

Modelling efforts in the early days of development in modern biology have proceeded apace to the point where new knowledge of the biology is actually driving the development of new mathematics. This explosion of biological knowledge has proceeded hand in hand with the development of mathematical modelling efforts to understand and explain it, leading to very complicated systems. Rapidly developing techniques of molecular biology and genetics produce large quantities of data that demand mathematical analysis and modeling. By using mathematical models one can analyze populations and biological systems at various levels, including cells, genes, and biomolecules. Nowadays mathematical modeling of biological processes is a central topic in theoretical biology and some biologists find that mathematical models are absolutely essential for research in modern biology. Although first mathematical methods appeared in demography, they have become increasingly important in almost all branches of biology including ecology, epidemiology and infectious diseases, genetics, physiology, immunology and cancer growth.

Our aim is to construct models of new biological phenomena which appear in population dynamics, molecular biology, genetics, and cells physiology, and to provide new mathematical tools to study existing biological models. Functioning of living cells depends on a variety of life processes at molecular level such as metabolism and reproduction, synthesis of macromolecules, regulation of gene activity, cellular differentiation, intercellular communication, as well as mutation, selection, and evolution. The nature of molecular interactions and processes imposes the need for modelling the molecular dynamics as a mixture of continuous state dynamics and discrete state dynamics together with stochastic effects. This type of dynamics is modeled and studied by stochastic hybrid systems and is successfully used to describe dispersal in biological systems, cell cycle, biochemical networks, gene expression, physiologically structured populations as well as neural activity.

In population biology, a population is usually heterogeneous. Thus it is important to divide it into homogeneous groups according to some significant parameters such as age, size, maturity, or proliferative state of cells, and to study interactions between such groups. Models of this type are called structured and they describe the time evolution of the distribution of the population according to the fixed parameters. This type of models are represented by differential equations and can model age and phenotypic structured population, fragmentation-coagulation processes, cancer growth and genome evolution.

The significance of scientific problems proposed by our project is related to its interdisciplinary character, going well beyond strictly mathematical research. We develop mathematical tools to describe and solve specific biological problems. We hope that mathematical analysis will be helpful in understanding mechanisms of biological processes. The most important issue of our research is to find mathematical results which can be biologically interpreted and can provide valuable biological information. For example, the existence of a stationary state and its global asymptotic stability is such a property, because we can expect that the real process should be close to a stationary state and then it is easy to estimate biological parameters. We hope to find general mathematical results which could be directly applied to study such problems. At the same time studying biological models has an inspiring impact on the development of new mathematical methods.