KEYNOTE: Biotic systems as multilevel dynamic information processing systems

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Highlights: Multilevel Modeling may simplyfy the modeling of complex biological processes

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Most studies of (information processing in) biological systems, focus on one level of organization, e.g. gene regulation, or ecosystem interactions. Such single level biological systems are already very complex, and even relatively simple models of them are hard to study, for example because of the large number of unknown or only partially known parameters.

In this talk I will argue that, extending such models to multiple levels can, paradoxically, make things simpler. Mutual interaction among levels may constrain the dynamics, tune parameters and/or make the dynamics more dependent on structure and less sensitive to parameters. Such extensions can be either by explicitly defining multiple levels in the model or allowing new levels of organization to emerge.

The argument will be illustrated in a number of case studies, focusing on gene regulation (adaptation to a varying environment at regulatory and evolutionary timescales; the role of bi-stability(van Hoek and Hogeweg 2006,2007)), genome evolution (the role of whole genome duplication, homeostasis (van Hoek and Hogeweg 2009, Cuypers and Hogeweg 2012, and in prep), development (the role of size and shape of cells and tissues in cell fate specification (Grieneisen et al 2007, 2012) and ecosystems (higher levels of organization and the role of mutualism and cheaters (Takeuchi and Hogeweg).

In these multilevel models counter-intuitive results are obtained, which often challenge conventional 'wisdom' and yet reflect observed but unexplained patterns in 'real' biological systems

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