Ex6: bulls and cows

Bulls and cows is a game of deduction that involves the system selecting a sequence of n digits, followed by the user trying to guess what the sequence is. Each digit in the sequence is unique, where the digits are 0,...,9 of course. Examples of sequences are [8], [9,1,3,0,2] and [0,1,2,3,4,5,6,7,8,9]. The sequence [1,4,3,1] is invalid as a digit repeats. Initially, the user knows only the length of the system's sequence.

The user can make as many guesses as he/she likes, but each guess must be a sequence that conforms to the same sequence requirements (same length, only digits and all unique). Each time, the user is told how many cows and bulls he/she has scored. A bull is defined as a correct digit in the correct position in the sequence, and a cow as a correct digit but in an incorrect position.

For example, if the system (secretly) selects the sequence [4,2,9,3,1], and the user guesses [1,2,3,4,5], then the user would be told that he/she has scored 1 bull and 3 cows, but not what they are of course. With this knowledge, the user makes another guess trying to improve his/her score. (The bull is digit 2, and the cows are 1, 3 and 4 by the way.) Eventually the user should be able to deduce what the sequence is, and in his/her last guess will score n bulls (and 0 cows of course). The aim is to make as few guesses as possible.

Bulls and cows is similar to mastermind, but predates it by many decades. You can play the game on www.mathsisfun.com/games/bulls-and-cows.html for a sequence of 4 digits.

The exercise: You do not have to code the game in Dafny. The exercise is to verify the calculation of the number of cows and bulls in the user's guess. Do this in two steps:

i) Write two functions:

```
function bullspec(s:seq<nat>, u:seq<nat>): nat
function cowspec(s:seq<nat>, u:seq<nat>): nat
```

which specify the number of bulls and cows in the user sequence u for selection s. The sequences u and s must satisfy the requirements of the game of course.

ii) Write a method with signature:

```
method BullsCows (s:seq<nat>, u:<seq<nat>) returns (b:nat, c:nat)
```

which computes the actual scores using Dafny code and verifies the code using the above functions.

Testing: Write a tester that provides a range of black-box tests for the functions and method. A sample testcase for a game of 5 digits is:

```
 \begin{array}{lll} \text{var sys:seq<nat>} := [4,2,9,3,1]; & \text{// system selection} \\ \text{var usr:seq<nat>} := [1,2,3,4,5]; & \text{// user guess} \\ \text{assert bullspec(sys, usr)} == 1; & \text{// verify the bulls} \\ \text{assert cowspec(sys, usr)} == 3; & \text{// verify the cows} \\ \text{var b:nat, c:nat} := \text{BullsCows(sys, usr)}; & \text{// calculate the bulls and cows} \\ \text{assert b} == 1 \&\& c == 3; & \text{// verify the calculation of bulls and cows} \\ \end{array}
```

I have included calls to the functions in the above tester to show how they work as well. You may write separate testers if you like. You may call your tester(s) anything you like, but not Main.

Ex7: DNA sequencing

In bio-chemistry, sequencing DNA means determining the order of the four chemical building blocks, called 'bases', that make up the DNA molecule. These bases are adenine (A), cytosine (C), guanine (G) and thymine (T). For the purpose of this work, assume that there may be any number of bases in a sequence (but greater than 0). (There are actually billions.)

i) Write a verified method that exchanges the bases at positions x and y in a sequence. A requirement is there must be bases at these positions. The first base in a sequence is at position 0

For example, if the sequence of bases is [A, C, A, T] then exchanging bases at positions 2 and 3 results in [A, C, T, A]. The signature of the method should be:

```
method Exchanger(s: seq<Bases>, x:nat, y:nat) returns (t: seq<Bases>)
```

where Bases is a datatype that represents the four DNA bases. The sequence t that is returned has the bases exchanged. The input sequence s is not altered.

Testing: Write a tester method that checks that Exchanger is working for a comprehensive range of testcases. A sample testcase is:

ii) Write a predicate with the following signature:

```
predicate bordered(s:seq<Bases>)
```

which returns true if the input sequence is base-ordered, and false otherwise. Base-order is alpha- betical: that is A, C, G, T. For example, the sequence s = [A, G, G, G, T] is in base-order so bordered(s) is true. The empty sequence is also base-ordered. The sequence t = [G, A, T] is not in base-order so bordered(t) is false.

iii) Write a verified method with signature:

```
method Sorter(bases: seg<Bases>) returns (sobases:seg<Bases>)
```

which sorts the sequence bases, creating and returning a new sorted sequence sobases. There must be at least one base in bases. The ordering of bases should be as in part ii of course. Some conditions:

- You should use predicate bordered to verify whether a sequence is ordered or not.
- The sorter must be linear in performance (quadratic sorts such as insertion sort are not suitable as they are too slow).
- You should not use an array anywhere in this exercise.

Testing: Write a tester method that checks that your sorter is working. Provide a comprehensive range of testcases. A sample testcase is:

For small testcases, such as the one above, you could have tested the new sequence is ordered simply using assert b == [A,G,T]. For technical reasons, however, this will not work in general, and instead you will need to use the code used above.

As usual, you may call the tester method anything you like (but not Main and not the same name as you used earlier in this exercise).