Big Data Analytics Mini - Project

Nutrient Analysis

Dataset: food.csv

1. Introduction

This project aims to analyze the nutritional composition of various food items using PySpark, focusing on understanding energy content, macronutrients, and correlations among vitamins and minerals. The dataset contains multiple food components and nutrient values that can reveal trends in food composition and health impacts.

2. Dataset Overview

The dataset used for this project is named 'food.csv'. It contains information such as **food category**, **description**, and **nutritional values like energy**, **protein**, **fat**, **carbohydrates**, **and various vitamins**. The data is processed using PySpark to handle large-scale analysis efficiently.

3. Data Preprocessing

Data preprocessing involved loading the CSV file into a PySpark DataFrame, identifying nutrient columns, and handling missing or malformed values using safe type casting. Rows with all null nutritional values were dropped.

MapReduce techniques were used conceptually by applying PySpark transformations (map, filter, reduceByKey) to extract and process nutrient-level data efficiently.

4. Analysis Performed

The following analyses were performed on the dataset:

- Descriptive statistics for key nutrients (Energy, Protein, Fat, Carbohydrates).
- Category-wise nutrient comparison.
- Correlation between nutrients (e.g., Energy vs. Protein).
- Identification of foods with the highest and lowest nutrient values.

5. Visualizations

This project provides the visual representation of the top particularly selected composition of nutrients in the food by the various visual analysis models

- 1: Energy Distribution across Food Categories
- 2: Top 10 High Protein Food Items

- 3: Correlation Heatmap of Nutrients
- 4: Carbohydrates vs. Energy Relationship

6. Workforce Characteristics

The project was developed through collaborative efforts involving multiple roles:

1. **Data Engineer:** Managed Spark setup, data loading, and cleaning using PySpark (try_cast, null handling, schema correction).

```
import findspark
 findspark.init()
 import pyspark
 from pyspark.sql import SparkSession
 spark = SparkSession.builder.appName("JupyterPySparkTest").getOrCreate()
 print("▼ PySpark is working in Jupyter!")
 print("PySpark version:", pyspark.__version__)
 print("Spark version:", spark.version)
 PySpark is working in Jupyter!
 PySpark version: 4.0.1
 Spark version: 4.0.1
[2]: from pyspark.sql import SparkSession
      from pyspark.sql.functions import expr, col
      from pyspark.sql import functions as F
      from pyspark.ml.feature import VectorAssembler, PCA
      from pyspark.ml.clustering import KMeans
      from pyspark.ml.stat import Correlation
      from pyspark.sql.functions import monotonically increasing id
      import matplotlib.pyplot as plt
1 [3]: # 1. Setup Spark session and load data
      spark = SparkSession.builder.appName("FoodAnalysis").getOrCreate()
      df = spark.read.csv("food.csv", header=True, inferSchema=True)
      df.printSchema()
      df
      # Clean column names for safe querying
      def clean column(name):
          return name.strip().replace(" ", "_").replace(".", "_").replace("-", "_")
      df = df.toDF(*[clean column(c) for c in df.columns])
```

```
root
    -- Category: string (nullable = true)
    -- Description: string (nullable = true)
    -- Nutrient Data Bank Number: string (nullable = true)
    -- Data.Alpha Carotene: string (nullable = true)
    -- Data.Beta Carotene: string (nullable = true)
   -- Data.Beta Cryptoxanthin: integer (nullable = true)
    -- Data.Carbohydrate: double (nullable = true)
-- Data.Cholesterol: double (nullable = true)
    -- Data.Choline: double (nullable = true)
   -- Data.Fiber: double (nullable = true)
    -- Data.Lutein and Zeaxanthin: double (nullable = true)
-- Data.Lycopene: double (nullable = true)
    -- Data.Niacin: double (nullable = true)
   -- Data.Protein: double (nullable = true)
    -- Data.Retinol: double (nullable = true)
    -- Data.Riboflavin: double (nullable = true)
    -- Data.Selenium: double (nullable = true)
   -- Data.Sugar Total: double (nullable = true)
    -- Data. Thiamin: double (nullable = true)
    -- Data.Water: double (nullable = true)
    -- Data.Fat.Monosaturated Fat: double (nullable = true)
    -- Data.Fat.Polysaturated Fat: double (nullable = true)
    -- Data.Fat.Saturated Fat: double (nullable = true)
    -- Data.Fat.Total Lipid: double (nullable = true)
    -- Data.Major Minerals.Calcium: double (nullable = true)
    -- Data.Major Minerals.Copper: double (nullable = true)
    -- Data.Major Minerals.Iron: double (nullable = true)
    -- Data.Major Minerals.Magnesium: double (nullable = true)
-- Data.Major Minerals.Phosphorus: double (nullable = true)
    -- Data.Major Minerals.Potassium: double (nullable = true)
    -- Data.Major Minerals.Sodium: integer (nullable = true)
    -- Data.Major Minerals.Zinc: double (nullable = true)
   -- Data.Vitamins.Vitamin A - RAE: double (nullable = true)
    -- Data. Vitamins. Vitamin B12: double (nullable = true)
    -- Data. Vitamins. Vitamin B6: double (nullable = true)
    -- Data. Vitamins. Vitamin C: double (nullable = true)
[5]: # 2. Data cleaning
    # Identify nutrient columns by prefix "Data_"
    nutrient cols = [c for c in df.columns if c.startswith("Data ")]
    # Safely cast nutrient columns to float
    for c in nutrient cols:
        df = df.withColumn(c, expr(f"try_cast({c} as float)"))
    # Drop rows where all nutrient columns are null
    df = df.dropna(how="all", subset=nutrient cols)
    # Show dataset after cleaning
    df.show()
    # Count rows and columns
    row_count = df.count()
    col count = len(df.columns)
    print(f"Row count: {row_count}")
    print(f"Column count: {col_count}")
    # Drop rows with any nulls (strict clean data)
    df_clean = df.dropna()
    row count clean = df clean.count()
    print(f"Row count after removing all nulls: {row count clean}")
    # Drop rows with nulls in vitamin columns only
    vitamin_cols = [c for c in df.columns if "Vitamin" in c]
    df vitamin clean = df.dropna(subset=vitamin cols)
    row_count_vitamin_clean = df_vitamin_clean.count()
    print(f"Row count after removing nulls in vitamin columns: {row_count_vitamin_clean}")
```

| Category| Description|Nutrient_Data_Bank_Number|Data_Alpha_Carotene|Data_Beta_Carotene|Data_Beta_Cryptoxant
a_Carbohydrate|Data_Cholesterol|Data_Choline|Data_Fiber|Data_Lutein_and_Zeaxanthin|Data_Lycopene|Data_Niacin|Data_Prot
a_Retinol|Data_Riboflavin|Data_Selenium|Data_Sugar_Total|Data_Thiamin|Data_Water|Data_Fat_Monosaturated_Fat|Data_Fat_Fated_Fat|Data_Fat_Fated_Fat|Data_Fat_Fated_Fat|Data_Fat_Fated_Fat|Data_Fat_Fated_Fat|Data_Fat_Fated_Fat

```
0.0
4.88
           11.0
                   14.6
0.172
           3.7
                              0.047
1.899
               3.31
                                  115.0
10.0
                     85.0
                                   0.036
47.0
0.3
     -----
only showing top 20 rows
Row count: 7083
Column count: 38
Row count after removing all nulls: 7078
Row count after removing nulls in vitamin columns: 7083
```

2. **Data Analyst:** Performed statistical analysis, trend identification, and summary generation.

```
# 3. Summary statistics & visualization

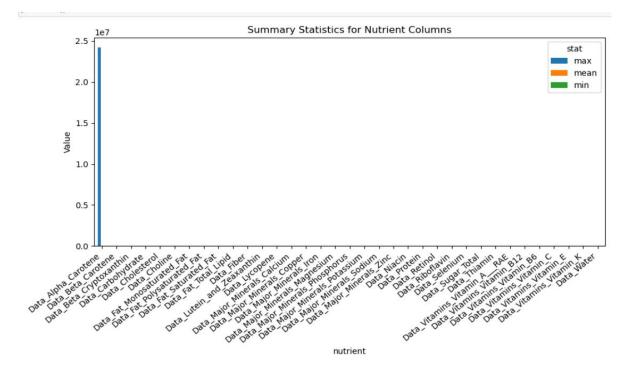
# Compute summary stats (mean, min, max) for all nutrient columns on cleaned df
summary_df = df_clean.agg(
    *[F.mean(c).alias(f"{c}_mean") for c in nutrient_cols],
    *[F.min(c).alias(f"{c}_min") for c in nutrient_cols],
    *[F.max(c).alias(f"{c}_max") for c in nutrient_cols]
)

# Convert summary to Pandas for plotting
summary_pd = summary_df.toPandas().T
summary_pd.columns = ['value']
summary_pd.rename(columns={'index': 'metric'}, inplace=True)
summary_pd['stat'] = summary_pd['metric'].str.split('_').str[-1]
summary_pd['nutrient'] = summary_pd['metric'].apply(lambda x: "_".join(x.split("_")[:-1]))

# Pivot dataframe for plotting
pivot = summary_pd_pivot(index='nutrient', columns='stat', values='value')
```

```
# Pivot dataframe for plotting
pivot = summary_pd.pivot(index='nutrient', columns='stat', values='value')

# Plot bar chart for nutrient summary statistics
pivot.plot(kind='bar', figsize=(10, 6))
plt.ylabel('Value')
plt.title('Summary Statistics for Nutrient Columns')
plt.title('Summary Statistics for Nutrient Columns')
plt.xticks(rotation=40, ha='right')
plt.tight_layout()
plt.show()
```

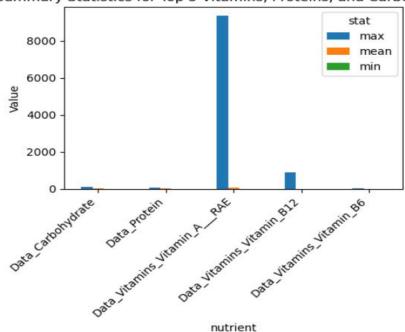


```
: # Select top 5 relevant nutrients (Vitamin, Protein, Carbohydrate)
  selected_cols = [
      c for c in df.columns
      if any(x in c for x in ["Vitamin", "Protein", "Carbohydrate"])
  # Summary stats for selected columns
  summary_selected = df.agg(
      *[F.mean(c).alias(f"{c}_mean") for c in selected_cols],
*[F.min(c).alias(f"{c}_min") for c in selected_cols],
      *[F.max(c).alias(f"{c}_max") for c in selected_cols]
  summary_selected.show()
  |Data_Carbohydrate_mean|Data_Protein_mean|Data_Vitamins_Vitamin_A___RAE_mean|Data_Vitamins_Vitamin_B12_mean|Data_Vi
  in_B6_mean|Data_Carbohydrate_min|Data_Protein_min|Data_Vitamins_Vitamin_A___RAE_min|Data_Vitamins_Vitamin_B12_min|I
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```

```
[9]: # Convert to Pandas for plotting
summary_pd = summary_selected.toPandas().T
summary_pd.columns = ['value']
summary_pd = summary_pd.reset_index()
summary_pd.rename(columns={'index': 'metric'}, inplace=True)
summary_pd['stat'] = summary_pd['metric'].str.split('_').str[-1]
summary_pd['nutrient'] = summary_pd['metric'].apply(lambda x: "_".join(x.split("_")[:-1]))
pivot = summary_pd.pivot(index='nutrient', columns='stat', values='value')

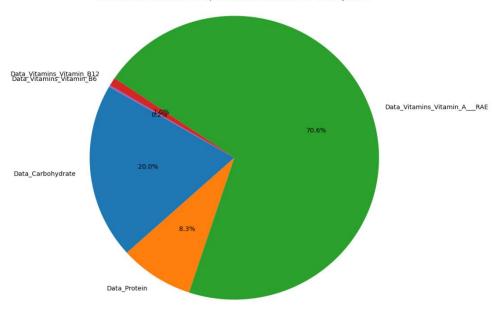
10]: # Plot bar chart
pivot.plot(kind='bar', figsize=(5, 5))
plt.ylabel('Value')
plt.title('Summary Statistics for Top 5 Vitamins, Proteins, and Carbohydrates')
plt.xticks(rotation=45, ha='right')
plt.tight_layout()
plt.show()
```

Summary Statistics for Top 5 Vitamins, Proteins, and Carbohydrates

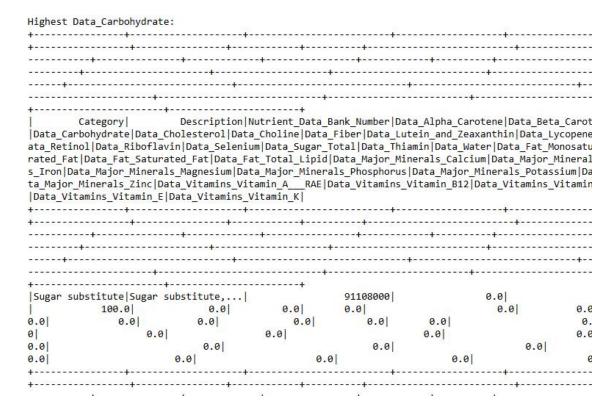


```
[11]: # Pie chart of mean distribution for selected nutrients
    mean_values = pivot['mean']
    plt.figure(figsize=(9, 9))
    plt.pie(mean_values, labels=mean_values.index, autopct='%1.1f%%', startangle=150)
    plt.title('Mean Value Distribution of Top 5 Vitamins, Proteins, and Carbohydrates')
    plt.axis('equal')
    plt.show()
```



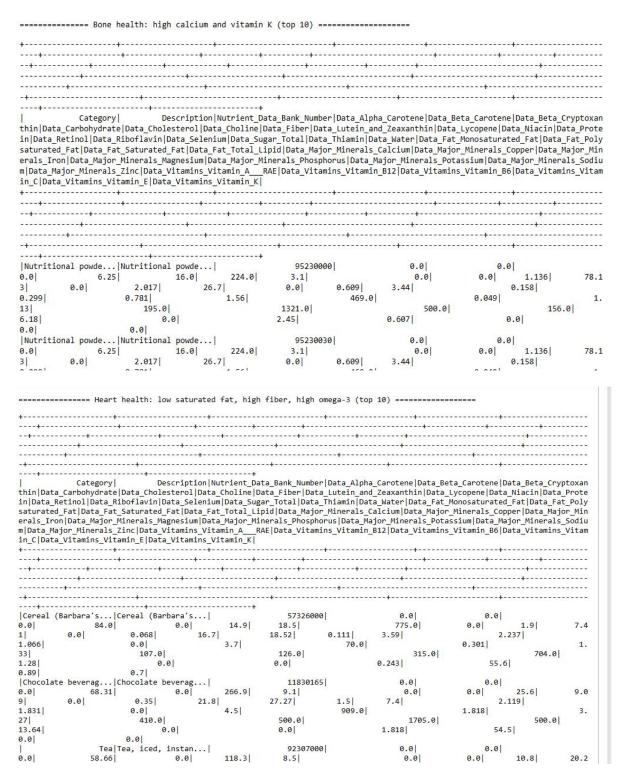


```
# 4. Highest and lowest values for selected nutrients
for col in selected_cols:
    print(f"\nHighest {col}:")
    df_clean.orderBy(df_clean[col].desc()).limit(1).show()
    print(f"Lowest {col}:")
    df_clean.orderBy(df_clean[col].asc()).limit(1).show()
```



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Category Desce Data_Cholest Riboflavin Dat t_Saturated_Fa Minerals_Magn _Zinc Data_Vintamin_E Data_V +	cription Nutrie terol Data_Chol ta_Selenium Dat at Data_Fat_Tot nesium Data_Maj tamins_Vitamin		umber Data_A: Data_Lutein Data_Thiamin Major_Minera osphorus Data itamins_Vitar +	lpha_Carotene and_Zeaxanthi Data_Water Da S_Calcium Data a_Major_Minera min_B12 Data_V	Data_Beta_Ca n Data_Lycop ta_Fat_Monos a_Major_Mine ls_Potassium itamins_Vita	rotene Data_Bet ene Data_Niacin aturated_Fat Da rals_Copper Dat Data_Major_Min min_B6 Data_Vit	a_Cryptoxanthi Data_Protein ta_Fat_Polysat a_Major_Minera erals_Sodium camins_Vitamin_ +	in Data_Carbo Data_Retino. Data_Retino. Data_Starbor_M: Cloata_Vitar	ohy l D Dat a_M ine min -+-

```
: # 5. Specialized food recommendations
  # High-protein foods (top 10)
  print("====== High Protein Food (top 10) =======")
  df_clean.orderBy(df_clean['Data_Protein'].desc()).limit(10).show()
  # Diabetes-friendly foods: low carbohydrates and sugars (top 10)
  print("====== Diabetes-friendly foods: low carbohydrates and sugars (top 10) =========")
  df_clean.orderBy(
        df_clean['Data_Carbohydrate'],
        df_clean['Data_Sugar_Total']
  ).limit(10).show()
  # Bone health: high calcium and vitamin K (top 10)
  print("-----Bone health: high calcium and vitamin K (top 10) ------")
  df_clean.orderBy(
       df_clean['Data_Protein'].desc(),
df_clean['Data_Vitamins_Vitamin_K'].desc()
  ).limit(10).show()
  # Heart health: low saturated fat, high fiber, high monounsaturated fat (top 10)
  print("====== Heart health: low saturated fat, high fiber, high omega-3 (top 10) =========""
  df_clean.orderBy(
        df_clean['Data_Fat_Saturated_Fat'],
        df_clean['Data_Fiber'].desc(),
        df_clean['Data_Fat_Monosaturated_Fat'].desc()
  | Nutritional powde...| Nutritional powde...| | |
| a | 6.25| 16.0| 224.0|
| 2.017| 26.7|
| 1.56|
  .....
                                                                                                                             0.0
                                                                                                                                         1.136
                                                                                                            0.0
                                                                                                      3.44
                                                                                                                                    0.158
                                                                                       0.6091
                                                                         0.01
                                                                                                                            9.9491
                                                                                           469.01
  13|
6.18|
6.0| 0.0| 0.0|
|Nutritional powde...|Nutritional powde...|
6.25| 16.0| 224.0|
2.017| 26.7|
                                  195.0|
                                                                        1321.0
                                                                       2.45|
                                                                                                                                     0.0
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                                                                                       0.609
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                                  195.0
                                                                        1321.0
                                                                                                               500.01
  13|
                                                                                                                                                156.01
 6.18
                                        0.01
                                                                       2.451
                                                                                                     0.607
                                                                                                                                     0.01
                               a al
  ====== Diabetes-friendly foods: low carbohydrates and sugars (top 10) =========
  | Category| Description|Nutrient_Data_Bank_Number|Data_Alpha_Carotene|Data_Beta_Carotene|Data_Beta_Cryptoxanthin|Data_Carbohydrate|Data_Cholesterol|Data_Choline|Data_Fiber|Data_LuteIn_and_Zeaxanthin|Data_Lycopene|Data_Niacin|Data_Protein|Data_Re
  tinol|Data_Riboflavin|Data_Selenium|Data_Sugar_Total|Data_Thiamin|Data_Water|Data_Fat_Monosaturated_Fat|Data_Fat_Polysaturated_Fat|Data_Fat_Polysaturated_Fat|Data_Fat_Data_Fat_Data_Major_Minerals_Calcium|Data_Major_Minerals_Iron_Fat_Data_Major_Minerals_Iron_Fat_Data_Major_Minerals_Iron_Fat_Data_Major_Minerals_Iron_Fat_Data_Major_Minerals_Iron_Fat_Data_Major_Minerals_Iron_Fat_Data_Fat_Data_Major_Minerals_Iron_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_Data_Fat_D
  |Data_Major_Minerals_Magnesium|Data_Major_Minerals_Phosphorus|Data_Major_Minerals_Potassium|Data_Major_Minerals_Sodium|Data_Major_Minerals_Sodium|Data_Major_Minerals_Sodium|Data_Major_Minerals_Zinc|Data_Vitamin_B6|Data_Vitamin_S_Vitamin_C|Data_Vitamin_B12|Data_Vitamins_Vitamin_B6|Data_Vitamins_Vitamin_C|Data_
  Vitamins_Vitamin_E|Data_Vitamins_Vitamin_K|
  Steak | Steak, NS as to t... |
                                                            21001000
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                                                                                         0.0
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  9.91
                    81.0
                                   93.0
                                                  0.0
                                                                                 0.0
                                                                                                 9.91
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                                                                                                                                              1.0
  0.237
                                                                                                                                 0.333
                    33.71
                                        0.01
                                                     0.082
                                                                  62.46
                                                                                                  2.926
                                                                                           0.083
  2.6431
                           6.75
                                                            16.0
                                                                                                                         2.381
                                     238.01
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                                                                                                        387.01
  23.0
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                                                                                                                                          0.0|
                               1.98
                                                           0.676
                                                                                         9.91
  1.0
                                                                                                               0.01
  |Beef steak | Beef steak, broil... |
                                                            21101120
                                                                                         0.0
                     87.0|
                                                                                 0.01
                                                                                                  0.0
                                                                                                                           27.06
                                                                                                                                              3.01
                                                             58.14
                                                     0.075
  0.2151
                   29.8
                                        0.01
                                                                                                 6.0051
                                                                                                                                0.595
  5.576
                          13.44
                                                            17.0|
                                                                                           0.079
                                                                                                                         2.26
  21.01
                                     218.0
                                                                        341.01
                                                                                                       382.01
                                                                                                                                      5.211
```



3. ML Engineer: Built clustering (KMeans) and dimensionality reduction (PCA) models for pattern detection.

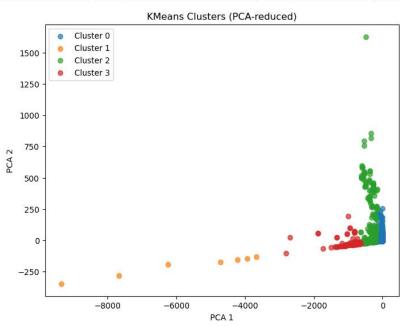
```
: # 6. Machine Learning Analysis
  # Feature selection (Vitamin, Protein, Carbohydrate, Fat, Fiber)
 features = [c for c in df.columns if any(x in c for x in ["Vitamin", "Protein", "Carbohydrate", "Fat", "Fiber"])]
 assembler = VectorAssembler(inputCols=features, outputCol="features")
 df features = assembler.transform(df).select("features")
 # KMeans clustering (k=4)
 kmeans = KMeans(k=4, seed=42)
 model = kmeans.fit(df_features)
 clusters = model.transform(df features)
 print(" Clustered Foods")
 clusters.show(5, truncate=False)
  # Find similar foods by Euclidean distance to the first food item
 from pyspark.ml.linalg import Vectors
 target = df_features.limit(1).collect()[0]["features"]
 similar = (df_features.rdd
            .map(lambda row: (float(Vectors.squared_distance(row["features"], target)), row["features"]))
            .sortByKey()
            .take(6))
 print("\n ▼ Top 5 similar foods:")
  for dist, feats in similar[1:]:
     print(f"Distance={dist:.4f}, Features={feats}")
 # Correlation matrix of nutrient features
 vector df = assembler.transform(df).select("features")
 corr_matrix = Correlation.corr(vector_df, "features").head()[0]
 corr_array = corr_matrix.toArray()
 print(corr array)

☑ Clustered Foods

 [6.889999866485596,0.0,1.0299999713897705,1.6579999923706055,0.4970000088214874,2.009000062942505,4.380000114440918,61.0,0.050
 00000074505806,0.010999999940395355,5.0,0.0799999821186066,0.30000001192092896
                                                                                      10
 [4.869999885559082,0.0,3.339999141693115,0.4259999990463257,0.06499999761581421,1.1640000343322754,1.9900000095367432,59.0,0.
  5600000023841858,0.05999999865889549,0.10000000149011612,0.029999999329447746,0.20000000298023224]|0
 00000214576721,0.061000000685453415,0.0,0.05000000074505806,0.30000001192092896]
  \lceil 4.460000038146973.0.0.3.0999999046325684.0.9990000128746033.0.12800000607967377.2.1540000438690186.3.4600000381469727.29.0.0.
 36000001430511475,0.03400000184774399,0.8999999761581421,0.0799999821186066,0.30000001192092896] 0
 00000214576721,0.061000000685453415,0.0,0.05000000074505806,0.30000001192092896]
                                                                                              T
 only showing top 5 rows
 Top 5 similar foods:
 Distance=4.0157, Features=[7.400000095367432,0.0,1.7200000286102295,1.3250000476837158,0.718999981880188,1.5119999647140503,3.5
 49999952316284,60.0,0.20000000298023224,0.0399999910593033,5.900000095367432,0.5899999737739563,0.0]
 Distance=4.0157, Features=[7.400000095367432,0.0,1.7200000286102295,1.3250000476837158,0.718999981880188,1.5119999647140503,3.5
 49999952316284,60.0,0.20000000298023224,0.03999999910593033,5.900000095367432,0.5899999737739563,0.0]
 Distance=4.0157, Features=[7.400000095367432,0.0,1.7200000286102295,1.3250000476837158,0.718999981880188,1.5119999647140503,3.5
 4999952316284,60.0,0.20000000298023224,0.0399999910593033,5.900000095367432,0.5899999737739563,0.0]
 Distance=4.0157, Features=[7.400000095367432,0.0,1.7200000286102295,1.3250000476837158,0.718999981880188,1.5119999647140503,3.5
 49999952316284,60.0,0.20000000298023224,0.0399999910593033,5.900000095367432,0.5899999737739563,0.0]
 Distance=4.0157, Features=[7.400000095367432,0.0,1.7200000286102295,1.3250000476837158,0.718999981880188,1.5119999647140503,3.5
 49999952316284,60.0,0.20000000298023224,0.03999999910593033,5.900000095367432,0.5899999737739563,0.0]
 Correlation matrix shape: (13, 13)
[[ 1.      0.32864258 -0.16771915     0.04580604     0.1000772      0.07554255
    -0.0913621 ]
  [ 0.32864258 1.
                       -0.02505399 0.20299966 0.27644682 0.03593452
    0.08350884 0.06331013 0.12199638 0.48191885 0.06784769 0.14478561
    0.036188661
  [-0.16771915 -0.02505399 1.
                                  0.22427035 0.08142519 0.18116615
    -0.09602871]
```

```
# 7. Cluster visualization with PCA
# Add row IDs to align DataFrames
df_with_id = df.withColumn("row_id", monotonically_increasing_id())
df_features_with_id = df_features.withColumn("row_id", monotonically_increasing_id())
clusters_with_id = clusters.withColumn("row_id", monotonically_increasing_id())
# Join cluster assignments to the original DataFrame
df_with_clusters = (
     df with id
     .join(clusters_with_id.select("row_id", "prediction"), on="row_id")
     .drop("row id")
     .withColumnRenamed("prediction", "cluster")
display(df_with_clusters)
# 2D visualization using PCA
pca = PCA(k=2, inputCol="features", outputCol="pca_features")
pca_model = pca.fit(df_features)
df_pca = pca_model.transform(df_features_with_id)
# Join cluster assignments to PCA DataFrame
df_pca = (
     df pca
     .join(clusters_with_id.select("row_id", "prediction"), on="row_id")
     .withColumnRenamed("prediction", "cluster")
# Convert to Pandas for matplotlib plotting
pdf = df_pca.select("pca_features", "cluster").toPandas()
pdf["x"] = pdf["pca_features"].apply(lambda v: v[0])
pdf["y"] = pdf["pca_features"].apply(lambda v: v[1])
import matplotlib.pyplot as plt
plt.figure(figsize=(8,6))
for cluster in sorted(pdf["cluster"].unique()):
    subset = pdf[pdf["cluster"] == cluster]
     plt.scatter(subset["x"], subset["y"], label=f"Cluster {cluster}", alpha=0.7)
plt.xlabel("PCA 1")
plt.ylabel("PCA 2")
plt.title("KMeans Clusters (PCA-reduced)")
plt.legend()
```

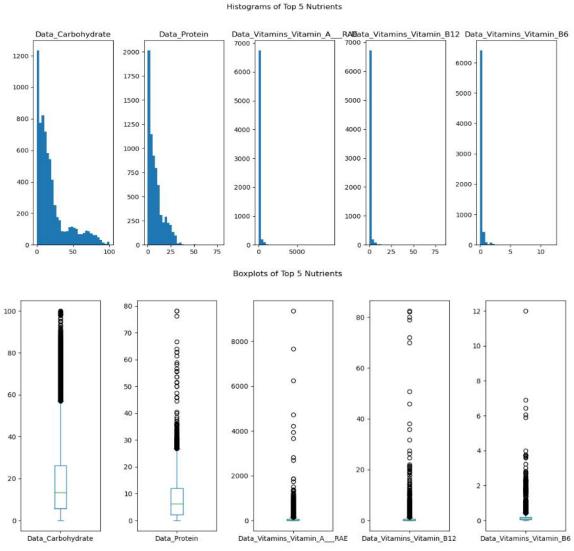
DataFrame[Category: string, Description: string, Nutrient_Data_Bank_Number: string, Data_Alpha_Carotene: float, Data_Beta_Carotene: float, Data_Beta_Cryptoxanthin: float, Data_Carobnydrate: float, Data_Cholesterol: float, Data_Choline: float, Data_Fiber: float, Data_Lutein_and_Zeaxanthin: float, Data_Lycopene: float, Data_Niacin: float, Data_Protein: float, Data_Retinol: float, Data_Riboflavin: float, Data_Selenium: float, Data_Sugar_Total: float, Data_Thiamin: float, Data_Water: float, Data_Fat_Monosatu rated_Fat: float, Data_Fat_Polysaturated_Fat: float, Data_Fat_Saturated_Fat: float, Data_Fat_Total_Lipid: float, Data_Major_Minerals_Copper: float, Data_Major_Minerals_Iron: float, Data_Major_Minerals_Magnesium: float, Data_Major_Minerals_Potasphorus: float, Data_Major_Minerals_Sodium: float, Data_Major_Minerals_Fat_Float, Data_Major_Minerals_Sodium: float, Data_Major_Minerals_Fotal_Lipid: float, Data_Major_Miner



Analysis on Normalized dataset(only on top-5 nutrients)

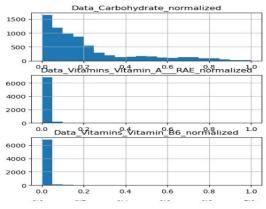
4. Visualization Specialist: Designed bar charts, boxplots, and PCA plots for clear interpretation.

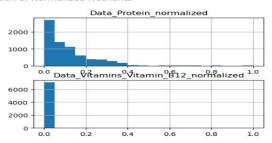
```
# Histograms and boxplots for selected nutrients
df plot = df clean.select(selected cols).toPandas()
df_plot.hist(bins=30, figsize=(12, 6), layout=(1, 5), grid=False)
plt.suptitle('Histograms of Top 5 Nutrients')
plt.tight layout(rect=[0, 0, 1, 0.95])
plt.show()
df_plot.plot(kind='box', subplots=True, layout=(1, 5), figsize=(12, 6), sharey=False)
plt.suptitle('Boxplots of Top 5 Nutrients')
plt.tight_layout(rect=[0, 0, 1, 0.95])
plt.show()
```

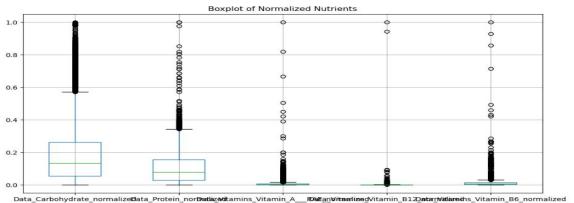


```
# Use only selected nutrient columns, e.g., top 5
selected_cols = [
    c for c in df.columns
     if any(x in c for x in ["Vitamin", "Protein", "Carbohydrate"])
][:5]
# Convert to RDD of Rows
rdd_rows = df.select(*selected_cols).rdd
# Convert each row to tuple of floats
rdd_tuples = rdd.map(lambda row: tuple(float(x) if x is not None else 0 for x in row))
# Compute column-wise min and max using reduce
min_values = rdd_tuples.reduce(lambda x, y: tuple(min(a,b) for a,b in zip(x,y)))
max_values = rdd_tuples.reduce(lambda x, y: tuple(max(a,b) for a,b in zip(x,y)))
print("Mins:", min_values)
print("Maxs:", max_values)
Mins: (0.0, 0.0, 0.0, 0.0, 0.0)
Maxs: (100.0, 78.12999725341797, 9363.0, 879.0, 14.0)
def normalize(row):
   normalized = []
   for i, val in enumerate(row):
       if max_values[i] != min_values[i]:
          norm_val = (val - min_values[i]) / (max_values[i] - min_values[i])
          norm_val = 0.0 # Handle constant columns
       normalized.append(norm_val)
   return tuple(normalized)
rdd_normalized = rdd_tuples.map(normalize)
from pyspark.sql.types import StructType, StructField, FloatType
# Define schema with FloatType for each selected column
schema = StructType([StructField(col, FloatType(), True) for col in selected_cols])
# Create DataFrame with schema
normalized_df = spark.createDataFrame(rdd_rows, schema)
normalized_df.show(5)
|Data_Carbohydrate|Data_Protein|Data_Vitamins_Vitamin_A___RAE|Data_Vitamins_Vitamin_B12|Data_Vitamins_Vitamin_B6|
             6.89 1.03
                                                     61.0
                                                                             0.05
             4.87
                         3.34
                                                     59.0
                                                                             0.56
                                                                                                     0.06
            4.67
                         3.28
                                                     32.0
                                                                             0.54
                                                                                                   0.061
            4.46
                                                     29.0
                                                                              0.36
                                                                                                   0.034
                          3.1
            4.67
                        3.28
                                                     32.0
                                                                              0.54
                                                                                                   0.061
only showing top 5 rows
normalized pd = df normalized.toPandas()
import matplotlib.pyplot as plt
# Histogram to view the distribution of each nutrient
normalized pd.hist(column=[c for c in normalized pd.columns if c != "Category"], bins=20, figsize=(12, 6))
plt.suptitle("Histogram view for the Distribution of Normalized Nutrients")
plt.show()
# Boxplot - visualize spread and outliers per nutrient
normalized pd.boxplot(column=[c for c in normalized pd.columns if c != "Category"], figsize=(12,6))
plt.title("Boxplot of Normalized Nutrients")
plt.show()
```

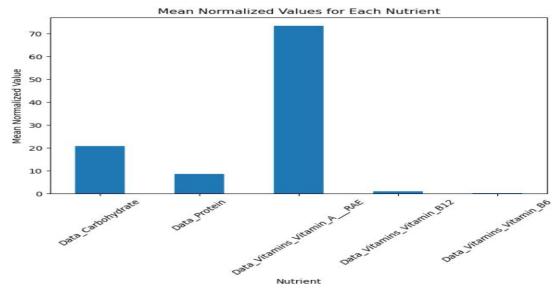
Histogram view for the Distribution of Normalized Nutrients







```
# Bar plot of mean normalized values per nutrient
mean_values = normalized_pd.mean()
mean_values.plot(kind='bar', figsize=(8, 5))
plt.title('Mean Normalized Values for Each Nutrient')
plt.ylabel('Mean Normalized Value')
plt.xlabel('Nutrient')
plt.xticks(rotation=45)
plt.show()
```



7. Insights and Observations

- Foods from categories such as snacks and fast food tend to have higher energy and fat content.
- Fruits and vegetables are rich in vitamins but low in energy content.
- A positive correlation was observed between protein and energy levels.
- Outliers in certain categories may indicate data recording inconsistencies or unique food compositions.

8. Conclusion

This project demonstrates how PySpark can be effectively used for large-scale nutritional data analysis. Through data cleaning, transformation, and visualization, we gain meaningful insights into food compositions that could inform health, diet planning, and food industry research.