Abstract. Reaction systems and population dynamics constitute two highly developed areas of research that build on well-defined model classes, both in terms of dynamical systems and stochastic processes. Despite a significant core of common structures, the two fields have largely led separate lives. The workshop brought the communities together and emphasised concepts, methods and results that have, so far, appeared in one area but are potentially useful in the other as well.

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Introduction by the Organisers

Background and focus: Reaction systems and population dynamics are two areas of research that have recently experienced many novel developments and currently attract increasing attention, which goes far beyond mathematical biology and (bio)chemistry. Reaction systems describe the time evolution of the composition of a mixture of different (bio)chemical species that undergo a variety of chemical reactions. Population dynamics is concerned with the time evolution of the composition of a population of individuals of different types that interact with each other; the interaction can be competition, symbiosis, predation, etc. Traditionally, it is assumed that the number of molecules of each species (or the number of individuals of every type) is so large that a law of large numbers applies that allows to neglect random fluctuations. The systems are then described deterministically by a system of nonlinear ordinary differential equations or, if spatial behaviour is taken into account, by partial differential equations. Recently, there
has been a boost of stochastic approaches in both areas, which lead to a wealth of new challenges, concepts, and results.

**The workshop:** In line with the above, the goal of the workshop was to bring together the two subcommunities, which have been somewhat separate so far, to provide the opportunity for mutual stimulation. Of the 26 participants, roughly equal proportions came from reaction networks and population dynamics; some, including the three organisers, had already worked in both areas. The workshop started with an expository talk by Hofbauer, who highlighted connections between the fields by means of illustrative examples. This set the scene for more detailed contributions to follow. Altogether, the following core of common structures led the way:

- In many cases, equations have similar or even identical structures and can be translated into each other. For example, the process of recombination in population genetics may be reformulated as a bi-molecular reaction; populations living in symbiosis may be understood as a reaction system with mutual catalysis.
- Both the transient and the asymptotic behaviour is relevant. For large subclasses of reaction systems and population models, the deterministic behaviour is captured by a Lyapunov function that is related to (relative) entropy.
- Scaling arguments are of importance for stochastic systems in both cases to achieve simplifications, model reductions, and limits. In particular, diffusion processes appear as limits, and separation of time scales plays a decisive role.
- Recently, there has been a boost of stochastic approaches in both areas, which lead to a wealth of new challenges, concepts, and results. Characteristically, the stochastic models of population genetics have a standard representation in terms of interacting particle systems, which also form the basis of reaction systems.
- The further development of the mathematical theory is also driven by a new quality and quantity of data acquisition (in particular via the high-resolution methods of *systems biology* in reaction systems and of *genome research* in population genetics) and the need to solve problems of inference.

Throughout the workshop, emphasis was on concepts, methods, and results that have, so far, appeared in one area but are potentially useful in the other as well. Let us summarise the most important topics.

- Many qualitative properties of deterministic reaction systems can already be deduced from the algebraic or graphical properties of the network. For example, the global attractor conjecture (Craciun) states that, for the so-called complex balanced systems, all trajectories converge to a unique stable equilibrium point. For certain classes of systems that are not complex-balanced, necessary and sufficient conditions for multistationarity may be
Given (Dickenstein). For others, such as the model of T-cell receptor phosphorylation (Rendall), no general results are available, so they must be considered on a case-by-case basis. High-dimensional reaction systems can often be reduced to lower dimensions with the help of algebraic methods (Walcher).

• Many processes of population genetics are much more accessible to analysis in terms of the ancestral processes than in terms of the original (forward-time) dynamics. This gives rise to processes of branching and pruning (Cordero), coalescence (Mölle), partitioning (M. Baake), or a mixture thereof (Jenkins). Closely-related growth-fragmentation equations appear in cell biology forward in time (Doumic).

• Stochastic aspects of reaction networks become increasingly important. For certain classes (namely, host-parasite reaction networks), the long-time asymptotics can now be characterised analytically (Majumdar). Noise might not always be a nuisance — in fact, an emerging paradigm is that it can have beneficial effects on biological processes (Gupta). Due to the high dimensionality, stochastic reaction systems call for new approaches to simulation (Williams) and inference (Rand, Hilfinger).

• Models taking into account spatial behaviour are much more developed for population models than for reaction networks. In genetics, for example, the theory of clines, which describes the spatial structure of a population under migration and selection, is well developed (Bürger). Likewise, the behaviour of populations under selection, mutation, and migration may be characterised, provided that there is time-scale separation due to rare mutations (Léman). There is a definite need to consider spatial structure in reaction systems, but this is more difficult due to the high dimensionality of the models and due to cell compartmentalisation.

• Deterministic and stochastic models do no longer belong to separate worlds. Rather, the connections between them are being increasingly recognised. This is true of several of the topics already mentioned above, but was in the centre of attention in the context of finite population models (Schreiber), where the quasistationary states of the stochastic system correspond to the stationary states of the deterministic one. Likewise, a stochastic model of adaptive dynamics which converges to an adaptive walk that jumps between Lotka–Volterra equilibria (Kraut). Results on complex-balanced reaction systems that have, so far, been available in the deterministic situation only, have recently been extended to the stochastic setting (Cappeletti).

Problem sessions were held on Thursday afternoon and evening, on the following topics:

• multiscale models
• spatial aspects of reaction networks
• moment closure
• Lyapunov functions
dualities, ancestries and hidden linearities in reaction systems

From the very first minute, the workshop was blessed with an extraordinarily intense atmosphere of discussion and curiosity. The coherence between the talks was astonishing, and additional connections were made by the speakers. Specifically, Paul Jenkins spontaneously changed the topic of his talk so as to blend in perfectly with the previous one. The intensity of the workshop under the spell of the MFO, added by the lively conversations in the warm midsummer nights, made this a very special week to most, if not all, participants, many of whom were newcomers to Oberwolfach or returning after many years.

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