

Section 6: Immunological Modeling/Semantic Web

The two readings introduce methods for understanding complex cellular dynamics. The first, by Perelson, is a review paper describing the essentials of mathematical modeling for quantitative events underlying the immune response. The second, by Antezana et al., presents the Cell Cycle Ontology- an integrated resource for answering scientific questions at a molecular or systems perspective. Both papers demonstrate the value of computational methods in integrating experimental and semantic data from experimental and community sources.

Perelson begins by describing how the complexity and heterogeneity of the immune system makes it a difficult subject to study, but also ideal for computational modeling. He introduces the basic model used in HIV (and other viruses), involving target cells that divide, die, and produce viral particles at various rates. Using experimental or clinical studies, along with data-fitting and parameter estimation techniques, researchers have been able to derive important information about biological bounds and other insights. Besides modeling viral progression, computational techniques have also successfully modeled the rise, peak, fall, and set point of antiviral immune responses. Perelson concludes with the argument that data-driven mathematical models have been able to reliably describe complex phenomena as part of a larger conceptual picture, and ends with the hope that new technologies, such as computers, databases, and high-throughput methods, will pave the way to greater use and understandings.

The Cell Cycle Ontology aims to integrate detailed information on the cell cycle from diverse sources. This is performed using semantic web technologies, allowing querying (using SPARQL) and analysis of data from sources such as Gene Ontology, Relations Ontology, the IntAct database, the NCBI taxonomy, and the OrthoMCL clustering algorithm. The integration of information allows researchers to link together questions about protein identity, location, and cell cycle phase all at once. This is especially useful for simulations and systems-level modeling. Lastly, the Cell Cycle Ontology uses description logic reasoners for consistency checking, classification, and redundancy reduction. All in all, the Cell Cycle Ontology offers a robust framework for accessing and updating cell cycle information.

- Perelson AS. Modelling viral and immune system dynamics. *Nat Rev Immunol*. 2002 Jan;2(1):28-36. PDF
- Antezana E, Egaña M, Blondé W, Illarramendi A, Bilbao I, De Baets B, Stevens R, Mironov V, Kuiper M. (2009) The Cell Cycle Ontology: an application ontology for the representation and integrated analysis of the cell cycle process. *Genome Biol*. 2009;10(5):R58. Epub 2009 May 29. PDF