BCB 567 - HW 2 Oct ??, 2010

4.1)

- INPUT: A set X of integers representing a sequence of DNA of length n, where $X_0 = 0$ and $X_k = n$ are the ends of the sequence and $X_1, X_2, ..., X_{k-1}$ represent k-1 restriction enzyme cleavage sites.
- FIND: The multiset ΔX of integers representing fragment lengths resulting from a partial restriction digest of the DNA sequence represented by X.

DoPartialDigest(Set *X*)

- 1. $\Delta X \leftarrow \emptyset$
- 2. for $i \leftarrow 1$ to |X|
- 3. for $j \leftarrow i + 1$ to |X|
- 4. Add $X_j X_i$ to ΔX
- 5. return ΔX

4.5)

Using the definitions of \oplus and \ominus , we can obtain the following equation demonstrating that the sets $U \oplus V$ and $U \ominus V$ are homometric.

$$\Delta(U \oplus V) = \{(u+v)_i - (u+v)_j : \forall (u_v)_{i,j} \in U \oplus V\}$$

= \{(u-v)_i - (u-v)_j : \forall (u-v)_{i,j} \in U \ightarrow V\}
= \Delta(U \ightarrow V)

4.8)

If the set X contains n elements, then the multiset ΔX will contain $\binom{n}{2}$ elements. We can therefore safely ignore sets with 1 element since $\binom{1}{2}=0$. Also, if sets X_1 and X_2 each contain 2 elements and generate the same ΔX , then X_2 is simply a shift of X_1 . We can therefore safely ignore sets with 2 elements. Therefore the smallest ΔX that satisfied the required criteria will contain at least $\binom{3}{2}=3$ elements.

Consider the multiset $\Delta X = \{1, 2, 3\}$ and the sets $X_1 = \{0, 1, 3\}, X_2 = \{0, 2, 3\}$. Performing a partial digest on X_1 and X_2 will generate the same multiset ΔX . Since X_1 and X_2 are not related by shift or reflection, and since we know ΔX cannot contain less than 3 elements, the given sets satisfy the given criteria.

4.9)

We first define the function "Map" that is used by the "BruteForceDDP" algorithm. Given a multiset of fragment lengths, the "Map" function creates the physical map that would result from concatenating the fragments in the given order.

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Map(Multiset Y, Integer n)

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\begin{array}{ll} \textbf{1.} \  \, Y' \leftarrow \{0,Y_1,Y_2,...,Y_n\} \\ \textbf{2.} \  \, X = \emptyset \\ \textbf{3.} \  \, \textbf{for} \  \, i \leftarrow 2 \  \, \textbf{to} \  \, n+1 \\ \textbf{4.} \qquad y \leftarrow Y_i' - Y_{i-1}' \\ \textbf{5.} \qquad \text{Add} \  \, y \  \, \textbf{to} \  \, X \\ \textbf{6.} \  \, \textbf{return} \  \, X \end{array}
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The "BruteForceDDP" algorithm then considers each possible order of fragments lengths from the two single digests, builds maps from those ordered fragments, combines the maps, and determines whether the digestion of the combined map matches the double digest.

BruteForceDDP(Multiset L_a , Multiset L_b , Multiset L_{ab})

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1. for each possible ordered permutation A of L_a
2. A' \leftarrow \operatorname{Map}(A,|A|)
3. for each possible ordered permutation B of L_b
4. B' \leftarrow \operatorname{Map}(B,|B|)
5. if \Delta(A' \cup B') = L_{ab}
6. return A' \cup B'
7. output "No solution"
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