

2 Bioinformatics (pl219)

- (a) Compute the global and local alignments for the following aminoacid sequences: SEPPT, CAPPR. Use the following scores: match = +2, mismatch = -2, gap penalty = -2. Then in the global alignment change to match = +4, mismatch = -4, gap penalty = -4. Compare and discuss the results. What is the general effect of the gap penalty? [5 marks]
- (b) Describe in outline the *Four Russians* algorithm. Give expressions for computational complexity as the number of tiles, t , is changed and compare the growth order with that of a tile-less approach. [6 marks]
- (c) Discuss with one example how an algorithm for RNA folding could use a dynamic programming approach. What are the cases when this will not work? [4 marks]
- (d) Is it possible to remove or add just one node (a species) from/to a phylogenetic tree without actually making the tree again? Discuss using different phylogenetic methodologies. [5 marks]