

Inferring the Demographic History of Wild House Mice

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Abstract

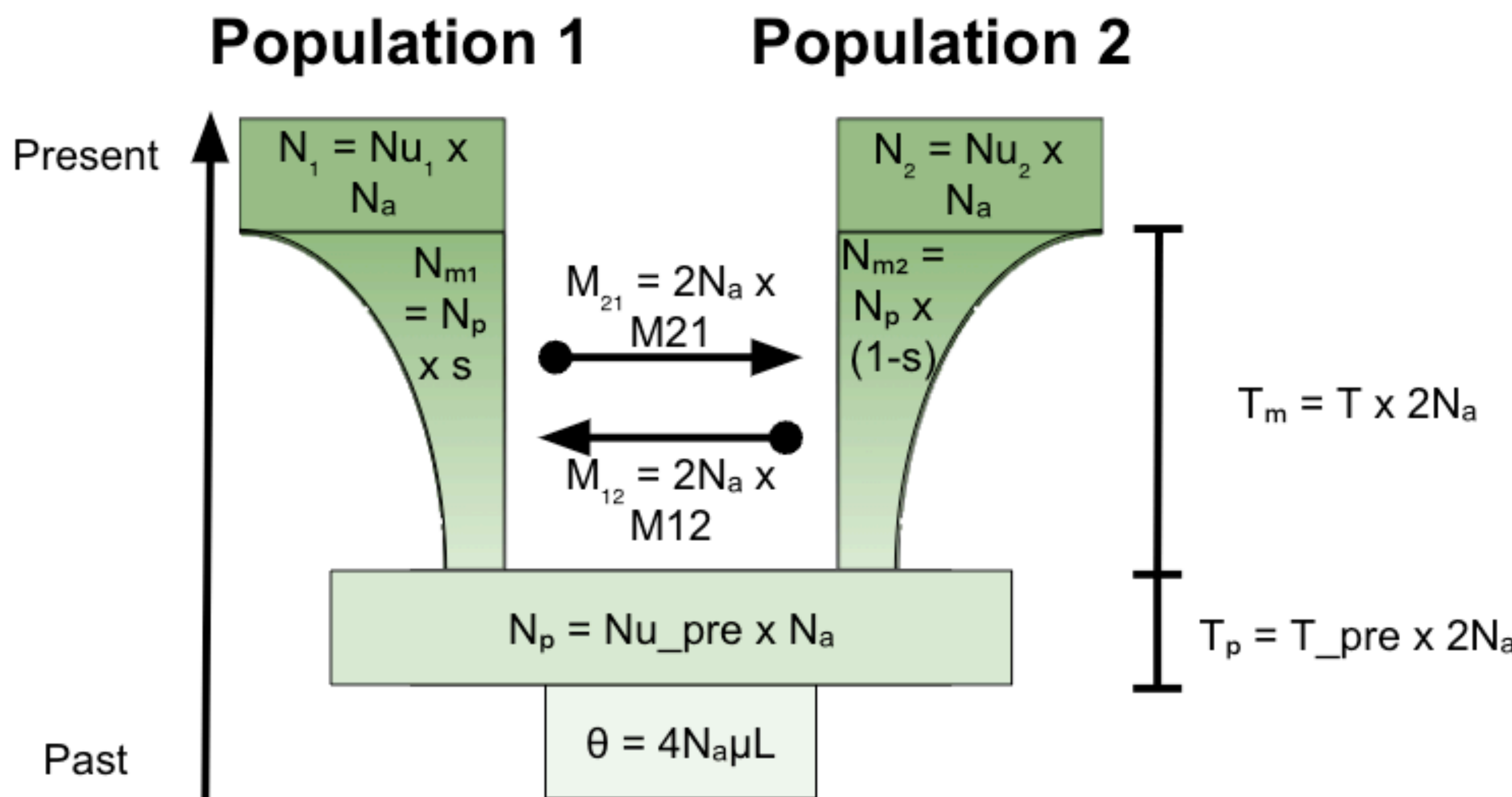
The distribution of fitness effects (DFE) of new mutations is a key input into the evolutionary process. We aim to infer the DFE among multiple populations of wild house mice, so that the extensive knowledge of mouse molecular biology can be leveraged to understand the biological basis of the DFE. To infer the DFE, we first use synonymous mutations to infer a model of demographic history. Here we present preliminary demographic history inferences for populations from Iran and France. We find the best models are those that include a distinct split between the two populations and account for inbreeding between closely related individuals.

Demography Inferences

Demography inferences involve learning about a population's history, specifically their size, migration and/or divergence over time, and whether there was inbreeding. Our preliminary results include demographic inferences for two populations of *Mus musculus domesticus* from France and Iran (1). We explored two population demographic history models using the software dadi and considered models that include inbreeding, migration, exponential growth, population splits, and isolation. The motivation for creating models that considered inbreeding is that prior research has shown significant evidence of inbreeding in populations of wild mice (2).

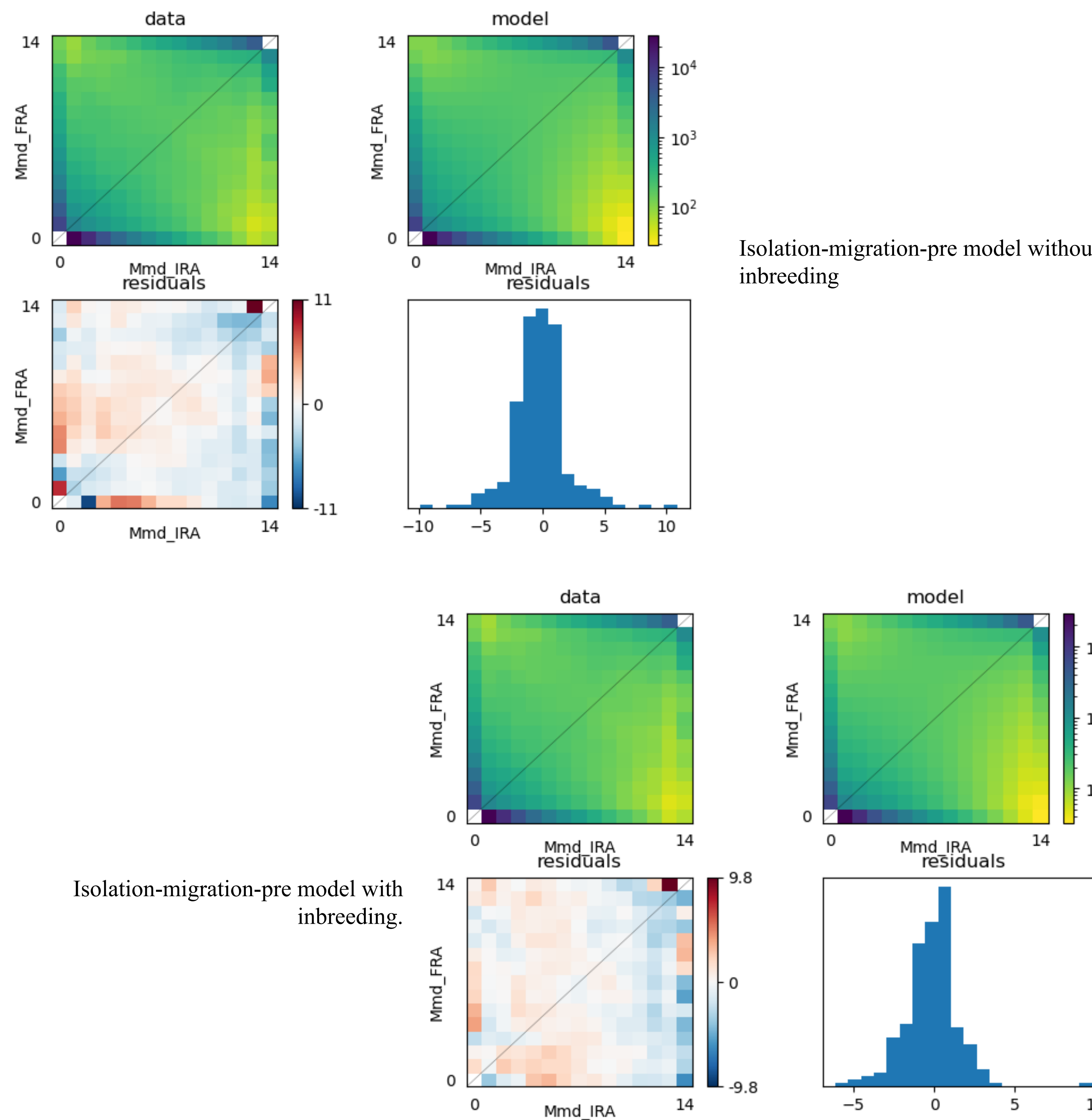
Isolation-Migration-Pre Model

Both when considering inbreeding and not considering inbreeding, the model with the best log likelihood estimate was the isolation-migration model with a size change prior to the split into two populations.



Results

The isolation-migration-pre model had a log likelihood estimate of -1386, almost 500 log likelihood units better than the next best fitting model. Because inbreeding has a strong effect on demography, especially in demographies including changes in population size, we expected the inclusion of inbreeding to improve our model's fit (3). After adding two inbreeding coefficients to our isolation-migration-pre model, F1 and F2 for populations 1 and 2 respectively, we saw about a 200 log likelihood unit improvement.

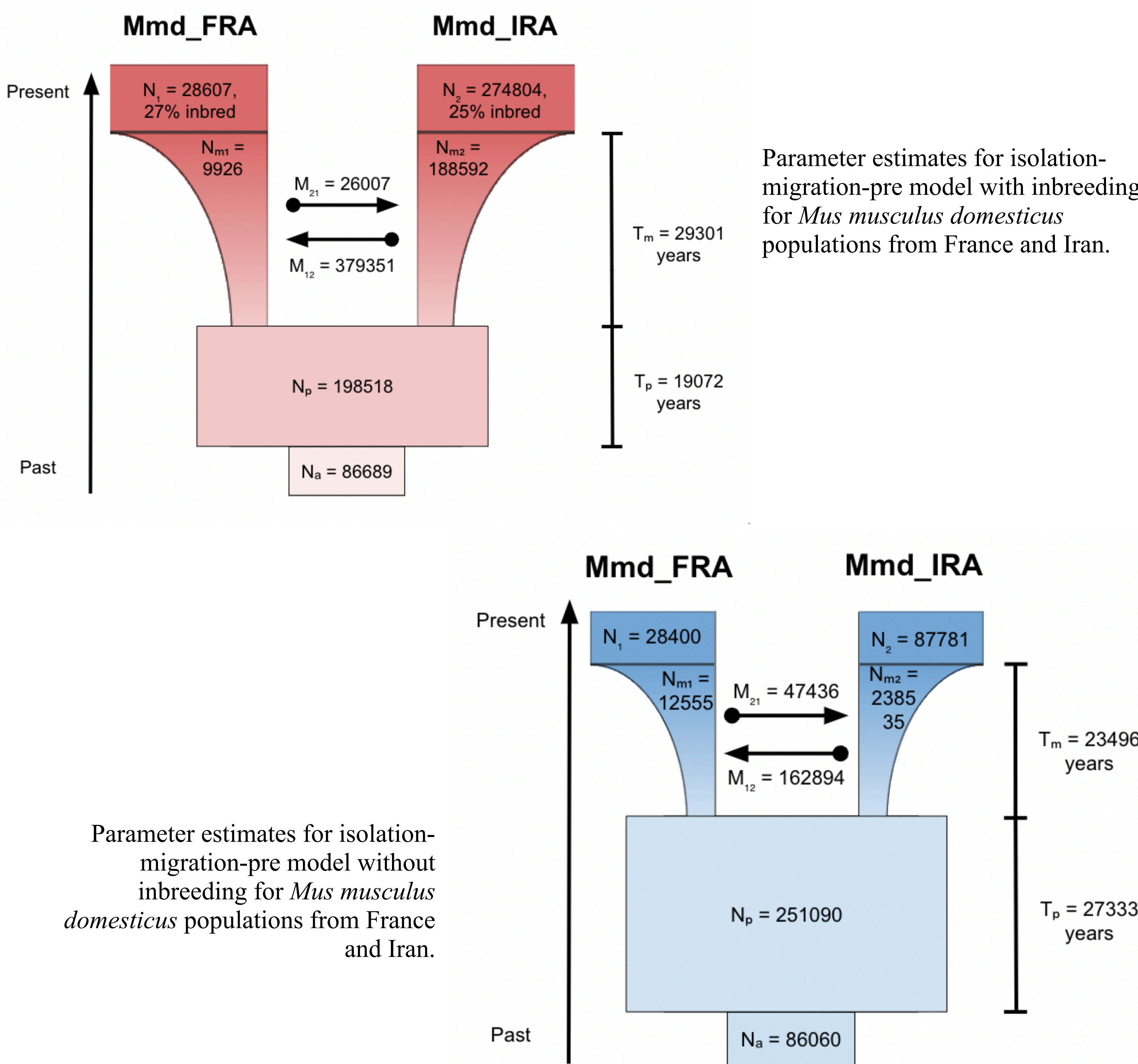


Discussion

While inferring the demographic history of these two populations is important, our primary focus is to infer the DFE, which builds on the demographic inferences made from synonymous mutations. Using the model of demographic history, we will now infer a joint DFE for the two populations, which will help us learn about the correlation between mutation fitness effects in the two populations (5). Our hope is that this work will help us gain a better understanding of the biological basis of the DFE by tapping into extensive mouse biology knowledge derived from laboratory mice, whose genomic origin is, on average, 92% *Mus musculus domesticus* (6).

Parameter Estimates

Both models estimated ancestral population sizes around 80000 individuals, which aligns with previous work that estimates the ancestral population size of wild mice to be between 58000 and 200000 (4). Our estimates for inbreeding coefficients around 0.25 match previous estimates for European populations of *Mus musculus domesticus* (2).



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Image: researchgate.net

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