CSCI 538 Computability

Assignment 4 (10 marks)

Question 1 (2 marks)

Let ϕ be a general boolean formula constructed from the boolean variables $x_1, x_2, ..., x_n, \neg, \lor, \land$ and parentheses. ϕ is a *tautology* if it evaluates to 1 for every assignment of 1 and 0 to the input variables. Define TAUTOLOGY as the languages of boolean formulas that are tautologies. Show that TAUTOLOGY \in co-NP.

Question 2 (3 marks)

Let $A_{LBA} = \{ \langle M, w \rangle | M \text{ is an LBA that accepts } w \}$. Show that $A_{LBA} \in PSPACE$.

Question 3 (2 marks)

Given a graph G, the MINIMUM COLORING problem asks one to color the vertices of G with the minimum number of colors (such that no two nodes connecting an edge have the same color). So this is a (minimization) optimization problem. Prove that there is no approximation algorithm for MINIMUM COLORING with factor less than 4/3, unless P=NP. (Hint: In assignment 3 we showed that even deciding whether the optimal color number is 3 is NPcomplete.)

Question 4 (3 marks)

In class we showed that the Zero Exemplar Breakpoint Distance problem is NP-complete, if each gene is allowed to repeat at most 3 times. In this problem, you are to study the approximability of the Exemplar Breakpoint Distance problem on *signed* genomes (defined below).

Given a set of distinct genes G, an exemplar signed genome is a signed permutation of the genes (i.e., without gene repetition but each gene could have a positive or negative sign). Example: $G = \{a, b, c, d, e\}$, then A = ac - dbe is an exemplar signed genome over G. Given two exemplar signed genomes A, B, if two consecutive genes xy appears in A but neither xy nor -y - x appears in B then xy is a breakpoint in A. (Note that -(xy) = -y - x and -(-x) = x.) The breakpoint distance between A and B is the number of breakpoints in A(symmetrically in B). Example: A = ac - dbe, B = ad - cbe, the breakpoint distance bd(A, B) = 2.

Now, given two signed genomes A', B' with gene repetitions, the *exemplar* breakpoint distance between A', B' is the minimum breakpoint distance between two exemplar genomes A, B obtained from A', B' by deleting redundant genes.

Show that if each gene appears in A'(B') at most twice, then the problem does not admit a factor 1.36 approximation via a reduction from Vertex Cover. (Vertex Cover is known to have no approximation with a factor 1.36 unless P=NP.)

Date Due: 8:30pm, Friday, Apr 12, 2024. You should upload your assignment in pdf format on D2L, under the "Assignment 4" directory.