

Abstract Submitted
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A general method for modeling biochemical and biomedical response¹ ROBERTO ORTIZ, JIA LERD NG, TYLER HUGHES, Texas A&M University, MICHEL ABOU GHANTOUS, OTHMANE BOUHALI, Texas A&M University at Qatar, ABDELILAH ARREDOUANI, Qatar Biomedical Research Institute, ROLAND ALLEN, Texas A&M University — The impressive achievements of biomedical science have come mostly from experimental research with human subjects, animal models, and sophisticated laboratory techniques. Additionally, theoretical chemistry has been a major aid in designing new drugs. Here we introduce a method which is similar to others already well known in theoretical systems biology, but which specifically addresses biochemical changes as the human body responds to medical interventions. It is common in systems biology to use first-order differential equations to model the time evolution of various chemical concentrations, and we as physicists can make a significant impact through designing realistic models and then solving the resulting equations. Biomedical research is rapidly advancing, and the technique presented in this talk can be applied in arbitrarily large models containing tens, hundreds, or even thousands of interacting species, to determine what beneficial effects and side effects may result from pharmaceuticals or other medical interventions.

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