

Abstract – English:

The ability to process information is as central to life as for instance reproduction. Biological systems can “run programs” of varying complexity. Examples of “biological programs” are, for instance, apoptosis, the activation of a T cell, the cell cycle, and development. While the interplay of biomolecules in such pathways is currently being unraveled at a rapid pace, it should be noted that in the case of complex dynamic systems, a merely qualitative description does not provide sufficient insight. Therefore, there is a need to develop quantitative mathematical models of such systems based on biophysical and chemical considerations, which will permit a deeper level of understanding. Such mathematical models will also allow predictions which are a prerequisite for creating new biological programs designed to perform certain desired tasks. The author suggests that such programs bear potential for future application as a new form of therapy e.g. for cancer and degenerative diseases.

The present dissertation (<http://www.bioprograms.org/thesis>) includes an introduction to information theory and the theory of computing with an emphasis on aspects relevant to biology and medicine. General physical principles of information storage, transport and processing are reviewed together with a comparison between the components of electronic and biological “circuits” and a description how these components are assembled to form complex systems capable of computing “programs”. It is shown that biological systems or “circuits” possess all the essential components required to process information and to compute programs i.e. logic gates, memory and I/O modules. This is followed by a review of several approaches to mathematical modeling of biological systems with an emphasis on metabolic control analysis, systems of non-linear differential equations and stochastic models based on matrices and Monte Carlo algorithms. Taken together, these considerations provide a theoretical framework for new approaches in medicine. The reason for this is as follows:

First, mathematical models permit a rigorous analysis of the biological “programs” that operate in states of health and disease, and they offer the possibility to identify previously unrecognized targets for future drug therapy capable of switching off “disease programs” e.g. by blocking certain signaling pathways. Second, the author suggests that biological programs and circuits could be created that perform desired tasks. While conventional pharmacotherapy can only aim at either blocking or activating receptors (a “simple one-step therapeutic algorithm”), biological programs make it possible to implement “complex, multi-step therapeutic algorithms”. As an example, a stochastic model of a biological circuit is presented that has been designed to be of possible clinical value: The circuit computes a program which allows the biological system to recognize the surface of target cells based on the *logical combination* of surface antigens. This toggles a biological switch that could trigger further effector programs. The example makes clear why creating biological programs constitutes an interesting approach for future medical therapy. Such a circuit could, for instance, help immune cells recognize cancer cells, or it could allow stem cells to settle down in appropriate environment. The circuit computes a logical operation on several inputs into an output, it contains a biological switch and a time delay, everything “built” exclusively from biological components. Although the biological molecules are fictitious, the example makes clear that a similar system could be built in reality. A stochastic model of the biological circuit has been implemented by the author in C programming language. Outputs from computer simulations of the stochastic model of the biological circuit are presented. To the authors knowledge, this is the first description of an “artificial” biological program designed for therapeutic purpose. The approach suggests a certain potential for the future application of “therapeutic biological programs” as a new form of medical therapy. The novel ideas are placed into a broad historical perspective, and analyzed critically from the viewpoint of medical ethics.