

Paper Reference:

Lui H, Franck P, Mancina A, Balloux F. (August 2006) A Geographically Explicit Genetic Model of Worldwide Human-Settlement History. *The American Journal of Human Genetics* 230:237

Abstract:

Over the course of time, mutations accumulate in populations of organisms, including duplications, deletions and substitutions. The difference of genomes across multiple populations is a function of the random drift of the DNA (rates of such mutations), selection for mutations, as well as the rate of migration of individuals between populations. Investigators create models of the spread of populations across different regions of the world based on the current genetic profile of populations in various areas, and estimations of the most recent divergence between the various areas (coalescence time).

This paper presents a model of the spread of the modern human population throughout the world beginning from a small population originating out of Eastern Africa using available human genetic variation from more than 1000 individuals originating from various parts of the world (data used in studies previously presented in class). By building a flexible model which incorporates previously described parameters (migration and mutation rates) along with carrying capacity of “demes” and coalescence times, they are able to avoid the need for fixing each parameter to an estimated value (as in other techniques), and were able to explore a range of values.

As a result, the authors determined which set of parameters matched a “best-fit” model, and were able to offer a wide variety of results, including an average growth rate and founder population, as well as the density of individuals per km², a migration rate, and very importantly, an estimate of the number of generations which have elapsed since the first set of modern humans left Africa to begin colonization.

Discussion:

The results in this paper clearly discuss the question of human migration through a population genetics approach. To determine the migratory pattern of early modern humans in an effort to populate the globe, the authors attempt to avoid the need for borrowing values from current literature (as in other papers presented) to use as parameters in this model. They do reuse widely recognized datasets and best-fit models to validate their results (shown in class).

The model is still not free of assumptions. It presumes that the population originates from Eastern Africa (even though it allows the initial population size to vary) and still fixes various mutation rates and demes (similar to previous methods presented). The variation in the initial population size is not a totally novel, as previous papers have allowed the same flexibility (albeit in a more limited fashion). In addition, there is also an exploration of the number of generations since the initial expansion, although it still conforms to the criterion that the expansion to South America not occur within a certain number of generations (deemed to be unreasonable according to archeological data). In addition, since the full parameter space cannot be explored, they decided to follow a “coarse-grid” search with a more granular search restricted to a smaller search space bounded by the initial search results.

The most weakly supported argument involves the carrying capacity and growth rate in new demes, considered equal in the model. It is unclear how each deme can reach the same carrying capacity. The authors acknowledge that initial growth rate is as a result of “extremely favorable conditions” which change over time as the settlers deplete the resources, recognizing that environment can affect growth rate. It seems contradictory to assume that all environments are able to support the same growth and carrying capacity since demes will vary in hospitability.