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A Complete Computational Model of the GC/ cGMP/PKG Pathway Between Calcium and Neuronal Gene Expression

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A Complete Computational Model of the GC/cGMP/PKG Pathway Between Calcium and Neuronal Gene Expression

The guanylate cyclase(GC)-cyclic guanosine monophosphate(cGMP)- protein kinase G(PKG) pathway is a fundamental controls system for neuronal gene expression regulation. While there is a tremendous amount of information regarding the species of this signaling pathway, there is a gap in the mathematical modeling and simulation of this pathway that can help elucidate the relationships and importance of interacting species. Our project aims to create a computational model of this pathway that connects calcium concentrations to neuronal gene expression that aids cell survival. We have constructed a wiring diagram via a literary search and analysis of biological papers, texts, and published articles, and include fundamental species including nitric oxide, soluble GC, and GC activator protein, the PKG pathway, and the synthesis of cyclic GMP from GTP. We will present our approach and methodology, mathematical model, and preliminary results that demonstrate the impact of calcium concentrations to cell survival.