Model-based demographic inference of recent invasions from genomic data

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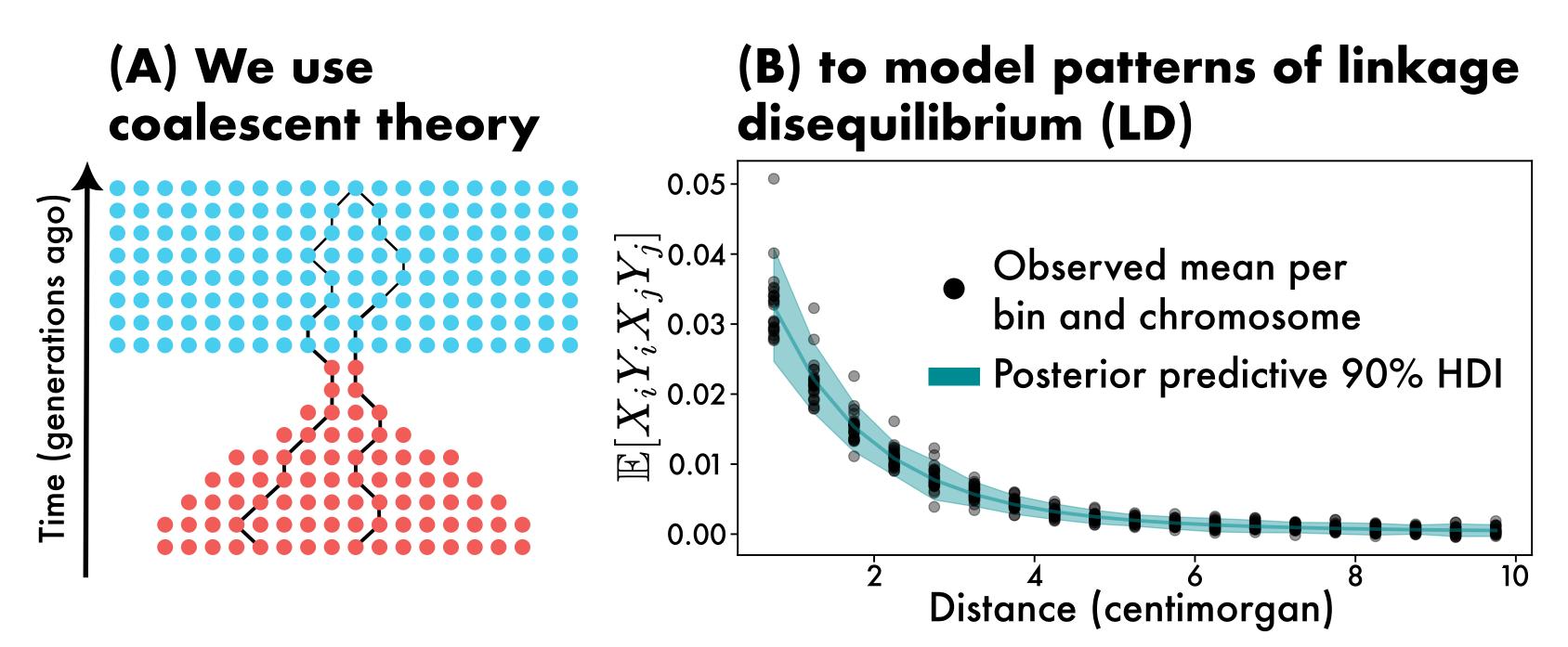
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Introduction

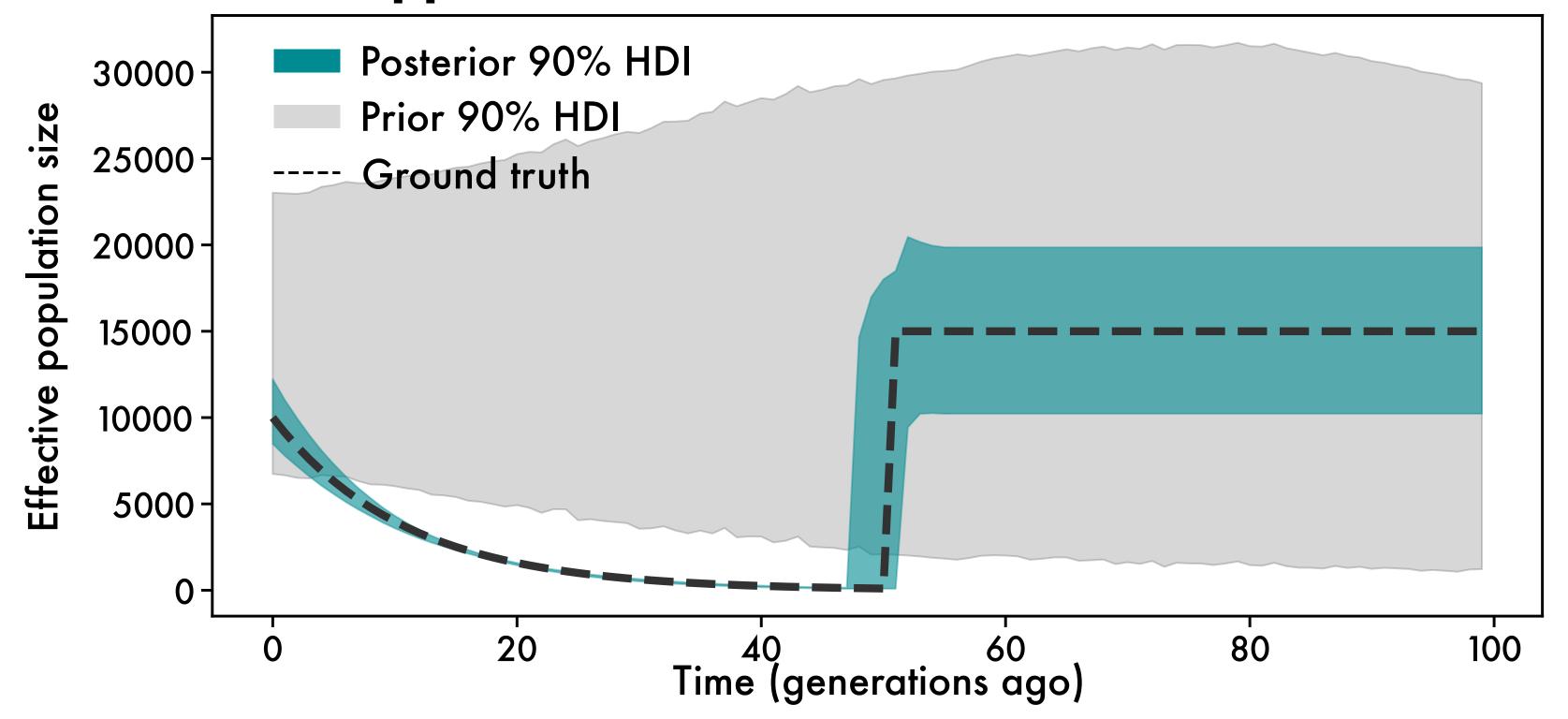
- Biological invasions are a major threat to biodiversity but also can be viewed as large-scale, unplanned experiments on how populations adapt to novel environments.
- Accurate estimates of recent effective population size (N_e) can guide conservation management plans and help disentangle the effects of selection and demography on genetic variation.
- Existing methods to infer very recent effective population size are not well-suited for realistic invasion scenarios.

Theoretical framework

We propose a method to infer recent evolution in N_e that can incorporate relevant prior information of the invasion process and the source population.



(C) and perform Bayesian inference through a pseudo-likelihood approach



Modelling multiple introductions

Multiple introductions are common in biological invasions, although difficult to model. In order to accommodate them, we leveraged recent advances in inhomogeneous phase-type distributions to compute approximate likelihoods.

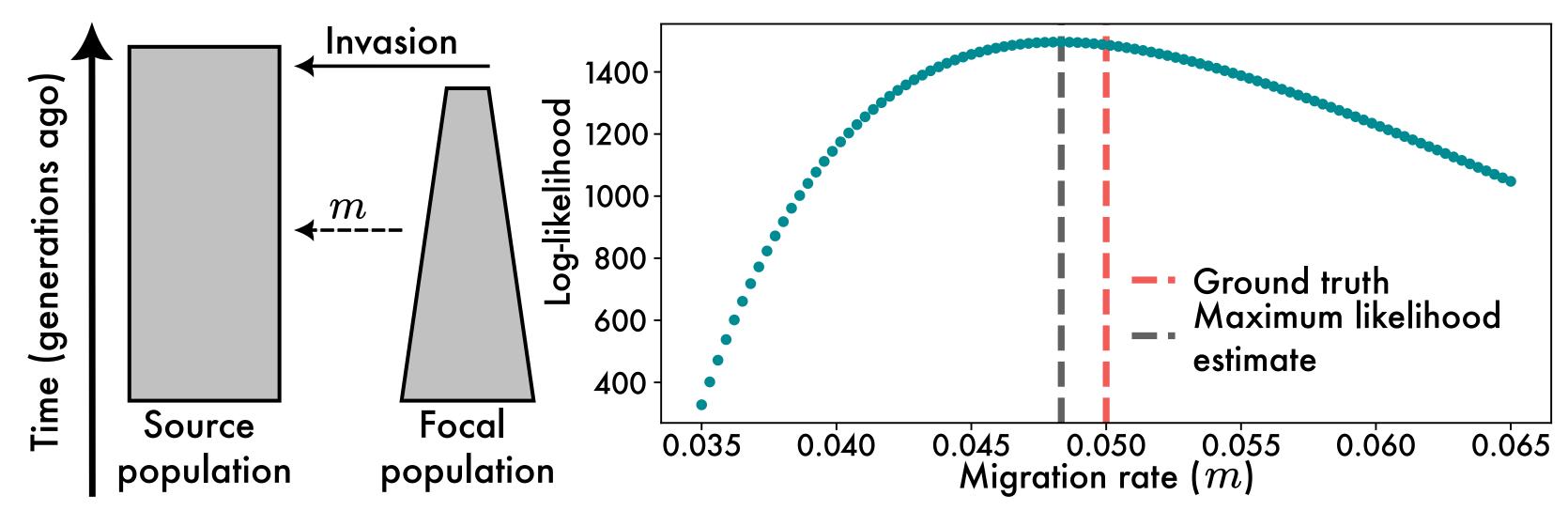


Figure 1: Likelihoods were obtained via numerical integration of the cumulative distribution function of the TMCRA using phasegen, keeping all other parameters fixed at their true values.

Preliminary results suggest we can estimate the migration rate m from LD data of the focal population solely. However, the posterior distribution for all other parameters is highly multimodal and raises concerns about identifiability.

Method comparison

The proposed method works better than existing state-of-the-art methods, at least in part because it does not penalize an abrupt change in N_e at the beginning of the invasion.

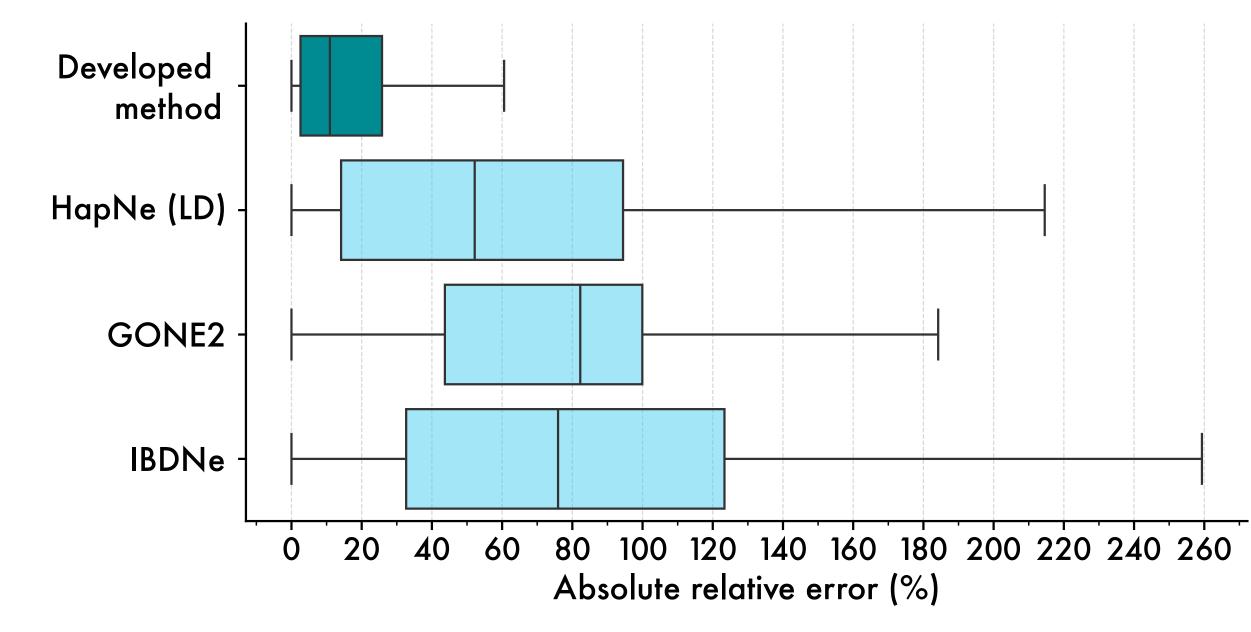


Figure 2: We computed the absolute relative error of N_e across the last 100 generations in 9 demographic scenarios (25 replicates each). Each dataset consisted of 200 diploid individuals and 25 chromosomes. HapNe-IBD has higher error than other methods (not shown).

Estimating key parameters

The time of invasion and the order of magnitude of the effective founder size can be estimated precisely, even without any a priori knowledge of the source population.

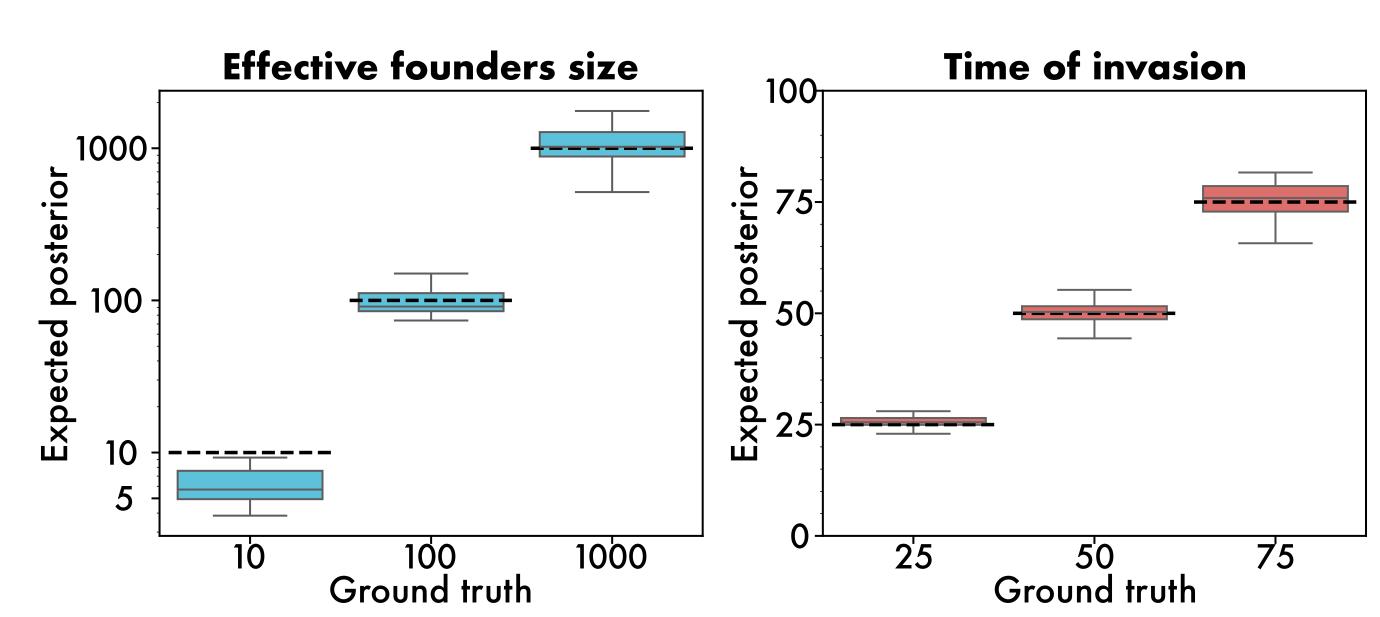


Figure 3: We compared the expected posterior with the ground truth of the effective founder size and time of invasion across 225 synthetic datasets. Doing inference, the prior of $N_{e(t)}$ was chosen to match observed genetic diversity.

Take home message

- Model-based methods based on LD data can provide better estimates of demographic parameters for invasion scenarios than existing methods.
- Recent advances in computational and statistical methods enable modeling more complex demographic scenarios and going beyond overly simplistic models.



