Developing Mathematical Models to Interpret Experimental Data and Infer the Underlying Mechanisms in Biological Systems

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4:00 p.m.
Marrs McLean Science Building 301

Abstract
Mathematical modeling and computational biology have emerged as new tools to explore new frontiers in biology. The application of mathematics and statistics are becoming an important integral component of biological sciences and research. In this talk, I will explain how to develop mathematical models to explain complex nonlinear biological processes and demonstrate how to use these models to interpret experimental data. Also, I will show how modeling can drive hypothesis generation and make testable predictions in specifically designed experiments. I will use two examples to illustrate how dynamical systems (system of ordinary differential equations) can be parameterized using statistical optimization methods for the models to faithfully reproduce the biological observations. In the examples, I will present (i) a novel mathematical/computational model that integrates gene expression data and biochemical systems theory to provide insights in the understanding of latent TB persistence. (ii) I will illustrate how models can be used to make immunological predictions and evaluate immune response assays. I will emphasize how mathematical modeling can be used to differentiate the underlying biological mechanisms that lead to disparate infection/disease progression patterns.

Dr. Magombedze is currently an Assistant Investigator at Baylor Institute for Immunology Research (BIIR). He has a PhD in Applied Mathematics. Prior to joining BIIR, he was a Research Associate at Imperial College in London (Department of Infectious Diseases Epidemiology), a Research Fellow at the National Institute for Mathematical and Biological Synthesis (University of Tennessee, Knoxville, TN), and a Post-doc Research Fellow at the University of Cape Town (Faculty of Health Sciences) in South Africa. His research interests are at the interface of Mathematics and Biology. He develops and uses mathematical and statistical models as a gateway to understand the interactions between infectious pathogens and the host immune responses.

Please join us for refreshments at 3:30.