

Watching the Daisies Grow: from Biology to Biomathematics and Bioinformatics — Alan Turing Centenary Special Issue

Preface

*We can only see a short distance ahead,
but we can see plenty there that needs to be done.*
Alan Turing

Year 2012 is both the centenary of Alan Turing's birth and the 60th anniversary of the famous paper *The Chemical Basis of Morphogenesis*, in which he established foundations of the mathematical theory of biological and chemical pattern formation.

The story started much earlier, in spring 1923, as documented by his mother in a caricature entitled *Hockey or Watching the Daisies Grow*. Crucial motif in the drawing is that, while most players are engaged by the game, Alan is investigating a flower emerging just off the field.

Always fascinated by the relationship between matter and spirit, especially in the processes of thinking, Turing started from the assumption that the operation of human brain is completely physical. This led him to invention of an abstract computing machine named after him, which laid the foundations of modern computer science. In recognition of his enormous contribution to the growth of the field, the most prestigious award in computer science, called "Nobel Prize of computing", is named after Turing.

Success has many fathers, but it was Alan Turing to whom we owe the final breaking of the Enigma code. He extended the idea of so-called "Cryptology bombs", i.e., machines aimed at breaking codes, constructed before World War II by Polish mathematicians: Rejewski, Różycki and Zygalski. His solution ensured the information advantage of the Allies during the Battle of the Atlantic, which had a direct bearing on the success of operations in Normandy and the defeat of Nazi Germany.

After the war, Turing took up marathon running to relieve the stress, studied why spots on the leopard's body are in the shape of a rosette or ring, and proposed a test to measure the machine's ability to exhibit intelligent behavior. For this last reason, Turing is regarded as a founder of artificial intelligence. He left this world prematurely in the age of 42, but managed to finish the race with the highest score, in fact more than one race. . .

In this special issue, we present a selection of papers commemorating Alan Turing and arguing that he should be also considered the co-founder of biomathematics and bioinformatics. His late works were

inspired by curiosity about the role of mathematics in natural phenomena. Turing's ideas on diffusion-driven instability leading to a formation of stable spatial structures provided mathematical explanations of symmetry break and *de novo* pattern formation during development, and the shapes of animal coat markings. They also led to the prediction of oscillating chemical reactions, the behavior which were first observed only about 10 years after Turing's death.

In this volume, various applications of mathematical theories inspired by Turing's work to natural phenomena are considered. The paper by Bertolusso and Kimmel is devoted to the interaction of spatial and stochastic effects in a model of viral infection. Reaction-diffusion systems can be viewed as mean-value approximations of random walk based stochastic systems of interacting molecules. However, as it turns out, the patterns developing in the stochastic system are different and generally richer than in the deterministic reaction-diffusion system.

Vakulenko and Radulescu present a mathematical formulation of Driesch and Wolpert's positional information theory of emergence of organization in multicellular organisms. The specific context is a model of control of a gene network, consisting of two types of nodes: centers and satellites. Satellites interact with each other only through the centers whereas the centers may interact with centers and satellites. The authors demonstrate that the model can be made "infinitely flexible", i.e., able to transition between any desired modes of qualitative behavior upon parameter change.

The main focus of the contribution of Archuleta *et. al* lies on three dimensional modeling of receptor signaling networks dynamics. Novel multi-resolution Monte Carlo technique allows the authors to observe an interesting mechanism, *adaptor protein hopping*, that explains the increase in signaling efficiency when receptors are colocated. Authors address the question how adaptor protein hopping enhances the immune response, which could constitute a mechanism exploited by pathogens to deregulate innate immune signaling for their own virulence strategies.

Błażewicz and Kasprzak consider several complexity issues inspired by computational biology. Among others, the similarities and differences between DNA computers and nondeterministic Turing machines are discussed.

The results by Setty *et. al* are clearly inspired by Turing's ideas. They describe the state-based modeling of morphogenesis, which results in a fully executable program for the interactions between chemical entities and morphogens. Furthermore they discuss a variant of the original Turing test for a machine's ability to demonstrate intelligence, as a future means to validate computerized biological models.

Finally, Batmanov *et. al* focus on the phenomenon of self-organized patterning during development of higher organisms. Often, a key role in this process is played by the community effect allowing the cell population to forge a common identity, originally observed in muscle differentiation in *Xenopus embryos*. The paper studies the dynamics of a community effect in space and its roles in two other processes of self-organized patterning by diffusible factors: Turing's reaction-diffusion system and embryonic induction by morphogens.

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