A basis for a visual language for describing, archiving and analyzing functional models of complex biological systems

ABSTRACT

Given available computer and internet technology, BioD may be implemented as an extensible, multidisciplinary language that can be used to archive functional systems knowledge and be extended to support both qualitative and quantitative functional analysis.

INTRODUCTION

Background Standard graphical representations of complex systems have been developed for many disciplines in order to communicate, archive and analyze systems knowledge. Electronic circuit diagrams and architectural plans, for instance, can be created, read and analyzed by knowledgeable persons, yet there is no such common graphical language for describing functional systems in biology. A variety of representations are used in print or online to archive knowledge in particular domains such as metabolic pathways, gene networks, signaling networks, and molecular interactions, yet are not sufficiently standardized to represent cross-disciplinary systems - the interactions of gene expression and metabolism at the inter- and intra-molecular levels, for instance. To describe such multidisciplinary biological problems at multiple levels of abstraction (for example, from intramolecular to disease phenotype), biologists customarily resort to informal cartoon diagrams which, although expressive, are often ambiguous and must be annotated to be interpreted properly. Here we suggest that a standardized visual biological description language would provide more readable and less ambiguous communication and, with computational implementation, provide a basis for distributed searchable archives of functional (as opposed to structural) knowledge, and serve as a 'computer-aided design' (CAD) language for simulating and analyzing biological systems. To explore these possibilities, we are developing a prototype biological description language, BioD, as a platform to test its conceptual basis, explore its utility and identify key issues surrounding its implementation.

CONCLUSION

Conclusions We have proposed that a generalized biological descriptive language akin to schematic diagramming languages in other disciplines is a necessary step in the evolution of functional bioinformatics. Toward this, we have developed a prototype language, BioD, that we have used to test the value of this approach and to explore the feasibility of computational implementation using object-oriented programming methods in the context of Internet-based communications. We suggest that a sufficiently formalized descriptive language built on the BioD concept of 'functional properties' can anchor a computational framework capable of supporting the archiving of extended, web-linked model networks and model analysis using hybrid qualitative reasoning and quantitative simulations.