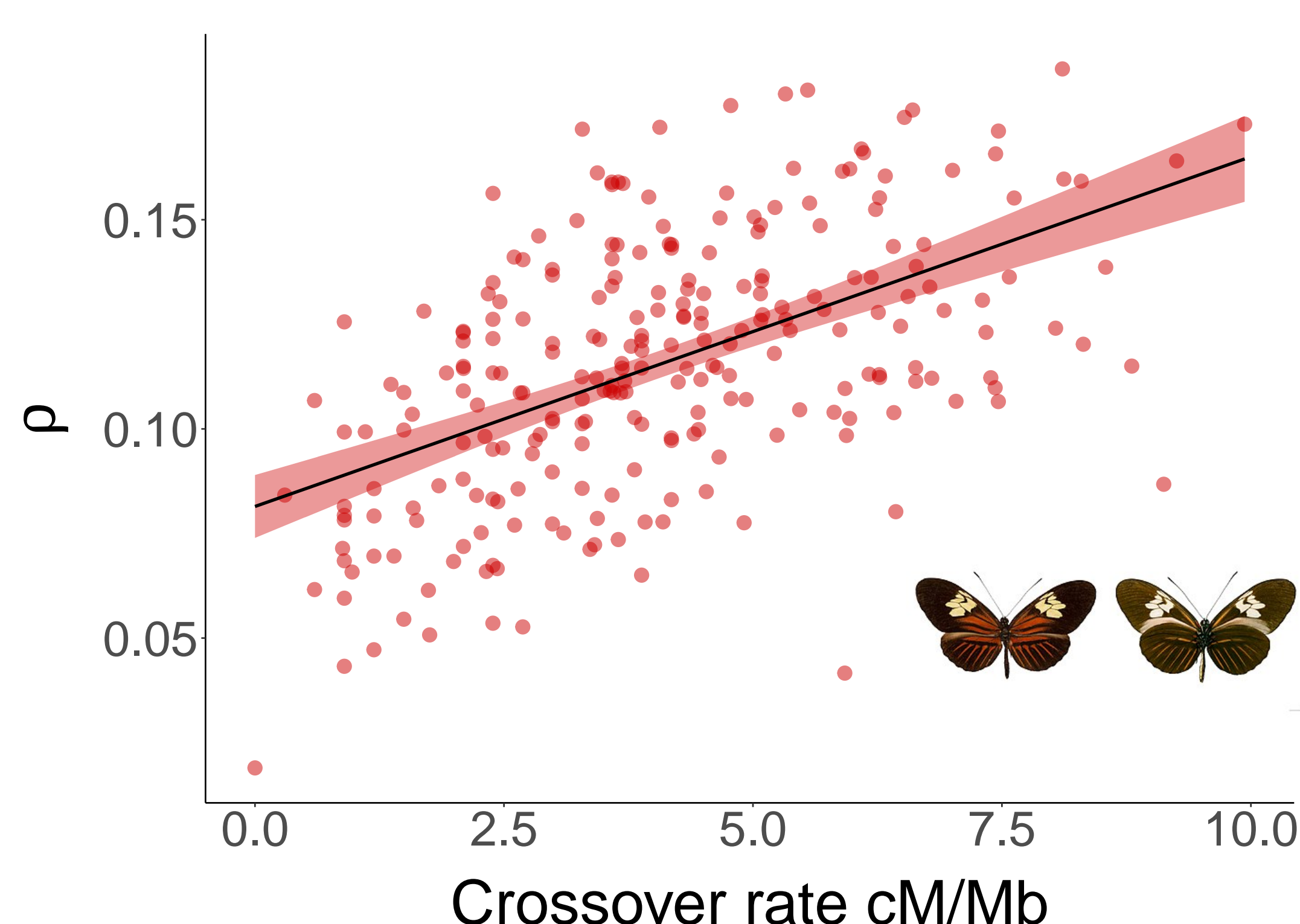


Figure 1: iSMC's estimates of ρ for *H. melpomene* compared to observed crossovers [2]

- *B. ino* has a lower and more variable recombination rate than *H. melpomene* (Figure 2).
- A putative fused chromosome in the *B. ino* genome has high ρ towards the ends but low ρ in the centre (Figure 3).

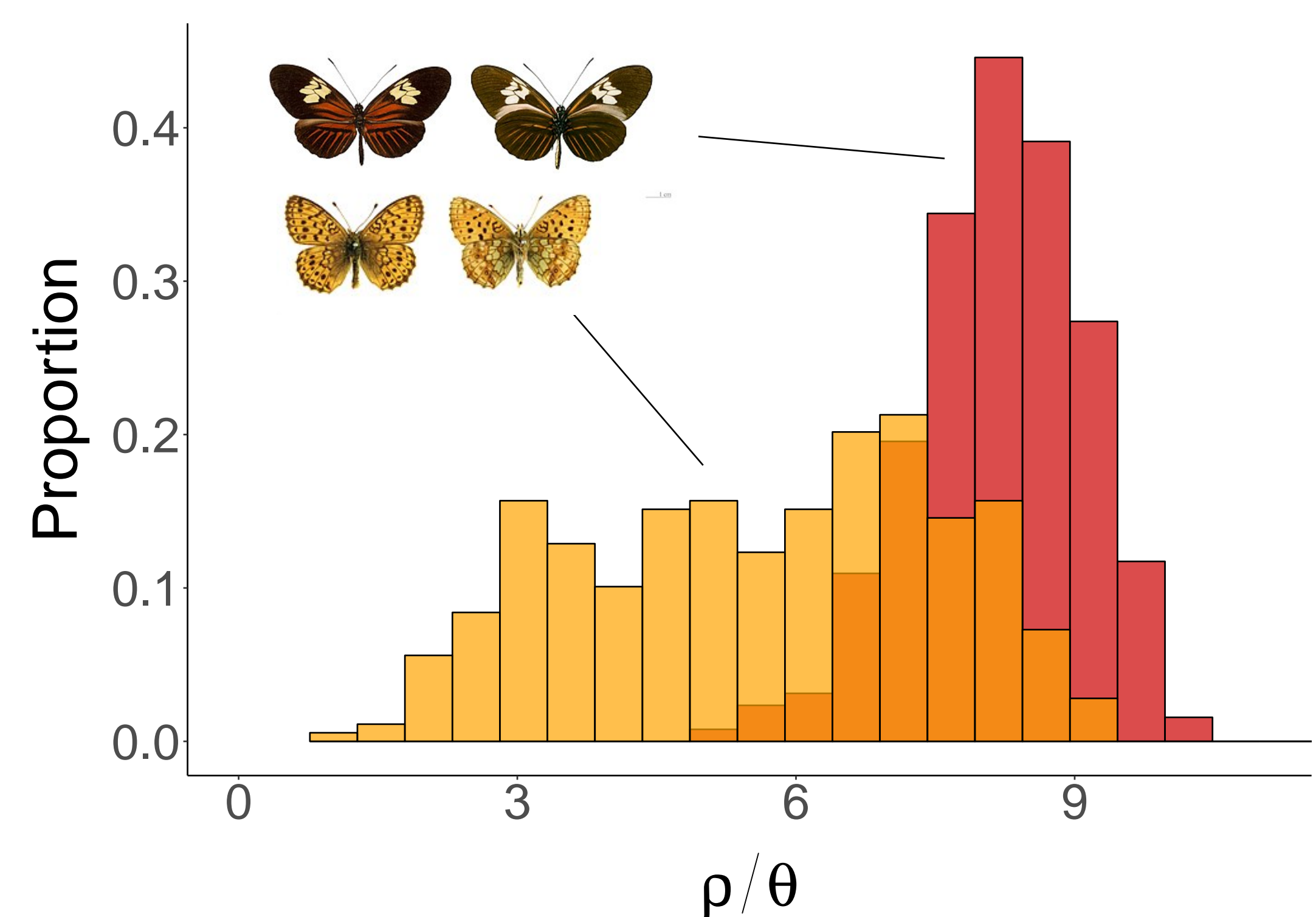


Figure 2: The distribution of ρ / θ for *H. melpomene* (red) and *B. ino* (orange)

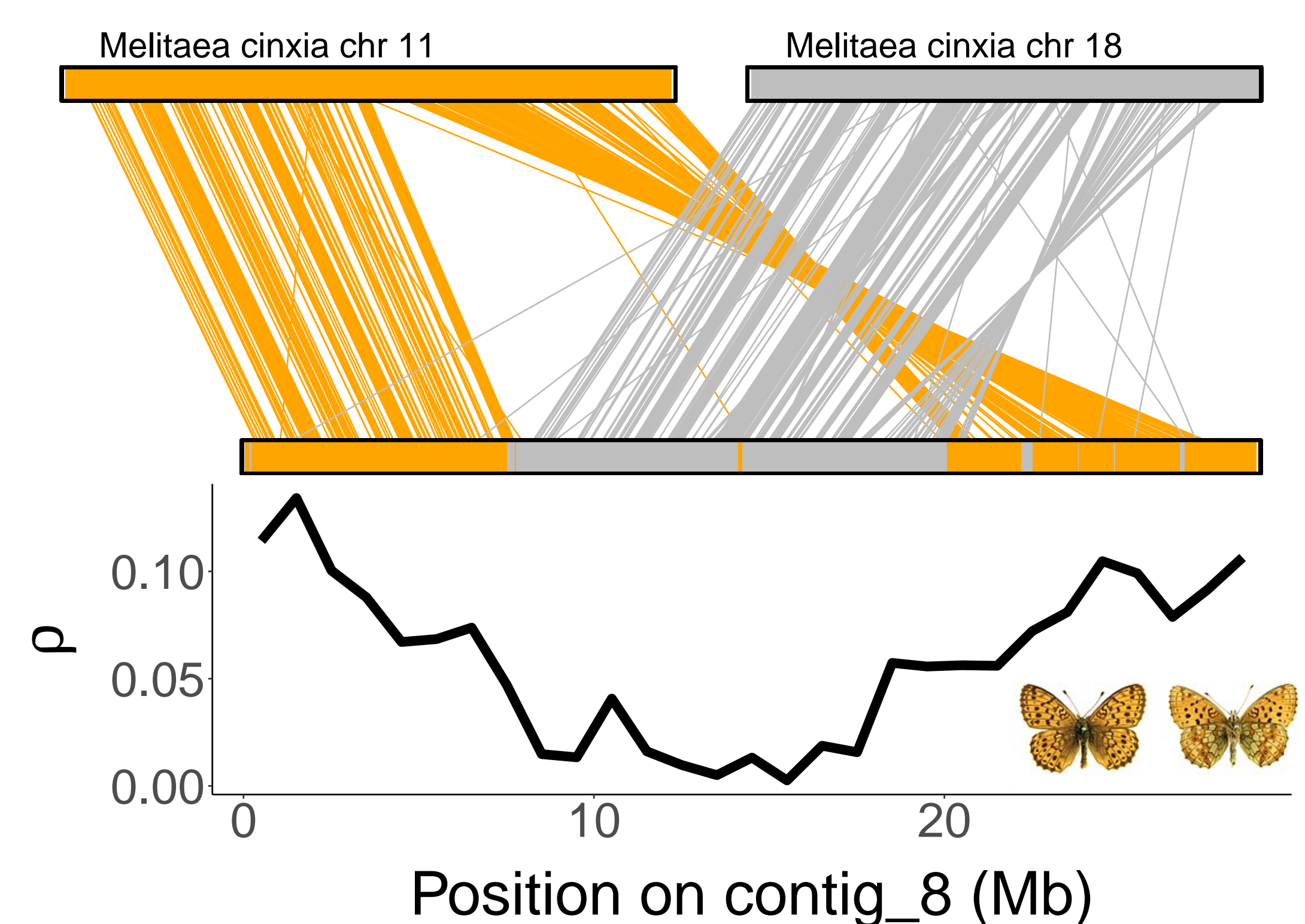


Figure 3: Contig 8 in the *B. ino* draft assembly aligned to *Melitaea cinxia* chromosomes (top) and estimates of ρ across the same contig (bottom)

Conclusions

- iSMC provides useful information about the rate of recombination but is limited when recombination is more common than mutation, as in butterflies.
- *B. ino* has a relatively low rate of recombination which is consistent with the effect of chromosome fusions.
- Loci in the centre of chromosomes may be disproportionately affected by fusions.

References

- [1] Gustavo V. Barroso, Nataša Puzović, and Julien Y. Dutheil. Inference of recombination maps from a single pair of genomes and its application to ancient samples. *PLOS Genetics*, 15(11):1–21, 11 2019.
- [2] John W. Davey, Sarah L. Barker, Pasi M. Rastas, Ana Pinharanda, Simon H. Martin, Richard Durbin, W. Owen McMillan, Richard M. Merrill, and Chris D. Jiggins. No evidence for maintenance of a sympatric heliconius species barrier by chromosomal inversions. *Evolution Letters*, 1(3):138–154, 2017.

Acknowledgements

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