Homework 3

CS 181, Fall 2023

Out: Oct. 14
Due: Oct. 20, 11:59 PM

Please upload your solutions on Gradescope. You can use LaTeX or a word document to write up your answers, but we prefer you use LaTeX. You can use the **tikz package** in LaTeX to draw the DFAs in this homework. This tool is a user-friendly way of generating tikz graphs. You may scan hand-written work or images for parts of solutions **only if** they are extremely clean and legible. Please ensure that your name does not appear anywhere in your handin.

Problem 1: Correctness of Knuth-Morris-Pratt

In class you have learned about the Knuth-Morris-Pratt algorithm for finding a pattern P in a larger text T. Recall that KMP's improvement over the naïve "sliding window" approach lies in the fact that in KMP we use the knowledge gained from earlier comparisons between P and T to avoid many unnecessary comparisons later on. To formalize this idea, we'll make the following definition.

Definition. *For each position k in the pattern P, let $s_k(P)$ denote the length of the longest proper suffix of $P_{1:k}$ that matches a prefix of P. (The notation $P_{1:k}$ is used to represent the first k characters of P.) If the pattern P is clear from context, we will simply write s_k. Note that $s_k(P)$ is essentially the failure function of P, which we will examine more later on.*

As an example, if $P = \texttt{abcxabcde}$, then $s_2 = s_3 = s_4 = 0$, $s_5 = 1$, $s_6 = 2$, $s_7 = 3$, and $s_8 = 0$.

If a mismatch between the pattern and the text is found at position $k + 1$ of P, then KMP responds by shifting the pattern $k - s_k$ places to the right. To see this rule in action, consider $P = \texttt{abcxabcde}$ and $T = \texttt{xyabcxabcxadcdqfeg}$. Suppose the left end of P is aligned with the third character of T. Then P and T match for 7 characters, but mismatch on the 8th character of P. So P is shifted to the right by $7 - s_7 = 7 - 3 = 4$ characters:

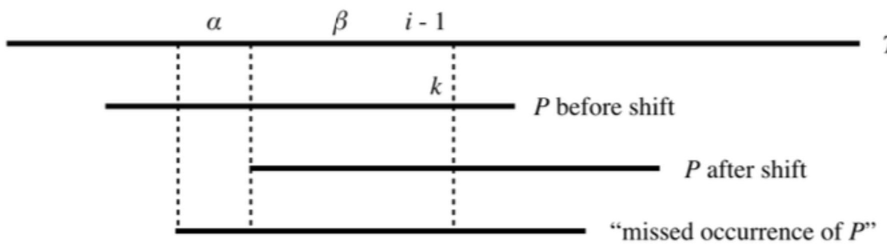
```
xyabcxabcxadcdqfeg
  abcxabcde
      abcxabcde
```

This shifting rule provides two advantages. First, we often shift the pattern by more than a single character, which is an improvement over the naïve algorithm. Second, after the shift is completed, we already know that the first s_k characters in P match their counterparts in T (see the example above). So we can start comparing P to T at position $s_k + 1$ of P, further saving ourselves from doing unnecessary work.

Everything sounds good so far. But hold on! How do we know that the KMP shift rule doesn't move the pattern too far to the right? In other words, how can we be sure that we don't inadvertently skip over the pattern we're looking for in the text? The purpose of this problem is to walk you through a proof of the following theorem, which should put your mind at ease.

Theorem. *For any alignment of P with T, if characters 1 through k of P match the opposing characters of T but character $k+1$ mismatches with T_i, then P can be shifted by $k - s_k$ places to the right without passing any occurrence of P in T.*

Our proof will proceed by contradiction. In other words, we shall assume that there *is* in fact an occurrence of P in T starting strictly to the left of the shifted P and show that this assumption leads to a contradiction. Our proof will be guided by the following picture. For further explanation, you can refer to this article.



In this diagram,

- α and β are the indicated substrings of T,
- the unshifted pattern P matches T up through position k of P and position $i-1$ and of T,
- $P_{k+1} \neq T_i$.

a. What is the relationship between β and P? What is the length of β? Give justification for both answers.

b. Which portion of the missed occurrence of P matches T? Which portion of the unshifted P matches T? What can you say about which portion matches between the unshifted P and the missed P as a result? Call this matching substring γ.

c. Is a γ a prefix of $P_{1:k}$? a proper prefix? a suffix? a proper suffix? Explain.

d. What can we say about the length of α?

e. Combine your results from (a), (c), and (d) to derive a contradiction and complete the proof.

Problem 2: Failure Function

For each of the following strings, draw the failure function table. There's no need to write out the prefixes and suffixes for full credit but it may save you from some confusion :).

a. `SAUSAURUS`

b. `ABRACADABRA`

Problem 3: Finite Automata for Pattern Matching

Congratulations! The CS 181 dino-rescue team has recruited you to go on their most recent mission. Having just rescued a nothosaurus on a distant seashore and named him Nathan, you and the team are headed back to Nathan's home. However, Nathan just woke up from a long nap with a sore throat and is ferociously rocking the boat. Fortunately, the team also brought a dino-geneticist, Sorin, on board last minute. Sorin says Nathan needs to be dropped off with some of his cousins to recover from his sickness. The cousins should have multiple repeats of the following nucleotide sequences in their housekeeping genes (which are essential for general cell functions): CGCGAT, CTCGCGT, and CTCGCGA. Could you help construct a DFA that recognizes dinos that could be Nathan's cousins, based on their housekeeping genes?

a. In particular, construct a DFA that will accept any input that contains at least one of the patterns below. Once any of the patterns is found, the DFA should reach an absorbing acceptance state. Remember to try out this tool.

```
CGCGAT
CTCGCGT
CTCGCGA
```

Note that there are many valid DFAs for this question. You should construct the simplest and most specific one possible; in other words, your DFA should include the smallest number of states possible, and it should not accept any strings that do not contain at least one of the patterns above.

b. Then, write the sequences of states visited when the machine is run on the text `CTCGCTCTCGCGAACC`. Assume that the finite automaton reads the whole string (i.e. there is no early stopping).

Problem 4: Languages

In the previous two problems, we have focused on building DFAs to recognize whether a pattern p appears anywhere in a text t. As a result, the DFAs constructed in these problems will accept languages of the form $L = \{\text{strings containing pattern } p\}$. However, what if we wanted to build a DFA that recognized a different language, such as $L = \{\text{strings ending with pattern } p\}$?

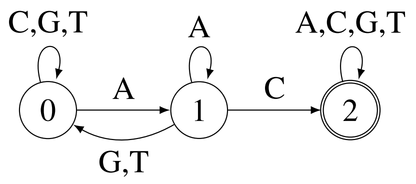
Our focus on DFAs accepting languages of the form $L = \{\text{strings containing pattern } p\}$ has enabled us to make two important assumptions to simplify our drawings of DFAs:

1. Once the entirety of p is found in t, the DFA should accept t regardless of what comes after p in t. Consequently, the acceptance state at the end of the DFA is also an *absorption state*, meaning that the

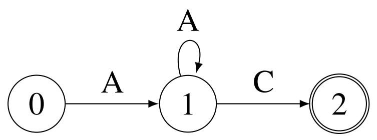
DFA will never exit this state once it is entered. The assumption that all acceptance states are absorption states allows us to exclude arrows from acceptance states to themselves in DFA diagrams.

2. The DFA should accept t if p is found in t, regardless of what comes before p in t. Consequently, whenever the next letter in t is not consistent with p, we can move several states backwards in the DFA and continue searching for p in t (this is the failure function). Because many incorrect next letters in t will send us back to state 0 (the beginning of p), we typically exclude these arrows from DFA diagrams and assume that all missing arrows from non-acceptance states go to state 0.

As an example of these simplifications, consider a DFA accepting $L = \{\text{strings containing the pattern } AC\}$ over the alphabet $\Sigma = \{A, C, G, T\}$. The complete version of this DFA is:



However, the two assumptions above allow us to simplify this DFA to:



For each of the following languages L over the alphabet $\Sigma = \{A, C, G, T\}$, either (i) construct a DFA that accepts L, or (ii) explain why it is not possible to construct a DFA that accepts L. List any assumptions you make that allow you to exclude arrows. *Hint: Think about how, if a string has permanently failed the language's criteria, you can transition to a "dump" state that rejects no matter what comes next.*

a. $L = \{\text{strings ending with pattern } CT\}$

b. $L = \{\text{DNA strings of length 4}\}$

c. $L = \{\text{palindromic DNA strings}\}$

d. $L = \{\text{strings containing } AC\text{, but not as the first or last two characters}\}$

e. **Bonus:** Recall from class that DFAs, NFAs, and regular expressions are equivalent in that they all represent the same set of languages—namely, the set of regular languages. In this problem, you will begin to prove the validity of this claim. Prove that every regular expression can be converted into a NFA that accepts the same language. *Hint: Consider each of the cases in the recursive definition of a regular expression to prove this claim recursively.*

Problem 5: Genetic Testing

Genetic testing can be used to determine whether someone possesses a genetic trait. Please read pages 1-3 of this paper about genetic testing (stop when you get to the Case Presentation header).

*Please try to make your answers as concise as possible! The italicized numbers are there so that you can keep track of the different parts of the question. They are **not** telling you how many sentences to make each part.*

Part I: Ethical Perspectives

a. List some similarities and differences of the utilitarian and libertarian perspectives, including their core values *(1)* and their views of genetic testing *(2)*. Which perspective do you think is the better framework for genetic testing *(3)*? Explain your reasoning *(4)*. Make sure to discuss all four points in your response (4-6 sentences).

b. In what ways does the justice principle align with the utilitarian view on genetic testing? In what ways does it align with the libertarian view? (3-4 sentences).

Part II: Case Study

Next, read the hypothetical case study below adapted from Kielstein and Sass (2002).

> *CASE STUDY: A 55-year-old female is a regular dialysis patient with autosomal dominant polycystic kidney disease (ADPKD). ADPKD is a dominant genetic disorder that causes cysts to grow in the kidney. Typically, kidney function slowly deteriorates in ADPKD patients to the point of kidney failure. There is no cure, although there are treatments to manage symptoms. If affected, patients usually begin to present symptoms between the ages of 30 and 40.*
>
> *The 55-year-old patient had 2 sons. The first son decided to undergo genetic screening while the second son decided not to. The genetic testing revealed that the oldest son possessed one of the genetic mutations known to cause the disease. The first son, who was 30 years old, divorced his wife and sold their home. He did not have problems until he was 54. The second son was 21 at the time, and several years later married and had two children. At the time of the case study's publication, he was 42 and had never experienced any symptoms.*

c. Do you think the individuals in the case study handled the situation appropriately *(1)*? Did any of them act in accordance with the utilitarian or libertarian perspectives *(2)*? Why or why not? Does this case study change how much you agree with the perspectives in the previous question *(3)*? Make sure your response touches on all three points (4-6 sentences).

Part III: Algorithmic Implications

One of the potential computational solutions to detect genetic markers is to use a pattern matching algorithm such as Knuth-Morris-Pratt. In the example case study, ADPKD is caused by mutations of many types (splice site, in-frame, and out-of-frame deletions and insertions, nonsense mutations, and missense mutations) in two different genes, *PKD1* and *PKD2*.

d. In one to two sentences, explain why the KMP algorithm might not be able to successfully detect ADPKD.