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## EE 434 Midterm Exam Spring 2009

Take home – due by Friday noon, 03/14/08; check the web for any corrections Open book, open notes, computer can be used. Your submitted results should be organized so they can be easily understood for grading purposes.

Signed submission declares that all of the work is your own and no consultation on the questions has occurred.

## #1. (50 points)

The transformation of molecules, x1 & x2, of two genes [around normalized base levels X1>>1 & X2>>1] can be represented by the coupled differential equations:

$$\frac{\mathrm{dx}_1}{\mathrm{dt}} = -\mathbf{k} \cdot \mathbf{x}_1 \cdot \mathbf{x}_2 + \mathbf{x}_2 - 1$$
$$\frac{\mathrm{dx}_2}{\mathrm{dt}} = -\mathbf{k} \cdot \mathbf{x}_1 \cdot \mathbf{x}_2$$

where the rate constant is also normalized to k=1. Assume initial conditions x(0)=[-1; 1].

- a) Set up a simulink representation of these equations and run for  $0 \le t \le 10$  sec.; submit the schematic and curves  $x_1 \& x_2$ . Save the data for part b) of this problem {as well as for the second problem}.
- b) A new type of neural network Ngt is proposed to represent this kind of gene transcription:

$$y(t) = \{2 \cdot 1_2 - (1_2 + e^{W_1 \cdot t} \cdot E)^{-1} \cdot (1_2 + e^{W_2 \cdot t} \cdot E)^{-1}\} \cdot x(0)$$
  
where  $1_2 = \begin{bmatrix} 1 & 0 \\ 0 & 1 \end{bmatrix}$ ,  $E = \begin{bmatrix} 0 & 1 \\ -1 & 0 \end{bmatrix}$ 

Here w<sub>1</sub> and w<sub>2</sub> are real (scalar) weights.

b1) Write out the term by term equations for  $y_1$  and  $y_2$  where  $y=[y_1; y_2]$ b2) Train Ngt (by varying  $w_1$  and  $w_2$ ) to minimize the mean square error over  $0 \le t \le 10$  subdivided into 10 equal intervals (of 1 sec each).

b3) Plot the output y(t) of Ngt and compare with that x(t) of part a). 2. (50 points)

Generalize the method of Lagaris {reference [1] below, discussed in class for a single differential equation} to a 2-vector differential equation; dx/dt=f(t,x) to be approximated by a neural network N<sub>f</sub> with output  $x_{Nf}(t)$ . Use t as the input,  $0 < t \le T$  subdivided into N intervals [t<sub>i</sub> t<sub>i+1</sub>], t<sub>o</sub>=0, t<sub>1</sub>=T/N, ...,t<sub>N</sub>=T, followed by a (hidden) Hx1 weight matrix, W<sub>H</sub>, and one bias u into H activation functions tanh(.), followed in turn by a 2xH (output) weight matrix, Wo, feeding 2 output neuron of activation functions purelin(.). Take that output, multiply by the input, t, and add the initial condition vector x(0) to get the output  $x_{Nf}(t)$ .

- a) Sketch a schematic of the neural network and give an equation for the final output  $x_{Nf}(t)$  in terms of the parameters and functions describing  $N_{f}$ .
- b) Explain why and how you can use the Matlab function newff to create and train  $N_{\rm f}$  .

c) Create such a neural network with H=5, N=10, to represent the differential equations of gene transcription given above part a) of problem 1, using the solution found in problem 1.

Some References:

[1]. I. Lagaris, A. Likas, D. I. Fotiadis, "Artificial Neural Networks for Solving Ordinary and Partial Differential Equatins," IEEE Transactions on Neural Networks, Vol. 9, No. 5, September 1998, pp. 987 – 1000.

[2]. S. Ando, E. Sakamoto, H. Iba, "Evolutionary modeling and inference of gene network," Information Sciences, Vol. 145, 2002, pp. 237 – 259.