CAB401   
  
  
PARALLELIZATION PROJECT REPORT

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Promoter

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**1. Original sequential application**

1.1 What it does

The application is utilized to identify different promoters – whose genes are listed in reference list – from the Ecoli bacteria genes.

For more information regarding the biology in this app, referenceGenes.list contains gene name and its gene sequence - the objectives this app needs to find in the bacteria genes. In the provided program, there are 8 reference genes in total. Each letter in the sequence corresponds to an amino acid – a basic building block of a protein sequence.

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*Figure 1 referenceGenes.list*

In each gene bank file (with .gbk tail), ORIGIN section is the DNA of a bacteria organism. The DNA can contain millions of DNA molecules represented by 4 letter a-t-g-c and triplet of DNA molecules encodes 1 protein. There are 20 different amino acids built from 64 possible combinations of a triplet, and they are the basic building block of proteins (Lee & Hain, 2021). Some sections of DNA don’t correspond directly to proteins so in between proteins, there are upstream region called promoters which are the objects we need to identify.

1.2 How it works

1.2.1 Important packages

Description and analysis of some important packages:

* SmithWatermanGotoh: contains utility classes that uses Smith-Waterman algorithm with Gotoh’s improvement for biological local pairwise sequence alignment. Note that classes in this package requires an intensive computation power to determine the similar regions between two strings of sequences.
* Sigma70Consensus: initializes the map and prediction of a sigma factor 70 consensus and contains utility functions to record results.
* BioPatterns: contains getBestMatch function which is responsible for searching the best match of a pattern in a nucleotide sequence.
* GenBankRecord: its instance contains a list of gene names, their strand, location and gene sequences and a nucleotide sequence. This package also has Parse method used to extract the mentioned data from a file.

1.2.2 Sequential

Through a brief analysis in run() function, the program first loads Ecoli DNA and reference genes using ParseReferenceGenes function.

After that, in the **first** **For** **loop** (number 1), the program iterates through each Ecoli DNA file to retrieve its gene record using Parse function.

Another **inner For loop** (number 2) iterates through the reference genes to compare it with each Ecoli gene in its **inner For loop** (number 3).

The comparation process is handled by Homologous function to determine if 2 genes serve the same purpose. In this case, they are an Ecoli gene from Ecoli records (from For loop 3) and another gene from reference genes (from For loop 2).

Inside the Homologous function, gene sequences are passed to align function of the SmithWatermanGotoh package.

If the Homologous function return true, the program proceeds to extract upstream region of the Ecoli gene by GetUpStreamRegion function and use it to predict if that Ecoli gene is a promoter. If true, the results are recorded in ‘consensus’ variable by adding 1 to the counter of that promoter type and the total matches.

**2. Potential parallelism analysis**

2.1 Profiler analysis

From the initial analysis of the given sequential program, Homologous function dominantly consumes 99.7% of the CPU computation. More specifically, it’s the align function in SmithWatermanGotoh class that get called by the Homologous function.

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*Figure 2 CPU hotspot from JProfiler*

Since SmithWatermanGotoh function is a computational-intensive algorithm and required a deep understanding of problem to rewrite for better performance, the work of this report mainly focuses to parallelize this part and increase performance at other parts where possible.

More importantly, this app uses 3-nested for loop which is being executed sequentially and contains both heavy (Honologous function) and light operations (extracting genes, gen bank records), read and write operations inside the For loops. As a consequence, the computing time takes a substantial amount of time and could be reduced if we apply parallelizing and restructuring.

2.2 Dependencies:

sigma70\_pattern is assigned value from Sigma70Definition.getSeriesAll\_Unanchored(). But the method itself getSeriesAll\_Unanchored() is also static which will cause data race when there are multiple threads trying to access sigma70\_pattern. So to parallelize, I made it a ThreadLocal variable to store data individually for each thread (except for Explicit Threading technique).

Control dependency (orange underlined): the condition statement in ‘if’ affects whether the code in it executes or not. However, the properties in Gene class are not static meaning values of its instance are separated from each thread so it can be safe to implement parallelization for this part.

2 data dependencies (yellow underlined) are also identified in the most inner section of the For loops. Specifically, they are of True Dependence type in which one statement reads a value written by an earlier statement. In this case, they are upStreamRegion and prediction.

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*Figure 3 Control (orange) and data dependencies (yellow)*

**3. Tools and techniques utilized**

3.1 Hardware specs:

* CPU: Intel Core i7-8565U @1.8GHz
* 4 cores
* 8 virtual cores
* 8GB RAM
* Cache
  + L1 Data 4x32KB, 8-way
  + L1 Instruction 4x32KB, 8-way
  + L2 4x256KB, 4-way
  + L3 8MB, 16-way

3.2 Software:

* Integrated development environment: IntelliJ
* Java 15
* Run on Window Operating System
* Profiler tool: Jprofiler

3.3 Techniques:

In this project, I restructured the For loops code block to parallelize (except for Explicit threading technique). I made For loop 2 wrap For loop 1 and 3. Now, the order of the 3 For loops looks like this:

2: referenceGene -> 1: filename -> 3: gene

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*Figure 4 For loops order changed (Parallel.java)*

The aim of this transformation is to increase spatial locality by reducing gap time between accessing ‘record’ in For loop 1 and 3 and therefore, increase the number of cache hits for ‘record’ when transiting from For loop 1 to 3

While this puts referenceGene further from the inner part (*if (Homologous(…){ …}*), the high frequency in calling the variable will keep its memory location stored in cache.

There are 3 parallelization approaches I have implemented in this project:

* Explicit Threading
* Parallel Stream
* Executor Service

3.3.1 Explicit Threading (in ExplicitThreading.java)

This is the first method I attempted for this application. From the sequential code, I thought the application can run faster by parallelizing and letting each thread handles one single input file instead of having them queue and running one by one. Therefore, I estimated this method can reduce the execution time by approximately 4 times (with 4 threads running parallelly to process 4 given Ecoli text files at once).

To apply explicit threading method, I created a new class called ExplicitThreading so that it can spawn a new thread of Sequential class by a separated For loop. To distribute the workload, that For loop also pre-processes ListGenBankFiles and assign each file for each thread. With this change, the Sequential class now only handle one file in each thread and 4 of them can run simultaneously.

With this approach, there are several changes in the original code structure. In order to prepare and extract the necessary data and add them as parameters to each Sequential call, 2 functions, ProcessDir and ListGenBankFiles, from Sequential class were moved down to my newly created class.

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*Figure 5 Newly created ExplicitThreading Class (ExplicitThreading.java)*

New private variables and constructors were also added in Sequential class to keep exclusive data from ExplicitThreading for each particular thread.

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*Figure 6 New private variables and constructors (ExplicitThreading.java)*

As for Homologous check – a critical part with most write operations, I used ReentrantLock to only allow 1 thread to access to it in any given time.

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*Figure 7 Critical part is protected with a lock (ExplicitThreading.java)*

3.3.2 Parallel stream (in Parallel.java)

Parallel Stream is an API that allows us to create multiple parallel streams, perform operations on them parallelly and as a result, utilize multiple processor cores. This technique especially comes in handy when the source of a stream is a Collection or an Array. In this case, we use parallelStream() method (baeldung, 2021).

3.3.2.1 Parallel stream 3rd For loop - runParallelStream3rd

As analyzed from the Jprofiler hotspot (Figure 2), 99.7% of execution time is spent on Homologous function so I decided to just parallelize the Homologous part using parallel stream following the 80-20 rule (Pareto principlpe).

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*Figure 8 parallelStream() 3rd For loop*

Note that the code block processing consensus value, the hotspot of many write statements during the process is now placed in a synchronized function to ensure only one thread can write on its value in any given moment and therefore, a correct final result.

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*Figure 9 synchronized addConsensus() function*

3.3.2.2 Parallel stream with pre-processing - runParallelStreamWithPrep

In addition to the approach in 3.3.2.1 Parallel stream 3rd For loop, **Divide and Conquer** technique is applied, which turns a block of 3 For loops into 2 sub-problems: one consists of block of 3 For loops to pre-process files, store outcomes (Figure 11) and utilizing ParallelStream to run Homologous check and promoter prediction (Figure 12).

In order to increase efficiency in storing data in the pre-process phase and accessing it in the second sub-problem, I created a new Class called TaskHandler (Figure 10) which takes each combination of reference gene, gene and gen bank record and then store it as an item in a List for later use.

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*Figure 10 TaskHandler class (TaskHandler.java)*

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*Figure 11 Pre-process code with List<TaskHandler> taskHandlers to store data*

Then, parallel stream can easily be implemented on a List as shown in Figure 12. Here, the tasks in List<TaskHandler> will be assigned to a thread and processed as soon as one becomes free. ‘filter’ expression of parallelStream() is also utilized instead of if condition to check whether if 2 gene sequences are Homologous or not.

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*Figure 12 Apply parallelStream() on taskHandlers*

3.3.3 Executor Service (Parallel.java - runExecutorService)

Executor Service is a JDK API that enables app to create a pool of threads and provides an API to assign tasks to it as threads become free. Number of threads is assigned when declaring an ExecutorService object. In this solution, tasks are objects of a class – RunnableTask – implementing Runnable Interface and each of which will keep a combination of referenceGene, gene, and record. Following the same approach with Parallel stream with pre-processing technique, thread pool will only be used for running Homologous code.

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*Figure 13 RunnableTask class*

In Executor service, Future represents pending completion of a task (Oracle, 2021). To assign tasks to a pool, these objects are first submitted to an executorService object, and they will then be added to a List<Future>.

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*Figure 14 Pre-process data: collecting List<Future>*

After having completed to getting all the futureTasks in List<Future>, the program iterates though each item in List<Future> and execute them asynchronously using the pool of threads we have declared in executorService.

3.4 Testing (CompareTests.java)

In my Tests, I declare a defaultConsensus variable of type HashMap<String, String> to store default result in the original Sequential run with given default input dataset. This helps speed up the testing time when comparing the final result of new parallelization techniques with Sequential code’s assuming input dataset is not changed. Nevertheless, tests that compares consensus result from an actual Sequential run is also covered.

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*Figure 15 Declare default consensus function*

Tests includes testing all 3 techniques. All the tests are conducted by going through each entry of consensus and comparing the 2 values correlating with the same entry key.

**4. Outcomes**

[ Discuss how you time your application (see in lecture for more) ]

First of all, all the parallelization techniques have achieved correct outcomes from the same input dataset. Below are the speedups of all techniques (on average of 10 runs each) mentioned in this report with best sequential time of 200 seconds:

*Table

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*Figure 16 Speedup of the parallelization techniques*

Chart, line chart

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*Figure 17 Speedup chart*

|  |  |
| --- | --- |
| *Chart, line chart  Description automatically generated*  *Figure 18 CPU utilization of ParallelStream with pre-processing running 12 threads* | *Chart  Description automatically generated*  *Figure 19 CPU utilization of ParallelStream 3rd For loop running 12 threads* |
| *Figure 20 CPU utilization of Executor Service running 12 threads* | *Figure 21 CPU utilization of Explicit Threading running 4 threads* |

Overall, from the above figures, Parallel Stream with pre-processing and Executor Service techniques achieved significantly better performance than Explicit Threading since CPU process load is utilized consistently at high percentage (>98% on average) during their execution periods. The reason for this is because data has been pre-processed, which enables constant input of data to the CPU cores, for checking Homologous to be specific.

However, at 12 threads, their speedup lines still leave a big gap with linear speedup line because the cost of overheads of creating threads and neckline issue in recording ‘consensus’. The more threads there are, the more overheads of creating threads and time for threads to wait and write to ‘consensus’.

Another interesting point is that, with no pre-process data, the CPU utilization seen in Explicit Threading and Parallel Stream 3rd For loop fluctuates strongly in a range of up to 20% due to the fact that program having to switching back and forth repeatedly between processing gene, referenceGene, record (which does not require much CPU power but inadvertently creates neckline) and checking Homologous (which requires a lot of CPU power). This can be observed more clearly when we compare Threads’ states in Parallel Stream with pre-processing and Parallel Stream 3rd For loop examples. Despite that, Parallel Stream 3rd For loop achieved a slightly better speedup performance than Parallel Stream with pre-processing

|  |  |
| --- | --- |
| *Chart  Description automatically generated*  *Figure 22 Threads state in PS 3rd For loop* | A picture containing graphical user interface  Description automatically generated  *Figure 23 Threads state in PS with pre-processing* |

During the execution time, threads in Parallel Stream 3rd For loop had to turn to Waiting state many times to wait for data preparation (gene, referenceGene, record) while they run continuously in Parallel Stream with pre-processing until running out of tasks

With 8 cores, both Parallel stream and Executor service techniques has achieved similar results and reached approximately 3.5-4 times speedup.

[ Calculate and add Amdahl’s law. Compare your outcome with the result ]

[ Discuss scalability ]

To conclude, Parallel stream and Executor service techniques clearly have more advantages than Explicit Threading in this app since it automates the process of distributing tasks between threads and then combine the results after finishing the task. While Explicit threading is capable of spawning more threads as we get inside the program to increase performance, it also gets more complicated with data and control dependencies at the same time.

**5. Limitations**

Changing For loop order is expected to increase locality and thus performance but this has not been tested and compared to unchanged version in Parallel Stream and Executor Service.

In each Homologous check, recording consensus result could add to an empty slot in an array and then be summed up after finishing the promoter identification phase. This would remove the neckline issue and increase performance of the app. So, this is a potential improvement for the app which I hope to discover.

**6. Difficulties**

6.1 Explicit Threading

The app can save some computation power if ParseReferenceGene is moved down to my new class ExplicitThreading. Because then, the referenceFile can now be processed once in ExplicitThreading and used multiple times by adding the variable as a parameter in every thread call instead of compute it every time a new Thread is call.

However, ParseReferenceGene depends on ‘consensus’ and functions, which makes the program much more complex. While attempting to do this, I got a data race error and did not manage to fix it.

Exception in thread "0" java.lang.NullPointerException: Cannot invoke "qut.Sigma70Consensus.addMatch(edu.au.jacobi.pattern.Match)" because the return value of "java.util.HashMap.get(Object)" is null

at qut.Sequential\_for\_explicit\_threading.run(ExplicitThreading.java:93)

So, this further development is stopped.

6.2 Parallel Stream

**Inefficient performance while parallelStream() every For Loop:**

My first approach to this Parallel Stream technique was to apply parallelStream() to every List instead of iterating through every item in List in every For loop without the pre-processing step.

However, later I found out that applying parallelStream() to every For loop does not increase performance as the app still spawns a pre-determined number of threads. So, this may be counterproductive because the app now has more overheads to run parallelStream() 3 times which brings no benefit in this case. The execution time is **62 seconds for 8 threads or 61 seconds for 12 threads**, which is much greater than the proposed Parallel Stream technique above that used parallelStream() once. So after discovering this, I only used parallelStream once in each run.

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*Figure 24 Initial approach for parallel stream: using parallelStream() 3 times*

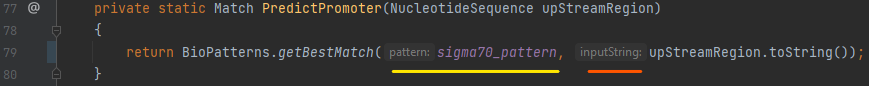
**Fixing data race while parallelStream() the app.**

While parallelizing the app with parallel stream, my app ran into an IndexOutOfBound error. So, I speculated this is a data race issue. I followed the error report and found the key cause of this error which is in PredictPromoter function.

A screenshot of a computer

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*Figure 25 Console screenshot with error*



*Figure 26 Identify error cause*

Data race in sigma70\_pattern between difference threads has cause IndexOutOfBound error. It could not be upStreamRegion.toString() because it is a String type which is not a popular cause of IndexOutOfBound error. And sigma70\_pattern is assigned values from a static function -Sigma70Definition.getSeriesAll\_Unanchored(0.7) - at the beginning of the program so its properties contain a lot of Integer and Array as we can see in the below code snippet in Sigma70Definition.java.

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*Figure 27 A look into getSeriesAll\_Unanchored() function*

After doing some research, I managed to solve it by making sigma70\_pattern a ThreadLocal<Series> variable because ThreadLocal is a special construct allows to store data that will be accessible only by the thread running it (baeldung, 2021).

6.3 Executor Service

The same issue with sigma70\_pattern was encountered in implementing Executor Service and easily resolved.

**7. Reflection**

**To parallelize an app well, we must have a deep understanding of the app** such as its data structure, purposes of the app in general, functions, classes, noticing small details like data type as well as knowing various parallelization techniques to use the most suitable one. For example, ThreadLocal protects data race between threads, but we do not apply it to all variables, but only to the exposed ones.

**Complicated program should often be used with implicit threading instead of explicit threading**. The reason for this is that threads can run and finished in different time, and we have little control over this. Therefore, it gets more complicated to organize and add tasks to threads so as to make the most of all CPU cores power. On the other hand, implicit threading solves this problem by automating task distribution for us.

**Finding the most optimized parallelization techniques requires much hand-on work**. There is no superior parallelization method that fits all cases or has the best performance. The original program also needs change to further optimize the runtime. For instance, changing program architecture or algorithm. Therefore, the performance of each technique varies in each program, so it needs trial and error to find the best parallelization technique.

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**9. Appendixes**

9.1 Instructions to run app with each technique

Step 1: Open Zip file and open the folder with IntelliJ

Step 2: Open src > qut

Step 3: Now we are in qut directory:

* To use Sequential code, run Sequential.java
* To use Explicit Threading Technique, run ExplicitThreading class in ExplicitThreading.java
* To use Parallel Stream 3rd For loop / Parallel Stream with pre-processing / Executor Service, change ‘choice’ value with number 1 / 2 / 3 accordingly at line 271 (and threadNum parameter to run on [threadNum] threads) in Parallel.java and run main function.

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Step 4: To test the result, you similarly change ‘choice’ value and run the test you want. Tests provided are:

* Compare a Parallel technique’s consensus with consensus from analyzing default dataset
* Compare ExplicitThreading technique’s consensus with consensus from analyzing default dataset
* Compare a Parallel technique’s consensus with Sequential code’s
* Compare a Parallel technique’s consensus with Sequential code’s

9.2 Others

9.2.1 Test script

class CompareResult {  
  
 private HashMap<String, String> defaultConsensus;  
  
 @BeforeEach  
 void declareDefaultConsensus() {  
 defaultConsensus = new HashMap<>();  
 defaultConsensus.put("all", " Consensus: -35: T T G A C A gap: 17.6 -10: T A T A A T (5430 matches)");  
 defaultConsensus.put("fixB", " Consensus: -35: T T G A C A gap: 17.7 -10: T A T A A T (965 matches)");  
 defaultConsensus.put("carA", " Consensus: -35: T T G A C A gap: 17.7 -10: T A T A A T (1079 matches)");  
 defaultConsensus.put("fixA", " Consensus: -35: T T G A C A gap: 17.6 -10: T A T A A T (896 matches)");  
 defaultConsensus.put("caiF", " Consensus: -35: T T C A A A gap: 18.0 -10: T A T A A T (11 matches)");  
 defaultConsensus.put("caiD", " Consensus: -35: T T G A C A gap: 17.6 -10: T A T A A T (550 matches)");  
 defaultConsensus.put("yaaY", " Consensus: -35: T T G T C G gap: 18.0 -10: T A T A C T (4 matches)");  
 defaultConsensus.put("nhaA", " Consensus: -35: T T G A C A gap: 17.6 -10: T A T A A T (1879 matches)");  
 defaultConsensus.put("folA", " Consensus: -35: T T G A C A gap: 17.5 -10: T A T A A T (46 matches)");  
 }  
  
 */\*\*  
 \* Compare a Parallel technique’s consensus with consensus from analyzing default dataset  
 \*/* @org.junit.jupiter.api.Test  
 void parallel\_n\_defaultResult() throws IOException, ExecutionException, InterruptedException {  
 Parallel.*main*(new String[0]);  
 for (Map.Entry<String, Sigma70Consensus> entry : Parallel.*getConsensus*().entrySet()) {  
 *assertEquals*(defaultConsensus.get(entry.getKey()), entry.getValue().toString());  
 }  
 }  
  
 */\*\*  
 \* Compare a Parallel technique’s consensus with consensus from analyzing default dataset  
 \*/* @org.junit.jupiter.api.Test  
 void explicit\_n\_defaultResult() throws InterruptedException {  
 ExplicitThreading.*main*(null);  
 for (Map.Entry<String, Sigma70Consensus> entry : ExplicitThreading.*getConsensus*().entrySet()) {  
 *assertEquals*(defaultConsensus.get(entry.getKey()), entry.getValue().toString());  
 }  
 }  
  
  
 */\*\*  
 \* Compare a Parallel technique’s consensus with Sequential code’s  
 \* Note: This test should only be run when input data set has been changed  
 \* as Sequential takes much time to run  
 \*/* @org.junit.jupiter.api.Test  
 void parallel\_n\_sequential() throws IOException, ExecutionException, InterruptedException {  
 Parallel.*main*(null);  
 Sequential.*main*(null);  
 HashMap<String, Sigma70Consensus> sequentialConsensus = Sequential.*getConsensus*();  
 for (Map.Entry<String, Sigma70Consensus> entry : Parallel.*getConsensus*().entrySet()) {  
 *assertEquals*(sequentialConsensus.get(entry.getKey()).toString(), entry.getValue().toString());  
 }  
 }  
  
 */\*\*  
 \* Compare a Parallel technique’s consensus with Sequential code’s  
 \* Note: This test should only be run when input data set has been changed  
 \* as Sequential takes much time to run  
 \*/* @org.junit.jupiter.api.Test  
 void explicitThreading\_n\_sequential() throws IOException, InterruptedException {  
 ExplicitThreading.*main*(null);  
 Sequential.*main*(null);  
 HashMap<String, Sigma70Consensus> sequentialConsensus = Sequential.*getConsensus*();  
 for (Map.Entry<String, Sigma70Consensus> entry : ExplicitThreading.*getConsensus*().entrySet()) {  
 *assertEquals*(sequentialConsensus.get(entry.getKey()).toString(), entry.getValue().toString()); } } }