1116-03-1664      **Solomon Feferman\*** (`feferman@stanford.edu`), Department of Mathematics, Stanford University, Stanford, CA 94305. *Many-sorted first-order model theory as a conceptual framework for complex dynamical systems.* Preliminary report.

When complex biological systems (among others) are conceived reductively, they are modeled in set-theoretical hierarchical terms from the bottom up. But the point of view of Systems Biology (SB) is to deal with such systems from the top down. So in this talk I will suggest the use of many-sorted first-order structures with downward nested sorts as an alternative conceptual framework for modeling them. In particular, the notion of a nested substructure allows one to study parts of a structure in isolation from the rest, while the notion of restriction allows one to study a structure relative to some of its parts treated as black boxes. The temporal dimension can be incorporated both as an additional sort and in the indexing of sorts, allowing for both static and dynamic views of a system. Furthermore, one may make use of a quite general theory of recursion on many-sorted first-order structures that includes both discrete and continuous computation. Some possible applications of this model-theoretic approach to SB include excision or substitution of a part as operations on structures, similarity of biological systems via similarity notions for structures, and homeostasis via fixed point recursion. (Received September 21, 2015)