1. [20 points] Read the paper “Hardware/Software Partitioning of Software Binaries” by G. Stitt and F. Vahid published in 2002 IEEE/ACM international conference on Computer-aided design. Answer the following questions in your own words:
   a) [5 points] What is the main idea of this paper and how is it different than techniques discussed in the lecture?
   b) [10 points] What are the advantages and disadvantages of partitioning from software binaries compared to program source code?
   c) [5 points] Explain how the authors interfaced their reconfigurable circuits with the main processor.

2. [30 points] One of the popular functions to accelerate using reconfigurable computing is the Edit Distance function. The edit distance function measures the difference between two strings by aligning them and estimating the cost of transforming one string, character by character, to the other. Consider two strings: TTGACATC and TTCAATGC. When comparing the two strings (please see the next figure), then at each position one of three cases can occur:

   a. a match can occur when the same character is present in both strings.
   b. a mismatch when there are two different characters at the same position in the two strings.
   c. A gap where there is an insertion of one character in only one string, or symmetrically a deletion in the other string.

An effective way to solve such problem is through *dynamic programming* which breaks the given problem into smaller sub problems and then solves the subproblems and combines the results to obtain the final solution. If we have two strings \( X = \{x_1, x_2, \ldots, x_n\} \) and \( Y = \{y_1, y_2, \ldots, y_n\} \) then we can define the function \( H(i, j) \) as the minimum difference between the two substrings \( x_1x_2\ldots x_i \) and \( y_1y_2\ldots y_j \). \( H(i, j) \) can be calculated as follows.

\[
H(i, j) = \min \left\{ H(i-1, j-1) + \text{cost of matching/mismatching } x_i \text{ to } y_j \ (= c(x_i, y_j)) \right. \\
H(i, j-1) + \text{cost of matching a gap ‘-’ in } X \text{ to } y_j \ (= c(\_, y_j)) \\
H(i-1, j) + \text{cost of matching a gap ‘-’ in } X \text{ to } x_i \ (= c(x_i, \_))
\]
A straight-forward pseudo-code to calculate the difference between the two strings is as follows

```plaintext
initialize array H[0→n] [0→n] to zero;
for (i = 1; i <= n; i++)
begin
  for (j = 1; j <= n; j++)
  begin
    H[i][j] = min(H[i-1][j-1]+c(x[i], y[j]),
                   H[i][j-1]+c(_, y[j]),
                   H[i-1, j]+c(x[i], _));
  end
end
```

Assume the presence of an instruction (\texttt{min}) that takes five inputs \(H[i-1][j-1]\), \(H[i-1][j]\), \(H[i][j-1]\), \(x[i]\), \(y[j]\) and produces the minimum result in 1 cycle.

a. [15 points] Assuming \(n = 3\), perform loop unrolling for both the outer and inner loops. Write down the sequence of \texttt{min} instructions that results from loop unrolling.

b. [15 points] Construct the data flow graph for the \texttt{min} instructions sequence that results from part (b).

Side note: The genome of living organisms can be symbolically represented by a string of four letters (A, C, G, T). Given two strings that correspond to the genomes of two organisms, the edit distance becomes a powerful tool in determining the closeness or similarity of the two organisms.