1117-92-128   **Andy Jenkins** (`leej@clemson.edu`), Department of Mathematical Sciences, Martin Hall, Clemson University, Clemson, SC 29634-0975, and **Matthew Macauley*** (`macaule@clemson.edu`), Department of Mathematical Sciences, Martin Hall, Clemson University, Clemson, SC 29634-0975. *A Boolean network model of the L-arabinose operon.* Preliminary report.

In genetics, an operon is a segment of DNA that contains several co-transcribed genes, which together form a functional regulatory unit. Operons have primarily been studied in prokaryotes, with both the lactose (lac) and tryptophan (trp) operons in E. coli having been classically modeled with differential equations and more recently, with Boolean networks. The L-arabinose (ara) operon in E. coli encodes proteins that function in the catabolism of arabinose. It differs from the lac and trp operons in that it exhibits both positive and negative gene regulation within a single operon. In this talk, we will describe our proposed Boolean network model for the ara operon, which consists of both a physical wiring diagram, and the logical functions that govern each node. Additionally, we will describe the results of model validation and current and future research. (Received January 08, 2016)