The time-scale hierarchies of a very general class of models in differential equations is analyzed. Classical methods for model reduction and time-scale analysis have been adapted to this formalism and a complementary method is proposed. A unified theoretical treatment shows how the structure of the system can be much better understood by inspection of two sets of singular values: one related to the stoichiometric structure of the system and another to its kinetics. The methods are exemplified first through a toy model, then a large synthetic network and finally with numeric simulations of three classical benchmark models of real biological systems.