# HealthVerity Claims Analysis Haltam

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## 0.1 Health Verity Analysis

#### 0.2 Jasmine Haltam

- 1. This analysis leveraged GCP Cloud Storage/BigQuery, GCP Vertex AI, Python, and SQL.
- 2. The initial Sample\_Claims dataset was loaded to BigQuery with Schema matching the Table\_Definitions guidelines, resulting in exclusion of 25 rows that did not meet the Schema. The final dataset was a matrix of 4,975 rows x 6 cols.

### Question 1

- 1a. What are the top 5 most common valid procedure codes?
- 1a. 88175, 87591, 87491, 87798, 85049.

```
#Code for Question 1. Subquery sorts by most prevalent procedure code________descending (Top 5). Returns only distinct procedure code

SELECT DISTINCT procedure_code
FROM
(select procedure_code, COUNT(procedure_code) as total
FROM `healthverityproject.sample_claims.notnull`
GROUP BY procedure_code
ORDER BY total DESC
LIMIT 5);
```

```
Query complete after 0.01s: 100%| | 4/4 [00:00<00:00, 1687.68query/s]
Downloading: 100%| | 5/5 [00:01<00:00, 4.92rows/s]
```

#### 1b. How many patients are associated with at least one of those procedures?

1b. 58 unique patients are associated with at least one of the procedure codes above.

```
#Query uses code above to return the distinct patients associated with top 5
procedures.

SELECT COUNT (DISTINCT patient_id) as total_patients
FROM `healthverityproject.sample_claims.notnull`
WHERE procedure_code in (SELECT DISTINCT procedure_code
FROM
(select procedure_code, COUNT(procedure_code) as total
FROM `healthverityproject.sample_claims.notnull`
GROUP BY procedure_code
ORDER BY total DESC
LIMIT 5))
ORDER BY total_patients DESC;
```

```
Query complete after 0.03s: 100%| | 9/9 [00:00<00:00, 2735.02query/s]
Downloading: 100%| | 1/1 [00:01<00:00, 1.13s/rows]
```

# [1]: total\_patients 0 58

# 1c. What is the percentage of records in sample\_claims that have valid procedure codes?

1c. We will define valid procedure codes as non-null procedure codes that successfully join the reference table.

1c. 66.4% of records contain a valid procedure code.

```
[18]: | %%bigquery
      ##Query divides the number of records successfully joining the cpt_codes table_
       ⇒by the total number of rows.
      SELECT (y.valid_codes/x.total_rows)*100 as PercentValid, Valid_Codes, Total_Rows
      FROM
      (SELECT COUNT(*) as Total_Rows
      FROM `healthverityproject.sampledataset5.
       →healthverityproject_sampledataset5_sampledsetf`) x
      JOIN
      (SELECT COUNT(*) as valid_codes
      FROM healthverityproject.sampledataset5.
       →healthverityproject_sampledataset5_sampledsetf master
       inner join healthverityproject.valid_cpt_codes.valid_cpt_codes cpt on cpt.codeu
       ⇒= master.procedure_code
      WHERE master.procedure_code IS NOT NULL) y
      on 1=1
```

Query complete after 0.00s: 100% | 6/6 [00:00<00:00, 1316.89query/s]

```
Downloading: 100% | 1/1 [00:00<00:00, 1.08rows/s]
[18]:
         PercentValid Valid Codes Total Rows
             66.41206
                              3304
                                           4975
     Question 2
     2a) What are the top 5 most common valid diagnosis codes? Note: Diagnosis code
     field needs to be split.
     We will define valid diagnosis codes as the ICD10 codes that successfully join the reference ICD10
     table.
     2a) Z11, Z34, Z01, E55, Z12.
[27]: | %%bigquery
      ##First, we unnest diagnosis codes by '^' delimiter.
      ##We use regex to split to the period to allow us to join to the reference \Box
       →ICD10 table.
      ##Alternative solutions included potentially adding a period after the first 3_{\sqcup}
       ⇔characters in the reference ICD10 table.
      CREATE TABLE healthverityproject.sampledataset5.extracted_icd as (
      WITH data AS
        (SELECT diagnosis_codes
        FROM healthverityproject.sampledataset5.
       healthverityproject_sampledataset5_sampledsetf)
      SELECT diagnosis_codes, substrings, REGEXP_EXTRACT(substrings, r'^[^\.]+') as_
       ⇒substrings_simplified
      FROM data, UNNEST(SPLIT(diagnosis_codes, '^')) substrings)
     Query complete after 0.01s: 100% | 3/3 [00:00<00:00, 1300.83query/s]
[27]: Empty DataFrame
      Columns: []
      Index: []
[34]: %%bigquery
      ##Return the top 5 most common valid ICD codes that match the icd_10_codes_
       ⇔reference table after cleanup above.
      SELECT substrings_simplified, COUNT(substrings_simplified) as total ##return_□
       ⇔count of substrings grouped by substring.
      from healthverityproject.sampledataset5.extracted icd as original
      inner JOIN healthverityproject.icd10codes.icd_10_codes as n ##use inner join tou
```

⇔filter unmatched values.

ON original.substrings\_simplified = n.string\_field\_0

```
where substrings_simplified is not null ##filter any null_
substrings_simplified_values
GROUP BY substrings_simplified
ORDER BY total DESC
LIMIT 5; ##limit to only the top 5 most frequent, valid diagnosis codes.
```

Query complete after 0.00s: 100%| | 4/4 [00:00<00:00, 1880.01query/s]
Downloading: 100%| | 5/5 [00:00<00:00, 5.17rows/s]

[34]: substrings\_simplified total
0 Z11 1466
1 Z34 855
2 Z01 525
3 E55 494
4 Z12 427

Question 2b. What are the top 5 invalid diagnosis codes? With and without special characters removed.

- 2b. With special character removed: Z86, Z87, Z91.
- **2b.** Without special character removed (after join): Z86.718, Z87.59, Z87.898, Z87.440, Z91.89.
- 2b. Without special character removed (pre-join): Z11.3, E55.9, Z01.419, Z11.8, Z34.81.

```
Query complete after 0.00s: 100% | 4/4 [00:00<00:00, 1566.94query/s]
Downloading: 100% | 3/3 [00:00<00:00, 3.16rows/s]
```

```
[37]: substrings_simplified total 0 Z86 32 1 Z87 23 2 Z91 1
```

### [45]: %%bigquery

#Note that to successfully join, the period needed to be removed pre-join.

SELECT substrings, substrings\_simplified, COUNT(substrings) as total ##return $_{\sqcup}$   $_{\hookrightarrow}$ count of substrings grouped by substring.

from healthverityproject.sampledataset5.extracted\_icd as original

left JOIN healthverityproject.icd10codes.icd\_10\_codes as n ##use left join to⊔
→return everything

ON original.substrings\_simplified = n.string\_field\_0

where string\_field\_0 is null ##filter to return only the invalid ICD10 values GROUP BY substrings\_simplified, substrings

ORDER BY total DESC

LIMIT 5;

Query complete after 0.00s: 100%| | 4/4 [00:00<00:00, 1457.87query/s]
Downloading: 100%| | 5/5 [00:00<00:00, 5.39rows/s]

#### [45]: substrings substrings\_simplified total

0	Z86.718	Z86	32
1	Z87.59	Z87	17
2	Z87.898	Z87	5
3	Z91.89	Z91	1
4	Z87.440	Z87	1

### [44]: | %%bigquery

##Without the special character "." removed, return the top invalid ICD10 codes\_ that do not join the reference table.

SELECT substrings, substrings\_simplified, COUNT(substrings) as total ##return $_{\sqcup}$   $_{\hookrightarrow}$ count of substrings grouped by substring.

from healthverityproject.sampledataset5.extracted\_icd as original

ON original.substrings = n.string field 0

where string\_field\_0 is null ##filter to return only the invalid ICD10 values GROUP BY substrings simplified, substrings

ORDER BY total DESC

LIMIT 5;

Query complete after 0.00s: 100% | 1/1 [00:00<00:00, 872.90query/s]
Downloading: 100% | 5/5 [00:01<00:00, 4.94rows/s]

```
substrings substrings_simplified total
[44]:
      0
              Z11.3
                                       Z11
                                               942
      1
             E55.9
                                       E55
                                               494
      2
           Z01.419
                                       Z01
                                               403
      3
             Z11.8
                                       Z11
                                               357
      4
            Z34.81
                                       Z34
                                               346
```

Question 2c. What is the percentage of records in sample\_claims that have valid diagnosis codes after split and with special characters removed?

Note that sample\_claims, after splitting the diagnosis codes, has 10,064 rows.

2c. 99.4%, or 10,008 records with ICD codes, successfully join the ICD10 reference table.

```
Query complete after 0.00s: 100%| | 6/6 [00:00<00:00, 2078.79query/s]
Downloading: 100%| | 1/1 [00:00<00:00, 1.02rows/s]
```

# [52]: PercentValid Valid\_Codes Total\_Rows 0 99.443561 10008 10064

#### Question 3.

Using the TableDefinitions provided and sample files, please write at least 1 data quality validation for each category below. Minimum 5 and no more than 10 validations required.

- 1. Formatting
- 2. Duplicates
- 3. Missing values
- 4.Referential
- 5.Date Distribution (trend in chronological order)
- 1. Formatting- Dates

```
[83]: | %%bigquery
      WITH query_result AS (
      SELECT * FROM healthverityproject.sampledataset5.
       →healthverityproject_sampledataset5_sampledsetf
      WHERE PARSE_DATE('%Y-%d-%m', FORMAT_DATE('%Y-%d-%m', date_service)) IS NULL)
      SELECT
      IF(COUNT(*) > 0, 'Validation Error: File fails date formatting.', 'Validation⊔
       ⇔Pass: File passes date formatting validation.') as Validation_Message from

¬query_result

                                            | 1/1 [00:00<00:00, 711.38query/s]
     Query complete after 0.00s: 100%
                           | 1/1 [00:00<00:00, 1.09rows/s]
     Downloading: 100%
[83]:
                                    Validation_Message
     O Validation Error: File fails date formatting.
     2. Duplicates- overall
[82]: | %%bigquery
      SELECT (
      WITH query_result AS (SELECT_
       apatient_id,claim_id,diagnosis_codes,procedure_code,date_service,date_received,count(*)
      FROM healthverityproject.sampledataset5.
       ⇔healthverityproject sampledataset5 sampledsetf
      GROUP BY
       patient_id,claim_id,diagnosis_codes,procedure_code,date_service,date_received
      HAVING count(*) > 1)
      SELECT
       IF(COUNT(*) > 0, 'Validation Error: File contains duplicate rows.',
       →'Validation Pass: No duplicate rows.') as Validation_Message from

query_result)
     Query complete after 0.00s: 100%
                                            | 1/1 [00:00<00:00, 483.88query/s]
     Downloading: 100%
                          | 1/1 [00:01<00:00, 1.17s/rows]
[82]:
      O Validation Pass: No duplicate rows.
     Duplicates- claim ID's
[76]: | %%bigquery
      SELECT (WITH query_result AS (WITH duplicate_rows AS (
        SELECT claim_id,
          ROW_NUMBER() OVER (PARTITION BY claim_id ORDER BY claim_id) as row_number_
       →##Ranks claim IDs. If duplicate, row_number > 1.
       FROM healthverityproject.sampledataset5.
       →healthverityproject_sampledataset5_sampledsetf)
```

```
SELECT claim_id
      FROM duplicate_rows
      WHERE row number > 1) ##Filter to return duplicate claim ID values.
      SELECT
      IF(COUNT(*) > 0, 'Validation Error: Duplicated Claim IDs.', 'Validation Pass:⊔
       File has no duplicates.') as Validation_Message from query_result)
     Query complete after 0.00s: 100%
                                         | 3/3 [00:00<00:00, 1261.57query/s]
     Downloading: 100%
                            | 1/1 [00:01<00:00, 1.02s/rows]
[76]:
                                             f0_
     O Validation Error: Duplicated Claim IDs.
     3. Missing values- ICD 10 Codes
[78]: | %%bigquery
      SELECT (WITH query_result AS (SELECT *
      FROM healthverityproject.sampledataset5.
       →healthverityproject_sampledataset5_sampledsetf
      WHERE diagnosis codes IS NULL)
      ##Filter for null diagnosis codes, if > 0, return validation error.
      SELECT
      IF(COUNT(*) > 0, 'Validation Error: Missing ICD10 Codes.', 'Validation Pass:
       File has no missing values.') as Validation_Message from query_result)
     Query complete after 0.00s: 100%
                                           | 2/2 [00:00<00:00, 685.23query/s]
                            | 1/1 [00:00<00:00,
     Downloading: 100%
                                                1.05rows/sl
[78]:
      O Validation Error: Missing ICD10 Codes.
     Missing values- Patient IDs
[79]: | %%bigquery
      SELECT(WITH query_result AS (SELECT *
      FROM healthverityproject.sampledataset5.
       →healthverityproject_sampledataset5_sampledsetf
      WHERE patient id IS NULL)
      ##Filter for null patient ID, if > 0, return validation error.
      SELECT
      IF(COUNT(*) > 0, 'Validation Error: Missing Patient IDs.', 'Validation Pass:
       File has no missing values.') as Validation Message from query result)
     Query complete after 0.00s: 100% | 2/2 [00:00<00:00, 789.29query/s]
```

Downloading: 100% | 1/1 [00:01<00:00, 1.01s/rows]

```
[79]:

0 Validation Error: Missing Patient IDs.

4.Referential
```

```
[80]: | %%bigquery
      SELECT (WITH query_result AS (SELECT (x.joined_total_count/y.
       →original_total_count)*100 as Percentage_of_validity
      (SELECT COUNT(*) as joined_total_count
          FROM healthverityproject.sampledataset5.
       →healthverityproject_sampledataset5_sampledsetf master
       inner join healthverityproject.valid cpt codes.valid cpt codes cpt on cpt.code
       ⇒= master.procedure_code
      WHERE master.procedure_code IS NOT NULL ) x
      JOIN
      (SELECT COUNT(*) as original_total_count
      FROM healthverityproject.sampledataset5.
       ⇔healthverityproject_sampledataset5_sampledsetf) y
      on 1=1)
      #If Inner join results in a decrease in rowcount, return validation error.
       →Values not successfully joining reference table.
      SELECT
       IF (Percentage_of_validity<100, 'Validation Error: Referential Join by CPT_
       Gode.', 'Validation Pass: Referential Join by CPT Code.') as ...
       →Validation_Message from query_result)
```

```
Query complete after 0.00s: 100%| | 6/6 [00:00<00:00, 2497.85query/s]
Downloading: 100%| | 1/1 [00:00<00:00, 1.01rows/s]
```

#### 5. Date Distribution

```
WHERE date_received < previous_date)
```

Query complete after 0.01s: 100% | 8/8 [00:00<00:00, 2120.34query/s]
Downloading: 100% | 1/1 [00:01<00:00, 1.02s/rows]

[81]: f0\_

O Validation Error: Dates not in chr. order.

#### Code:

Note that Code output below compiles the validation checks to produce a list of validation checks in a single table, per guidelines.

```
[71]: | %%bigquery
      #The following list of queries produce a single table containing all of the \Box
       ⇒validation checks performed for this question.
      ----"Formatting - DATE"-----
      #Check the date formatting. If the date does not meet the "Y-%d-%m format, __
       ⇔return a validation fail.
      WITH query_result AS (
      SELECT * FROM healthverityproject.sampledataset5.
       →healthverityproject_sampledataset5_sampledsetf
      WHERE PARSE DATE('%Y-%d-%m', FORMAT DATE('%Y-%d-%m', date service)) IS NULL)
      SELECT
       IF(COUNT(*) > 0, 'Validation Error: File fails date formatting.', 'Validation ∪
       →Pass: File passes date formatting validation.') as Validation_Message from
       ⊶query_result
      UNION ALL
                  #Duplicate Overall Analysis.
      ----"Duplicates - Overall"-----
      \#Check if the file contains duplicate rows across the entire dataset. If there \sqcup
       →are duplicates, return a validation error.
      SELECT (
      WITH query_result AS (SELECT_
       apatient_id,claim_id,diagnosis_codes,procedure_code,date_service,date_received,count(*)
      FROM healthverityproject.sampledataset5.
       ⇔healthverityproject_sampledataset5_sampledsetf
       apatient_id,claim_id,diagnosis_codes,procedure_code,date_service,date_received
      HAVING count(*) > 1)
```

```
SELECT
IF(COUNT(*) > 0, 'Validation Error: File contains duplicate rows.',
 →'Validation Pass: No duplicate rows.') as Validation Message from
 →query_result)
UNION ALL
----"Duplicates - Claim ID"-----
\#Check if the file contains duplicate claim IDs. If there are duplicate row_{\sqcup}
 →IDs, return validation error.
SELECT (WITH query_result AS (WITH duplicate_rows AS (
 SELECT claim_id,
   ROW_NUMBER() OVER (PARTITION BY claim_id ORDER BY claim_id) as row_number_
 →##Ranks claim IDs. If duplicate, row_number > 1.
 FROM healthverityproject.sampledataset5.
 →healthverityproject_sampledataset5_sampledsetf)
SELECT claim id
FROM duplicate rows
WHERE row_number > 1) ##Filter to return duplicate claim ID values.
SELECT
IF(COUNT(*) > 0, 'Validation Error: Duplicated Claim IDs.', 'Validation Pass:
 →File has no duplicates.') as Validation Message from query result)
UNION ALL
---- "Missing values - Diagnosis Codes"-----
#Check for null diagnosis codes.
SELECT (WITH query_result AS (SELECT *
FROM healthverityproject.sampledataset5.
 →healthverityproject_sampledataset5_sampledsetf
WHERE diagnosis codes IS NULL)
##Filter for null diagnosis codes, if > 0, return validation error.
SELECT
IF(COUNT(*) > 0, 'Validation Error: Missing ICD10 Codes.', 'Validation Pass:
 →File has no missing values.') as Validation_Message from query_result)
UNION ALL
```

```
---- "Missing values - Patient IDs"-----
#Check for null patient IDs.
SELECT(WITH query_result AS (SELECT *
FROM healthverityproject.sampledataset5.
 ⇔healthverityproject_sampledataset5_sampledsetf
WHERE patient_id IS NULL)
##Filter for null patient ID, if > 0, return validation error.
SELECT
IF(COUNT(*) > 0, 'Validation Error: Missing Patient IDs.', 'Validation Pass:
 File has no missing values.') as Validation_Message from query_result)
UNION ALL
---- "Referential Analysis - CPT Code"-----
#Referential Analysis - Check if join to CPT code table successfully works. If __
 ⇒join is not a 1-1 match, return validation error.
SELECT (WITH query_result AS (SELECT (x.joined_total_count/y.
 →original_total_count)*100 as Percentage_of_validity
FROM
(SELECT COUNT(*) as joined_total_count
   FROM healthverityproject.sampledataset5.
 →healthverityproject_sampledataset5_sampledsetf master
inner join healthverityproject.valid_cpt_codes.valid_cpt_codes cpt on cpt.codeu
 ⇒= master.procedure_code
WHERE master.procedure_code IS NOT NULL ) x
JOIN
(SELECT COUNT(*) as original_total_count
FROM healthverityproject.sampledataset5.
 ⇔healthverityproject_sampledataset5_sampledsetf) y
on 1=1)
#If Inner join results in a decrease in rowcount, return validation error.
 →Values not successfully joining reference table.
SELECT
IF (Percentage_of_validity<100, 'Validation Error: Referential Join by CPT_
 ⇔Code.', 'Validation Pass: Referential Join by CPT Code.') as⊔
 →Validation_Message from query_result)
UNION ALL
```

```
----"Date Distribution - Chronological Order"-----
      #First, we sort by date received ascending. If there is a date gap, return an
      #Then, use the lag function to check for chronological order of dates in the
       →dataset.
      SELECT (
      WITH query_result AS (
        SELECT date_received,
               LAG(date received) OVER (ORDER BY date_received) as previous_date_
       ⇒##compare each row with the row behind it
       FROM healthverityproject.sampledataset5.
       ⇔healthverityproject_sampledataset5_sampledsetf
      )
      SELECT
        IF(COUNT(*) = 0, 'Validation Error: Dates not in chr. order.', 'Validation□
       →Pass: Dates in chro. order.') as Validation_Message
      FROM query_result
      WHERE date_received < previous_date)</pre>
     Query complete after 0.00s: 100%|
                                            | 26/26 [00:00<00:00, 8811.56query/s]
                           | 7/7 [00:01<00:00, 6.62rows/s]
     Downloading: 100%
[71]:
                                      Validation_Message
                 Validation Error: Missing ICD10 Codes.
      1 Validation Error: Referential Join by CPT Code.
                 Validation Error: Duplicated Claim IDs.
                 Validation Error: Missing Patient IDs.
      3
      4
                     Validation Pass: No duplicate rows.
      5
          Validation Error: File fails date formatting.
              Validation Error: Dates not in chr. order.
[69]: #Date - Trend in Chronological Order
      from google.cloud import bigquery
      import matplotlib.pyplot as plt
      #Leveraged Python's GCP BigQuery library to pull distinct patient id,
       →date_received and use matplotlib to produce a bar chart
      client = bigquery.Client()
      query = '''
      SELECT date_received, COUNT(DISTINCT patient_id) as total_patients
      FROM healthverityproject.sampledataset5.
       ⇔healthverityproject_sampledataset5_sampledsetf
      GROUP BY date_received
      ORDER BY date_received;
```

```
results = client.query(query).to_dataframe()

results.plot(x='date_received', y='total_patients', kind='bar')
plt.title("Trend of Total Patients by Date Received")
plt.xlabel("Date Received")
plt.ylabel("Total Patients")
```

[69]: Text(0, 0.5, 'Total Patients')

