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## Abstract

Much can be learned about a species' recent evolutionary past by fitting models to contemporary patterns of genetic variation. There are two categories of models we fit, models of demographic history and distributions of fitness effects. When we fit a demographic history model, we use synonymous mutations and infer a model to learn about things like population size, divergence time, and rates of inbreeding. A distribution of fitness effects provides information about what proportions of mutations in nonsynonymous sites are deleterious, neutral, and advantageous, which can provide key input into the evolutionary process (1). 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. Here we present our demographic inferences along with preliminary DFEs.

## 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. We explored demographic history models using the software dadi. The demographic histories inferred here are for four populations of *Mus musculus domesticus* from Iran, France, Germany, and Heligoland. Because there is prior knowledge of migration of this wild mice from Iran to France to Germany to Heligoland, we considered joint demographic histories of Iranian and French mice, French and German mice, and German and Heligolandic mice (2). Across all three groups, our results showed a consistent pattern of an ancestral population splitting into the two present day populations, low levels of inbreeding in each population, and some migration between the two populations in a pair.

## Distributions of Fitness Effects

To infer the DFEs for all three population pairs, we use our models of demographic history to set up frequency distribution of nonsynonymous sites under a range of selection coefficients. For all three population pairs, we find that the best distribution was a lognormal distribution that inferred equal selection coefficients for each mutation in both populations. Our DFE investigations are not complete, but our current results suggest that mutations that are harmful in one population of *Mus musculus domesticus* are also harmful in the other populations of *Mus musculus domesticus*.

## Discussion

The next steps in our project are to continue investigating the DFEs and hopefully begin to develop an understanding of the biological basis of the DFE. *Mus musculus domesticus* are a perfect species to use for tackling these kinds of questions because they are close relatives of the common laboratory mouse. Laboratory mice are thought to have a genomic origin that's 92% *Mus musculus domesticus* and we have extensive biological knowledge of them that we expect will help us understand the DFE patterns we see in their wild counterparts.

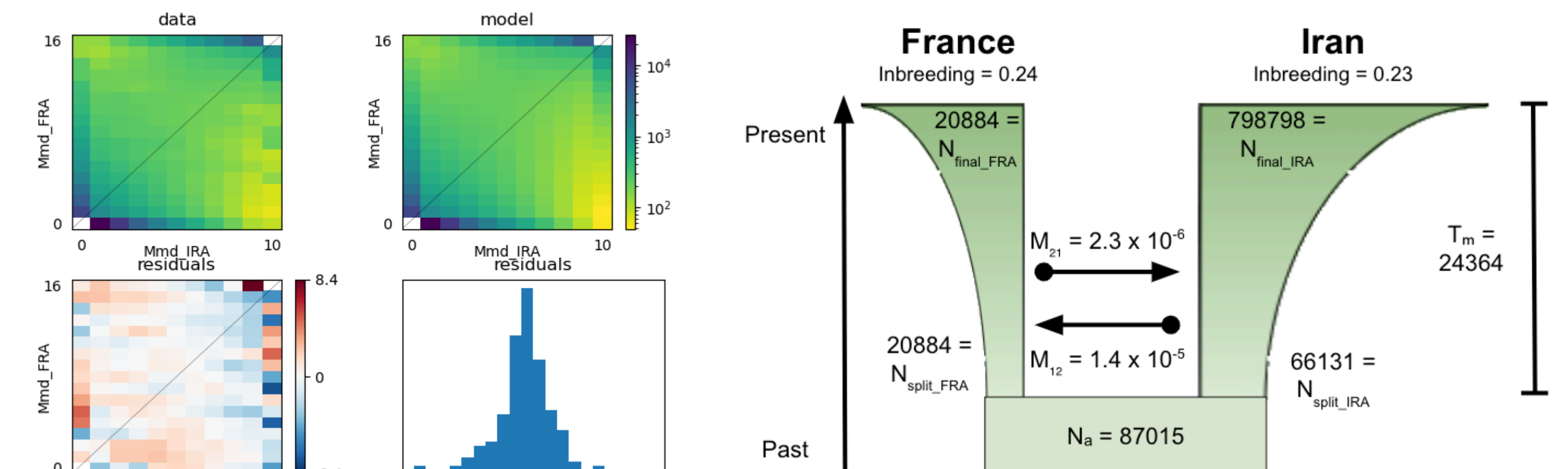
## References

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Image: [researchgate.net](https://www.researchgate.net)
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## Demography Results

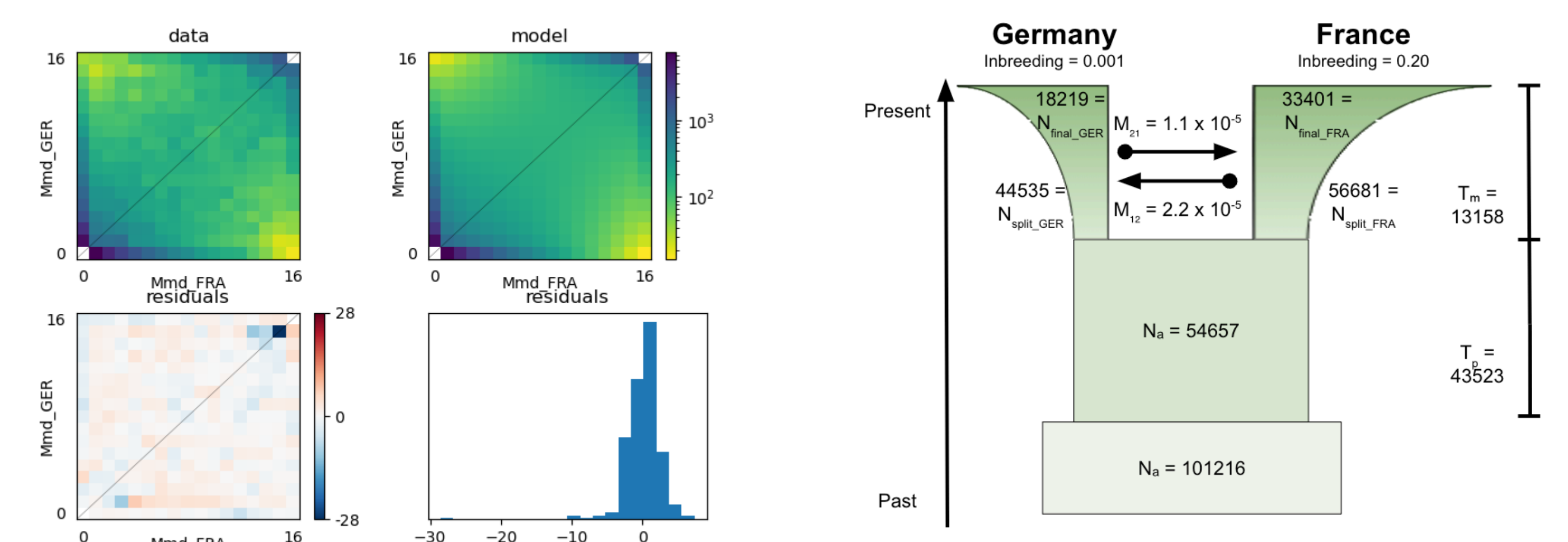
### Iran vs. France

For the populations from Iran and France, there were four models that fit reasonably well: an isolation migration model, an isolation migration pre model, a split asymmetric migration model, and a split delay migration model, all with the inclusion of inbreeding. The four models had similar likelihoods with the isolation migration model being the best. Each model estimated an ancestral population size of about 87000 individuals, which matches previous estimates of the ancestral population size for *Mus musculus domesticus* (3). All four models also estimated low - moderate levels of inbreeding in both populations.



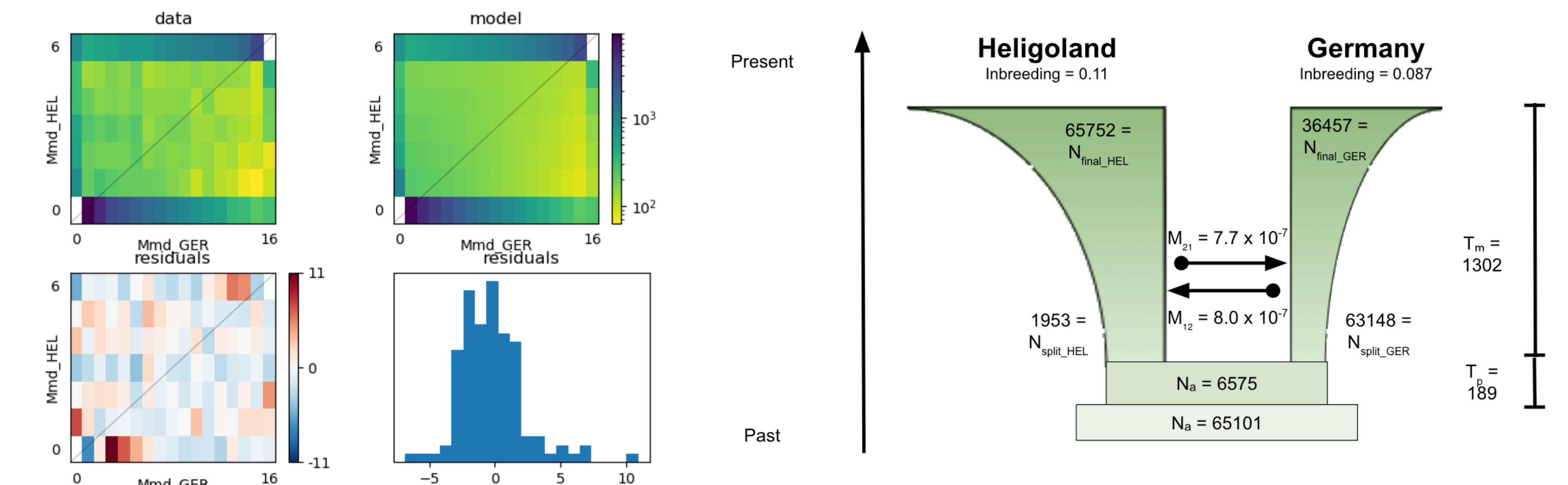
### France vs. Germany

The populations from France and Germany had two models that fit fairly well: an isolation migration pre model and a split asymmetric migration model, both with the inclusion of inbreeding. The likelihood estimate was significantly better for the isolation migration pre model with inbreeding. This model estimated an ancestral population size of about 101000 individuals, similar inbreeding in the French population to our Iran vs. France results, and almost no inbreeding in the German population.



### Germany vs. Heligoland

Because the Heligoland population is an island population, these results are of particular biological interest. In comparing the Heligoland population with the Germany population, one model stood out, the isolation migration pre model with inbreeding. This model estimated an ancestral population size of about 65000 individuals and low levels of inbreeding in both the German and Heligolandic populations.



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