

Biology's next revolution

The emerging picture of microbes as gene-swapping collectives demands a revision of such concepts as organism, species and evolution itself.

Nigel Goldenfeld and Carl Woese

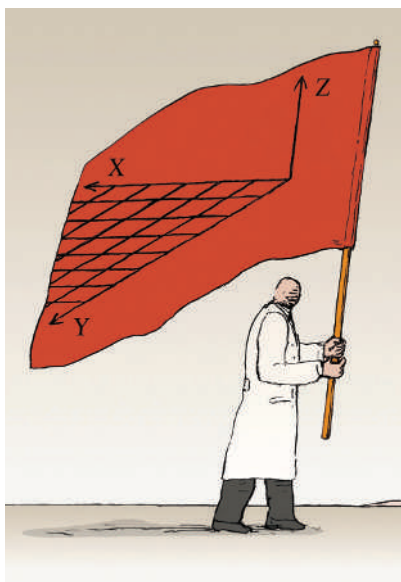
One of the most fundamental patterns of scientific discovery is the revolution in thought that accompanies a new body of data. Satellite-based astronomy has, during the past decade, overturned our most cherished ideas of cosmology, especially those relating to the size, dynamics and composition of the Universe.

Similarly, the convergence of fresh theoretical ideas in evolution and the coming avalanche of genomic data will profoundly alter our understanding of the biosphere — and is likely to lead to revision of concepts such as species, organism and evolution. Here we explain why we foresee such a dramatic transformation, and why we believe the molecular reductionism that dominated twentieth-century biology will be superseded by an interdisciplinary approach that embraces collective phenomena.

The place to start is horizontal gene transfer (HGT), the non-genealogical transfer of genetic material from one organism to another — such as from one bacterium to another or from viruses to bacteria. Among microbes, HGT is pervasive and powerful — for example, in accelerating the spread of antibiotic resistance. Owing to HGT, it is not a good approximation to regard microbes as organisms dominated by individual characteristics. In fact, their communications by genetic or quorum-sensing channels indicate that microbial behaviour must be understood as predominantly cooperative.

In the wild, microbes form communities, invade biochemical niches and partake in biogeochemical cycles. The available studies strongly indicate that microbes absorb and discard genes as needed, in response to their environment. Rather than discrete genomes, we see a continuum of genomic possibilities, which casts doubt on the validity of the concept of a 'species' when extended into the microbial realm. The uselessness of the species concept is inherent in the recent forays into metagenomics — the study of genomes recovered from natural samples as opposed to clonal cultures. For example, studies of the spatial distribution of rhodopsin genes in marine microbes suggest such genes are 'cosmopolitan', wandering among bacteria (or archaea) as environmental pressures dictate.

Equally exciting is the realization that viruses have a fundamental role in the biosphere, in both immediate and long-term evolutionary senses. Recent work suggests that viruses are an important repository and



memory of a community's genetic information, contributing to the system's evolutionary dynamics and stability. This is hinted at, for example, by prophage induction, in which viruses latent in cells can become activated by environmental influences. The ensuing destruction of the cell and viral replication is a potent mechanism for the dispersal of host and viral genes.

It is becoming clear that microorganisms have a remarkable ability to reconstruct their genomes in the face of dire environmental stresses, and that in some cases their collective interactions with viruses may be crucial to this. In such a situation, how valid is the very concept of an organism in isolation? It seems that there is a continuity of energy flux and informational transfer from the genome up through cells, community, virosphere and environment. We would go so far as to suggest that a defining characteristic of life is the strong dependency on flux from the environment — be it of energy, chemicals, metabolites or genes.

Nowhere are the implications of collective phenomena, mediated by HGT, so pervasive and important as in evolution. A computer scientist might term the cell's translational apparatus (used to convert genetic information to proteins) an 'operating system', by which all innovation is communicated and realized. The fundamental role of translation, represented in particular by the genetic code, is shown by the clearly documented optimization of the code. Its special role in any form of life leads to the striking prediction that early life evolved in a lamarckian way, with vertical descent marginalized by the

more powerful early forms of HGT.

Refinement through the horizontal sharing of genetic innovations would have triggered an explosion of genetic novelty, until the level of complexity required a transition to the current era of vertical evolution. Thus, we regard as regrettable the conventional concatenation of Darwin's name with evolution, because other modalities must also be considered.

This is an extraordinary time for biology, because the perspective we have indicated places biology within a context that must necessarily engage other disciplines more strongly aware of the importance of collective phenomena. Questions suggested by the generic energy, information and gene flows to which we have alluded will probably require resolution in the spirit of statistical mechanics and dynamical systems theory. In time, the current approach of post-hoc modelling will be replaced by interplay between quantitative prediction and experimental test, nowadays more characteristic of the physical sciences.

Sometimes, language expresses ignorance rather than knowledge, as in the case of the word 'prokaryote', now superseded by the terms archaea and bacteria. We foresee that in biology, new concepts will require a new language, grounded in mathematics and the discoveries emerging from the data we have highlighted. During an earlier revolution, Antoine Lavoisier observed that scientific progress, like evolution, must overcome a challenge of communication: "We cannot improve the language of any science without at the same time improving the science itself; neither can we, on the other hand, improve a science without improving the language or nomenclature which belongs to it." Biology is about to meet this challenge. ■

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FURTHER READING

Frigaard, N., Martinez, A., Mincer, T. & DeLong, E. *Nature* **439**, 847–850 (2006).
 Sullivan, M. et al. *PLoS Biol.* **4**, e234 (2006).
 Pedulla, M. et al. *Cell* **113**, 171–182 (2003).
 Vetsigian, K., Woese, C. & Goldenfeld, N. *Proc. Natl Acad. Sci. USA* **103**, 10696–10701 (2006).

For other essays in this series, see <http://nature.com/nature/focus/arts/connections/index.html>

KAPUSTA

CONNECTIONS

Making connections

A series of essays is launched in *Nature*.

There are times in the development of science when a shift in approach is sufficiently extensive that only a collection of thoughts and perspectives from many different practitioners can do justice to it. This issue sees the launch of a themed series of essays, called Connections, which take such an approach to the interdisciplinary study of complex, dynamic systems (see page 369).

Scientists in almost every discipline are grappling with the problem of how best to model such systems. Cell biologists are being driven to do so, for example, by the surge of data from techniques that reveal biological processes in unprecedented detail, and quantum physicists by properties exhibited by collections of particles that would not have been anticipated on the basis of how a single particle behaves. Across these fields and beyond, deeper insight requires a systems-level approach that seeks to understand interactions and make connections. Although the goal is clear enough, the way to reach it is not.

Many researchers recoil from terms such as 'systems biology' and 'complexity', interpreting them as euphemisms for things we don't adequately understand. Research on problems involving dynamic interactions between large numbers of entities is often directed by the availability of the data, rather than by a carefully considered question. And a rush of studies claiming to uncover simplifying prin-

ciples that unite complex networks has sometimes generated more heat than light.

In some cases, attempts to understand networks and whole systems are driving researchers to cross disciplinary boundaries. Social and physical scientists are often more accustomed to such collective activity than molecular biologists, for whom the borrowing of techniques and expertise is now becoming commonplace.

The essays in the Connections series will illustrate some of the insights that are emerging as researchers pursue more holistic approaches to problems, while engaging in an unprecedented degree of collaboration between biological, social and physical scientists. They will raise provocative ideas about how to probe dynamic systems, illustrating, for example, how systems approaches can challenge assumptions established within the more reductionist framework of twentieth-century science.

The series begins just a few weeks after the popular Essay page returned to *Nature*. It will reiterate the tradition of this format as a forum for scientists to reflect on new ideas, or re-evaluate old ones. The Connections essays will also be collated on the web, where access to the first four will be free. We hope that, week by week, a greater story develops than could be told by a single article — and that over the coming year, the Essay page will continue to provide scientists with a valuable opportunity to say exactly what they think. ■

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