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Abstract

Computational modelling of morphogenesis: from genes to organism

One of the most spectacular developments in biology is the discovery of genes and regulatory networks controlling morphogenesis in animals. Nüsslein-Volhard, Wieschaus and Lewis shared the Nobel price in medicine and physiology in 1995 for their discovery of the genes regulating the early development of the *Drosophila* embryo. These genes controlling development appeared to be highly conserved throughout the animal kingdom. The development of individual body parts (eyes, limbs, the heart, etc) is regulated by similar genes within the animal kingdom. Disruptions in the developmental regulatory networks play an important role in the development of malformations and the emergence of cancer.

An important next step is to understand the structure and dynamics of regulatory networks, this may lead to fundamental new insights in developmental biology, evolution and new medical applications. Most of these networks are characterized by very complicated structures. An additional complication is that these networks change in space and time. A simple graph representation showing the connections between genes, does not provide insight in how these connections are changing quantitatively in space and time. For research on these networks and gene regulation of morphogenesis, simulation models are indispensable.

Within the metazoans, sponges and cnidarians represent the phyla with the simplest body plan and a relatively simple regulatory network controlling the development. This makes these organisms an excellent case study for understanding morphogenesis and the physical translation of the genetic information into a growth form, using a combination of biomechanical models of growth and form and a model of the spatial and temporal expression of developmental genes. During this talk we will give an overview of the ongoing work within the MORPHEX project on modelling and simulation of growth and form in sponges and cnidarians (examples the sea anemone *Nematostella vectensis* and scleractinian corals). For modelling the developmental biology of these organisms it is required to combine models at very different spatio-temporal scales: gene regulation and cellular level, bio-mineralisation, physiology, growth of the organism and the impact of the physical environment (water movement and availability of light). We will briefly discuss:

- Modelling gene regulation and cell movement in early development of the cnidarian *Nematostella vectensis* and the sponge *Lubomirskia baikalensis* and methods for inferring gene networks from spatio-temporal gene expression data stemming from in-situ hybridizations.
- Modelling accretive growth and gene regulation in a sponge and the impact of the physical environment