CSCI.4430/6430 Programming Languages Fall 2016
Programming Assignment #2

*This assignment is to be done either **individually** or **in pairs**. **Do not show your code to any other group** and **do not look at any other group's code**. Do not put your code in a public directory or otherwise make it public. However, you may get help from the TAs or the instructor. You are encouraged to use the LMS Discussions page to post problems so that other students can also answer/see the answers.*

DNA Sequence Matching

In this programming assignment, you will implement a concurrent and distributed DNA Sequence Matching counter. The counter should take two DNA sequences: an *input* sequence which will be grouped together by the chemical bases that would be present in a *target* sequence. The program should return the total number of inversions we need to perform for a sequence match between the input and target sequences. Your assignment should be created using the actor model to allow for concurrent and distributed computation of the number of inversions needed to match the target DNA sequence.

Note : The DNA sequence is made up of four chemical bases: adenine (**a**), guanine (**g**), cytosine (**c**), and thymine (**t**).

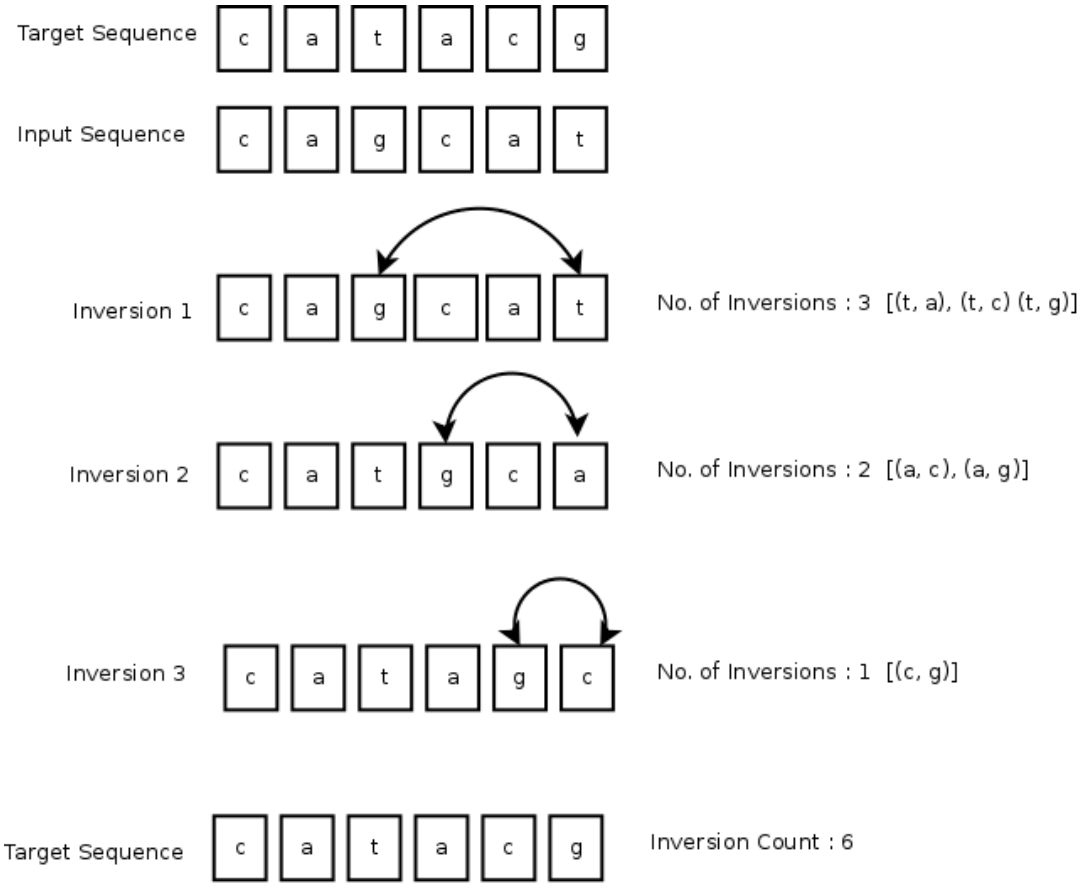
Inversion Count

An inversion is a pair of consecutive places of a sequence where the elements on these places are out of their natural order. Inversion count is defined by the total number of inversions needed to convert an input to a target sequence.

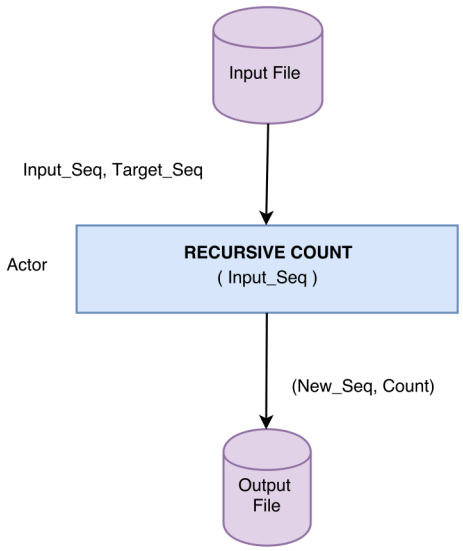
Example results

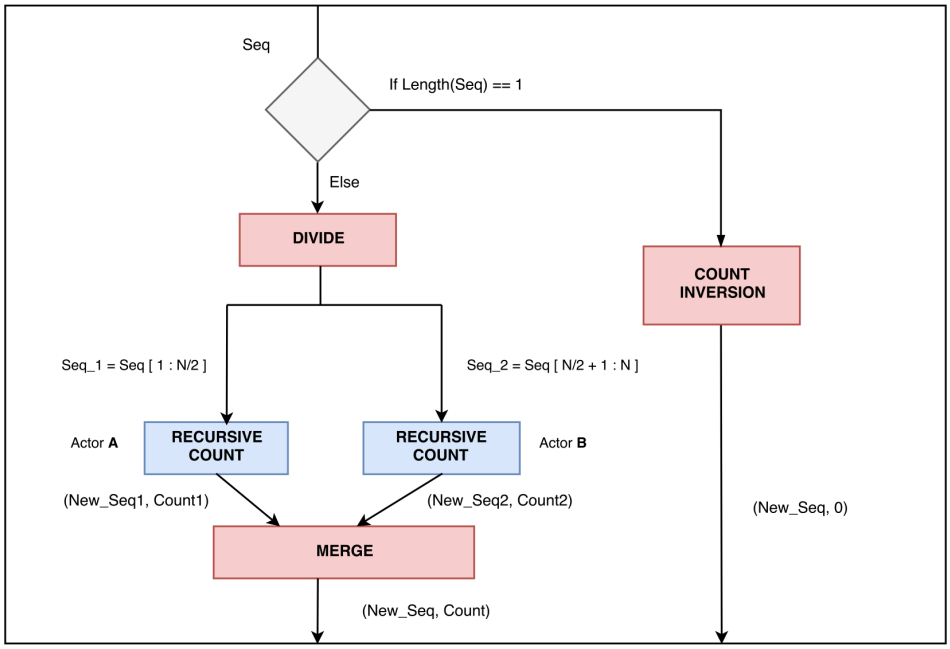
Target Seq	Input Seq	Inversion Count	Inversions
ga	ga	0	-
ga	ag	1	[(a,g)]
gat	tga	2	[(t,g), (t,a)]
gat	tag	3	[(t,a), (t,g), (g,a)]
gtca	tacg	4	[(g,c), (g,a), (g,t), (c,a)]

Illustrated Sample Inversion Count



High-level Design & Program Flow





Hint: You can view inversion count as a modified sorting problem and use a correspondingly modified recursive merge-sort algorithm.

Program I/O

Input : Your program should accept a text file that contains two strings on separate lines, the first of which is the input sequence and the second the target sequence.
Output : Your program should return the inversion count to transform the input sequence into the target sequence.

Sample Interactions

```
$ ./run.sh < ./input1.txt
0
$ ./run.sh < ./input2.txt
2

$ cat ./input1.txt
ga
ga

$ cat ./input2.txt
gaag
agga
```

Notes for Salsa Programmers

Your concurrent program should be run in the following manner:

```
$ salsac dna/*
$ salsa dna.InversionCount < input2.txt
2
```

where `input2.txt` specifies the name of input file. `salsac` and `salsa` are UNIX aliases or Windows batch scripts that run `java` and `javac` with the expected arguments: See .cshrc for UNIX, and salsac.bat salsa.bat for Windows. And your distributed program should be run in the following manner:

```
$ salsac dna/*
$ salsa dna.DInversionCount theaters.txt < input.txt
```

where `input.txt` specifies an input file name, and `theaters` is a name server and theater description file. See a sample name server and theaters description file, the first line of which specifies the name server location and each of the remaining lines specifies a theater location.

Time Saving Hints

1. For reference, please see the SALSA webpage, including its FAQ. Read the tutorial and a comprehensive example illustrating distributed programming in SALSA.
2. The module/behavior names in SALSA must match the directory/file hierarchical structure in the file system. e.g., the `InversionCount` behavior should be in a relative path `dna/InversionCount.salsa`, and should start with the line `module dna;`.
3. Messaging is asynchronous. `m1(...);m2(...);` does not imply `m1` occurs before `m2`.
4. Notice that in the code `m(...)@n(...);`, `n` is processed after m is executed, but not necessarily after messages sent *inside* `m` are executed. For example, if inside `m`, messages `m1` and `m2` are sent, in general, `n` could happen before `m1` and `m2`.
5. (Named) tokens **can only be used** as arguments to messages.

Running as a distributed system

To run your program as a distributed system, you must:

1. First, run the name server and the theaters:

   ```
   [host0:dir0]$ wwcns [port number 0]
   [host1:dir1]$ wwctheater [port number 1]
   [host2:dir2]$ wwctheater [port number 2]
   ...
   ```

   where `wwcns` and `wwctheater` are UNIX aliases or Windows batch scripts: See .cshrc for UNIX, and wwcns.bat wwctheater.bat for Windows.
2. Make sure that the theaters are run where the actor behavior code is available, that is, the `dna` directory should be visible in directories: `host1:dir1` and `host2:dir2`. Then, run the distributed program as mentioned above.

Please put the modified program in the file `DInversionCount.salsa`. Be sure to attempt to evenly distribute your workload across the nodes; a good way to do this is a random, uniform sampling of an array containing all nodes.

Notes for Erlang Programmers

Please find the starting code on Github: Fall16_PA2_Erlang.

When submitting, make sure your `main:start()` launches your program. It should read two strings from the command line, and output the number of inversions it takes to make the first string into the second string.

Running as a distributed system

To make your code run on multiple machines (in a distributed network), you must use spawn/4 and related functions. Then you just need to make sure you launch Erlang with the same cookie set on all the machines. To run your program on multiple hosts, execute it as follows:

```
machine1$ erl -sname example1@localhost -setcookie thecookiemonster
machine2$ erl -sname example2@localhost -setcookie thecookiemonster
machine3$ erl -sname example3@localhost -setcookie thecookiemonster
machine4$ erl -sname example4@localhost -setcookie thecookiemonster -pa ./main.erl -run main -run init stop -noshell
```

You can use the following code to dynamically find available nodes:

```
get_random_node() ->
  rget_random_node(rand:uniform(length(net_adm:world())), net_adm:world()).

rget_random_node(1, [H|_]) -> H;
rget_random_node(_, [H|[]]) -> H;
rget_random_node(N, [_|T]) -> rget_random_node(N-1, T).
```

Things to watch out for

- Make sure the main thread does not exit until the answer is printed out; if run with -noshell, erl will kill other threads once the main thread terminates. The starter code gives a solution to avoid this.
- Your output must match the examples given, exactly. Please be sure to include a newline after the integer.

Documentation for Erlang

Please look at http://erlang.org/doc/ for Erlang examples, function documentation, and usage. Pay special attention to http://erlang.org/doc/man/io.html, and remember Google is your friend (but don't copy and paste code!).

Due date and submission guidelines

Due Date: Thursday, 10/27, 7:00PM

Grading: The assignment will be graded mostly on correctness, but code clarity / readability will also be a factor (comment, comment, comment!).

Submission Requirements: Please submit a ZIP file with your code, including a README file. README files must be in plain text; markdown is acceptable. Your ZIP file should be named with your LMS user name(s) and chosen language as the filename, either userid1_erlang.zip (or userid1_salsa.zip) or userid1_userid2_erlang.zip (or userid1_userid2_salsa.zip). Only submit one assignment per pair via LMS. In the README file, place the names of each group member (up to two). Your README file should also have a list of specific features / bugs in your solution.

Do not include unnecesary files. Test your archive after uploading it. Name your source files appropriately: `InversionCount.salsa` for SALSA, and `main.erl` for Erlang.