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Inference of demographic parameters using importance sampling on coalescence history

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State of our art

We developed and evaluated the performance of maximum likelihood (ML) analysis of allele frequency data in a linear array of populations under isolation by distance (IBD) and in a model of isolation with migration (IM) between two populations.

Implementation in the software MIGRAINE

The Algorithms used in this study are implemented in MIGRAINE, a free program for likelihood analyses of genetic data, with a focus on spatially structured populations. The demographic models currently implemented in this program are:

1. A simple model of isolation by distance in a linear habitat, as described in Rousset & Leblois (2007), which includes the infinite island model as a special case;
2. An isolation with migration (IM) model with two populations. Note that this IM algorithm is still under development but will soon be available.

At the heart of the program is the importance sampling algorithm defined by de Iorio & Griffiths (2004). Some approximate procedures ("PAC-likelihood") are also available and have been shown to be at least as efficient than exact maximum likelihood for time constant models.

MIGRAINE is currently designed for allelic type mutation data sets only: a K-alleles mutation model is implemented for all demographic models and a strict stepwise mutation model (SMM) is implemented to some extent for models with one or two populations (not yet published).

However, we plan to adapt MIGRAINE for sequence data in a “near” future.

Preliminary results under the IM model

We implemented a simple IM model with two populations with potentially different sizes and asymmetric migration rates. This model has 6 parameters which are the total population size scaled by migration rate, the relative populations sizes, the two migration rates scaled by total population size, the time of divergence scaled by total population size and the ancestral population size scaled by migration rate (Fig. 3).

Our first results on simulated data sets are quite interesting because they show that:

1. Our algorithm is able to infer all 6 parameters meaning that it will be able to detect asymmetric population sizes and migration rates, even if the precision is not equal for all parameters.
2. Graphical output (likelihood points as shown on Fig. 4 and soon likelihood and likelihood ratio plots) can help a lot in understanding what information is available in the data. One illustration on Fig. 4 is that microsatellite data will not have much information on large divergence time and ancestral populations when the population split is not very recent. It is thus quite easy to understand why some parameters are more or less well estimated depending on the marker used and the time of divergence of the populations studied.

Few other demographic models such as single population with size fluctuations in time, n-population with constant migration and the possibility to consider multiple samples in time are almost ready to be tested. We are looking for students or post-docs to develop those models. Do not hesitate to contact us if you are potentially interested. Migraine will thus be regularly updated to consider more demographic and mutational models so

Check the Migraine web page regularly to find new model implementations and Download Migraine at:

http://kimura.univ-montp2.fr/~rousset/Migraine.htm

References

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