

Advanced Programming Languages and Techniques

April 21, 2024

Guidelines

- Submit a single compressed file `tar.gz` file containing all your solutions.
- Inside the compressed file include a separate file for each question of the assignment. Name your Haskell files with the name of the function in question.
- You can use Haskell's standard library if you want.

Assignment 1

1. You are given an integer `num`. You can swap two digits at most once to get the maximum valued number. Create the function `maxSwap` that returns the maximum valued number you can get

```
maxSwap :: Int -> Int
```

For example,

```
ghci> maxSwap 9973
9973
ghci> maxSwap 1123
3121
ghci> maxSwap 1222
2221
```

2. An interval is a pair of integer (l, h) such that $l \leq h$. The pair (l, h) represents all the integers x that are between l and h , ie., $l \leq x \leq h$. Two intervals (l_1, h_1) and (l_2, h_2) are overlapping if $l_1 \leq l_2 \leq h_1$. Given a list of intervals, create the function `mergeIntervals` that merges all overlapping intervals and returns a list of non-overlapping intervals that covers all the intervals in the input.

```
mergeIntervals :: [(Int, Int)] -> [(Int, Int)]
```

For example,

```
ghci> mergeIntervals [(3,4), (1,5), (7,10), (2,3), (6,8)]
[(1,5), (6,10)]
```

3. The DNA sequence is composed of a series of nucleotides abbreviated as A, C, G, and T. For example, the string "ACGAATTCCG" is a DNA sequence.

When studying DNA, it is useful to identify repeated sequences within the DNA.

Given a string that represents a DNA sequence, return all the 10-letter-long sequences (substrings) that occur more than once in a DNA molecule. You may return the answer in any order.

```
repDNASeq :: String -> [String]
```

For example,

```
ghci> repDNASeq "AAAAACCCCCAAAAACCCCCAAAAAGGGTTT"
["AAAAACCCCC", "CCCCAAAAA"]
ghci> repDNASeq "AAAAAAAAAAAAA"
["AAAAAAAAA"]
```