Abstract. The meeting was devoted to mathematical aspects of population genetics, a branch of theoretical biology that is concerned with the genetic structure of populations under the influence of various evolutionary processes such as genetic drift, mutation, selection, recombination, and migration. The main focus was on probabilistic aspects of the dynamics, with the Moran model and its relatives as a central theme, and the corresponding stochastic processes forward and backward in time as a unifying point of view.

Mathematics Subject Classification (2000): 92D15, 60xx.

Introduction by the Organisers

One of the aims of population genetics is to explain how the genetic variation within and between biological populations is generated and maintained. Population genetics theory describes the change in the genetic composition of populations under the influence of various evolutionary processes such as genetic drift, mutation, selection, recombination, and migration. Elements of randomness turn out to be essential in the modelling of these processes. Random genetic drift, for example, is a consequence of the fact that, even without fitness differences, some individuals may, by chance, have more offspring than others, so that the offspring of one genotype may displace another.

The basic processes of evolution are known in principle, along with fundamental equations which describe the effects of interactions between genes. Indeed, of the biological sciences, genetics – and population genetics in particular – is the one with the most clearly defined mathematical models, with a strong emphasis on
probability. This fact has increasingly attracted probabilists who have given the theory a new impetus through powerful modern methods. Thus there is now an increasingly large community of biologists and mathematicians speaking a common language, learning from each other, and identifying problems that should be attacked. This spirit was manifest in our meeting, with its small group of senior mathematicians and biologists, and its larger fraction of young researchers.

The topics presented during the workshop crystallized into the following thematic groups:

- Genetic hitchhiking and selective sweeps (Stephan, Schweinsberg, Etheridge);
- Mutation-selection systems (Evans, Stannat);
- Speciation and adaptation (Bürger, Champagnat);
- Spatially structured systems (Birkner, Swart, Hutzenhaker);
- Stochastic processes associated with the coalescent (Krone, Pfaffelhuber);
- Poisson-Dirichlet distributions (Spano, Feng);
- Sampling formulae and coalescent-based inference (Ewens, Griffiths, Wakeley, Möhle, Hudson);
- Recombination, gene-rearrangement and sequence alignment (M. Baake, Berestycki, Metzler)

Stimulated by these lectures, there were many discussions and a rich scientific exchange during the workshop, between generations as well as between disciplines. Last not least, the meeting also profited greatly from the friendly and serene Oberwolfach atmosphere.