USING MAPREDUCE IN THE 1000 GENOMES DATASET

1. INTRODUCTION

The 1000 genomes project is an international research project that created a catalogue of common human genetic variation. Their data is available for free in their website (https://www.internationalgenome.org/)

This practical session aims to determine the distribution of samples across different populations in the 1000 Genomes dataset. Nevertheless, for the session a small portion of the dataset called "we will use a small sample file called integrated_call_male_samples_v3.20130502.ALL.panel" was used. This file contains information about the samples in the dataset, which are grouped into populations and super populations based on their geographic origin.

This is how the data looks like:

sample	рор	super_po	ор	gender
HG00096	GBR	EUR	male	
HG00101	GBR	EUR	male	
HG00103	GBR	EUR	male	
HG00105	GBR	EUR	male	
HG00107	GBR	EUR	male	
HG00108	GBR	EUR	male	
HG00109	GBR	EUR	male	
HG00112	GBR	EUR	male	
HG00113	GBR	EUR	male	
HG00114	GBR	EUR	male	
HG00115	GBR	EUR	male	
HG00116	GBR	EUR	male	
HG00117	GBR	EUR	male	
HG00119	GBR	EUR	male	
HG00126	GBR	EUR	male	
HG00129	GBR	EUR	male	
HG00131	GBR	EUR	male	

The objective of this session is to count how many samples are there for each country implementing the **MapReduce** with AWS in a simple way.

MapReduce is a programming model and associated implementation for processing and generating large datasets that are parallelizable. Here is a brief overview:

 <u>Mapping</u>: In the mapping phase, data is broken down into smaller chunks and distributed across multiple machines in a cluster. Each machine performs a specific task (map) on its subset of data and generates intermediate key-value pairs.

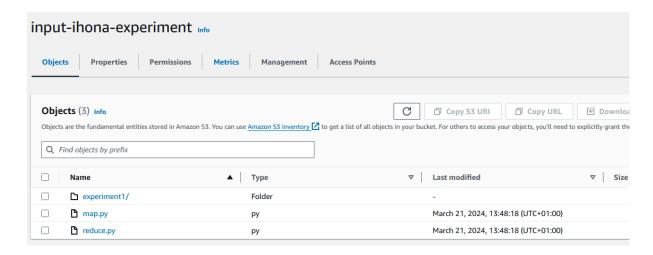
- 2. <u>Shuffling</u>: In this phase, the intermediate results from the mapping phase are shuffled and sorted based on keys. This process ensures that all values associated with a particular key are grouped together.
- 3. <u>Reducing</u>: In the reducing phase, the shuffled intermediate data is processed to produce the final output. Each reducer machine processes a subset of keys and their associated values, aggregates them, and generates the final output.

On the other hand, **Hadoop** is an open-source distributed computing framework designed for storing and processing large datasets across clusters of commodity hardware, which uses the MapReduce as its processing engine. In AWS, we can use **EMR** (Amazon Elastic MapReduce), that simplifies the deployment and management of Hadoop and other distributed computing frameworks, including support for the MapReduce programming model. It enables users to efficiently process and analyze large datasets using parallel computing techniques across a dynamically scalable cluster of virtual servers.

For this exercise, we will use EMR for processing our dataset. Moreover, **Python** is used for the MapReduce codes that will process the data.

2. CREATING THE BUCKETS

Before starting with the EMR, we must create two buckets, one for storing the input data (dataset, map and reduce python codes) and another one to store the results of the MapReducer. We have to take into consideration that the buckets will need to be in the same region as the cluster.



The map and reduce functions can either be in the same code, or separately. In this exercise, it has been used two separate functions, map.py for the map function, and reduce.py for the reducer function:

- map.py: This code goes line by line, and if the line is not a comment (#) it launches the map function. The map function splits the line using a separator and stores the population and the super population (which according to the dataset, they are in the second and third column) in separate variables.

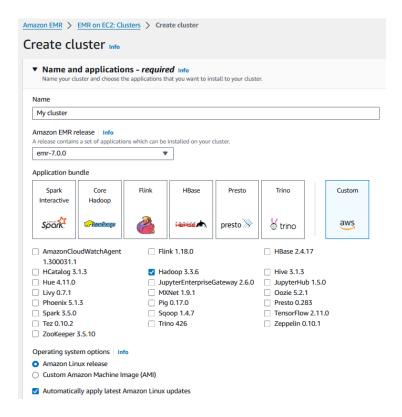
```
#!/usr/bin/env python3
1
2
     import sys
3
4
     def map function(record):
5
         fields = record.split('\t')
6
         population = fields[1]
 7
         super_population = fields[2]
8
         print(f'{population}\t{super_population}\t1')
9
10
     for line in sys.stdin:
11
         if not line.startswith('#'):
12
             map_function(line.strip())
```

 reduce.py: The reducer reads everything received from the maper and groups it together using the key. Once it has all the groups together, it sums the number of occurrences.

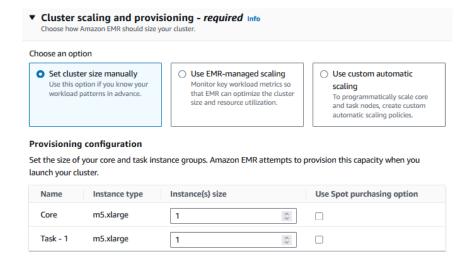
```
#!/usr/bin/env python3
 1
 2
    import sys
 3
     from itertools import groupby
    from operator import itemgetter
 4
 5
     def read_mapper_output(file, separator='\t'):
 6
 7
         for line in file:
             yield line.rstrip().split(separator, 2)
 8
 9
10
     def main(separator='\t'):
         data = read_mapper_output(sys.stdin, separator=separator)
11
         for current_key, group in groupby(data, itemgetter(0)):
12
             total_count = sum(int(count) for _, _, count in group)
13
14
             print(f"{current_key}{separator}{total_count}")
15
     if __name__ == "__main__":
16
17
         main()
```

3. EMR

Now, we have to go to the EMR service and configure it to use these buckets. To make it simpler and for the demo purpose, we select the hadoop cluster:

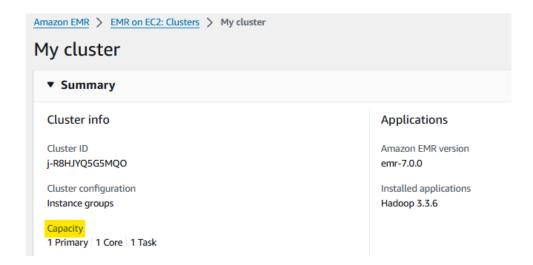


We set the cluster size manually:

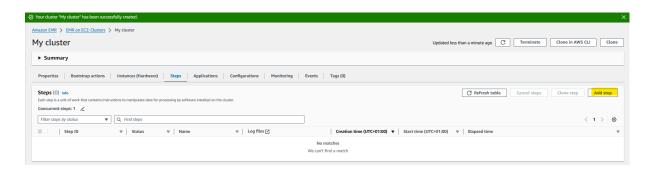


After created, the cluster can take some minutes to start. When creating a cluster, the logs of that cluster will be saved in an s3 bucket automatically created.

With the configuration selected, we have specified 3 nodes (primary, code and task):

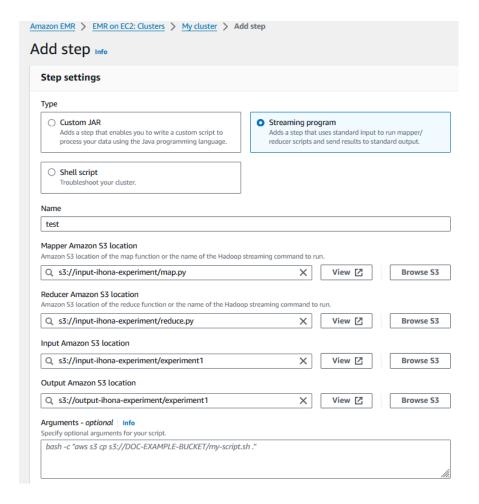


The next step is to prepare the job to be run. For that, we need to add a step to the cluster:



When creating the step, we have to select the "streaming program" because in this way we will be able to use the standard input (remember that tmap.py and reduce.py read and write in the standard input). Besides the streaming program, we specify:

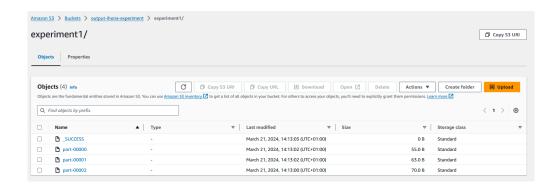
- The mapper (map.py), located in the input bucket.
- The reducer (reduce.py), also located in the input bucket.
- The bucket where the dataset is located.
- The output bucket to store the results. It is really customizable, we can specify that in the output file, it should create a new folder named "experiment1" to store there the results.



We save the task:



Once the task has finished, it stores the result in the bucket specified:



It is possible to see that the MapReducer has created inside the output bucket a folder named experiment1 and it has stored there the results. There are 3 results (or parts), because we have a cluster with 3 nodes.

If we open one of the files we can see the count for each country:

CELL	40	
CEU	49	
ESN	53	
FIN	38	
ITU	59	
KHV	46	
MSL	42	
PJL	48	
pop	1	

4. VISUALIZE RESULTS WITH JUPYTER NOTEBOOK

Finally, we will visualize the results of the MapReducer in a jupyter notebook inside an EC2 instance.

To do that, we first need to connect from our terminal, via SSH, to that EC2 instance. Then, we activate our Python environment, which has Jupyter already installed. Afterwards, we open jupyter from the terminal by running the following command:

After that, we can access jupyter via the Public IPv4 DNS of the instance, specifying the port :8888 and entering the token received in the terminal.

Since we will have to retrieve the data through the s3 bucket, we have to also run the command "aws configure" and set the aws_access_key_id, aws_secret_access_key and aws_session_token to grant access for different AWS services to interact.

Once everything is set, we create a new notebook, install and import the necessary libraries and set the destination where our results from the MapReducer were saved:

```
[2]: #!pip install boto3
    #!pip install pandas

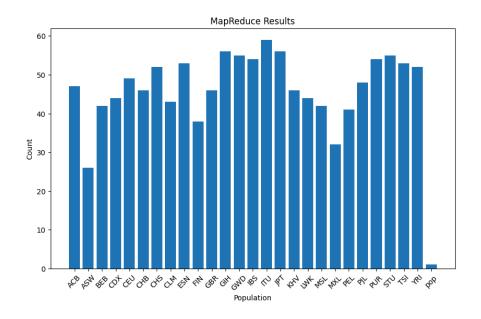
[4]: import boto3
    import matplotlib.pyplot as plt
    import pandas as pd

[10]: s3 = boto3.client('s3',region_name='us-east-1')
    # Define the S3 bucket name and prefix
    bucket_name = 'output-ihona-experiment'
    prefix = 'experiment1'
```

Then, we get a list of all object keys in the bucket with the specified prefix and initialize an empty list to store the data. The code loops through the object keys and reads the data into a list. Afterwards, we parse the line into the population and count columns.

Finally, the data is transformed into a dataframe, we group the data by the population column and sum the count column.

We can create a bar plot with the results:



5. REFERENCES

This exercise was proposed and provided by Jordi Mateo, professor of the subject High Performance and Distributed Computing for Big Data (URV).

https://github.com/JordiMateoUdL