# Substring Search with application to Genomics Advanced Computer Architecture - Project

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## 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
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 files in a unique output one.
- 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



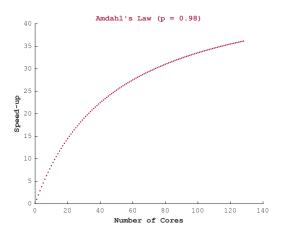
These are the data sent by the master process to the other processes:

- send: an array containing bufsize, that is the length of text each core has to analyze, M that is the length of the pat, and the rest of  $\frac{N}{\text{bufsize}}$  where N is the overall length of the txt 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



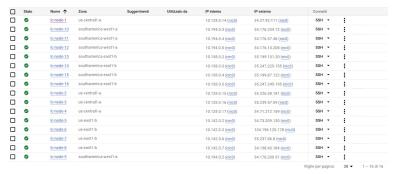
Each process sends his frequency to the master process by using the MPI\_Gather function.

```
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  $\sim 3.15$  sec.
- § Light cluster, 4 cores each 2 vCPUs (N2 series) each core in one different region. Execution time  $\sim 3.50$  sec.
- 4 Fat cluster, multi-region, 2 cores each 16 vCPUs (N2 series). Execution time  $\sim 1.35$  sec.



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

## 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	0.02
1 MB	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.

#### Individual Contribution



We both worked on writing serial and parallel code. Then we decided to split the remaining work according to our own knowledge:

- Diego Mastella was in charge of managing the repository on GitHub during the development of the code.
- Matteo Ragni took care of the report and the presentation using LATEX;



Thanks for your attention