# **Health Care POC**

# **Objective:**

To study data processing of Patient's Data.

# **Input Data:**

Pdf File (With over 3000 Records)

# **Input Data Format:**

PATIENTID PATINENT\_NAME AGE GENDER DISEASE\_INFO HOSPITALNAME ADMITED\_DATE ADDRESSOFPATIENT

Eg: (Tab Separated Records)

100001 SarathSexsena 39 Male Cancer CareHospital 2015-15-04 2ndCross,BTRoad,Mumbai

## Task:

## Task 1: Use MapReduce Code

The input data from pdf is to extracted and placed into 5 different files according to following conditions:

If Patient Age > 35 and Gender is 'Male'

- And if DISEASE\_INFO is Cancer or TB then store the details in "EmergencyCareSection" file.
- And if ADMITED\_DATE is in BETWEEN 2015-04-01 to 2015-07-31 then store the details in "SeasonalCareSection" file.

If Patient Age >50 and Gender is 'Male' or 'Female'

- And if Address is 'Jarkhand' then store the details in "DengueCareSection" file.
- And if ADMITED\_DATE is in BETWEEN 2015-09-01 to 2015-12-31 then store the details in 'WinterSeasonalCareSection' file.

#### Else

Store the details in "GeneralCareSection" file.

## **Task 2: Use Pig Script to write Pig Commands**

Develop a PIG Script to filter the Map Reduce Output in the below fashion

- Store Unique data in a HDFS Directory.
- Sort the Unique data based on PatientID and Store it in a different HDFS Directory.

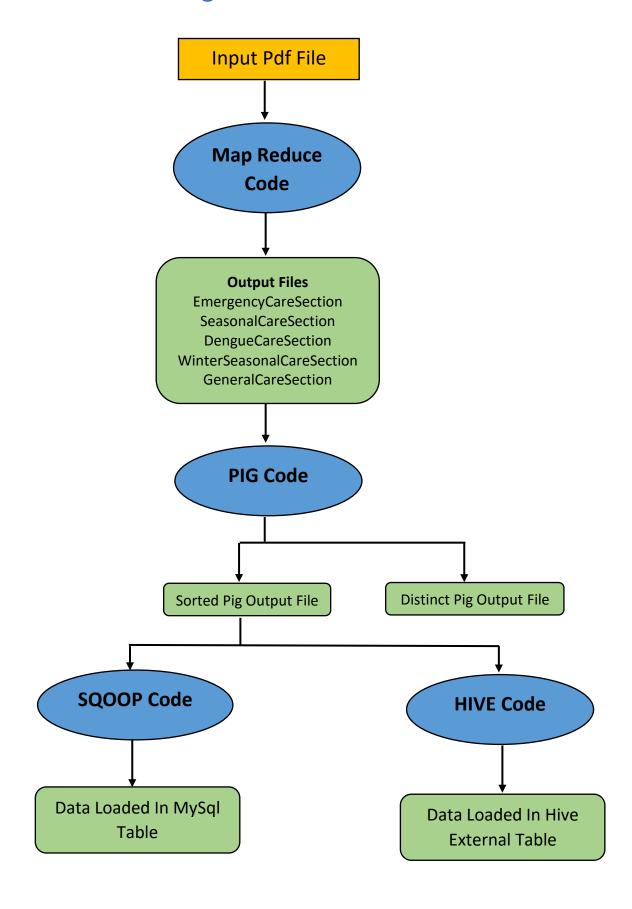
## **Task 3: Use Sqoop Commands**

EXPORT the same PIG Sorted Output from HDFS to MySQL using SQOOP.

## Task 4: Use Hive Commands

Store the same PIG Sorted Output in a HIVE External Table.

# **Architectural Flow Diagram:**



# **Technical Deployment:**

The whole Use Case is executed by executing the script file "healCarePoc.sh", provided the input file "InputPdfPoc1.pdf", Pig Script "HealthCarePoc.pig", and the Jar file "PdfProcessing.jar" of MapReduce Job is present in the same directory as that of the Script.

The commands used inside this script are explained below:

#### Some variables used are initializes first:

## #Input File Detail

inputFileName=InputPdfPoc1.pdf

#### **#DataBase And Tables Created**

mysqlDbName=health\_db mysqlTableName=health\_tab hiveDbName=health\_care\_db hiveTableName=health\_care\_tab

## #Input and Output HDFS Location Names

InputPdfLocation=/Poc1Input
MRLogLocation=/HealthCareLog
MROutputLocation=/HealthCareOut
PigDistinctOutputLocation=/PigDistinctOut
PigSortOutputLocation=/PigSortOut

## **#Mysql Connection Details**

mysqlUser=root mysqlPass=root

#### **Actual Code:**

## #Removing HDFS Directories

hadoop fs -rmr \$PigDistinctOutputLocation \$PigSortOutputLocation \$InputPdfLocation

This code will remove the mentioned directories enabling us run the same Use Case on a machine again and again, without getting an error that "Directory already exists".

### #Placing Input Pdf File On HDFS

hadoop fs -mkdir \$InputPdfLocation hadoop fs -put InputPdfPoc1.pdf \$InputPdfLocation

To run our "**Task 1**" which is execution of a MapReduce job using a Jar file, we first need our input file to be on HDFS location. Thus this code will create a directory on HDFS and then place the input file into this directory.

## #Running MapReduce Job

hadoop jar PdfProcessing.jar com/pdfprocess/poc1/PdfDriver \$InputPdfLocation/\$inputFileName \$MRLogLocation \$MROutputLocation

This MapReduce Job perform our "Task 1", which is extracting the data from pdf file according to the given conditions and place them in respective 5 files.

## #Running Pig Script

pig -p Input=\$MROutputLocation/\* -p DistinctLoc=\$PigDistinctOutputLocation -p SortLoc=\$PigSortOutputLocation HealthCarePoc.pig

This code will perform out "Task 2".

This code will run the mentioned pig script, which will filter the distinct data from the output of MapReduce Job and then will Sort the filtered data according to Patient\_Id and will store this in a HDFS location.

### The content of Pig Script is described below:

```
inputData = load '$Input' using PigStorage('\t');
```

Above line will load the data, which is the output of MapReduce Job, into a variable *inputData*.

```
distinctData = DISTINCT inputData;
```

Above code will load the Distinct data of variable *inputData* into the variable *distinctData*.

```
sortData = ORDER distinctData BY $0:
```

Above code will load the data present in *distinctData* variable after Sorting it by Patient\_Id into the variable *sortData*.

```
store distinctData into '$DistinctLoc';store sortData into '$SortLoc';
```

Above code will Store the data in the variables distinctData and sortData into the mentioned HDFS directories.

## #Creating MySql Table

```
mysql -u $mysqlUser -p$mysqlPass << EOF
drop database if exists $mysqlDbName;
create database $mysqlDbName;
create table $mysqlDbName.$mysqlTableName(
pid int, pname varchar(20), page int, pgender varchar(6),
pdisease varchar(10), hname varchar(20), adate varchar(10),
paddress varchar(30));
grant all privileges on $mysqlDbName.* to "@'localhost';
EOF
```

The above code is the prerequisit of our "Task 3".

Yes, before exporting the data into a MySql table, first we need to have a table. This code will first delete the database of MySql if it already exists and then will create the database and the table inside that database.

## #Exporting Pig Output to MySql Table

```
sqoop export --connect jdbc:mysql://localhost/$mysqlDbName --table $mysqlTableName --fields-terminated-by '\t' --export-dir $PigSortOutputLocation/part*;
```

This code will perform our "Task 3", that is it will export the output of Task 2, that also the sorted output, into the MySql table created above.

## #Exporting Pig Output to Hive Table

```
hive << EOF
drop database if exists $hiveDbName cascade;
create database $hiveDbName;
create external table $hiveDbName.$hiveTableName(pid int,pname string,page int,pgender
string,pdisease string,
hname string,adate string,paddress string)
row format delimited
fields terminated by '\t'
lines terminated by '\n'
stored as textfile location '$PigSortOutputLocation';
FOF
```

The above code will perform our "Task 4". This code will create a hive table, and then will load the Sorted Output of Task 2 (that is pig script execution task), into this hive table.

## At the end we will have the following things:

- 1. 5 Output files of MapReduce Job in a HDFS Directory.
- 2. 2 Output files of Pig Script execution.
- 3. A MySql table with Sorted output of Pig task loaded in it.
- 4. A Hive table with Sorted output of Pig task loaded in it.

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