ASSESSMENT REPORT

ON

Big Data Tools & Techniques

Submitted by

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Big Data Tools & Techniques

For

MASTER OF SCIENCE IN ARTIFICIAL INTELLIGENCE

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TASK 1

ANALYSIS OF THE CLINICAL TRIAL AND PHARMA DATASET

INTRODUCTION

In today's digital world, we deal with a lot of data. This brings both opportunities and challenges for businesses. The increasing number of devices like smartphones and computers results in a larger amount of data being generated. Smart devices can provide insights into people's behaviors. To manage this growing volume of data, specialized tools and methods have been developed. They help collect, store, analyze, and show data, often in real-time. These tools let businesses find important insights hidden in big datasets. This era marks a transition from an Informational Society to a Knowledge-Based Society, where the strategic utilization of big data plays a pivotal role. (Youssra et al, 2018).

The analysis will use PySpark methods in RDDs and DataFrames, followed by SQL queries. PySpark is a Python library for large-scale data processing that works well with distributed systems like Apache Spark, allowing parallel computation across multiple nodes. It helps process extensive datasets quickly and efficiently. RDDs are foundational in PySpark, representing distributed object collections processed in parallel, with fault tolerance for seamless recovery from failures. DataFrames organize data in tabular form for structured manipulation. SQL, a common language for database operations, allows analysts to query, filter, and aggregate data efficiently. PySpark enhances SQL operations by offering an SQL interface for RDDs and DataFrames.

Data Cleaning and Preparation

The investigation revealed null values in the Clinical Trials and Pharma CSV files. Removing these nulls might distort analysis results by also eliminating non-null values. These files were imported into the Databricks filesystem, and a notebook was generated, considering the implementation approach (SQL or Python). The listed process was carried out during data cleaning and preparation.

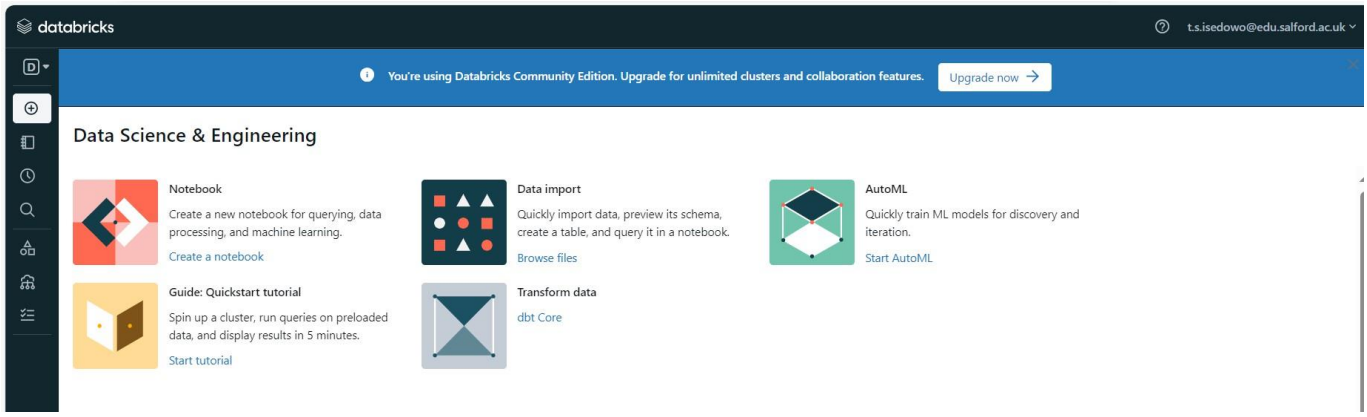
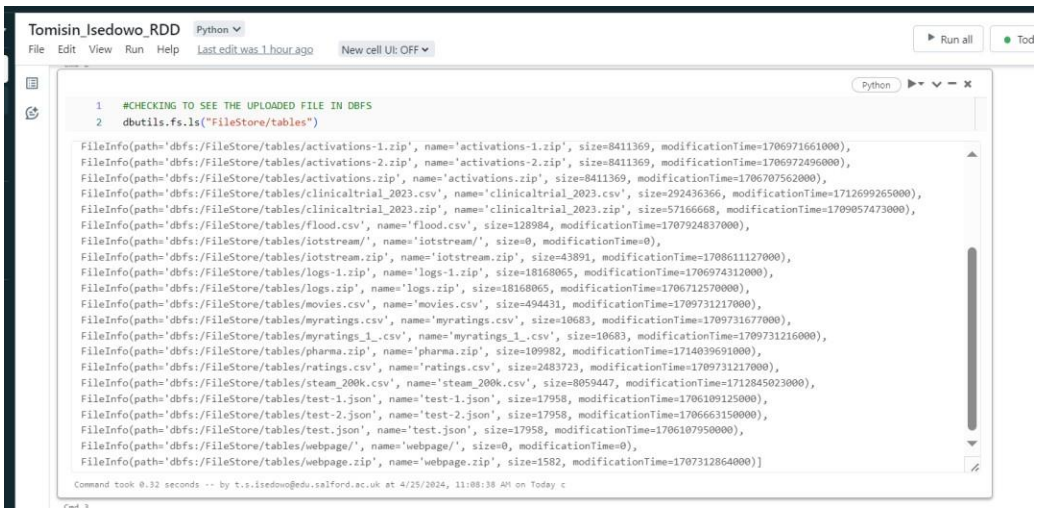


Fig 1: Databricks Environment

The utilization of the ‘dbutils.fs.ls’ function was pivotal in assessing the presence of the imported CSV files. Upon examination, it was noted that the clinical trials CSV files were successfully uploaded.



This line of code sets an environment variable named "fileroot" to the value stored in the variable fileroot. Environment variables are key-value pairs that can be accessed by programs running on a computer. They provide a way to customize the behavior of programs and scripts without modifying their code directly. In this case, the code appears to be assigning a value to an environment variable named "fileroot" using the Python os.environ module. The value assigned to "fileroot" is taken from the variable fileroot, which should be defined elsewhere in the code. This allows other parts of the program or scripts to access the value of "fileroot" using os.environ['fileroot'].

```
Cmd 2
#remove clinical trial csv should in case it is available
dbutils.fs.rm("/FileStore/tables/clinicaltrial_2023.csv")
#declare a variable called fileroot
fileroot = "clinicaltrial_2023"
# copy the file to the local cluster to unzip the file
dbutils.fs.cp("/FileStore/tables/" + fileroot + ".zip", "file:/tmp/")

Out[2]: True

Command took 1.62 seconds -- by t.s.isedowo@edu.salford.ac.uk at 5/2/2024, 12:40:39 AM on Task1
Cmd 3
import os
os.environ['fileroot'] = fileroot

Command took 0.13 seconds -- by t.s.isedowo@edu.salford.ac.uk at 5/2/2024, 12:40:47 AM on Task1
Cmd 4
```

Moreso, the existence of the CSV file was checked, and some actions were performed based on its presence.

The existence of the file with the name "${fileroot}.csv" was confirmed in the "/tmp" directory. "${fileroot}" is a variable that holds a filename prefix.

If the CSV file exists, the condition [-f "/tmp/${fileroot}.csv"] evaluates to true, the script proceeds to remove it using the rm command.

Then, the script unzips a file located at "/tmp/${fileroot}.zip" and extracts its contents into the "/tmp" directory using the unzip command with the -d flag specifying the target directory.

```
Cmd 4
%sh
# Check if the CSV file exists
if [ -f "/tmp/${fileroot}.csv" ]; then
    # If the CSV file exists, remove it
    rm "/tmp/${fileroot}.csv"
fi

# Unzip the ZIP file
unzip -d "/tmp" "/tmp/${fileroot}.zip"

Archive:  /tmp/clinicaltrial_2023.zip
  inflating: /tmp/clinicaltrial_2023.csv

Command took 2.44 seconds -- by t.s.isedowo@edu.salford.ac.uk at 5/2/2024, 12:41:04 AM on Task1
Cmd 5
dbutils.fs.cp("file:/tmp/" + fileroot + ".csv", "/FileStore/tables")

Out[5]: True

Command took 20.35 seconds -- by t.s.isedowo@edu.salford.ac.uk at 5/2/2024, 12:41:12 AM on Task1
Cmd 6
```

myRDD1 is a Resilient Distributed Dataset (RDD) created by reading a CSV file located at "FileStore/tables/clinicaltrial_2023.csv" using the sc.textFile() function. Each line in the CSV file becomes an element in myRDD1. It undergoes various Spark operations like map(), filter(), and reduce() to preprocess rows, ensuring consistent formatting and addressing discrepancies in column lengths. Then, a map transformation is applied again to create myRDD2, retaining only the original elements without the indexThe take(5) action is then called on myRDD2 to retrieve the first 5 elements of the RDD,

```python
#THIS COMMAND HELP TO READ THE CSV FILE AS AN RDD
myRDD1= sc.textFile("FileStore/tables/clinicaltrial_2023.csv")
```

Command took 0.91 seconds -- by t.s.isedowo@edu.salford.ac.uk at 4/28/2024, 8:11:25 AM on sunday

Cmd 8

```python
#THIS COMMAND ASSISTS IN DEFINING A FUNCTION DEDICATED TO CLEANING AND TRANSFORMING INDIVIDUAL ROWS WITHIN THE CLINICALTRIAL DATASET
def clean_and_transform(row):
    #THIS AIDS IN ELIMINATING SURPLUS TRAILING COMMAS AND UNNECESARY DOUBLE QUOTES THROUGH THE UTILIZATION OF THE STRIP METHOD.
    cleaned_row = row.strip(",").strip('"')
    #THIS COMMAND FACILITATES THE SPLITTING OF THE ROW BY THE SPECIFIED DELIMITER, WHICH IN THIS CASE IS THE TAB ('\t').
    cleaned_row = cleaned_row.split('\t')

    return cleaned_row

# RDD containing rows with varying column lengths

def fill_empty_columns(row):
    # Check if the row has less than 14 columns
    if len(row) < 14:
        # Fill up the remaining columns with empty strings
        row += [''] * (14 - len(row))
    return row


```

Command took 0.14 seconds -- by t.s.isedowo@edu.salford.ac.uk at 4/28/2024, 8:14:38 AM on sunday

Cmd 9

Python

```python
#THIS COMMAND MAP THE CLEAN_AND_TRANSFORM FUNCTION TO myRDD2.
myRDD2 = myRDD1.map(clean_and_transform) \
      .map(fill_empty_columns)\
     .zipWithIndex().filter(lambda x: x[1] > 0).map(lambda x: x[0])

myRDD2.take(5)
```

The function replace_empty_with_null takes a list as input. It uses a list comprehension to iterate over each field in the input list. If a field is an empty string (""), it replaces it with the Python keyword "None" to indicate a null value. Otherwise, the field remains unchanged. This function is then applied to each element of an RDD called "myRDD2" using the "map" transformation. Two other functions are also defined.The clean_date(date) function appends "-01" to short date strings to complete them, returning the modified or original date.The fill_empty_date(date, default_value) function returns the default value if the date string is empty; otherwise, it returns the original date string.

```python
# Function to replace empty strings with None
def replace_empty_with_null(line):
    return [None if field == "" else field for field in line]

# Replace empty fields with null values
replace_with_null = myRDD2.map(replace_empty_with_null)
```

Command took 0.14 seconds -- by t.s.isedowo@edu.salford.ac.uk at 4/28/2024, 8:17:38 AM on sunday

Cmd 11

Python

```python
def clean_date(date):
    if len(date) < 8:
        date = date + "-01"
    return date

def fill_empty_date(date, default_value):
    return default_value if not date else date

# Select the column indices
column_indices = [12, 13]

# Clean up the start and completion dates
default_date = "2024-01-01"

# First RDD: Fill up empty date columns
myRDD3 = replace_with_null.map(lambda row: [
    fill_empty_date(row[i], default_date) if i in column_indices else row[i] for i in range(len(row))
])

# Second RDD: Format the date columns
myRDD4 = myRDD3.map(lambda row: [
    clean_date(row[i]) if i in column_indices else row[i] for i in range(len(row))
])

myRDD4.take(5)
```

(1) Spark Jobs

STATEMENT OF PROBLEM ONE

GETTING THE NUMBER OF STUDIES IN THE CLINICAL TRIAL DATASET

ASSUMPTION MADE

It was assumed that the" Id" serves as the unique identifier in the clinical trial dataset, it is being utilized to ascertain the number of studies contained within the dataset. This approach suggests prioritizing the Id over the study title for its distinctiveness and reliability in accurately representing each study entry.

IMPLEMENTATION IN RESILIENT DISTRIBUTED SYSTEM (RDD)

The implementation counts the number of studies in myRDD4, an RDD with study data. It extracts unique study IDs, removes duplicates, and counts them using the distinct().count() function. This is a typical operation in big data processing for distributed datasets. In this case, it reveals that there are 483,422 distinct studies in the clinical trial dataset of 2023.

```
#Q1 IMPLEMENTATION IN RDD

# Extract Id
Id_rdd =myRDD4.map(lambda x: x[0])

# Count the total number of Id

distinct_Id = Id_rdd.distinct().count()

print("Number of Studies: ", distinct_Id)
```

```
(1) Spark Jobs
Number of Studies:  483422
```

IMPLEMENTATION IN DATAFRAME

The DataFrame was made with PySpark, a Python tool for Apache Spark, a distributed data processing system. We imported modules like pyspark.sql.types for data type definitions. We converted an RDD (myRDD4) to a DataFrame (Clinicaltrial_df) using a preset schema (mySchema). In Spark, it's typical to use DataFrames for organized and efficient distributed data handling.

```python
#Using Dataframe
from pyspark.sql.types import*

mySchema = StructType([
            StructField("Id", StringType()),
            StructField("Study Title", StringType()),
            StructField("Acronym", StringType()),
            StructField("Status", StringType()),
            StructField("Conditions", StringType()),
            StructField("Interventions", StringType()),
            StructField("Sponsor", StringType()),
            StructField("Collaborators", StringType()),
            StructField("Enrollment", StringType()),
            StructField("Funder Type", StringType()),
            StructField("Type", StringType()),
            StructField("Study Design", StringType()),
            StructField("Start", StringType()),
             StructField("Completion", StringType()),
])


Clinicaltrial_df =spark.createDataFrame(myRDD4, mySchema)

Clinicaltrial_df.show(5)
```

(1) Spark Jobs

Clinicaltrial_df: pyspark.sql.dataframe.DataFrame = [Id: string, Study Title: string ... 12 more fields]

```
+-----------+-----------------+---------+-----------------+-----------------+-----------------+-----------------+-----------+---------+-----------+-----------------+----------+----------+
|         Id|         Study Title|   Acronym|           Status|          Conditions|       Interventions|            Sponsor|       Collaborators|Enrollment|Funder Type|          Type|        Study Design|     Start|Completion|
+-----------+-----------------+---------+-----------------+-----------------+-----------------+-----------------+-----------+---------+-----------+-----------------+----------+----------+
|NCT03630471|Effectiveness of ...|     PRIDE|        COMPLETED|Mental Health Iss...|BEHAVIORAL: PRIDE...|           Sangath|Harvard Medical S...|     250.0|      OTHER|INTERVENTIONAL|Allocation: RANDO...|2018-08-20|2019-02-28|
|NCT05992571|Oral Ketone Monoe...|      null|       RECRUITING|Cerebrovascular F...|OTHER: Placebo|DI...| McMaster University|Alzheimer's Socie...|      30.0|      OTHER|INTERVENTIONAL|Allocation: RANDO...|2023-10-25|2024-08-01|
|NCT00237471|Impact of Tight G...|      null|       TERMINATED|Myocardial Infarc...|DRUG: Insulin (ti...|   Melbourne Health|National Health a...|      40.0|      OTHER|INTERVENTIONAL|Allocation: RANDO...|2005-10-01|2006-05-01|
|NCT03820271|New Prognostic Pr...| SUPERMELD|       RECRUITING|Decompensated Cir...|    OTHER: SuperMELD|Assistance Publiq...|      null|     500.0|      OTHER|INTERVENTIONAL|Allocation: NA|In...|2020-10-01|2023-10-01|
|NCT06229171|InTake Care: Deve...|InTakeCare|NOT_YET_RECRUITING|Hypertension|Trea...|OTHER: adherence ...|Istituto Auxologi...|Istituti Clinici ...|     206.0|      OTHER|INTERVENTIONAL|Allocation: RANDO...|2024-10-01|2026-04-01|
+-----------+-----------------+---------+-----------------+-----------------+-----------------+-----------------+-----------+---------+-----------+-----------------+----------+----------+
only showing top 5 rows
```

Command took 4.53 seconds -- by t.s.isedowo@edu.salford.ac.uk at 4/28/2024, 8:49:16 AM on sunday

Then "Id" column from the DataFrame, removes duplicate Ids, and then counts the number of unique Ids, providing a count of distinct studies present in the DataFrame.

Cmd 10

```python
collect_Id_rdd = Clinicaltrial_df.select("Id")

# Count the number of distinct study titles
distinct_study_count = collect_Id_rdd.distinct().count()

# Print result
print("Number of Studies: ", distinct_study_count)
```

(3) Spark Jobs

collect_Id_rdd: pyspark.sql.dataframe.DataFrame = [Id: string]

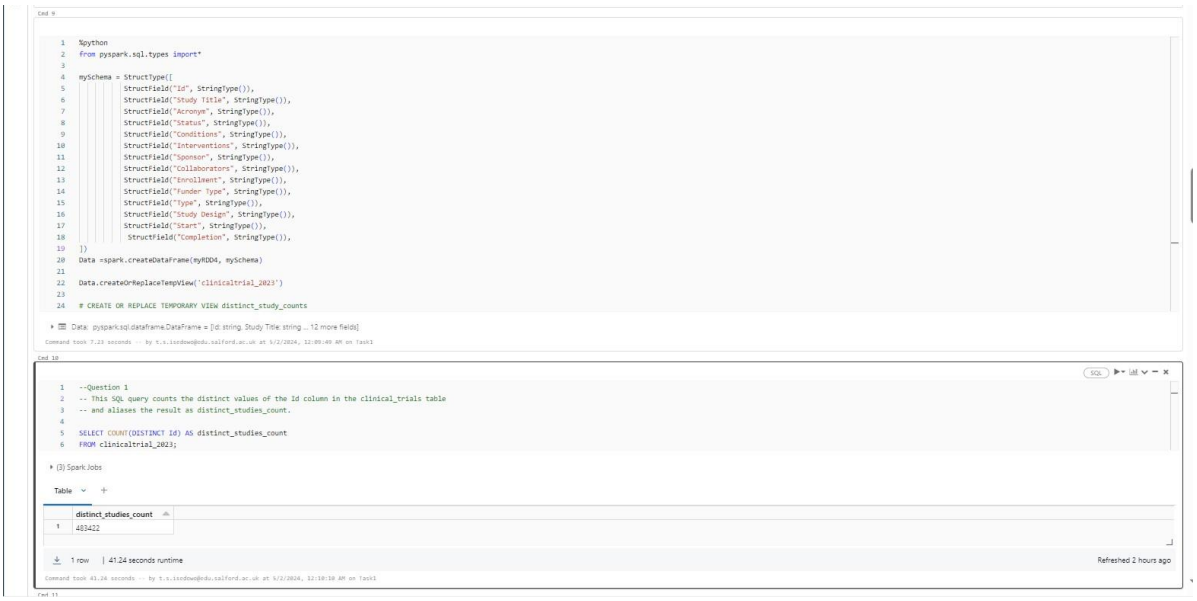
```
Number of Studies:  483422
```

Command took 20.14 seconds -- by t.s.isedowo@edu.salford.ac.uk at 5/2/2024, 12:36:36 AM on Task1

Cmd 11

IMPLEMENTATION IN SQL

The code converts RDD myRDD4 into a DataFrame Clinicaltrial_df using schema mySchema. Using DataFrame is common in Spark for structured and optimized data handling. A temporary view called clinicaltrial_2023 is created from Clinicaltrial_df for Spark SQL operations. The SQL query retrieves the count of distinct values in the "Id" column from the clinicaltrial_2023 table, assigning the result the alias "distinct_studies_count".



```python
%python
from pyspark.sql.types import*

mySchema = StructType([
            StructField("Id", StringType()),
            StructField("Study Title", StringType()),
            StructField("Acronym", StringType()),
            StructField("Status", StringType()),
            StructField("Conditions", StringType()),
            StructField("Interventions", StringType()),
            StructField("Sponsor", StringType()),
            StructField("Collaborators", StringType()),
            StructField("Enrollment", StringType()),
            StructField("Funder Type", StringType()),
            StructField("Type", StringType()),
            StructField("Study Design", StringType()),
            StructField("Start", StringType()),
             StructField("Completion", StringType()),
])
Data =spark.createDataFrame(myRDD4, mySchema)

Data.createOrReplaceTempView('clinicaltrial_2023')

# CREATE OR REPLACE TEMPORARY VIEW distinct_study_counts
```

Data: pyspark.sql.dataframe.DataFrame = [Id: string, Study Title: string ... 12 more fields]

Command took 7.23 seconds -- by t.s.isedowo@edu.salford.ac.uk at 5/2/2024, 12:09:40 AM on Task1

```sql
--Question 1
-- This SQL query counts the distinct values of the Id column in the clinical_trials table
-- and aliases the result as distinct_studies_count.

SELECT COUNT(DISTINCT Id) AS distinct_studies_count
FROM clinicaltrial_2023;
```

(3) Spark Jobs

Table

	distinct_studies_count
1	483422

1 row | 41.24 seconds runtime

Refreshed 2 hours ago

Command took 41.24 seconds -- by t.s.isedowo@edu.salford.ac.uk at 5/2/2024, 12:10:10 AM on Task1

DISCUSSION OF THE RESULT

In our analysis, we used three methods to extract and count distinct studies from a clinical trial dataset represented in RDD, DataFrame, and SQL formats within the Spark framework. Despite employing different approaches, all yielded consistent results, showcasing Spark's reliability across different abstraction levels, from RDD to SQL queries.

STATEMENT OF PROBLEM TWO

LIST OF ALL TYPES OF CLINICAL TRIAL 2023 DATASET AND THEIR FREQUENCIES FROM THE MOST FREQUENT TO THE LEAST FREQUENT

ASSUMPTION MADE

It was assumed that the RDD (myRDD4) contains rows of data, each with a 'Type' field indicating a certain category. The goal of the operation is to determine the frequency of occurrence of each unique type within the RDD. This will show the number of times the unique type occurs in the dataset.

IMPLEMENTATION IN RDD

The process begins by extracting the 'Type' field from each row of RDD (myRDD4) and creating key-value pairs, where the key represents the 'Type', and the value is 1, indicating one occurrence of each type.

Next, a reduction by key operation (reduceByKey) is performed to aggregate the counts for each type. The frequencies of each type are then sorted in descending order based on their occurrence frequency. Finally, the sorted frequencies are collected into a list, providing a sorted list of types with their respective frequencies.

```python
#Q2 IMPLEMENTATION IN RDD
# Extract 'Type' field and create key-value pairs
type_counts_rdd = myRDD4.map(lambda row: (row[10], 1))

# get the frequencies of reach type
type_frequency = type_counts_rdd.reduceByKey(lambda x, y: x + y)

# Sorting the result by frequency in descending order
sorted_frequencies = type_frequency.sortBy(lambda x: x[1], ascending=False)

sorted_frequencies.collect()
```

```
(3) Spark Jobs
Out[32]: [('INTERVENTIONAL', 371382),
 ('OBSERVATIONAL', 110221),
 ('EXPANDED_ACCESS', 928),
 (None, 891)]
Command took 12.81 seconds -- by t.s.isedowo@edu.salford.ac.uk at 4/28/2024, 8:27:19 AM on sunday
```

Cmd 14

IMPLEMENTATION IN DATAFRAME

This snippet helps to count the occurrences of each unique value in the "Type" column of a DataFrame (Clinicaltrial_df), sort the counts in descending order, and display the results. This from command pyspark.sql.functions import col, helps to import the col function from pyspark.sql.functions which is used to create a Column object representing a column in a DataFrame. The groupBy(). Count() function helps to group the DataFrame by the "Type" column and counts the number of occurrences of each unique value in the "Type" column.

```python
#Question 2
from pyspark.sql.functions import col

type_counts_df = Clinicaltrial_df.select(col("Type").alias("Type")).groupBy("Type").count()

# Sorting the result by frequency in descending order
sorted_frequencies_df = type_counts_df.orderBy("count", ascending=False)

sorted_frequencies_df.show()
```

```
(2) Spark Jobs
type_counts_df: pyspark.sql.dataframe.DataFrame = [Type: string, count: long]
sorted_frequencies_df: pyspark.sql.dataframe.DataFrame = [Type: string, count: long]
+---------------+------+
|           Type| count|
+---------------+------+
| INTERVENTIONAL|371382|
|  OBSERVATIONAL|110221|
|EXPANDED_ACCESS|   928|
|           null|   891|
+---------------+------+

Command took 20.18 seconds -- by t.s.isedowo@edu.salford.ac.uk at 4/28/2024, 8:46:28 AM on sunday
```

IMPLEMENTATION IN SQL

The SQL query effectively analyzes the table to identify the distribution of studies across various types. It groups studies by type and calculates the frequency of each type, providing insights into the most prevalent study categories within the dataset. The snippet retrieves the count of occurrences of each unique value in the Type column from the clinicaltrial_2023 table and presents the results in descending order of count.

```sql
-- Question 2
SELECT
    Type,
    COUNT(*) AS count
FROM
    clinicaltrial_2023
GROUP BY
    Type
ORDER BY
    count DESC;
```

(2) Spark Jobs

Table

	Type	count
1	INTERVENTIONAL	371382
2	OBSERVATIONAL	110221
3	EXPANDED_ACCESS	928
4	null	891

4 rows | 23.99 seconds runtime

Refreshed 2 hours ago

DISCUSSION OF THE RESULT

The analysis showed the same results across three methods: RDD, DataFrame, and SQL. They all found the top 5 types of studies and how often they appear. Types like INTERVENTIONAL, OBSERVATIONAL, and EXPANDED_ACCESS give us a good idea of how common different kinds of clinical research are. Seeing "None" shows us we might need to check the data's quality. Getting consistent results from different methods makes us more confident that our findings are reliable. This helps make better decisions in healthcare and research.

STATEMENT OF PROBLEM THREE

LIST OF THE TOP 5 CONDITIONS AND THEIR PREQUENCY OF OCCURRENCE

ASSUMPTION MADE

Prior to performing the extraction, splitting, and counting operation on the 'Conditions' column of the RDD, it is assumed that the RDD (`myRDD4`) contains rows where each row represents a record, and the 'Conditions' column in each row is a string consisting of multiple conditions separated by the '|' character. Additionally, it is assumed that the RDD is structured such that the first element of each row uniquely identifies the record, and the fifth element contains the 'Conditions' column. This assumption is necessary for the subsequent operations to effectively extract and process the relevant data.

IMPLEMENTATION IN RDD

This script extracts values from the 'Conditions' column of an RDD, splits them by '|' character, counts each condition's occurrences, and sorts them in descending order. It then retrieves the top 5 most frequent conditions. First, a maps function is used to map each row of myRDD4 to a tuple containing the first and fifth elements of the row, where row[0] holds a unique identifier and row[4] holds the 'Conditions' column. Next, the split string function is applied to each element of the RDD from the previous step. This step flattens the resulting list of lists into a single list. Finally, reduceByKey is used to sum up the values (counts) for each key (condition) in the RDD.

Python

```python
#Q3 IMPLEMENTATION IN RDD
# Step 1: Extract the 'Conditions' column

def split_string(text):
    if text and text != '':
        return text.split('|')
    return ''

conditions_rdd = myRDD4.map(lambda row: (row[0],row[4])).flatMap(lambda x: split_string(x[1])).map(lambda x: (x,1)).reduceByKey(lambda a,b: a+b)
sorted_rdd = conditions_rdd.sortBy(lambda x: x[1], ascending=False)
# filter_cond_rdd = conditions_rdd.filter(lambda x: x == '')

sorted_rdd.take(5)
```

(3) Spark Jobs

```
Out[33]: [('Healthy', 9731),
 ('Breast Cancer', 7502),
 ('Obesity', 6549),
 ('Stroke', 4071),
 ('Hypertension', 4020)]
```

Command took 15.81 seconds -- by t.s.isedowo@edu.salford.ac.uk at 4/28/2024, 8:27:37 AM on sunday

Cmd 15

IMPLEMENTATION IN DATAFRAME

In PySpark DataFrame analysis of clinical trial data, we start by importing necessary functions from pyspark.sql.functions. Then, we select only the 'Id' and 'Conditions' columns from the DataFrame Clinicaltrial_df, filtering out rows with null or empty 'Conditions'. Next, we explode the array into separate rows, duplicating the 'Id' column for each condition. After that, we group the DataFrame by 'Conditions' and count the occurrences of each condition, displaying the top 5 most frequent ones in descending order.

```python
#Question 3
from pyspark.sql.functions import split, explode, col, lit

# Split the string by '|' delimiter if it's not empty
# Then, explode the resulting array into separate rows
# Finally, count the occurrences of each element
conditions_df = Clinicaltrial_df.select(Clinicaltrial_df['Id'], Clinicaltrial_df['Conditions']) \
                                .filter(col('Conditions').isNotNull() & (col('Conditions') != '')) \
                                .withColumn('Conditions', split(col('Conditions'), '\|')) \
                                .withColumn('Conditions', explode(col('Conditions'))) \
                                .groupBy('Conditions').count()

# Sort the DataFrame by count in descending order
sorted_df = conditions_df.orderBy(col('count').desc())

# Take the top 5 rows from the sorted DataFrame
top_5_rows = sorted_df.limit(5)

# Show the top 5 elements
top_5_rows.show()
```

```
(2) Spark Jobs
conditions_df: pyspark.sql.dataframe.DataFrame = [Conditions: string, count: long]
sorted_df: pyspark.sql.dataframe.DataFrame = [Conditions: string, count: long]
top_5_rows: pyspark.sql.dataframe.DataFrame = [Conditions: string, count: long]

+-------------+-----+
|   Conditions|count|
+-------------+-----+
|      Healthy| 9731|
|Breast Cancer| 7502|
|      Obesity| 6549|
|       Stroke| 4071|
| Hypertension| 4020|
+-------------+-----+

Command took 23.39 seconds -- by t.s.isedows@edu.salford.ac.uk at 5/2/2024, 12:38:02 AM on Task1
```

IMPLEMENTATION IN SQL

This SQL query identifies the top 5 most common conditions mentioned in a clinical trials dataset along with their counts. It uses a CTE called condition_counts to explode the Conditions column, separating multiple conditions with a delimiter '|'. Then, it counts occurrences of each condition using COUNT(*) and groups them by condition, ordering the results by count in descending order and limiting output to the top 5 conditions.

```sql
--Question 3
-- It first line explodes the 'Conditions' column by '|' delimiter, to separate each condition and filters out non-empty and non-null values.
-- Then, it counts the occurrences of each condition and groups the results by condition.
-- Finally, it selects the top 5 conditions based on the count of occurrences, sorting them in descending order.
WITH condition_counts AS (
    SELECT
        condition,
        COUNT(*) AS count
    FROM (
        SELECT
            Id,
            explode(split(Conditions, '\\|')) AS condition
        FROM
            clinicaltrial_2023
        WHERE
            Conditions IS NOT NULL AND Conditions != ''
    ) exploded_conditions
    GROUP BY
        condition
)
SELECT
    condition,
    count
FROM
    condition_counts
ORDER BY
    count DESC
LIMIT 5;
```

(2) Spark Jobs

Table

	condition	count
1	Healthy	9731
2	Breast Cancer	7502
3	Obesity	6549
4	Stroke	4071
5	Hypertension	4020

5 rows | 22.84 seconds runtime

Refreshed 2 hours ago

Command took 22.84 seconds -- by t.s.isedown@edu.salford.ac.uk at 5/2/2024, 12:11:29 AM on Task1

DISCUSSION OF THE RESULT

We've identified the top 5 prevalent health conditions in our clinical trial dataset. This information is crucial for healthcare providers, researchers, and policymakers to allocate resources effectively and design interventions. Using RDD, DataFrame, and SQL methods, we ensured consistent results, validating the accuracy of our analysis. This consistency highlights the robustness of our approach in exploring and summarizing the dataset.

STATEMENT OF PROBLEM FOUR

LIST OF THE 10 MOST COMMON SPONSOR THAT ARE NOT PHARMACEUTICAL COMPANIES

ASSUMPTION MADE

To ensure our analysis is reliable, we trust that both the clinical and pharmaceutical datasets are accurately curated, providing a thorough record of clinical studies and pharmaceutical companies. We also assume the pharmaceutical datasets are free from major omissions or biases. Furthermore, we presume the classification of companies as pharmaceutical or non-pharmaceutical is correct according to industry standards and available information. These assumptions are vital for accurately identifying the top ten sponsors that are not pharmaceutical companies.

IMPLEMENTATION IN RDD

The pharmaceutical data file was imported into the Databricks environment. However, the file was in a compressed format which needed to be unzipped. The process of unzipping the file was carried out to ensure its accessibility for further analysis.

```
dbutils.fs.cp("/FileStore/tables/pharma.zip" , "file:/tmp/")

Out[22]: True
Command took 0.34 seconds -- by t.s.isedowo@edu.salford.ac.uk at 4/28/2024, 8:22:47 AM on sunday
Cmd 16
Python
%sh

unzip -d /tmp/  /tmp/pharma.zip

ls /tmp

  inflating: /tmp/pharma.csv
Rserv
RtmpV6V3Ux
chauffeur-daemon-params
```

Then, the pharmaceutical dataset named "pharma.csv" was processed and extraction of the unique pharmaceutical company names was initiated. The sc.textFile() function reads the file line by line and creates an RDD where each line is a string and map() was used to split each line by commas, effectively converting each line into a list of fields. The lambda function was used to remove and strip any leading or trailing double quotation marks from each field in the row, whitespace from each field in the row before he company name was extracted. The distinct () was used to remove duplicate entries from the RDD.

```
Cmd 17
Python
dbutils.fs.cp("file:/tmp/pharma.csv" , "/FileStore/tables")

Out[17]: True
Command took 0.38 seconds -- by t.s.isedowo@edu.salford.ac.uk at 5/2/2024, 12:44:08 AM on Task1
Cmd 18

pharma_rdd = sc.textFile("/FileStore/tables/pharma.csv") \
    .map(lambda line: line.split(",")) \
    .map(lambda row: [field.strip('"') for field in row]) \
    .map(lambda row: [field.strip() for field in row]) \
    .map(lambda x: x[1])

pharma_companies_rdd = pharma_rdd.distinct()

Command took 0.25 seconds -- by t.s.isedowo@edu.salford.ac.uk at 5/2/2024, 12:44:13 AM on Task1
Cmd 19
```

For the implementation, two RDDs are used which is myRDD4 and pharma_companies_rdd. myRDD4 contains data where the 6th element is the identifier for a clinical trial while the pharma_companies_rdd

contains data related to pharmaceutical companies, likely with an identifier field. The data allows for joining clinical trials with pharmaceutical companies based on some relationship. The left outer join was performed between clinicalTrial_pairs and pharma_companies_rdd. In the left outer join, all keys from the left table (clinical trials) are kept, even if there's no match in the right table (pharma companies). The resulting value for unmatched keys in the right table will be None.

Cmd 19

Python

```python
#Q4 IMPLEMEMTATION IN RDD
filtered_col = myRDD4.map(lambda x: x[6])
clinicalTrial_pairs = filtered_col.map(lambda x: (x, 1))
pharma_pairs = pharma_companies_rdd.map(lambda x: (x, 1))

join_rdd = clinicalTrial_pairs.leftOuterJoin(pharma_pairs)

filtered_rdd = join_rdd.filter(lambda x: x[1][1] is None)
result = filtered_rdd.map(lambda x: (x[0], 1)).reduceByKey(lambda a,b: a+b)

result = result.map(lambda x: (x[1], x[0]))

result = result.sortByKey(False).take(10)

print(result)
```

(3) Spark Jobs

```
[(3410, 'National Cancer Institute (NCI)'), (3335, 'Assiut University'), (3023, 'Cairo University'), (2951, 'Assistance Publique
- Hôpitaux de Paris'), (2766, 'Mayo Clinic'), (2702, 'M.D. Anderson Cancer Center'), (2393, 'Novartis Pharmaceuticals'), (2340,
'National Institute of Allergy and Infectious Diseases (NIAID)'), (2263, 'Massachusetts General Hospital'), (2181, 'National Taiw
an University Hospital')]
```

Command took 15.44 seconds -- by t.s.isedowo@edu.salford.ac.uk at 4/28/2024, 8:32:43 AM on sunday

IMPLEMENTATION IN DATAFRAME

For this implementation, the clinical trial sponsors that are not found in the pharma company dataset were filtered out. Then counts the occurrence of each sponsor, sorts the result by count, selects the top 10 sponsors and displays the result. The pharma dataset was read into DBFS and the column ‘c1’ was named Parent_company before joining with the clinical trial dataset.

```python
pharma_data = spark.read.csv("/FileStore/tables/pharma.csv", header=False)

# Rename the column
pharma_df = pharma_data.withColumnRenamed("_c1", "Parent_company")

# Left Anti Join to find entries that exist in Clinical Trial Sponsor but not in Pharma Companies
filtered_df = Clinicaltrial_df.join(pharma_df, Clinicaltrial_df.Sponsor == pharma_df.Parent_company, "left_anti")

# Count occurrences again after filtering
result_df = filtered_df.groupBy("Sponsor").count()

# Sort the result in descending order of counts
sorted_result_df = result_df.orderBy("count", ascending=False)

# Take the top 10 records
top_10_sponsors = sorted_result_df.limit(10)

top_10_sponsors.show()
```

(4) Spark Jobs

pharma_data: pyspark.sql.dataframe.DataFrame = [_c0: string, _c1: string ... 32 more fields]
pharma_df: pyspark.sql.dataframe.DataFrame = [_c0: string, Parent_company: string ... 32 more fields]
filtered_df: pyspark.sql.dataframe.DataFrame = [Id: string, Study Title: string ... 12 more fields]
result_df: pyspark.sql.dataframe.DataFrame = [Sponsor: string, count: long]
sorted_result_df: pyspark.sql.dataframe.DataFrame = [Sponsor: string, count: long]
top_10_sponsors: pyspark.sql.dataframe.DataFrame = [Sponsor: string, count: long]

```
+--------------------+-----+
|             Sponsor|count|
+--------------------+-----+
|National Cancer I...| 3410|
|   Assiut University| 3335|
|    Cairo University| 3023|
|Assistance Publiq...| 2951|
|          Mayo Clinic| 2766|
|M.D. Anderson Can...| 2702|
|Novartis Pharmace...| 2393|
|National Institut...| 2340|
|Massachusetts Gen...| 2263|
|National Taiwan U...| 2181|
+--------------------+-----+
```

Command took 22.22 seconds -- by t.s.isedowo@edu.salford.ac.uk at 4/28/2024, 8:53:37 AM on sunday

Cmd 14

IMPLEMENTATION IN SQL

This SQL code is implementing a query to find the top 10 clinical trial sponsors that exist in the "Clinical Trial Sponsor" dataset but not in the "Pharma Companies" dataset. A temporary view called filtered_df was created where it selects the sponsor names (Sponsor) from the clinicaltrial_2023 and counts the occurrences of each sponsor.

The LEFT ANTI JOIN operation was used to find entries that exist in the clinicaltrial_2023 but not in the pharma based on the condition that c.Sponsor = p.Parent_company. This operation ensures that only sponsors that are present in clinicaltrial_2023 but not in pharma are considered.

After finding the sponsors that meet the criteria, they are sorted in descending order of counts. This means sponsors with the highest number of occurrences will appear first.

Cmd 14

```python
%python
#This should run on Python cell

# Load data from CSV into a temporary view
spark.read.csv("/FileStore/tables/pharma.csv", header=True, inferSchema=True).createOrReplaceTempView("pharma")
```

(2) Spark Jobs

Command took 2.76 seconds -- by t.s.isedowo@edu.salford.ac.uk at 5/2/2024, 12:13:43 AM on Task1

Cmd 15

```
%sql
--Q4 IMPLEMENTATION IN SQL
-- Step 3: Left Anti Join to find entries that exist in Clinical Trial Sponsor but not in Pharma Companies
CREATE OR REPLACE TEMP VIEW Filtered_df AS
SELECT
    c.Sponsor,
    COUNT(*) AS count
FROM
    clinicaltrial_2023 c
LEFT ANTI JOIN
    pharma p ON c.Sponsor = p.Parent_company
GROUP BY
    c.Sponsor;

-- Step 4: Sort the result in descending order of counts
CREATE OR REPLACE TEMP VIEW sorted_result_df AS
SELECT
    Sponsor,
    count
FROM
    Filtered_df
ORDER BY
    count DESC;

-- Step 5: Take the top 10 records
CREATE OR REPLACE TEMP VIEW top_10_sponsors AS
SELECT
    Sponsor,
    count
FROM
    sorted_result_df
LIMIT 10;

-- Show the top 10 sponsors
SELECT * FROM top_10_sponsors;
```

(3) Spark Jobs

Table

	Sponsor	count
1	National Cancer Institute (NCI)	5470
2	Assiut University	3339
3	Cairo University	3023
4	Assistance Publique - Hôpitaux de Paris	2951
5	Mayo Clinic	2766
6	M.D. Anderson Cancer Center	2702
7	Novartis Pharmaceuticals	2391
8	National Institute of Allergy and Infectious Diseases (NIAID)	2340
9	Massachusetts General Hospital	2268
10	National Taiwan University Hospital	2181

10 rows | 24.35 seconds runtime

Refreshed 2 hours ago

Command took 24.35 seconds -- by t.a.lawlawu@edu.salford.ac.uk at 5/2/2024, 12:14:23 AM on Task1

```
%sql
--Q5 IMPLEMENTATION IN SQL
```

DISCUSSION AND COMPARISON OF THE RESULT

The result across the three implementations were consistent. Based on the results, it can be observed that the National Cancer Institute has topped the Non-Pharmaceutical Sponsors list. The analysis sheds light on the prominent role of non-pharmaceutical sponsors in clinical research and underscores the importance of collaboration and resource allocation to drive innovation and address healthcare challenges effectively.

STATEMENT OF PROBLEM FIVE

VISUALS DISPLAYING THE NUMBER OF COMPLETED STUDIES IN THE YEAR 2023

ASSUMTION MADE

We assume that the completion dates recorded in the dataset are consistent and follow a standard format. We trust that these dates truly represent when the studies were completed. Also, we believe that the status assigned to each study accurately indicates whether it's completed or not.

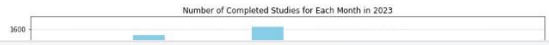
Moreover, we're working on the assumption that the dataset includes all studies completed in 2023 without any important missing or incorrect entries. These assumptions are essential to ensure that our analysis accurately shows how many studies were completed each month in 2023.

IMPLEMENTATION IN RDD

This PySpark script analyzes and visualizes the count of completed studies per month in 2023 using RDDs. It employs matplotlib, datetime, and calendar libraries, with completion_index set to 13 for identifying completion dates. The count_completed_studies function extracts completion dates, checks if studies are completed in 2023, and returns a tuple with the month and 1 if conditions are met, else (0, 0). Data integrity is ensured by filtering out rows with less than 14 fields. The map transformation applies count_completed_studies to each row, while reduceByKey aggregates counts for each month. Results are collected into a dictionary using collectAsMap. The matplotlib creates a bar plot with month names on the x-axis and completed study counts on the y-axis.

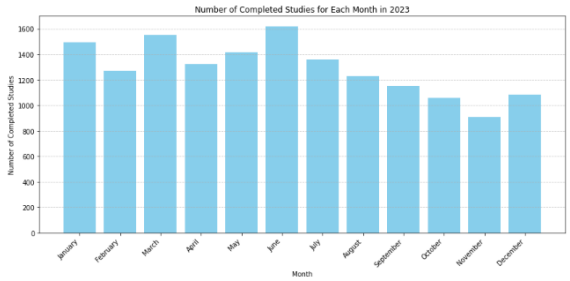
```python
#Q5 IMPLEMEMTATION IN RDD
import matplotlib.pyplot as plt
from collections import defaultdict
from datetime import datetime
import calendar

completion_index = 13
# Function to parse completion date and count completed studies for each month

def count_completed_studies(row):
    completion_date = datetime.strptime(row[completion_index], '%Y-%m-%d')
    if row[3] == 'COMPLETED' and completion_date.year == 2023:
        return (completion_date.month, 1)
    else:
        return (0, 0)

filter_less_row = myRDD4.filter(lambda fields: len(fields) == 14)

filter_less_row.take(5)

# Count completed studies for each month
completed_studies_by_month = filter_less_row.map(count_completed_studies) \
                                .reduceByKey(lambda x, y: x + y) \
                                .collectAsMap()

# Plotting
months = range(1, 13)
study_counts = [completed_studies_by_month.get(month, 0) for month in months]

# Convert month numbers to month names
month_names = [calendar.month_name[month] for month in months]

plt.figure(figsize=(12, 6))
plt.bar(month_names, study_counts, color='skyblue')
plt.title('Number of Completed Studies for Each Month in 2023')
plt.xlabel('Month')
plt.ylabel('Number of Completed Studies')
plt.xticks(rotation=45, ha='right')  # Rotate the x-axis labels for better readability
plt.grid(axis='y', linestyle='--', alpha=0.7)
plt.tight_layout()
plt.show()

# Table of values
print("Month\t\t\t\tCompleted Studies")
for month in range(1, 13):
    count = completed_studies_by_month.get(month, 0)
    print(f"{calendar.month_name[month]:<24}{count}")
```

(2) Spark Jobs



```
for month in range(1, 13):
    count = completed_studies_by_month.get(month, 0)
    print(f"{calendar.month_name[month]:<24}{count}")
```

(2) Spark Jobs



Month	Completed Studies
January	1494
February	1272
March	1552
April	1324
May	1415
June	1619
July	1360
August	1230
September	1152
October	1058
November	909
December	1082

Command took 23.36 seconds -- by t.s.isedowo@edu.salford.ac.uk at 5/2/2024, 12:44:40 AM on Task1

Cmd 21

IMPLEMENTATION IN DATAFRAME

The pyspark.sql.functions were imported which helps to manipulate park dataframe. The calendar, which is a standard python library provides various calendar functions, completion_year and completion_status are variables used to filter the clinical trial data which filter the data based on completion year. (2023) and status completed.

The filtered_df filters the Clinicaltrial_df DataFrame to include only rows where the 'Status' column matches the completion_status and the year of the 'Completion' column matches the completion_year. Then, the formatted_df function covert the completion column to a date format.

The completed_studies_by_month_dict converts the result of the previous step into a dictionary where the keys are the month numbers, and the values are the corresponding counts of completed studies. The matplotlib then visualizes the number of completed studies in a bar plot.

```python
#Q5 IMPLEMEMTATION IN RDD
import matplotlib.pyplot as plt
from pyspark.sql.functions import month, year, to_date
import calendar

# Define completion date and status filters
completion_year = 2023
completion_status = 'COMPLETED'

# Filter the DataFrame to include only rows with the correct number of fields
filtered_df = Clinicaltrial_df.filter(Clinicaltrial_df['Status'] == completion_status) \
                              .filter(year('Completion') == completion_year)
# Convert the completion column to a date format
formatted_df = filtered_df.withColumn('Completion', to_date('Completion', 'yyyy-MM-dd'))

# Group by month and count completed studies for each month
completed_studies_by_month = formatted_df.groupBy(month('Completion').alias('month')) \
                                         .count() \
                                         .orderBy('month') \
                                         .collect()

# Convert the result to a dictionary
completed_studies_by_month_dict = {row['month']: row['count'] for row in completed_studies_by_month}

# Plotting
months = range(1, 13)
study_counts = [completed_studies_by_month_dict.get(month, 0) for month in months]

# Convert month numbers to month names
month_names = [calendar.month_name[month] for month in months]

plt.figure(figsize=(12, 6))
plt.bar(month_names, study_counts, color='skyblue')
plt.title('Number of Completed Studies for Each Month in 2023')
plt.xlabel('Month')
plt.ylabel('Number of Completed Studies')
plt.xticks(rotation=45, ha='right')  # Rotate the x-axis labels for better readability
plt.grid(axis='y', linestyle='--', alpha=0.7)
plt.tight_layout()
plt.show()

# Table of values
print("Month\t\t\tCompleted Studies")
for month in range(1, 13):
    count = completed_studies_by_month_dict.get(month, 0)
    print(f"{calendar.month_name[month]:<24}{count}")
```

(4) Spark Jobs

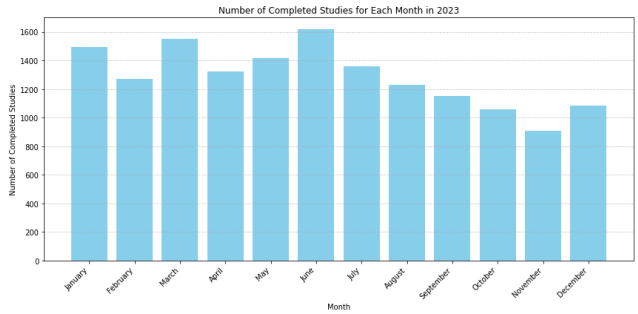
filtered_df: pyspark.sql.dataframe.DataFrame = [Id: string, Study Title: string ... 12 more fields]

formatted_df: pyspark.sql.dataframe.DataFrame = [Id: string, Study Title: string ... 12 more fields]

Number of Completed Studies for Each Month in 2023

File Edit View Run Help Last edit was 21 hours ago New cell UI: OFF

formatted_df: pyspark.sql.dataframe.DataFrame = [Id: string, Study Title: string ... 12 more fields]




```
Month                   Completed Studies
January                 1494
February                1272
March                   1552
April                   1324
May                     1415
June                    1619
July                    1360
August                  1230
September               1152
October                 1058
November                909
December                1082
```

Command took 21.08 seconds -- by t.s.isedowo@edu.salford.ac.uk at 4/28/2024, 8:54:39 AM on sunday

IMPLEMENTATION IN SQL

A temporary view named completed_studies is created to store the aggregated results. This view aggregates the completed studies count for each month in the year 2023.

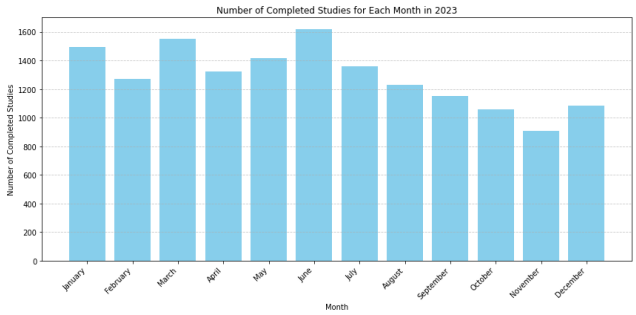
The MONTH() function extracts the month from the Completion date column and the COUNT(*) function counts the number of records for each month. The WHERE clause filters the data to include only completed studies (STATUS = 'COMPLETED') and studies completed in the year 2023 (YEAR(Completion) = 2023). The GROUPBY and ORDER BY group the data by month and order the result by month.

```python
%python
#QS IMPLEMENTATION IN SQL(PLOTTING OF THE GRAPH)

import matplotlib.pyplot as plt
import calendar

#Query the completed_studies view and convert the result into a DataFrame
completed_studies_df = spark.sql("SELECT * FROM completed_studies")

#Collect the results to the driver as a list of Row objects
completed_studies_rows = completed_studies_df.collect()

#Convert the result to a dictionary
completed_studies_by_month_dict = {row['month']: row['completed_count'] for row in completed_studies_rows}

#Plotting
months = range(1, 13)
study_counts = [completed_studies_by_month_dict.get(month, 0) for month in months]

#Convert month numbers to month names
month_names = [calendar.month_name[month] for month in months]

plt.figure(figsize=(12, 6))
plt.bar(month_names, study_counts, color='skyblue')
plt.title('Number of Completed Studies for Each Month in 2023')
plt.xlabel('Month')
plt.ylabel('Number of Completed Studies')
plt.xticks(rotation=45, ha='right')  # Rotate the x-axis labels for better readability
plt.grid(axis='y', linestyle='--', alpha=0.7)
plt.tight_layout()
plt.show()

#Table of values
print("Month\t\t\tCompleted Studies")
for month in range(1, 13):
    count = completed_studies_by_month_dict.get(month, 0)
    print(f"{calendar.month_name[month]:<24}{count}")
```

(4) Spark Jobs

completed_studies_df: pyspark.sql.dataframe.DataFrame = [month: integer, completed_count: long]

completed_studies_df: pyspark.sql.dataframe.DataFrame = [month: integer, completed_count: long]




```
Month                   Completed Studies
January                 1494
February                1272
March                   1552
April                   1324
May                     1415
June                    1619
July                    1360
August                  1230
September               1152
October                 1058
November                909
December                1082
```

Command took 20.48 seconds -- by t.s.isedowo@edu.salford.ac.uk at 4/28/2024, 9:13:18 AM on sunday

DISCUSSION OF THE RESULT

The consistent outcomes achieved through all three implementation approaches (RDD, DataFrame, and SQL) highlight the dependability and resilience of the analysis. The tabulated data showcases the quantity of completed studies for each month throughout 2023, revealing fluctuations in completion rates. For instance, June recorded the highest number of studies completed (1619), while November exhibited the lowest (909). These fluctuations might be influenced by factors like funding availability, seasonal variations in research endeavors, or specific project timelines. Moreover, presenting the data visually via a bar chart could offer a clearer depiction of the distribution of completed studies across months, facilitating the identification of any noticeable patterns or trends. In sum, the consistency in findings across diverse

implementation methods bolsters the credibility of the results and underscores the reliability of the analysis conducted.

FURTHER ANALYSIS

REASONS FOR FURTHER ANALYSIS

The initial analysis focused on identifying the top 5 conditions and their frequencies within the clinical trial dataset. However, the broader aim extends beyond merely listing existing conditions. It emphasizes the significance of understanding the current interventions available for preventing, managing, or eliminating these conditions. This understanding can reveal the most common and effective methods currently in use, as well as identify areas where new interventions are needed. By knowing what interventions are already in place, we can work towards contributing to advancing healthcare outcomes and fostering the development of impactful solutions.

EXECUTION STRATEGY

The additional analysis was implemented using the PySpark RDD, the Interventions column data was retrieved from the clinical trial RDD named “myRDD2”. The Intervention column was in the 6th element of myRDD2 which corresponds to index 5. To extract the Intervention column data from myRDD2, I used the map transformation on the myRDD2. to return a new RDD named “interventions_rdd” that only contains the Intervention column data. The interventions_rdd.take(20) retrieves the first 20 elements from the interventions_rdd and the take action retrieves a specified number of elements from the interventions_rdd and returns them as a list

Cmd 21

Python

```
#Further analysis 1

#extracting interventions and their frequencies
interventions_rdd = myRDD2.map(lambda x: x[5])
interventions_rdd.take(10)

```

(1) Spark Jobs

```
Out[21]: ["BEHAVIORAL: PRIDE 'Step 1' problem-solving intervention|BEHAVIORAL: Enhanced usual care",
 'OTHER: Placebo|DIETARY_SUPPLEMENT: β-OHB',
 'DRUG: Insulin (tight blood glucose control)',
 'OTHER: SuperMELD',
 'OTHER: adherence support system based on a vocal assistant',
 'BEHAVIORAL: Person-centered inhibitory control training|BEHAVIORAL: Active behavioral response training',
 'DRUG: Propranolol|DRUG: Placebo',
 'BEHAVIORAL: Computerized brief alcohol intervention + IVR booster calls|BEHAVIORAL: Computerized brief alcohol intervention|BEHAVIORAL: Attention Control',
 'OTHER: Pharmacist - Smoking Cessation Support',
 'PROCEDURE: Biospecimen Collection|OTHER: Genetic Testing|OTHER: Medical Chart Review']
```

Command took 1.27 seconds -- by t.s.isedowo@edu.salford.ac.uk at 5/2/2024, 12:45:13 AM on Task1

Cmd 22

After isolating the Intervention column from the clinical trial RDD, some cleaning was performed. A filter operation was performed on interventions_rdd to remove any elements (interventions) from the RDD where the value is an empty string ' ' and the take (10) collect the first 10 element from the filtered RDD "interventions_rdd1" and display them

```
Cmd 22
Python
#remove empty column
interventions_rdd1 = interventions_rdd.filter(lambda x: x !='')
interventions_rdd1.take(10)

(1) Spark Jobs
Out[111]: ["BEHAVIORAL: PRIDE 'Step 1' problem-solving intervention|BEHAVIORAL: Enhanced usual care",
 'OTHER: Placebo|DIETARY_SUPPLEMENT: β-OHB',
 'DRUG: Insulin (tight blood glucose control)',
 'OTHER: SuperMELD',
 'OTHER: adherence support system based on a vocal assistant',
 'BEHAVIORAL: Person-centered inhibitory control training|BEHAVIORAL: Active behavioral response training',
 'DRUG: Propranolol|DRUG: Placebo',
 'BEHAVIORAL: Computerized brief alcohol intervention + IVR booster calls|BEHAVIORAL: Computerized brief alcohol intervention|BEHAVIORAL: Attention Control',
 'OTHER: Pharmacist - Smoking Cessation Support',
 'PROCEDURE: Biospecimen Collection|OTHER: Genetic Testing|OTHER: Medical Chart Review']
Command took 1.42 seconds -- by t.s.isedowo@edu.salford.ac.uk at 5/1/2024, 12:35:32 PM on BDDTT
Cmd 23
```

The elements of interventions_rdd1 were split by comma, the flatMap transformation applies a function to each element of the interventions_rdd1 and flattens the result. take(10) action is used to retrieve the first 10 elements of the resulting interventions_rdd2.

```
Cmd 23
Python
#split by comma
interventions_rdd2 = interventions_rdd1.flatMap(lambda x: x.split(","))
interventions_rdd2.take(10)

(1) Spark Jobs
Out[30]: ["BEHAVIORAL: PRIDE 'Step 1' problem-solving intervention|BEHAVIORAL: Enhanced usual care",
 'OTHER: Placebo|DIETARY_SUPPLEMENT: β-OHB',
 'DRUG: Insulin (tight blood glucose control)',
 'OTHER: SuperMELD',
 'OTHER: adherence support system based on a vocal assistant',
 'BEHAVIORAL: Person-centered inhibitory control training|BEHAVIORAL: Active behavioral response training',
 'DRUG: Propranolol|DRUG: Placebo',
 'BEHAVIORAL: Computerized brief alcohol intervention + IVR booster calls|BEHAVIORAL: Computerized brief alcohol intervention|BEHAVIORAL: Attention Control',
 'OTHER: Pharmacist - Smoking Cessation Support',
 'PROCEDURE: Biospecimen Collection|OTHER: Genetic Testing|OTHER: Medical Chart Review']
Command took 1.34 seconds -- by t.s.isedowo@edu.salford.ac.uk at 5/2/2024, 12:50:12 AM on Task1
Cmd 24
```

Another flatMap transformation is applied to split each intervention record by the '|' delimiter. This transformation flattens the resulting nested lists into a single list. For each record x, the split("|") function is used to split the interventions separated by '|'.

```
Cmd 24
Python
#split by  pipe
interventions_rdd3 = interventions_rdd2.flatMap(lambda x: x.split("|"))
interventions_rdd3.take(10)

(1) Spark Jobs
Out[48]: ["BEHAVIORAL: PRIDE 'Step 1' problem-solving intervention",
 'BEHAVIORAL: Enhanced usual care',
 'OTHER: Placebo',
 'DIETARY_SUPPLEMENT: β-OHB',
 'DRUG: Insulin (tight blood glucose control)',
 'OTHER: SuperMELD',
 'OTHER: adherence support system based on a vocal assistant',
 'BEHAVIORAL: Person-centered inhibitory control training',
 'BEHAVIORAL: Active behavioral response training',
 'DRUG: Propranolol']
Command took 1.41 seconds -- by t.s.isedowo@edu.salford.ac.uk at 5/1/2024, 2:21:13 PM on TASK2
Cmd 25
```

A new RDD (interventions_rdd3) was created by transforming each element of the interventions_rdd2 RDD into a tuple where the intervention is the key, and the value is 1. Essentially, it's mapping each intervention to the number 1, indicating that each intervention has occurred once.

```python
#pair rdd to count the frequency
interventions_rdd4 = interventions_rdd3.map(lambda c: (c, 1))
interventions_rdd4.take(10)
```

(1) Spark Jobs

```
Out[50]: [("BEHAVIORAL: PRIDE 'Step 1' problem-solving intervention", 1),
 ('BEHAVIORAL: Enhanced usual care', 1),
 ('OTHER: Placebo', 1),
 ('DIETARY_SUPPLEMENT: β-OHB', 1),
 ('DRUG: Insulin (tight blood glucose control)', 1),
 ('OTHER: SuperMELD', 1),
 ('OTHER: adherence support system based on a vocal assistant', 1),
 ('BEHAVIORAL: Person-centered inhibitory control training', 1),
 ('BEHAVIORAL: Active behavioral response training', 1),
 ('DRUG: Propranolol', 1)]
```

Command took 1.24 seconds -- by t.s.isedowo@edu.salford.ac.uk at 5/1/2024, 2:22:22 PM on TASK2

Cmd 26

The reduceByKey transformation in PySpark was used to sum up the values associated with each key in the RDD interventions_rdd4.

Cmd 26

```python
#reduce by key to sum up the values
interventions_rdd5 = interventions_rdd4.reduceByKey(lambda x,y: x+y)
interventions_rdd5.take(10)
```

(1) Spark Jobs

```
Out[44]: [('BEHAVIORAL: Enhanced usual care', 25),
 ('BEHAVIORAL: Attention Control', 66),
 ('OTHER: Pharmacist - Smoking Cessation Support', 1),
 ('OTHER: Blood draw', 86),
 ('BEHAVIORAL: 5waysA Inactive wait-list control', 1),
 ('DRUG: human fetal-derived Neural Stem Cells (hNSCs)', 1),
 ('DRUG: PREDNISOLONE', 1),
 ('PROCEDURE: Doing Different ICU techniques and skills', 1),
 ('DEVICE: rTMS', 107),
 ('OTHER: Intra-abdominal pressure during laparoscopy', 1)]
```

Command took 10.73 seconds -- by t.s.isedowo@edu.salford.ac.uk at 5/1/2024, 2:17:31 PM on TASK2

Cmd 27

In addition, each intervention is split by ":" using the split(":") method, and only the first part (intervention type) is extracted. The strip() method is used to remove any leading or trailing whitespace that is still present. The reduceByKey() transformation is applied to aggregate the counts for each intervention type and sortBy() was used to sort the interventions by their count in descending order. The take() action is used to extract the top 10 interventions after sorting.

Cmd 27

```python
# Split each intervention by ":" and extract the intervention type
interventions_rdd5_cleaned = interventions_rdd5.map(lambda x: (x[0].split(":")[0].strip(), x[1]))

# Aggregate the counts for each intervention type
interventions_rdd5_aggregated = interventions_rdd5_cleaned.reduceByKey(lambda x, y: x + y)

# Sort the aggregated interventions by count in descending order
interventions_rdd5_sorted = interventions_rdd5_aggregated.sortBy(lambda x: x[1], ascending=False)

# Take the first 20 interventions after aggregation and sorting
interventions_rdd6 = interventions_rdd5_sorted.take(10)

# Display the top 20 interventions
interventions_rdd6
```

(3) Spark Jobs

```
Out[45]: [('DRUG', 353617),
 ('OTHER', 135985),
 ('DEVICE', 81400),
 ('BEHAVIORAL', 74219),
 ('PROCEDURE', 71472),
 ('BIOLOGICAL', 40817),
 ('DIETARY_SUPPLEMENT', 24422),
 ('DIAGNOSTIC_TEST', 19660),
 ('RADIATION', 10937),
 ('GENETIC', 3557)]
```

Command took 2.39 seconds -- by t.s.isedowo@edu.salford.ac.uk at 5/1/2024, 2:17:46 PM on TASK2

Cmd 28

Finally, each pair has its elements swapped, so that the count comes first, and the intervention type comes second.

Cmd 28

```python
# Swap the positions of count and intervention type
interventions_top_10 = [(count, intervention) for intervention, count in interventions_rdd6]

# Display the top 20 interventions with count first
interventions_top_10
```

```
Out[47]: [(353617, 'DRUG'),
 (135985, 'OTHER'),
 (81400, 'DEVICE'),
 (74219, 'BEHAVIORAL'),
 (71472, 'PROCEDURE'),
 (40817, 'BIOLOGICAL'),
 (24422, 'DIETARY_SUPPLEMENT'),
 (19660, 'DIAGNOSTIC_TEST'),
 (10937, 'RADIATION'),
 (3557, 'GENETIC')]
```

Command took 0.04 seconds -- by t.s.isedowo@edu.salford.ac.uk at 5/1/2024, 2:18:31 PM on TASK2

Cmd 29

After further analysis was carried out to understand the current interventions available for preventing, managing, or eliminating the conditions, it was discovered that the highest intervention to the clinical trial conditions is Drug based on the analysis of the Top 10 interventions.

TASK 2

COLLABORATIVE FILTERING RECOMMENDER SYSTEM

BUILDING A COLLABORATIVE FILTERING RECOMMENDER SYSTEM FOR GAME RECOMMENDATIONS USING MLLIB AND MLFLOW

In the realm of recommendation systems, collaborative filtering stands out as a powerful technique for suggesting items based on user preferences and behaviors. Leveraging Apache Spark's MLlib, we embark on a journey to construct a collaborative filtering recommender system. This guide navigates through the process of utilizing the steam-200k.csv dataset, a rich collection of user interactions with video games on the Steam platform.

DESCRIPTION OF THE SET UP USED FOR THE TASK.

1. **Databricks Account Creation**

The initial phase commenced with registering for a Databricks account, granting access to the platform's workspace for managing project-related tasks. In this experiment, we opted for the community edition to fulfill our requirements.

2. **Cluster Configuration**

We configured a Databricks cluster optimized to meet the computational requirements of training our recommender system. For this experiment, we selected Databricks runtime version 15.0 ML (Scala 2.12, Spark 3.5.0), ensuring compatibility and performance for our machine learning tasks.

3. **Notebook Creation:**

Within our Databricks workspace, we established a notebook named "Tomisin_Isedowo_ml" to facilitate the development of our collaborative filtering recommender system. This notebook served as an interactive environment for writing and executing code, allowing for seamless development and experimentation.

4 **Data Preparation:**

We imported the "steam-200k.csv" dataset, which captures user interactions with video games on the Steam platform, into the Databricks workspace. The dataset was stored in the DBFS file layer with the file path "/FileStore/tables".

5 Library Installation:

We ensured the installation of essential libraries and dependencies within the Databricks cluster to support the development process. This included installing Apache Spark's MLflow, which plays a crucial role in managing the machine learning lifecycle. Additionally, MLLib, a component of Apache Spark, was readily available within the Databricks platform to support our recommender system development.

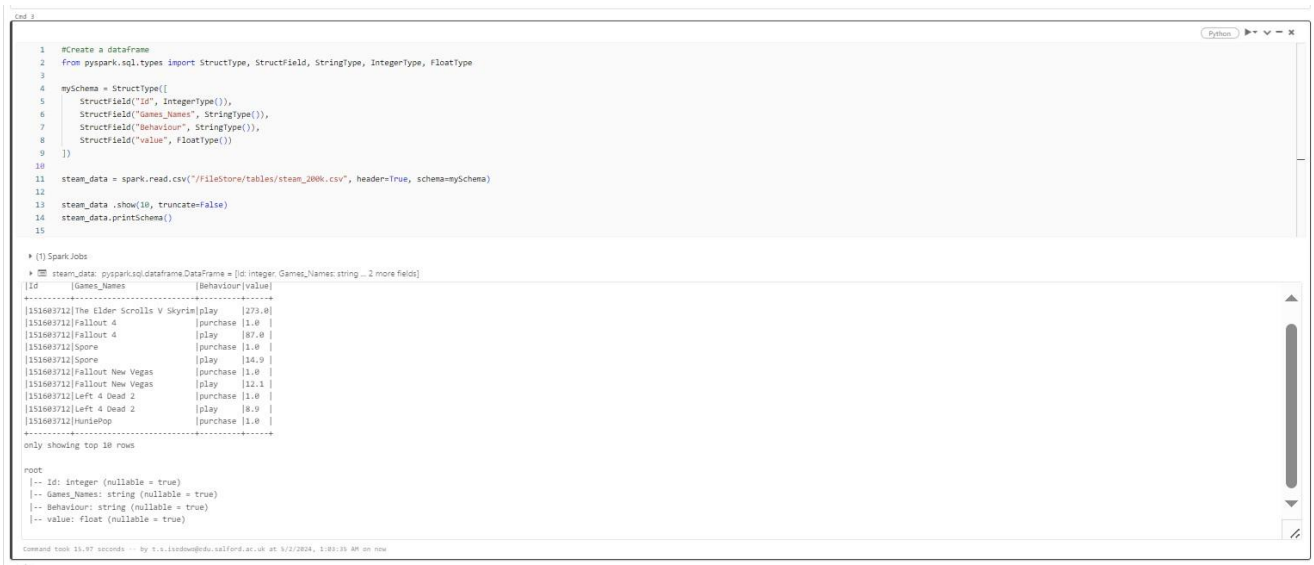
LOADING DATA INTO SPARK DATAFRAME AND ANY EXPLORATORY ANALYSIS OR VISUALISATION CARRIED OUT PRIOR TO TRAINING.

1) **Checking Dataset Availability:** We use a code dbutils.fs.ls("/FileStore/tables") in Databricks to see what files are in a specific directory (/FileStore/tables). This helps us confirm if our dataset is there before we start working with it.

2) **Preparing for Data Analysis:** Before diving into analyzing the data, we set up a plan for how the data should look. This plan, called a schema, tells us what kind of information each column in our dataset should contain. For example, we decided that our dataset should have columns named "Id", "Games_Names", "Behaviour", and "value", each with specific types of data like numbers or text.

3) **Loading the Dataset**: Once we've made our plan, we read the actual dataset into our analysis environment. The dataset is a CSV file located at "/FileStore/tables/steam_200k.csv". We use the plan we made (our schema) to make sure the data is organized correctly. By setting header=True, we tell the system that the first row of the CSV file has the names of the columns. This helps the system understand how the data is organized.

4) **Everythingthe Data:** After we load the data, we take a quick look at the first 10 rows to see if everything looks right. This helps us make sure that the data was loaded correctly and matches our schema.



```
#Create a dataframe
from pyspark.sql.types import StructType, StructField, StringType, IntegerType, FloatType

mySchema = StructType([
    StructField("Id", IntegerType()),
    StructField("Games_Names", StringType()),
    StructField("Behaviour", StringType()),
    StructField("value", FloatType())
])

steam_data = spark.read.csv("/FileStore/tables/steam_200k.csv", header=True, schema=mySchema)

steam_data .show(10, truncate=False)
steam_data.printSchema()
```

```
(1) Spark Jobs
steam_data: pyspark.sql.dataframe.DataFrame = [Id: integer, Games_Names: string ... 2 more fields]
|Id        |Games_Names                |Behaviour|value|
+---------+---------------------------+---------+-----+
|151603712|The Elder Scrolls V Skyrim|play     |273.0|
|151603712|Fallout 4                  |purchase |1.0  |
|151603712|Fallout 4                  |play     |87.0 |
|151603712|Spore                      |purchase |1.0  |
|151603712|Spore                      |play     |14.9 |
|151603712|Fallout New Vegas          |purchase |1.0  |
|151603712|Fallout New Vegas          |play     |12.1 |
|151603712|Left 4 Dead 2              |purchase |1.0  |
|151603712|Left 4 Dead 2              |play     |8.9  |
|151603712|HuniePop                   |purchase |1.0  |
+---------+---------------------------+---------+-----+
only showing top 10 rows

root
 |-- Id: integer (nullable = true)
 |-- Games_Names: string (nullable = true)
 |-- Behaviour: string (nullable = true)
 |-- value: float (nullable = true)
```

DATA PREPARATION AND PRE-PROCESSING CARRIED OUT PRIOR TO TRAINING THE MODEL.

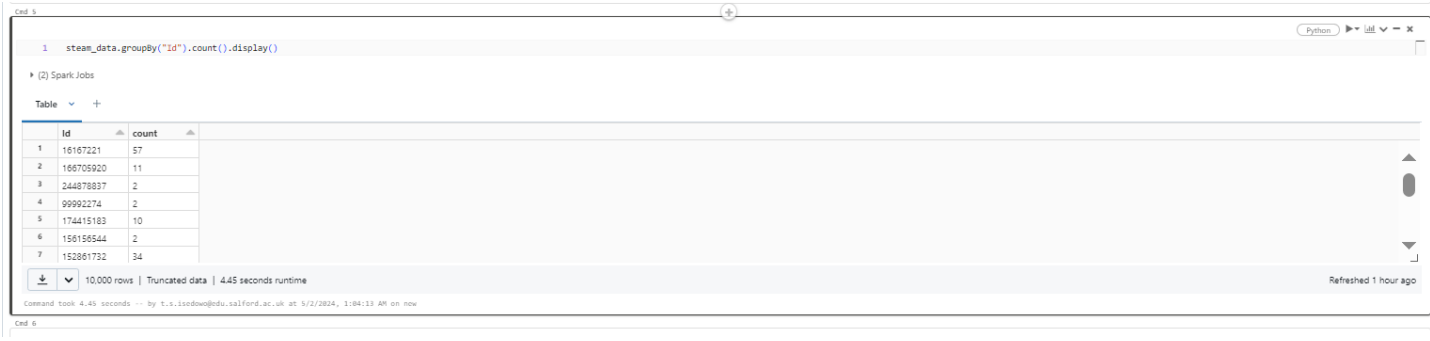
Prior to training the model, data preparation and preprocessing were undertaken to ensure the dataset's suitability for training a machine learning model. The following grouping was done to understand the structure of the dataset.

1) **Grouping by "Behaviour" Column**

The groupBy("Behaviour”) function groups the data in the steam_data based on the unique values in the "Behaviour" column. This operation creates groups where all rows with the same value in the "Behaviour" column are grouped together. The count() function is applied to each group, which calculates the number of rows in each group. This results in steam_data with two columns: "Behaviour" and "count". The "Behaviour" column contains unique values from the original "Behaviour" column, and the "count" column contains the number of rows corresponding to each unique "Behaviour" value. Then the display() function is used to display the result of steam_data in a visually appealing format.

2) Grouping by "Id" Column

The groupBy("Id") function collects all rows with the same value in the "Id" column into groups. After grouping by "Id", the count() function is applied to each group. This function calculates the number of rows in each group, effectively counting the occurrences of each unique "Id" value in the dataset. Then, the display() function is used to visually display the result.



3) Grouping by "Games_Names" Column

The groupBy("Games_Names") function collects all rows with the same value in the "Games_Names" column into groups. Then, the count() function is applied to each group. This function calculates the number of rows in each group, effectively counting the occurrences of each unique game name in the dataset and the display() function is used to visually display the result

```
steam_data.groupBy("Games_Names").count().display()
```

(2) Spark Jobs

Table

	Games_Names	count
1	Dota 2	9682
2	METAL GEAR SOLID V THE PHANTOM PAIN	134
3	LEGO Batman The Videogame	17
4	RIFT	236
5	Anodyne	14
6	Legend of Grimrock	93
7	Divinity Original Sin	138
8	Meltdown	4
9	SanctuaryRPG Black Edition	6
10	Snuggle Truck	14
11	Lunar Flight	16
12	Dungeons 2	12
13	Zuma's Revenge	7
14	HassleHeart	1
15	Ihf Handball Challenge 12	1

5,155 rows | 3.21 seconds runtime

Refreshed 1 hour ago

Command took 3.21 seconds -- by t.s.isedowo@edu.salford.ac.uk at 5/2/2024, 1:04:21 AM on new

The dropna() function was applied to steam_data, which removes all rows containing any missing values.

The resulting DataFrame with missing values removed is assigned to a new variable df_cleaned. The df_cleaned, contains only the rows from the original DataFrame steam_data where all values are present (i.e., no missing values).

Cmd 7

```
df_cleaned = steam_data.dropna()
```

df_cleaned: pyspark.sql.dataframe.DataFrame = [Id: integer, Games_Names: string ... 2 more fields]

Command took 0.15 seconds -- by t.s.isedowo@edu.salford.ac.uk at 4/30/2024, 10:57:46 PM on anoo

Cmd 8

Moreso, The DataFrame df_cleaned contains rows representing user interactions with video games. The filter() function is applied to this DataFrame to select only those rows where the value in the "Behaviour" column is equal to "purchase". After filtering, the select() function is used to retain only specific columns from the filtered DataFrame.

In this case, the "Id", "Games_Names", and "value" columns are selected. These columns represent the user ID, the name of the game purchased, and any associated value respectively which is the focus for the task. The filtered and selected DataFrame is assigned to a new variable data. This new DataFrame contains only the rows where users have made purchases and includes the selected columns: "Id", "Games_Names", and "value".

```
Cmd 9
#Training the recommender system using Purchase
# This checked the dataset and find the behaviour column. Then it picks all parameter with purchase
data = df_cleaned.filter(col("Behaviour") == "purchase").select("Id", "Games_Names", "value")
```

data: pyspark.sql.dataframe.DataFrame = [Id: integer, Games_Names: string ... 1 more field]

Command took 0.22 seconds -- by t.s.isedowo@edu.salford.ac.uk at 5/1/2024, 12:48:07 AM on ooo

Cmd 10

The line window = Window.orderBy("Games_Names") defines a window specification for ordering rows by the "Games_Names" column. This window specification is used in subsequent operations involving window functions. The unique_gameID = data.select("Games_Names").distinct() selects the distinct game names from the DataFrame data. Then, withColumn("GameID", row_number().over(window)) adds a new column "GameID" to the DataFrame unique_gameID. This column is populated with unique row numbers assigned to each distinct game name based on the order specified by the window. This effectively assigns a unique ID to each game name. After that, joined_data = data.join(unique_gameID, "Games_Names", "left") performs a left join between the original DataFrame data and the DataFrame unique_gameID on the "Games_Names" column. This helps to join the unique game IDs with the corresponding game names in the original DataFrame and .drop("Games_Names").withColumnRenamed("GameID", "GameID") drops the original "Games_Names" column from the joined DataFrame and renames the newly generated "GameID" column to "GameID". The joined_data.display() function is used to visually display the joined DataFrame joined_data with the game names replaced by their corresponding IDs.

```
# Window function help to assign IDs to the game names
window = Window.orderBy("Games_Names")
#We get the distinct game names so that the game name is not reapeated.
unique_gameID = data.select("Games_Names").distinct().withColumn("GameID", row_number().over(window))
#The new dataframe is joined with existing dataframe, then replace the Game_names with the GameID genarated in the new dataframe
joined_data = data.join(unique_gameID, "Games_Names", "left").drop("Games_Names").withColumnRenamed("GameID", "GameID")

joined_data.display()
```

(4) Spark Jobs

unique_gameID: pyspark.sql.dataframe.DataFrame = [Games_Names: string, GameID: integer]

joined_data: pyspark.sql.dataframe.DataFrame = [Id: integer, value: float ... 1 more field]

Table

	Id	value	GameID
1	151603712	1	1679
2	151603712	1	3998
3	151603712	1	1680
4	151603712	1	2476
5	151603712	1	2194
6	151603712	1	3115
7	151603712	1	3214

10,000 rows | Truncated data | 5.77 seconds runtime

Refreshed 1 hour ago

Command took 5.77 seconds -- by t.s.isedowo@edu.salford.ac.uk at 4/30/2024, 11:02:39 PM on anoo

Cmd 11

Data Splitting

The dataset was split into training and test sets to evaluate the model's performance on the dataset. The joined_data.randomSplit([0.8, 0.2]), splits the DataFrame into two sets, training set and test set. The first argument [0.8, 0.2] specifies the proportions for splitting the data, with 80% allocated to the training set and 20% to the test set. Then the test.show() displays the content of the test set.

Cmd 11

Python

```python
# This split the dataset into training and test sets (80% training, 20% test)
(training, test) = joined_data.randomSplit([0.8, 0.2])
# Display the content of the training set
print("Training set:")
training.show()
# Display the content of the test set
print("Test set:")
test.show()
```

(4) Spark Jobs

training: pyspark.sql.dataframe.DataFrame = [Id: integer, value: float ... 1 more field]

test: pyspark.sql.dataframe.DataFrame = [Id: integer, value: float ... 1 more field]

```
|  5250|  1.0|  2073|
|  5250|  1.0|  2075|
|  5250|  1.0|  3224|
|  5250|  1.0|  3532|
| 76767|  1.0|  1180|
| 76767|  1.0|  4259|
| 76767|  1.0|  4545|
| 76767|  1.0|  4547|
|103360|  1.0|   981|
|103360|  1.0|  2077|
|103360|  1.0|  4259|
|181212|  1.0|   985|
|181212|  1.0|  1180|
|181212|  1.0|  2071|
|181212|  1.0|  2075|
|298950|  1.0|    39|
|298950|  1.0|   177|
|298950|  1.0|   215|
+------+-----+------+
only showing top 20 rows
```

Command took 2.61 seconds -- by t.s.isedowo@edu.salford.ac.uk at 4/30/2024, 11:07:13 PM on anoo

Cmd 12

SELECTION OF HYPERPARAMETERS AND MODEL TRAINING AND EVALUATION AND MLFLOW EXPERIMENT TRACKING.

TRAINING A RECOMMENDATION MODEL USING THE ALTERNATING LEAST SQUARES (ALS) ALGORITHM

This ALS (maxIter=5, regParam=0.01, userCol="Id", itemCol="GameID", ratingCol="value", coldStartStrategy="drop"), initializes an ALS (Alternating Least Squares) model object. ALS is a collaborative filtering algorithm commonly used for recommendation systems. The maxIter=5 specifies the maximum number of iterations to run during training. In this case, the model will run for a maximum of 5 iterations and regParam=0.01 which is a regularization parameter was used to prevent overfitting by penalizing large parameter values. Also, the userCol="Id", itemCol="GameID", ratingCol="value"specify the names of the columns in the DataFrame training that represent the user ID, item ID (game ID), and rating (value) respectively. The coldStartStrategy="drop specifies the strategy to handle cold-start scenarios, where new users or items are encountered during prediction. Setting it to "drop" ensures that rows with missing values in the user or item columns are dropped during prediction.

The model = als.fit(training), fits the ALS model to the training data. The fit() method takes the training data (training DataFrame) as input and learns the model parameters (user and item embeddings) based on the specified configuration and optimization objective resulting in a trained recommendation model (model) that can be used to make predictions on unseen data.

MODEL EVALUATION

Before evaluation was initiated, predictions = model.transform(test) generates predictions on the test dataset using the trained ALS model (model). The transform() method applies the model to the test dataset and adds a new column "prediction" to the DataFrame predictions containing the predicted ratings for each user-item pair.

Evaluation was done using RMSE, the evaluator = RegressionEvaluator(metricName="rmse", labelCol="value", predictionCol="prediction"), initializes a regression evaluator object ‘evaluator’ to compute the Root Mean Square Error (RMSE) metric. The rmse = evaluator.evaluate(predictions), computes the RMSE by comparing the actual ratings (labelCol="value") in the test dataset with the predicted ratings (predictionCol="prediction") generated by the model. The RMSE is a measure of the differences between predicted and observed values, providing an indication of the model's accuracy.

The print("Root-mean-square error = " + str(rmse)), helps to prints out the computed RMSE, indicating the level of error in the model's predictions on the test dataset and predictions.show() displays the predictions DataFrame, showing the actual ratings, predicted ratings, and other relevant columns.

Cmd 13

```python
# Evaluate the model by computing the RMSE on the test data
predictions = model.transform(test)
evaluator = RegressionEvaluator(metricName="rmse", labelCol="value",
                                predictionCol="prediction")
rmse = evaluator.evaluate(predictions)
print("Root-mean-square error = " + str(rmse))
predictions.show()
userRecs = model.recommendForAllUsers(5)
userRecs.show(truncate=False)
```

(10) Spark Jobs

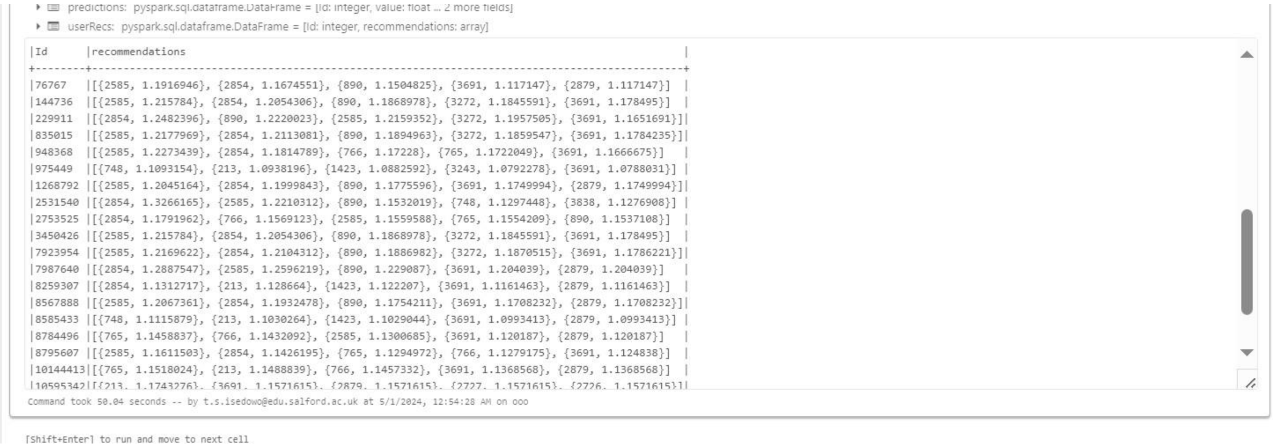
predictions: pyspark.sql.dataframe.DataFrame = [Id: integer, value: float ... 2 more fields]

userRecs: pyspark.sql.dataframe.DataFrame = [Id: integer, recommendations: array]

```
Root-mean-square error = 0.06912668456713267
+------+-----+------+----------+
|    Id|value|GameID|prediction|
+------+-----+------+----------+
|  5250|  1.0|   228| 1.0039171|
|  5250|  1.0|  1132|0.95531964|
| 76767|  1.0|   443| 1.0123292|
| 76767|  1.0|   742|  0.951943|
| 76767|  1.0|  4541| 1.0252277|
| 76767|  1.0|  4543| 1.0308981|
|181212|  1.0|  1180| 0.9584445|
|181212|  1.0|  2072| 0.9899501|
|298950|  1.0|   176| 1.0010703|
|298950|  1.0|   207|0.99800795|
|298950|  1.0|   258|0.99228364|
|298950|  1.0|   619|0.99340993|
|298950|  1.0|   669| 1.0018195|
|298950|  1.0|   982| 0.8935823|
|298950|  1.0|  1105| 0.9942115|
|298950|  1.0|  1248| 1.0006379|
|298950|  1.0|  1505| 0.9993739|
Command took 50.04 seconds -- by t.s.isedowo@edu.salford.ac.uk at 5/1/2024, 12:54:28 AM on ooo
```

Cmd 14

Recommendations for the test dataset



```
▸ predictions:  pyspark.sql.dataframe.DataFrame = [Id: integer, value: float ... 2 more fields]
▸ userRecs:  pyspark.sql.dataframe.DataFrame = [Id: integer, recommendations: array]
|Id      |recommendations                                                                          |
+--------+-----------------------------------------------------------------------------------------+
|76767   |[{2585, 1.1916946}, {2854, 1.1674551}, {890, 1.1504825}, {3691, 1.117147}, {2879, 1.117147}]  |
|144736  |[{2585, 1.215784}, {2854, 1.2054306}, {890, 1.1868978}, {3272, 1.1845591}, {3691, 1.178495}]  |
|229911  |[{2854, 1.2482396}, {890, 1.2220023}, {2585, 1.2159352}, {3272, 1.1957505}, {3691, 1.1651691}]|
|835015  |[{2585, 1.2177969}, {2854, 1.2113081}, {890, 1.1894963}, {3272, 1.1859547}, {3691, 1.1784235}]|
|948368  |[{2585, 1.2273439}, {2854, 1.1814789}, {766, 1.17228}, {765, 1.1722049}, {3691, 1.1666675}]   |
|975449  |[{748, 1.1093154}, {213, 1.0938196}, {1423, 1.0882592}, {3243, 1.0792278}, {3691, 1.0788031}] |
|1268792 |[{2585, 1.2045164}, {2854, 1.1999843}, {890, 1.1775596}, {3691, 1.1749994}, {2879, 1.1749994}]|
|2531540 |[{2854, 1.3266165}, {2585, 1.2210312}, {890, 1.1532019}, {748, 1.1297448}, {3838, 1.1276908}] |
|2753525 |[{2854, 1.1791962}, {766, 1.1569123}, {2585, 1.1559588}, {765, 1.1554209}, {890, 1.1537108}]  |
|3450426 |[{2585, 1.215784}, {2854, 1.2054306}, {890, 1.1868978}, {3272, 1.1845591}, {3691, 1.178495}]  |
|7923954 |[{2585, 1.2169622}, {2854, 1.2104312}, {890, 1.1886982}, {3272, 1.1870515}, {3691, 1.1786221}]|
|7987640 |[{2854, 1.2887547}, {2585, 1.2596219}, {890, 1.229087}, {3691, 1.204039}, {2879, 1.204039}]   |
|8259307 |[{2854, 1.1312717}, {213, 1.128664}, {1423, 1.122207}, {3691, 1.1161463}, {2879, 1.1161463}]  |
|8567888 |[{2585, 1.2067361}, {2854, 1.1932478}, {890, 1.1754211}, {3691, 1.1708232}, {2879, 1.1708232}]|
|8585433 |[{748, 1.1115879}, {213, 1.1030264}, {1423, 1.1029044}, {3691, 1.0993413}, {2879, 1.0993413}] |
|8784496 |[{765, 1.1458837}, {766, 1.1432092}, {2585, 1.1300685}, {3691, 1.120187}, {2879, 1.120187}]   |
|8795607 |[{2585, 1.1611503}, {2854, 1.1426195}, {765, 1.1294972}, {766, 1.1279175}, {3691, 1.124838}]  |
|10144413|[{765, 1.1518024}, {213, 1.1488839}, {766, 1.1457332}, {3691, 1.1368568}, {2879, 1.1368568}]  |
|10595342|[{213, 1.1743276}, {3691, 1.1571615}, {2879, 1.1571615}, {2727, 1.1571615}, {2726, 1.1571615}]|
Command took 50.04 seconds -- by t.s.isedowo@edu.salford.ac.uk at 5/1/2024, 12:54:28 AM on ooo

[Shift+Enter] to run and move to next cell
```

Top 5 recommendations for all users in the dataset

HYPERPARAMETER TUNING

In building a collaborative filtering recommender system for game recommendations, the hyperparameters: rank, maxIter, and regParam have significant impacts on the performance and effectiveness of the model.

Rank

The rank hyperparameter represents the number of latent factors in the model. These latent factors capture the underlying features of users and items, (in this case, games) in a lower-dimensional space. A higher rank allows the model to capture more complex patterns in the data but also increases the risk of overfitting. Alternatively, a lower rank might lead to underfitting as the model may not capture enough information to make accurate predictions. In your case, the best model has a rank of 5, indicating that a lower-dimensional representation suffices to capture the essential user-item interactions for game recommendations.

Max Iterations

This parameter determines the maximum number of iterations the ALS algorithm will perform before converging to a solution. Convergence occurs when the model's parameters no longer change significantly between iterations. A higher number of iterations allows the model to potentially reach a more optimal solution, especially in complex datasets or when using higher ranks. In this task, I tested max iterations of 5 and 7. The best model selected had a max iteration of 7, suggesting that a slightly longer training time

was beneficial for improving model performance.

Regularization Parameter (RegParam)

Regularization is a technique used to prevent overfitting by penalizing large parameter values. The regularization parameter controls the strength of this penalty. A higher regularization parameter imposes a stronger penalty, which can help prevent the model from fitting the noise in the data but may also lead to underfitting if set too high. Alternatively, a lower regularization parameter allows the model to fit the training data more closely but risks overfitting. In this task, I tested regularization parameters of 0.01 and 0.1. The best model selected had a regularization parameter of 0.01, indicating that a relatively low regularization strength was sufficient to prevent overfitting while still allowing the model to capture the underlying patterns in the data effectively.

Cmd 14

```python
from pyspark.ml.tuning import CrossValidator, ParamGridBuilder

# Define the parameter grid
param_grid = ParamGridBuilder() \
    .addGrid(als.rank, [5,7]) \
    .addGrid(als.maxIter, [5,7]) \
    .addGrid(als.regParam, [0.01, 0.1]) \
    .build()

# Define evaluator
evaluator = RegressionEvaluator(metricName="rmse", labelCol="value", predictionCol="prediction")

# Define cross-validator
cross_validator = CrossValidator(estimator=als,
                                 estimatorParamMaps=param_grid,
                                 evaluator=evaluator,
                                 numFolds=5)  # 5-fold cross-validation

# Fit cross-validator to the training data
cv_model = cross_validator.fit(training)

# Get the best model from cross-validation
best_model = cv_model.bestModel

# Evaluate the best model on the test set
predictions = best_model.transform(test)
rmse = evaluator.evaluate(predictions)
print("Root-mean-square error (Best Model) = " + str(rmse))
predictions.show()

# Print the best hyperparameters
print("Best Rank: ", best_model.rank)
print("Best Max Iterations: ", best_model._java_obj.parent().getMaxIter())
print("Best Regularization Parameter: ", best_model._java_obj.parent().getRegParam())
```

(21) Spark Jobs

(9) MLflow runs

Logged 9 runs to an experiment in MLflow. Learn more

(21) Spark Jobs

(9) MLflow runs

Logged 9 runs to an experiment in MLflow. Learn more

predictions: pyspark.sql.dataframe.DataFrame = [id: integer, value: float ... 2 more fields]

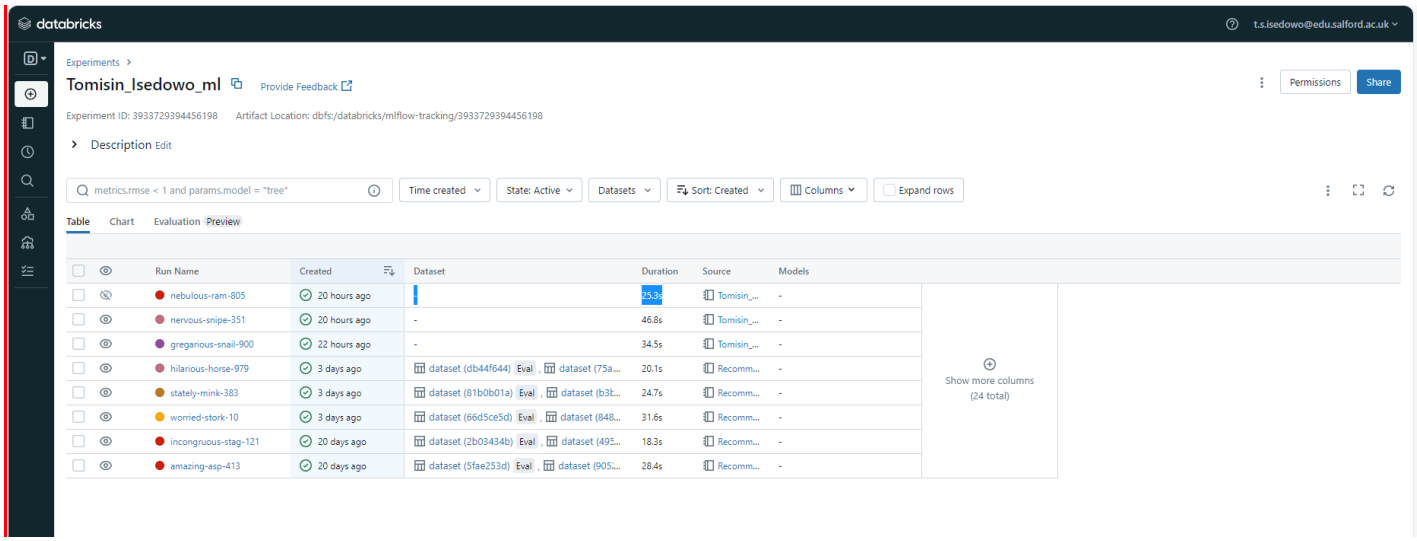
```
2024/05/01 20:50:55 INFO mlflow.utils.autologging_utils: Created MLflow autologging run with ID 'dc2137139d0f41a89b1c0811e5fb49ee', which will track hyperparameters, performance metrics, model artifacts, and lineage information for the current pyspark.ml workflow
2024/05/01 21:06:59 WARNING mlflow.pyspark.ml: Model CrossValidatorModel_4da514fec01d will not be autologged because it is not allowlisted or or because one or more of its nested models are not allowlisted. Call mlflow.spark.log_model() to explicitly log the model, or specify a custom allowlist via the spark.mlflow.pysparkml.autolog.logModelAllowlistFile Spark conf (see mlflow.pyspark.ml.autolog docs for more info).
Root-mean-square error (Best Model) = 0.048343038428550915
+------+-----+------+----------+
|    Id|value|GameID|prediction|
+------+-----+------+----------+
|  5250|  1.0|  1132| 0.9635958|
| 76767|  1.0|   323| 0.9865943|
| 76767|  1.0|   727| 0.9677381|
| 76767|  1.0|   744|0.97113115|
| 76767|  1.0|  4547| 1.0026014|
|103360|  1.0|   979| 0.9759166|
|103360|  1.0|  1132|0.97558707|
|103360|  1.0|  2070| 0.992193 6|
|103360|  1.0|  2079| 0.9932321|
|181212|  1.0|  2070|0.98570704|
|298950|  1.0|   175|0.98243535|
|298950|  1.0|   176|0.98423177|
|298950|  1.0|   215| 0.9871077|
|298950|  1.0|   308| 0.9893474|
|298950|  1.0|   619| 0.9833505|
|298950|  1.0|   659| 0.9905615|
|298950|  1.0|   982|  0.951398|
```

Command took 16.30 minutes -- by t.s.iezdow@edu.salford.ac.uk at 5/1/2024, 9:50:55 PM on Taskkkk

Cmd 15

MLFLOW EXPERIMENT TRACKING

MLflow plays a crucial role in machine learning development by ensuring transparency, reproducibility, and accountability. It allows us to track experiment details comprehensively, including parameters and metrics. This capability enables users to recreate experiments and validate results effectively.



CONCLUSION

The RMSE value of approximately 0.069 indicates the average difference between the actual ratings and the predicted ratings on the test dataset. The low RMSE value indicates that the ALS model performs well in predicting user ratings for video games, as the model's predictions are generally close to the actual ratings. The model's ability to generate accurate predictions and relevant recommendations demonstrates its effectiveness in capturing user preferences and delivering personalized content in the gaming domain. the results suggest that the ALS recommendation model trained on the dataset has the potential to improve user satisfaction and retention by providing tailored recommendations for video games.

The hyperparameter tuning process identified a combination of hyperparameters (rank=5, max iterations=7, regularization parameter=0.01) that resulted in a lower root-mean-square error (RMSE) on the test data compared to the initial model. This suggests that the tuned model is better at predicting user-item interactions. Additionally, the impact of each hyperparameter can be understood in terms of its effect on model complexity, training time, and regularization strength.