Substring Search with application to Genomics Advanced Computer Architecture - Project

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January 31^{th} , 2023

The Algorithm



- Rabin-Karp fingerprint search;
- Linear-time for substring searching O(M+N);
- Constant time for hash computation of a M-character string.

Rolling Hashing



- D: alphabet's dimension
- Q: large prime number

Serial Program Functionalities



It has two major routines:

- read_txt: the one that reads the txt file and saves it into an array;
- rabin_karp: the one that develops Rabin-Karp substring search in the given text.

gprof outcome:

	% time	comulative seconds	self seconds	calls	self s/call	total s/call	name
ſ	100.00	15.17	15.17	1	15.17	15.17	rabin_karp
	0.00	15.17	0.00	1	0.00	0.00	read_file

Strategies for Parallelization



- Divide the txt string among several cores, allowing each core to look for a specific pattern within the text string's allocated part. Every process prints its results on the stdout file.
- Same as before but every process prints on its own file and then the master process merges all the file in a unique outout file.
- Assign a single core to a single pattern (in the case of a multi-pattern search) and then search in the txt string for that specific pattern. (not implemented).

Communication and Syncronization Strategy



These are the data sent by the master process to the other processes:

- send: an array containing bufsize, that is the length of text each core has to analyze, M that is length of the pat, and the rest of Note of bufsize where N is the overall length of the txt string and string;
- pat: the actual string to be searched into the txt file;

When M > bufsize + rest + 1, the number of cores is decreased because otherwise the chunk of txt given to each core is smaller than the pattern to be found.

Theoretical Assessment



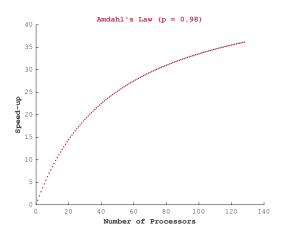


Figure 1: speedup = $\frac{n}{n+p(1-n)}$

Communication between cores



The master process is in charge of opening the communication between processes: it sends the necessary information to all the others to allow them to begin the execution. This was accomplished through the use of the MPI_Scatter and MPI_Bcast functions.

```
1 //Sending preliminary variables in send array
2 MPI_Bcast(send, 3, MPI_INT, 0, MPI_COMM_WORLD);
3
4 //Sending the pattern
5 MPI_Bcast(pat,pat_len,MPI_CHAR,0,MPI_COMM_WORLD);
6
6 //Sending the flag variable
8 MPI_Scatter(flag, 1, MPI_INT, &flag_send, 1, MPI_INT, 0, MPI_COMM_WORLD);
```

File management



The file pointer is unique so that all cores could open the file through the MPI_File_open function. Then each process, once the file is opened, moves to the indicated location through the MPI_File_set_view function. Then reads its chunk of text thanks to MPI_File_read function.

```
MPI_File_open(MPI_COMM_SELF, text_name, MPI_MODE_RDONLY,MPI_INFO_NULL, &file_in);

MPI_File_set_view(file, position, MPI_CHAR, MPI_CHAR, "native", MPI_INFO_NULL);

MPI_File_read(file, seq, bufsize+M-1, MPI_CHAR, &status);
```

Frequency computation

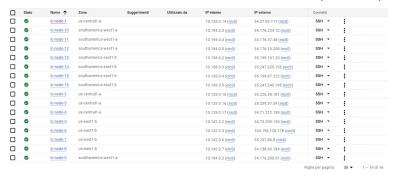


Each process sends his frequency to the master process by using the MPI_Gather function.

```
1 MPI_Gather(&freq, 1, MPI_INT, rec_freq, 1, MPI_INT, 0, MPI_COMM_WORLD);
2 if(myrank == 0){
3    int total_freq = 0;
4    for(int i = 0; i < size; i + +) {
5        total_freq = total_freq + rec_freq[i];
6    }
7    printf("PATTERN FOUND %d TIMES\n", total_freq);</pre>
```

Strong scaling analysis

1 Light cluster, multi-region, 16 cores each 2 vCPUs (N2 series).





Strong scaling analysis (cont.)

N. of cores	Execution time (sec.)		
1	17.96		
2	10.97		
3	10.00		
4	6.96		
5	5.97		
6	4.84		
7	4.23		
8	3.68		
9	3.36		
•			
31	1.35		
32	1.23		

Strong scaling analysis (cont.)



- 2 Light cluster, single-region (us-central1-a), 4 cores each 2 vCPUs (N2 series). Execution time ~ 3.15 sec.
- § Light cluster, 4 cores each 2 vCPUs (N2 series) each core in one different region. Execution time ~ 3.50 sec.
- 4 Fat cluster, multi-region, 2 cores each 16 vCPUs (N2 series). Execution time ~ 1.35 sec.



6 Fat cluster, single-region (southamerica-west1), 2 cores each 16 vCPUs (N2 series). Execution time ~ 1.35 sec.

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Strong scaling analysis (cont.)





After approved, Quotas can take up to 15 min to be fully visible in the Cloud Console and available to you.

Weak scaling analysis



We performed a few tests with different text file without changing the setup of the VMs instances (fat cluster, 2 cores each 16 vCPUs (N2 series)).

Text size	Execution time (sec.)
1 KB	0.01
100 KB chars	0.02
1 MB chars	0.02
2 GB	1.35

Table 1: Weak scalability

Consideration about speed-up



Given that the serial program run with one vCPU takes almost 18 seconds and the fastest VM configuration takes 1.23 seconds, we can estimate that running a parallel program produce a speed-up of \sim 14.6, almost as the theoretical speed-up of the Amdahl's Law.



Thanks for your attention