Modelling Information Flow in Biological Coding Systems

COST Action CA21169
DYNALIFE WG1 Meeting

BOOK OF ABSTRACTS

Editor: Nataša Mišić

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About DYNALIFE

In the mid-twentieth century two new scientific disciplines emerged forcefully: molecular biology and information-communication theory. At the beginning cross-fertilisation was so deep that the term genetic code was universally accepted for describing the meaning of triplets of mRNA (codons) as amino acids. However, today, such synergy has not taken advantage of the vertiginous advances in the two disciplines and presents more challenges than answers. These challenges are not only of great theoretical relevance but also represent unavoidable milestones for next generation biology: from personalized genetic therapy and diagnosis, to artificial life, to the production of biologically active proteins. Moreover, the matter is intimately connected to a paradigm shift needed in theoretical biology, pioneered long time ago in Europe, and that requires combined contributions from disciplines well outside the biological realm. The use of information as a conceptual metaphor needs to be turned into quantitative and predictive models that can be tested empirically and integrated in a unified view. The successful achievement of these tasks requires a wide multidisciplinary approach, and Europe is uniquely placed to construct a world leading network to address such an endeavour. The aim of this Action is to connect involved research groups throughout Europe into a strong network that promotes innovative and high-impact multi and inter-disciplinary research and, at the same time, to develop a strong dissemination activity aimed at breaking the communication barriers between disciplines, at forming young researchers, and at bringing the field closer to a broad general audience.

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2023

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Modeling the Non-Linear Dynamics of Information Flows in Neuro-Endocrine Systems

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Abstract

Nonlinear feedback loops inherent to *neuroendocrine systems* are among the most important information flows at the organism level. They support high sensitivity and responsiveness of the living beings to external perturbations. Moreover, nonlinear feedback loops enable efficient control over dynamic physiological states. Often, they can be recognized through emergence of various dynamic phenomena, such as *biological rhythmicity*. Typical examples of such neuroendocrine systems are the hypothalamic-pituitary-adrenal (*HPA*) *axis* and the hypothalamic–pituitary–thyroid (*HPT*) *axis*. They are characterized by rhythmic dynamics with two characteristic periods, circadian (~ 24 h) and ultradian (20 min – 120 min), which allows living organisms to quickly adjust their neuroendocrine activity to fluctuations in their surroundings and/or their internal physiology.

We focus our research on mechanistic modelling of biochemical transformations that underlay complex neuroendocrine networks. Thus far, we have developed several variants of low-dimensional and extended models for the *HPA axis*, as well as, one medium scale model of the *HPT axis*. Both of them are assembled by combinations of the pseudo-reaction steps, describing in essence the information flow through the network of chemical transformations. Their role in physiological system is to maintain basal levels of hormone concentrations, and enable their functionally reasonable change when some need emerges. Our models enable one to emulate in numerical simulations changes in blood level of relevant hormones that constitute the HPA or HPT axis (Jelić et al. 2005, Marković et al. 2011, Čupić et al. 2017, Kolar-Anić et al. 2023).

The high predictive value of our models paves the way for their use in medical diagnostics of neuroendocrine diseases and for more efficient corticosteroid treatment that is applied in various illnesses, by harnessing the power of the underlying nonlinear feedback loops to the dosage of corticosteroid drugs could be significantly decreased, while preserving their efficacy. We pay special attention to the Stoichiometric Network Analysis of reaction network models to identify conditions ensuring the existence of unstable steady states, and in particular, Hopf bifurcation as a most plausible path leading to the oscillatory dynamics. The simplest way to use this template is to replace the text in this file with your own words using the styles provided as far as possible.

Keywords

Neuro-endocrine systems, oscillatory reactions, bifurcations, reaction networks, biological rhythmicity, nonlinear feedback loops.

Reference

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