1. model
   1. Initial implementation of the code from the first Jupyter notebook
   2. Includes
      1. pH
      2. Intramitochondrial binding polynomials
      3. J\_F1F0 – ATP synthesis/hydrolysis in mito matrix
      4. J\_ANT – adenine nucleotide exchanger
      5. J\_ATPase – general ATP consumption in cytosol
      6. J\_PiC – Pi/H+ cotransporter
      7. J\_CK – creatine kinase
2. Model2
   1. Dan’s implementation of the model
   2. Added extramitochondrial binding polynomials
   3. Changed J\_ANT to incorporate absolute concentrations of [ATP4-]e, [ADP3-]e, [ATP4-]x, [ADP3-]x
   4. Changed J\_PiC equation
   5. Let J\_ATPase be constant
   6. Included data values for volumes and added Vmito and Vcyto
3. Model3
   1. Added J\_C1, J\_C3, and J\_C4 to the model
   2. Added states QH2, NADH\_x, and cytCred
      1. Don’t have initial conditions for these values
      2. I couldn’t find them in the paper nor were the in the code Dan sent. It looks like loads them from co.mat
      3. FIXED – made ICs ½ of the total concentration of each species
4. Model4
   1. Added differential equation for DPsi
   2. Added J\_DH equations
   3. Problem
      1. Phosphate increasing without bound. Most likely due to the J\_CK equations?