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POLYMORPHISM AND MIGRATION RATE DIFFERENCE IN FRAGMENTED HABITAT

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In natural population migration is not always symmetrical. An example is matrilocality, in which a married couple resides with or near the wife's parents. In a matrilocal population, the Y-chromosomes should have higher migration rate than the X-chromosomes. We can also imagine a population living in a fragmented habitat and was founded by merging of two genetically diverged populations. In such population, if migration rates of the two ancestral populations differ, migration rate of an individual should depend on the genetic background. The natural questions are: How the migration rate difference could have influences on genomic diversity? Is it possible to infer such difference from genomic polymorphism data? Here, I will present a population genetic model of allele-dependent migration in fragmented habitat. The Wright's island model with allele-dependent migration rate was introduced. The probability of fixation of a mutant throughout the habitat was obtained by the diffusion process limit. Then, I introduced a random graph, which is an analogue of the coalescent genealogy, as a dual process of the diffusion model. In the strong migration limit, the population becomes panmictic and the difference in migration rate is equivalent to directional selection. By using the random graph, I developed an algorithm to compute likelihood of a given sample, which is based on the importance sampling with the perfect simulation.

Keywords: fragmented habitat, population genetics, migration, diffusion model