

Structural Bioinformatics 2004-05 Semester B Assignment 4.

Due to April 12

1. Devise an algorithm that answers in $O(n \log(n))$ time whether two point sets in R^2 of size n are congruent (i.e. exact congruence under rigid (translation + rotation) transformation).
2. Given two ordered point sets (u_1, \dots, u_n) and (v_1, \dots, v_m) and ϵ give an algorithm that detects a largest alignment which preserves the sequence order, i.e. the goal is to detect a maximal cardinality set $S = \{(u_{i_k}, v_{j_k})\}_{k=1}^t$, such that $\forall k \|u_{i_k} - v_{j_k}\| \leq \epsilon$ and matching indices are in ascending order $i_{k+1} > i_k$ and $j_{k+1} > j_k$.
(!!! no optimization on transformations is needed, the points are fixed in 3D).
3. Given a weighted bipartite graph, $G = (V \cup U, E)$, $w : E \rightarrow R$, devise an approximation bipartite matching algorithm which guarantees to find a matching of weight at least half of the maximal weight matching. Give an algorithm with running time $O(E \cdot \log(V))$.
4. Given two sets of 3-D points $\{u_i\}_1^n$ and $\{v_i\}_1^n$ assume that the minimal distance between points in each set is strictly more than $\epsilon * 2$. Also assume that the diameter (maximal distance between two points) is bounded by D . Give a linear time algorithm (linear in the number of points and $(D/\epsilon)^3$) that detects the sequence order independent alignment of maximal size. The distance between the matched points should be less than ϵ . (no optimization on transformations is needed, the points are fixed in 3D).