Introduction

Historically, the Life Sciences have provided stimulation for a number of important developments in different branches of mathematics. In particular, significant progress in Probability Theory is the result of problems that have been raised in the theory of population genetics (Mendel, Fisher, Kimura, and others). Furthermore, classical statistical theory arose largely because of the need to interpret data from biological and medical investigations. Today, there are newer topics such as morphogenesis, which is a source of problems that require new tools from Geometry and Complex Analysis. The biological use of fractal mathematics is also very common.

Mathematics and the Life Sciences have always interacted in both directions, and it is inevitable for the progress of science that they must do so. In the first place, mathematics represents an indispensable tool for the biologist or the physician. Important work is yet to be done in order to provide more elaborate and sophisticated mathematical methodologies capable of treating data and problems in the life sciences area. For example, the treatment of censored survival data to be correctly carried out needs an approach founded on martingale theory. The establishment of the human genome map requires the tools of complex combinatorics. In a similar manner, the analysis of more and more complex data demands ever-increasing computer support, including the methodology of expert systems to help with decision making, artificial intelligence, and medical image processing. Thus a whole new field opens itself to a collaboration between mathematicians and physicians.

The second and main point is that the Life Sciences are set to play the same role as did physics in the nineteenth century and early twentieth century for fundamental mathematics, that is to say, to raise to some questions. This is already happening, as for instance with the development of neural networks or again in the newer uses of mathematics in biochemistry. Mathematical models underlying many of the processes in the field of molecular biology are still to be devised. When they are, they will have to account for some extremely complex phenomena, such as the role of enzymes, phenomena occurring in membranes and retroactions. These models will certainly be linked to various mathematical studies such as the stability of the solutions to partial differential equations, bifurcations, models of chaos, etc.
For some 50 years we have experienced a transition from “smooth” mathematical tools (e.g., classical analysis, deterministic systems, differentiability, ...) to more “chaotic” tools (e.g., randomness, singularities, fractals, self-similarity, ...), which enables the mathematician to refocus a field of application from physics in a broad sense to biology.

The originality of the phenomena then considered introduces a very “decentralized” behaviour: the different components of a biological system, whether they be living creatures in a population or cells in an organ, determine their behaviour with a given independence. Their study requires the development of “statistical biology” similar to the established statistical mechanics; obviously this independence can be modelled by the same independence which underlies brownian motion, with bifurcations looking like phase transitions. Taking advantage of the development of modern computers, one can work to extend a whole speculative field, going from the more sophisticated theory of point processes to the stability of stochastic partial differential equations to explain some evolutions, or change point theory to express some imbalances.

**Invited participants**

Elja Arjas (Oulu)
Gilbert Chauvet (Angers)
Albert Goldbeter (Brussels)
Niels Keiding (Copenhagen)
Jonathan Swinton (London)
Petr Tautu (Heidelberg)