

## Chapter 6

### Epilogue

Population genetics is one of the constitutive parts of evolution. It provides mechanisms by which populations change given demography, environmental pressures and interactions with other populations, mutations and crossovers, not mentioning such exotic mechanisms as retro-transpositions, horizontal transfer and other. Population geneticists built great and logical machinery, which is propelled by abstract forces of drift, selection, mutation and recombination. The principles are simple, and encompass various versions of the Wright-Fisher and Moran Models of drift, with Markovian mutations, Haldane model for recombination and several types of selection. However, when combined, these principles lead to very complicated and frequently puzzling models; some with very complicated mathematics. This mathematics is not mere embellishment; it is needed in the same way it is needed in physics. Hence our belief in importance of approaches such as in this book. It is possible to paraphrase Theodosius Dobzhansky and state that nothing in population genetics makes sense except in view of demography. Models in the current book underscore the importance of population growth and decline and their influence on gene flow. The classical hypothesis of constant population time embedded in Wright-Fisher model has to be relaxed if we are to understand peculiar genetic structure of our own species, which expanded dramatically over the past 12,000 years. Expansion resulted in populations highly diversified with respect to genetic make-up, language and culture. One important fact is that because of this change, the human population is in genetic imbalance, which among other results in a high proportion of rare variants underlying common genetic diseases such as cardiovascular diseases, cancer, dementias and other. Demographic and genetic history of modern humans can be now better traced because of availability of methods of sequencing of ancient DNA. These exciting methodologies will become progressively less expensive. Methods of population genetics (mainly the Moran Model) have been already used to study evolution of cell populations in tumors. Therefore the issues considered here are not of purely academic interest. Dynamics of populations endowed with genetic structure are amenable for study by methods typical for dynamical systems, such as for example the semigroup theory of operators. In many cases these will be probabilistic semigroups. We hope that this short monograph will make population genetics more popular among applied mathematicians and also help them understand the importance of searching for real-life research problems.