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Short Communication

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Short Communication on Semantics for Biological Processes

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Abstract

Models as abstract representations of observed or hypothesized phenomena are not new to the life sciences. They have long been used as tools for organizing and communicating information. However, these models take in systems biology has changed dramatically. Traditional representations of biomolecular networks have been used for natural language narratives augmented with block-and-arrow diagrams. While useful for describing hypotheses about a system's components and their interactions, those representations are increasingly recognized as inadequate vehicles for understanding complex systems Instead, formal, quantitative models replace these static diagrams as integrators of knowledge, and serve as the centerpiece of the scientific modeling and simulation cycle

Keywords

Gene; DNA; Biological Process; Semantics

By systematically describing how biological entities and processes interrelate and unfold, and by the adoption of standards for how these are defined, represented, manipulated and interpreted, quantitative models can enable 'meaningful comparison between the consequences of basic assumptions and the empirical facts.

Computational models, expressed in representation formats such as the Systems Biology Mark up Language (SBML, CellML and NeuroML), still require much human interpretation. While syntax standards define the format for expressing the mathematical structure of models (i.e. the variables and their mathematical relationships), they define neither what the variables and the mathematical expressions represent, nor how they were generated. Where this critical information is communicated through free-text descriptions or non-standard annotations, it can only—if at all—be computationally interpreted with complex text-mining procedures (and hardly even with those Existing modeling tools that work only with unannotated models are therefore restricted to a fraction of the overall model information available, omitting the crucial semantic.Portion encoded in non-standard annotations. Furthermore, textual

Descriptions of semantics can be ambiguous and error-prone.

Subsequent activities such as model searching, validation, integration, analysis and sharing all suffer as a result; software tools are of limited use without standardized, machine-readable data. The extent of semantic information associated with models which is potentially unlimited and susceptible to rapid evolution. Thus, to provide for maximum flexibility, semantic information should be defined independently of the standard formats used for model encoding. This allows for easy updates and extensions of the vocabulary as science evolves, without invalidating previously encoded models. Making use of ontologies, as one approach of encoding semantics, has gained momentum in life sciences over the last decade Ontologies are formal representations of knowledge with definitions of concepts, their attributes and relations between them expressed in terms of axioms in a well-defined logic. Ontologies include information about their terms, especially definitional knowledge, and provide a single identifier for each distinct entity, allowing unambiguous reference and identification. In addition, ontologies can be augmented with terminological knowledge such as synonyms, abbreviations and acronyms. Widely used and established examples include the Gene Ontology , the Foundational Model of Anatomy and BioPAX. Ontologies used in conjunction with standard formats provide a rich, flexible, fast-evolving semantic layer on top of the stable and robust standard formats.

Cellular processes of semantics are mostly studied at the molecular scale. In that case, describing a cellular process from the functional point of view consists in describing the molecular activities that underpin it, as well as the influences these activities have on each other. Such descriptions are generally represented in the form of *influence graphs*. Describing the cellular processes from the mechanistic point of view involves describing the molecular processes and molecular entities that take part in the cellular process. These descriptions are mainly represented in the form of reaction networks. In reaction networks, nodes represent molecular entities and arcs represent reactions or influences of some molecular entities on reactions. Reaction networks allow to model a large variety of biological processes, such as metabolic or signaling processes. The majority of available reaction networks model metabolic processes. Yet, comprehensive networks modeling signaling processes with several hundreds of nodes have been built during this last decade

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