

Exercise 2: Exercise on State Machines

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Task 1

DNA Processing

Deoxyribonucleic Acid (DNA) is the building block of life. It contains the information a cell requires to synthesize protein and to replicate itself, to be short it is the storage repository for the information that is required for any cell to function. The famous double-helix structure is composed out of four nucleotide bases:

- Adenine (A)
- Guanine (G)
- Thymine (T)
- Cytosine (C).

Each base has its complementary base, i.e. A will have T as its complimentary and similarly G will have C.

A DNA sequence looks some thing like this:

•	ATTGCTGAAGGTGCGG																	
								I						I	I	I		
		Τ	Α	Α	C	G	Α	C	Т	Т	С	С	Α	C	G	С	С.	

The previous sequence can also be written shortly as ATTGCTGAAGGTGCGG.

Figure 1 shows a simple state machine for checking if GAAG is part of a specific DNA sequence. The state machine has 5 states. When the state GAAG is reached an output

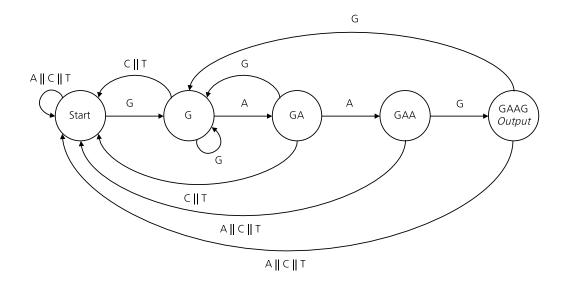


Fig. 1: Simple State Machine for the Regex /GAAG/

will be given.

First, you should implement the given state machine as an SC_MODULE with the class name stateMachine. The module should have the following inputs:

- sc in<char> input;
- sc in<bool> clk;

The provided module stimuli will provide a new DNA symbol on its output in each clock cycle. The DNA symbols are implemented with the char datatype. For the internal states of the state machine an enumeration should be used:

The module state machine should have an SC_METHOD called process that implements the behavior of the state machine (e.g. by using a switch/case construct). The process should not be called during the initialization phase by using the dont_initialize() function call in the constructor after the sensitivity list. Use the provided testbench in order to test your program. When your FSM is in the GAAG state a printout should be done.

Second, can you estimate how often and also at which position in the string the searched pattern occurs? Implement it in your current code.