INNOVATION IN SOFTWARE FOR SYSTEMS BIOLOGY. IS THERE ANY?

Herbert M. Sauro

Keck Graduate Institute
535 Watson Drive,
Claremont, CA 91711, U.S.A.

ABSTRACT

Software for systems biology has been under development since the 1950s and has accelerated considerably in the last five years. However, much of the development has been repetitive and there has been little genuine innovation. In this talk I wish to briefly discuss the history of software provision in systems biology and will try to address the question why the academic community has found it so difficult to innovate. In many cases the software developed today is little different in functionality from the first packages that were written in the 1950s. Ironically is it industry that seems to be taking the lead. In particular, Microsoft is funding new theoretical developments at their systems biology centers and MathWorks has developed a substantial dynamics software package (SimBiology 2.0) for their Matlab product.

AUTHOR BIOGRAPHY

HERBERT SAURO was originally educated as a bio-chemist/microbiologist but became interested in simulation and theory to understand cellular networks after accidentally coming across a paper by David Garkfinkel on the simulation of glycolysis. He wrote one of the first bio-chemical simulators for the PC (SCAMP) in the 1980s to assist work on extending metabolic control analysis (a theory closely related to biochemical systems theory). However, with the lack of community interest in systems biology during the late 80s and early 90s, he left science to start a software company and offer consultancy work to finance firms in the UK. With the surge in interest in systems biology in the US in the late 90s, he secured a position at Caltech to assist in the development of the Systems Biology Markup Language. Since then he moved to a faculty position at the Keck Graduate Institute where he continues to do research on network motifs, theory and software. His email address is `<hsauro@kgi.edu>`.