Computational Methods in Systems Biology
Coursework 2, 17 March 2005
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This coursework contributes to 50% of the total coursework marks for the module.

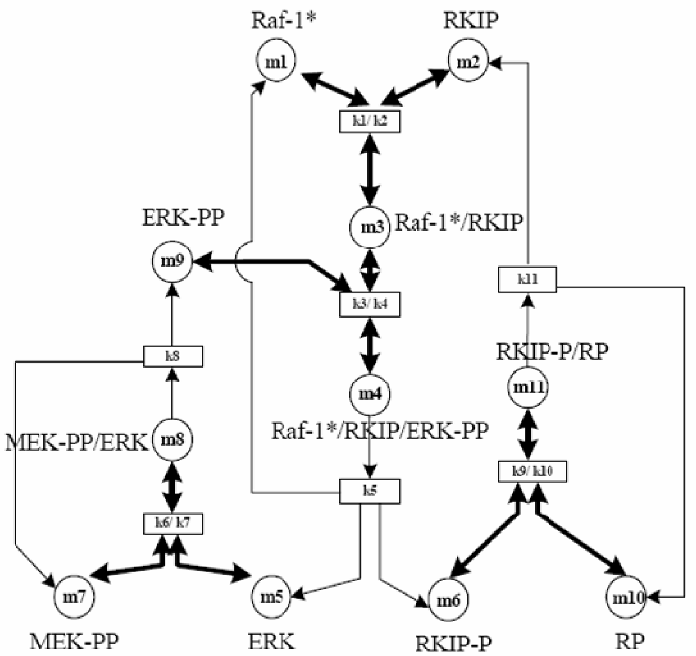
The solution to the coursework should be handed in by 14 April 2005, as hard copy to the course office.

(1) Implement Runge Kutte's method to numerically solve differential equations, and give runs on the examples in (2) above. Runge Kutte's method has as the essential step

$$y_1 = y_0 + h*f(t_0+0.5*h, y_0+0.5*h*f(t_0,y_0))$$

You should provide the commented source code of the program, and also email an executable form with instructions for its use to drg@brc.dcs.gla.ac.uk

(2) Consider the following biochemical system:



(i) Show how you can model this network as a 2-dimensional table of concentrationsXreactions where each cell holds one term of a differential equation, and a row represents the differential equation describing the behaviour of the concentration for one species (protein).

(ii) Given the following rate values
k1=0.53; k2=0.0072; k3=0.625; k4=0.00245; k5=0.0315; k6=0.8; k7=0.0075; k8=0.071; k9=0.92; k10=0.00122; k11=0.87;

Give the results of 2 runs on the system, one for each your two differential equation solvers (euler, runge-kutte) for a time interval from 0..10 and initial concentrations, and comment on any differences between the results obtained using the two methods.

m1=2.5, m2=2.5, m3=0, m4=0, m5=0, m6=0, m7=2.5, m8=0, m9=2.5, m10=3, m11=0