Demographic inference using the SFS with Moments and Demes

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Abstract

Placeholder

1 Introduction

What moments is, what type of data it uses, general framework for inference

1. The SFS – how its shape is sensitive to population, selection and genome biological parameters
2. Demographic inference from the SFS
3. Extensions: inference of selection, mutation rates, etc
4. Extensions: Multi-allele and multi-locus models

2 Interface with Demes

1. Manipulating and plotting Demes-specified demographic models
2. Computing statistics given a Demes model
3. Inferring history on a demes model, including specifying parameters to be fit

3 Examples

Two examples, one using simulated data with known parameters, which we try to reinfer. And another with actual data (humans + neanderthal). We briefly describe these, highlighting the high-level components of the fits. For detailed information for each, including managing data, specifying models, performing inference, and visualizing results, we refer readers to the GitHub (), which is maintained with up-to-date versioning.

3.1 Inferring parameters in a simulated isolation-with-migration model

A python snippet:

```
dbg = msprime.DemographyDebugger(
  population_configurations=population_configurations,
  migration_matrix=migration_matrix,
  demographic_events=demographic_events)
dbg.print_history()
ts = msprime.simulate(
  population_configurations=population_configurations,
  migration_matrix=migration_matrix,
  demographic_events=demographic_events)
```

or

```
dbg = demography.debug()
dbg.print_history()
ts = msprime.simulate(demography=demography)
```

This was in discussion of Kelleher et al. (2016).

3.2 Inferring human-Neanderthal demographic parameters

```
def myFunc():
    pass
```

4 Considerations and caveats

Incluce here general ideas about the strengths and weaknesses of various approaches in population genetic inference, including when using the SFS.

Challenges in finding local/global optima. Challenges in exploring parameter space.

References

Jerome Kelleher, Alison M Etheridge, and Gilean McVean. Efficient coalescent simulation and genealogical analysis for large sample sizes. *PLoS computational biology*, 12(5):e1004842, 2016.