Reverse-Engineering Gene Networks That Can Remember Using the Manifold Boundary Approximation Method[1] ANDREW WHITE, MARK TRANSTRUM, Department of Physics and Astronomy, Brigham Young University — Observable behaviors in biology result from the collective interactions of many microscopic elements. These microscopic elements make up complex biological systems that we can model mathematically. Ideally, mechanistic models should predict the system's behavior without misrepresenting the system's biochemistry. The computational method of model reduction known as the Manifold Boundary Approximation Method (MBAM) can help us identify which parts of a model are relevant for explaining a particular behavior. This project attempts to apply MBAM to gene transcription networks that are responsible for ensuring the permanence of cellular decisions to activate or silence genes. This behavior is known as "memory," and our goal is to use MBAM to reverse-engineer genetic design motifs that could produce memory in developmental transcription networks.

Andrew White
Department of Physics and Astronomy, Brigham Young University