

BOOK REVIEW

Mathematical, biological, and computational explanations

Making Sense of Life: Explaining Biological Development Models, Metaphors, and Machines

EF Keller

Harvard University Press, Cambridge, Massachusetts; 2002.
388 pp. £19.95, hardback. ISBN 0-674-00746-8

Heredity (2005) 94, 458. doi:10.1038/sj.hdy.6800630

Reviewed by L Leydesdorff

Although the narrative in the study is developed as a history of the field, Evelyn Fox Keller discusses a problem of the philosophy of science in her quest of 'making sense of life.' The author does not hide that this puzzle emerged from her own background as a physicist, once involved in proposing a mathematical model to explain the onset of aggregation in cellular slime molds. At that time (the 1960s), she found that the biological audience was not receptive to the model at all. The puzzles and problems were differently defined by biologists. One could not appreciate a model that abstracted from the biological question of what life is. Fox Keller points to important contributions from mathematical biology like those of Nicolas Rashevsky in the 1930s and Alan Turing in the 1950s that failed to reach their intended audience among biologists because the mathematical principles required translation into a discourse, which focuses on material observation and accordingly formulates its problems in empirical terms.

In the opening chapter, the author contrast this with the relative success of Stéphane Leduc and other scholars who in the beginning of the 20th century developed 'physico-chemical theories of life', which could be illustrated with experiments using osmosis. In this context, the biologist Gruenberg (1911) wrote a two-part overview in the *Scientific American* in 1911 (!) under the title 'The Creation of 'Artificial Life''. Nowadays, this same title is used by a research tradition in computational biology (Langton, 1986). How have the meanings of the terms shifted? How has the puzzle of combining material elements, biological questions about the dynamics, mathematical models and computational devices been solved in the research practiced differently in the various developmental stages of biology. How is this reflected in the texts?

The historical topic of Keller's study is the tension in the models between genetics and embryology during the development of biology in the 20th century. She shows at great length how the problem formulations shifted, for example, when the DNA-model became available and when Jacob & Monod's operon model was elaborated. In the latter model, the epigenetic understanding of development made it possible to solve the problem by translating concepts that had been developed in cybernetics into the discourse of biology. The latter requires a substantive understanding in addition to the mathematical model.

From the perspective of the mathematician and the physicist, the use of a metaphor may seem like blurring an

analytical distinction. However, the change of the context and therefore the meaning of the words may generate trading zones between discourses in which new puzzles can be generated. During the processes of change in the scientific discourses and practices, the very concepts used change meaning. For example, the word 'activation' invoked a context different from 'action.' The author elaborates on the example of what 'positional information' meant to various authors who used this concept for explaining developmental processes like segmentation in *Drosophila*. How does language mediate in changing our encounter with an external world in the scientific enterprise? How has this mediation been different for those who were socialized with the Galileian dictum that the book of nature is written in math, and for those who were socialized in the tradition of natural history with its focus on 'watching' and empirical observation?

In the final part of the book, the author describes how two recent developments in the computer sciences have contributed to building a new bridge between these traditions. First, the visualization techniques have changed the notion of what one can see. Under the microscope, the substance of life had to be cut and stained – and thus deprived of 'living' – but computer-aided visualizations enable us to grasp the dynamics of life. Secondly, the new discipline of 'artificial life' promises to explain the principles of life by using computer simulations. Unlike the mathematical models of the previous era, the cellular automata provide us with a material sense of what life 'could' be by specifying possible mechanisms. The author envisages that a meeting point between these two research programs (computational biology and biological computation) will be found when one agrees upon puzzles about synthetic life forms.

The puzzles are guided by the problem formulations. The author wishes to tell the history of modern biology in terms of the meeting points where different discourses could carefully be 'interlocked' (Clark, 1996, p 263). When the elaborate discourses enable us to receive signals in the specialist discourses on either side of a divide, science can move forward by redefining the problems from new perspectives. The past is then overwritten with a new semantics. The author, who once failed to infuse biology from the perspective of mathematics and the physical sciences, achieves this bridging of a divide by using the language of the discipline's history in a philosophical reflection.

References

- Clark A (1996). Happy couplings: emergence and explanatory interlock. In: MA Boden (ed) *The Philosophy of Artificial Life*. Oxford University Press: Oxford. pp 262–281.
- Gruenberg BC (1911). The creation of 'artificial life'. *Sci Am* 105: 231–237 and 272–286.
- Langton C (1986). Studying artificial life with cellular automata. *Physica* 22D: 120–149.

L Leydesdorff

Amsterdam School of Communications Research (ASCoR),
Kloveniersburgwal 48, 1012 CX Amsterdam, The Netherlands
E-mail: loet@leydesdorff.net; http://www.leydesdorff.net