1086-37-2025 **Danilo R Diedrichs*** (danilo.diedrichs@wheaton.edu), Wheaton College, Department of Mathematics, 501 College Ave., Wheaton, IL 60187. *Reverse Engineering of the Unfolded Protein Response Network using Polynomial Dynamical Systems.*

The Unfolded Protein Response (UPR) is a regulatory mechanism in cell biology that has senses perturbations in the protein-folding capacity of the endoplasmic reticulum and takes corrective steps to restore homeostasis. A mathematical model of the UPR in mammalian cells was recently developed based on extensive prior knowledge of the architecture of the UPR network with parameters calibrated by time course experimental data. In this study, we propose to reverse-engineer the mammalian UPR network using only the data, without making any assumptions on the structure of the network. We use computational algebra techniques to determine a class of models given by polynomial dynamical systems over \mathbb{Z}_p consistent with the data. The resulting optimal network provides valuable insights on structural elements of the original model that may not have been considered during the classical forward engineering approach. (Received September 24, 2012)