Towards an ‘Oceans Systems Biology’

The twentieth century has largely been a ‘reductionist century’ in biological sciences. With the successes of physics and chemistry, molecular biology was dominated by the idea that Nature could be understood by reducing its complexity to that of molecular interactions, if not to the fundamental principles of quantum mechanics. However, complex systems, and living organisms in particular, emerge from dynamical processes occurring simultaneously at various spatio-temporal scales. This requires a conceptual framework capable of bridging scales to explain the emergence of complexity. Although the analysis of individual interactions between a small number of molecules is useful to explain simple causal relationships, understanding what life requires a more holistic approach. This has been progressing slowly over the past 20 years with the rise of systems biology. Operationally, systems biology is by essence interdisciplinary and aims to understand how interactions between populations of molecules, cells and organisms give rise to complex biological processes such as cell division, developmental, behavioral and ecological patterns.

To apply such approaches to the study of biological systems, a series of conceptual and technological ‘toolbox’ has been developed (Box 1). Fascinatingly, these various approaches can be applied at any organization level of living organisms, from molecular interactions to the patterning of ecosystems and evolution.

Before metazoans appeared, life evolved in the oceans for more than 2.5 billion years as a world of unicellular organisms composed of viruses, bacteria and protists. The massive number of these microorganisms still represents today more than 98% of life in the oceans. These organisms are a key actor of our planet’s ecology. Not only do we originate from them through cellular and developmental evolution, but we also owe our existence to their impact on the chemistry of our atmosphere. Without them, there would be no O₂, no oil and no twenty first century scientists to think about it. Yet we know virtually nothing of these microscopic ecosystems. Quantitative data on the relative composition in viruses, bacteria, protists and metazoans of the oceanic drifting organisms collectively named ‘plankton’ are missing. It remains largely unknown how the various species in these kingdoms are distributed and interact as a function of environmental parameters. Such biogeographical data have been difficult to obtain because of technical limitations associated with oceanic sampling and because the required high-throughput methods were lacking. Until 5 years ago, sequencing methods were too expensive, too slow and not sensitive enough. Quantitative, automated imaging methods to identify protists and metazoans were still in their infancy. Data storage, informatics and bioinformatic were limiting and tools borrowed from physics for the analysis of complex dynamical systems were just being applied to the fields of cell and developmental biology. Since a couple of years these approaches have considerably matured and can now be applied to ocean biology.

One of the great challenges in ocean biology is to understand how populations of organisms are structured by their interaction with the environment and how such complex systems have evolved. Oceans are not homogeneous; they are structured by rotating currents or gyres, generated by temperature gradients, the rotation of the earth and the position of the continents. There are great variations, both in time and in space, of temperature, oxygen content, pH, nutrients, light and so on. The degree of mixing between surface layers and the deep ocean also varies dramatically. This great diversity of environments and, at the same time, the transport of species from one environment to the next is reminiscent of the great changes that occurred during
evolutionary times. This is a typical systems biology problem that requires the integration of quantitative systematic data obtained from imaging and large-scale metagenomics and metatranscriptomics efforts with high-content environmental data.

TARA OCEANS (http://oceans.taraexpeditions.org/) is the first expedition that carried out a comprehensive worldwide sample collection campaign (Figure 1) with a coherent strategy to record all the information necessary to the study of the emergent properties of plankton ecosystems. Indeed, the expedition has quantitatively sampled organisms ranging from viruses to small metazoans all around the world using real-time satellite imagery to select the proper water masses, a range of physico-chemical sensors and the proper set of sampling tools for each size class of organisms. Moreover, all data are connected together using a barcoding system that makes the downstream correlation analysis more straightforward than in previous similar environmental projects. Such quantitative data analyzed by genomics, imaging and physical oceanography will inform computational models of the functional biodiversity of plankton organisms and their evolution as well as physical models of the dynamical evolution of their biogeography. Although it is too early to say how well these models will perform, it is clear that the data collected are of sufficiently high quality to support this type of analysis. Correlative analysis of quantitative measurements of phages, virus, bacterial populations, protists and metazoans with complex environmental variables are being done on more than 30 stations around the world (the whole expedition will bring back samples and data from 155 stations from all the main oceans of our planet). Promising preliminary results begin to provide new information about the global biodiversity of plankton ecosystems and insights into the unknown diversity of viruses, giruses and protists as well as on potential symbiotic and parasitic relationships between kingdoms and species.

While the ship finishes the collection phase on the 31 March 2012, when it arrives in Lorient France, the land-based investigation is picking up speed. With the data and samples amassed during the 2.5 years of the TARA OCEAN expedition, the analysis promises to provide exciting results over the next few years in the fields of marine ecology, evolution, biogeography and adaptation to climate change by integrating data using the global methods of systems biology.

Eric Karsenti
EMBL, Heidelberg, Germany
E-mail: karsenti@embl.de

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