

2 Bioinformatics (pl219)

(a) Genetic toggle switches are systems of two proteins that repress each other's production. Such systems typically exhibit bistability and switching behaviours. Let's suppose that gene a produces an mRNA that translates into a protein A that inhibits gene b , which produces an mRNA that translates into a protein B , that inhibits gene a .

(i) Describe how the Gillespie algorithm models this circuit. [8 marks]

(ii) What factors affect the accuracy or robustness of the model output? [2 marks]

(b) Contrast Progressive Multiple sequence Alignment (PMA) with the Smith-Waterman (S/W) algorithm, using a common example. (The example needs to contain at least three sequences, at least 3-4 bases each.) Is a scoring matrix important in either algorithm? [4 marks]

(c) You are sequencing a new pathogenic bacterium.

(i) How would you proceed to carry out phylogenetic analysis to characterise the taxonomy of the bacterium? [3 marks]

(ii) In practice, many researchers compare results from multiple methods to see which species are robustly supported, rather than relying on a single approach. If you use parsimony and distance methods (for example neighbour joining) would you get the same information or different? [3 marks]