## Structural identifiability of weak-form ODE systems

## Nora Heitzman-Breen (Nora.Heitzman-Breen@colorado.edu) and David Bortz (David.Bortz@colorado.edu)

Compartmental modeling of biological systems provides insights on biological interactions and mechanisms not easily observed *in vivo*. Accurate and robust parameter estimation is critical to studying such biological problems. A common approach to parameter estimation is nonlinear least squares using a forward solver. However, as model size and noise in data increase these methods become computationally expensive to maintain accuracy in parameter estimates. The recently proposed Weak-form Estimation of Nonlinear Dynamics (WENDy) method is more accurate, robust to noise, and computational efficient than forward solver-based approaches (even for higher dimensional systems). This method involves using carefully chosen test functions to convert the strong form representation of a model to its weak form, and estimating parameters by solving an equation error-based generalized least squares problem.

The reliability of parameter estimates is dependent on both the data available and the formulation of the model. In particular, biological data is often noisy, infrequent, and not observed for all model compartments. Model identifiability refers to the ability to recover unique parameter estimates for a given model and available data, and is a critical step to understanding uncertainty in parameter estimation. Determining the structural identifiability, or the well-posedness of the data-fitting problem, has been well studied for ordinary differential equations (ODEs), but not for weak form equation error methods. In this talk, we show that the differential algebraic methods used to test the structural identifiability of ODEs can be adapted to study their weak form counterparts. Time permitting we will also discuss preliminary efforts to apply differential elimination algorithms to enable WENDy to be applied when only a subset of variables are measured. These results provide insight on parameter estimation using weak form approaches and inform experimental design for biological systems.