EEL851: Major Test (Part B; Systems Biology)

May 5, 2014

Maximum Marks: 20

1. Briefly describe any two broad approaches for modelling regulatory interactions between genes. State what, according to you, might be the strengths and weaknesses of each approach. [**4**]

2. Consider a regression model which tries to predict the expression of an output gene y as a function of a bunch of input genes $\mathbf{x} = \{x_1, ..., x_n\}$; say $y = \boldsymbol{\beta}.\mathbf{x}$, where $\boldsymbol{\beta}$ is a vector of coefficients (all variables are real-valued). This model treats each gene x_i as an independent factor affecting y. But often biological regulation involves pairwise or groupwise interactions between multiple input genes. Show how, by including pairwise $min(x_i, x_j)$ terms amongst the inputs to your regression model, you can learn certain kinds of logical pairwise interactions between genes. Give at least three examples of interaction types that can be captured, with justification. **[6]**

3. In class, we discussed the type-1 coherent feed-forward loop motif, and showed how, with AND logic at the output Z, it becomes a sign-sensitive delay element, with delayed response to ON (but not OFF) pulses in the input X. Now suppose that X is constantly present, and instead there are pulses/steps in the second input, Y. How would these affect the expression dynamics of Z? Will there be delays in the expression of Z for ON or OFF steps of Y? What would be the response time of Z for such steps? **[8]**

4. What do you think are the implications of Leslie Valiant's notion of evolution as a form of learning for the 'nature vs. nurture' debate in biology/psychology? **[2]**