

Some tools for scaling: modelling hierarchies

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Any biological system has an inherent hierarchy of structures, each being subject to modelling. Hence, it can be modelled at different scales, or coarse graining levels. Making sure that two different models at different scales describe the time evolution of the same biological system can be achieved by perfect aggregation, pioneered in ecology in the late 80's. The first part of the talk will present this tool, and show that it displays several nice mathematical properties, which suggest that it can be studied with a high level of generality, over a whole biological hierarchy. In a second and more speculative part, a link will be sketched with so called 'dynamical clustering': recent numerical simulations show that for large sets of maps coupled by diffusion on a lattice, clusters of highly correlated cells can emerge, such that the whole system can be analyzed as a spontaneous network of clusters. These recent examples suggest that perfect aggregation may be more often met in biological systems than what could be spontaneously assumed.

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