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Algorithms Homework 1  
Boinformatics

1. The algorithm that I took some time to think about and develop in my head first would take all the values shown on this chart

Size	Seq1		Seq2		Seq3		Seq4		Seq5		Seq6
200											
150											
100											
75											
60											
50											

And reduce them down to simple smallest-to-largest orders lists of size values. For example Seq1 would be turned into 60,75,100,150. Now in order to find the sequences that go together you would have to combine a choice of any two of these lists/sequences and then compare it to how a complete list would look like (50,60,75,100,150,200.) the two sequences do not match if any duplicate values are present or there are any missing sections of size for fragments . All this being said the only two sequences that are a fit for each other are sequence 5 and sequence 6 because once you combine their size values you get a perfect 50,60,75,100,150,200. Alternatively an of a pair that do not match would be sequence 4 and 5 where the algorithm would find the list of values to be 60,100,100,200,200. As we can see here from this incorrect match there are duplicate values and missing ones as well (50,75,150.)

\*\*Duplicate size values simply mean that the fragment sequences would overlap.