

# Text2Cohort: Democratizing the NCI Imaging Data Commons with Natural Language Cohort Discovery

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## Abstract

### Purpose

The Imaging Data Commons (IDC) is a cloud-based database that provides researchers with open access to cancer imaging data, with the goal of facilitating collaboration in medical imaging research. However, querying the IDC database for cohort discovery and access to imaging data has a significant learning curve for researchers due to its complex nature. We developed Text2Cohort, a large language model (LLM) based toolkit to facilitate user-friendly and intuitive natural language cohort discovery in the IDC.

### Materials and Methods

Text2Cohort translates user input into IDC database queries using prompt engineering and autocorrection and returns the query's response to the user. Autocorrection resolves errors in queries by passing the errors back to the model for interpretation and correction. We evaluate Text2Cohort on 50 natural language user inputs ranging from information extraction to cohort discovery. The resulting queries and outputs were verified by two computer scientists to measure Text2Cohort's accuracy and F1 score.

### Results

Text2Cohort successfully generated queries and their responses with an 88% accuracy and F1 score of 0.94. However, it failed to generate queries for 6/50 (12%) user inputs due to syntax and semantic errors.

### Conclusion

Our results indicate that Text2Cohort succeeded at generating queries with correct responses, but occasionally failed due to a lack of understanding of the data schema. Despite these shortcomings, Text2Cohort demonstrates the utility of LLMs to enable researchers to discover and curate cohorts using data hosted on IDC with high levels of accuracy using natural language in a more intuitive and user-friendly way.

## Introduction

The National Cancer Institute's Imaging Data Commons (IDC) is a cloud-based data commons that provides researchers with open access to large-scale cancer imaging datasets and tools for analysis, with the goal of facilitating the sharing of imaging data and promoting collaboration in the field of medical imaging research [1]. Not only would a data commons leverage economies of scale in providing high-quality networking and storage infrastructure, it would facilitate new opportunities for translational research through big-data analytics and collaborations in the research community [2, 3].

The IDC is hosted on the Google Cloud Platform (GCP), which provides a secure and scalable infrastructure for data storage and processing [4]. Furthermore, the DICOM metadata across all the datasets hosted on IDC (known as collections) is indexed in the form of a BigQuery database to enable powerful queries and cohort discovery for any IDC user [5]. However, curating cohorts by querying the BigQuery database can be a time-consuming task requiring extensive knowledge of the data schema. In addition, users also require knowledge of Structured Query Language (SQL) and a sandbox environment with Python to download and access the imaging data. This is a major bottleneck for users without extensive knowledge of the data schema or technical skills to effectively query these datasets and curate multi-collection cohorts.

Recently, large language models (LLMs) have emerged that can understand and respond to natural language queries, which can help alleviate the problems associated with BigQuery. The most advanced large language models, like OpenAI's Generative Pre-trained Transformer (GPT), have billions of parameters and have been trained on enormous corpus' of text data, such as news articles, books, and web pages on the entire internet [6–8]. At their core, LLMs learn to identify patterns and relationships between words and phrases in the text and develop an understanding of the structure and grammar of language. Consequently, fine-tuning LLMs provides a powerful interface to extend their capabilities to language translation, chatbot development, or query generation [8–10].

To that end, we developed Text2Cohort, a LLM based toolkit to facilitate cohort curation by interpreting natural language queries. By using natural language to query data as shown in **Figure 1**, Text2Cohort enables researchers to interact with and discover cohorts from multiple collections simultaneously in a more intuitive and user-friendly way, thus eliminating the learning curve associated with current solutions. In this work, we developed and evaluated Text2Cohort for generating a diverse range of queries from information extraction to cohort discovery.

Question:

How many collections have lung CT images hosted on IDC?

Generated Query:

```
SELECT COUNT(DISTINCT collection_id)
FROM bigquery-public-data.idc_current.dicom_all
WHERE modality = 'CT'
      AND LOWER(BodyPartExamined) LIKE '%lung%'
```

Result:

9

**Figure 1.** The Text2Cohort toolkit on an example natural language user input. Text2Cohort first transforms the user input into a query, uses the generated query to query the BigQuery table, and returns the response back to the user.

## Materials and Methods

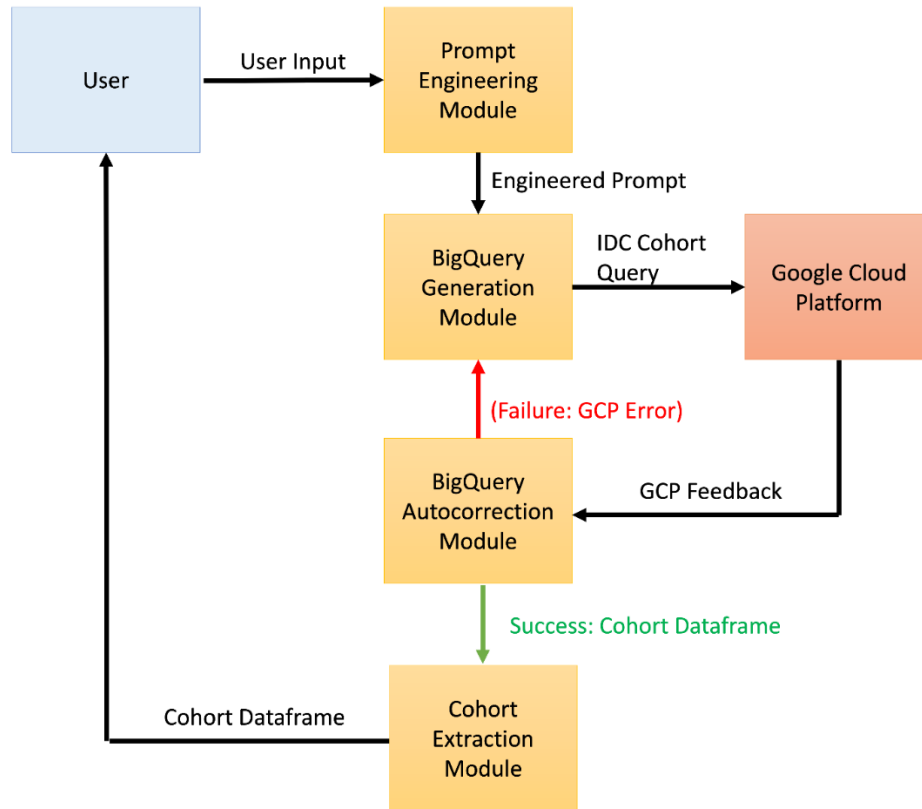
### Text2Cohort

The Text2Cohort toolkit is built using GPT-3.5, the state-of-the-art language model that also powers ChatGPT, and consists of four major components: (1) prompt engineering, (2) BigQuery generation, (3) BigQuery autocorrection, and (4) cohort extraction, as illustrated in **Figure 2**.

### Prompt Engineering

While GPT-3.5 provides a state-of-the-art interface for natural language processing, it is crucial to prime the model via prompt engineering to provide contextual information and focus the model's responses for the task at hand. In other words, this enables a zero-shot fine-tuning of the model's capabilities for the given task. In Text2Cohort, we utilize prompt engineering to prime GPT-3.5 for query generation as follows:

1. Query from the public BigQuery database “idc\_current.dicom\_all”, which contains DICOM metadata for all collections hosted by the IDC.
2. Queries should be as specific as possible without providing explanations behind responses to reduce time taken to generate queries.
3. Queries must be generated enclosed within fixed delimiters to simplify query extraction.
4. Queries should utilize regular expressions in queries to prevent exact matches, thus resulting in a more generalizable query structure.



**Figure 2.** Illustration of the Text2Cohort toolkit.

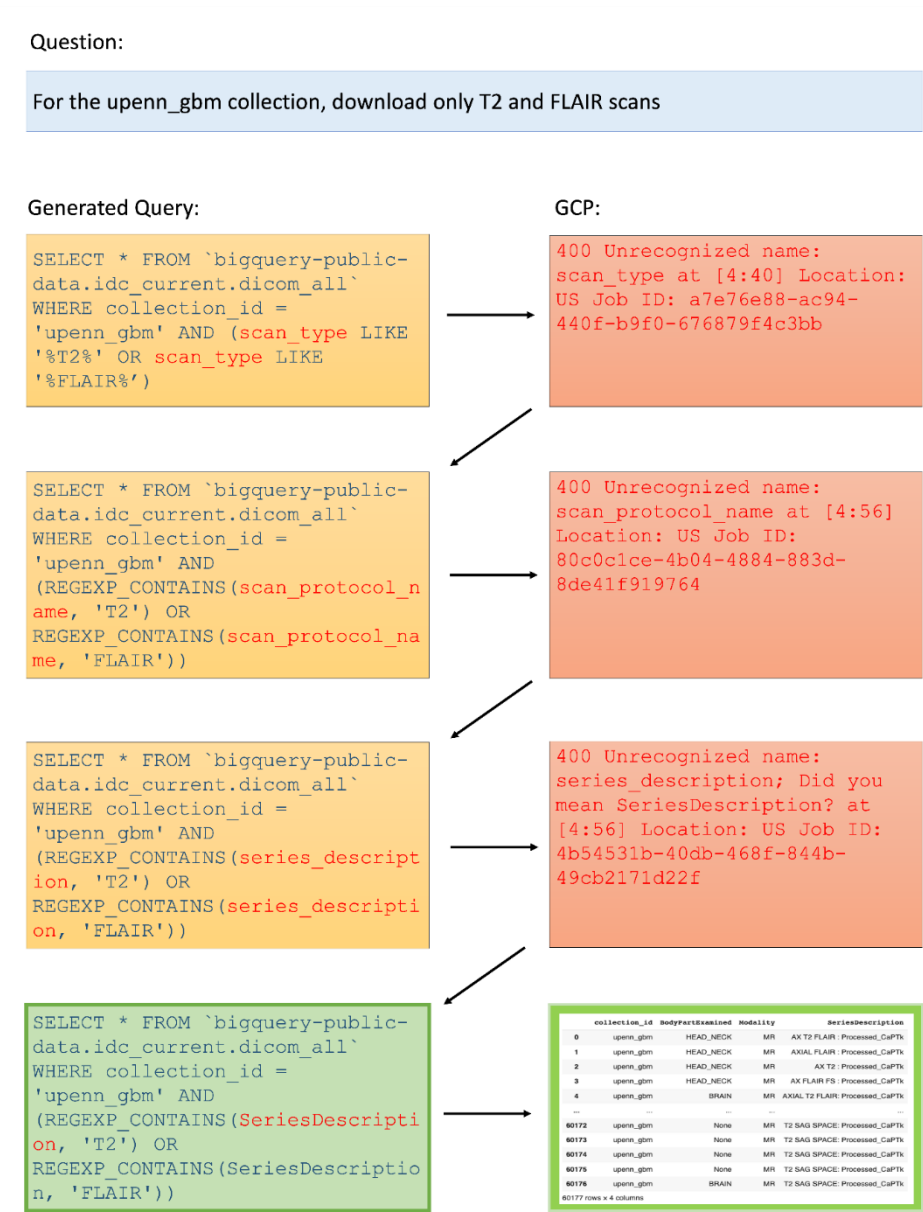
## BigQuery Generation

Once GPT-3.5 is primed for query generation, the user can enter a free-text query such as "How many male brain MRI images are hosted on IDC?" or "I want all images in the nsclc\_radiomics collection". This input is fed to the model for interpretation and query generation. The resultant query is extracted from the response and queried to IDC's BigQuery database using the GCP's BigQuery client.

## BigQuery Autocorrection

In many cases, GPT-3.5 generates an incorrect query containing errors that can be classified under two groups: (1) syntax errors and (2) semantic errors. Syntax errors can occur due to a typo or an incorrectly labeled field, while semantic errors can occur due to an incorrect interpretation of the input text. Text2Cohort implements an autocorrect pipeline to address both errors. The autocorrection pipeline ingests the associated error message when the generated query is incorrect and passes back to GPT-3.5 to interpret the error and attempt to fix it. Text2Cohort's autocorrect pipeline is implemented recursively to attempt query autocorrection

until the query is executed successfully. However, there are a few limitations to our autocorrection pipeline: (1) In some cases, semantic errors may not be corrected if the underlying query is executed successfully, thus resulting in an incorrect response, and (2) we limit autocorrection to at most  $K = 10$  attempts to prevent token usage from exceeding OpenAI's API token limit. **Figure 3** illustrates how the Text2Cohort toolkit autocorrects a query.



**Figure 3.** Illustration of the autocorrection pipeline for an example user input. The example demonstrates how the autocorrection pipeline recursively autoengineers the prompt to guide the LLM towards using the keyword SeriesDescription to filter different MRI sequences.

## Cohort Extraction

The cohort extraction component of the Text2Cohort toolkit uses the generated and autocorrected query to query the BigQuery database and extracts the resultant table as a Pandas dataframe in Python.

## Experiments

To initiate our study, we curated a dataset of  $N = 50$  natural language user inputs ranging from information extraction to cohort discovery to evaluate the Text2Cohort toolkit, with queries like "How many male and female patients are present in the NSCLC Radiomics dataset?" and "Please curate a dataset of all male brain MRI patients hosted on IDC" (**Supplementary Table 1**). The Text2Cohort toolkit was evaluated on these natural language user inputs and the resultant queries and responses were expert-verified by consensus between two computer scientists as either correct or incorrect; disagreements were adjudicated by a third computer scientist. The efficacy of the Text2Cohort toolkit was consequently measured by its accuracy and F1 scores across all user inputs. For user inputs that generated incorrect queries and responses, the query was corrected by an expert and the Levenshtein distance between the corrected query and the incorrect query was calculated. In short, the Levenshtein distance measures the minimum number of character modifications to change one string into another [11].

## Results

Our results indicate that on all  $N = 50$  curated natural language user inputs, across information extraction and cohort discovery tasks, Text2Cohort demonstrates excellent performance with an accuracy of 88% and F1 score of 0.94 in generating correct responses to the user inputs. The performance of Text2Cohort on an example set of information extraction and cohort discovery queries is illustrated in **Table 1**. In other words, the Text2Cohort generated correct queries and responses to 44 out of 50 user inputs (88%) but failed to do so for six user inputs (12%), as shown in **Table 2**. Out of these six incorrect responses, one (17%) resulted in a query that exceeded the maximum number of autocorrection attempts, while five (83%) failed due to semantic errors within the generated queries. Furthermore, out of the five responses containing semantic errors, three (60%) failed due to the generated query using an incorrect field for the task. These six incorrect queries were manually corrected by an expert with  $12.83 \pm 5.81$  character-edits determined by the Levenshtein distance between the corrected and incorrect queries, as shown in **Table 2**. In short, our results demonstrate that despite failing to correct 10%

of all queries due to semantic errors, the Text2Cohort toolkit was able to generate queries with correct structure and autocorrect syntax errors within them with a 98% success rate. The complete list of curated natural language user inputs with the resultant queries is provided in the **Supplementary Results**.

## Discussion

Text2Cohort yields excellent results in translating natural language user input into powerful database queries, and subsequently into responses, through prompt engineering and autocorrection. Furthermore, it demonstrates the utility of LLMs to facilitate natural language information extraction and cohort discovery by enabling a more intuitive and user-friendly interface to the IDC and other similar databases. It eliminates the need for a technical understanding of databases and the underlying data schema. In other words, our work demonstrates that not only does Text2Cohort revolutionize how researchers can discover cohorts, interact with, and access imaging data hosted on the IDC, it also democratizes access to the IDC.

However, the utility of the Text2Cohort toolkit is limited due to a few bottlenecks. Firstly, Text2Cohort requires an understanding of the entire data schema to reach its full potential. In our study, we observed that all incorrect responses were due to the lack of an understanding of the data schema (e.g., incorrectly interpreting collections as studies). While it is evident that LLM can encode certain facts, they are also prone to fabricating them without appropriate supervision [12]. Text2Cohort's autocorrection pipeline functions as a form of weak supervision by allowing the model to interpret and correct any errors generated while querying. However, autocorrection is limited in its utility when handling semantic errors. For example, a query containing semantic errors may successfully execute, bypass autocorrection, and return an incorrect response. Despite being held back by a limited knowledge of the data schema, our results indicate that Text2Cohort always generates queries with correct structure and any queries with syntax or semantic errors can be corrected by an expert with minimal character-edits.

Recently, the paradigm of in-context learning has enabled zero-shot fine-tuning of LLMs using contextual information as a method for supervision [13–17]. For example, the open-source package Llamaindex implements data connectors to pass various data sources, such as tables, schemas, radiology reports, etc. as context to a GPT model [18]. For future work, we intend to explore these in-context learning techniques to address these limitations in Text2Cohort, while comparing them with other state-of-the-art language models. We also invite others in the research

community to experiment with other techniques and language models. The Text2Cohort implementation and our dataset is available on <https://github.com/UM2ii/text2cohort>.



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**Table 1.** Text2Cohort generated queries on an example set of 10 natural language user inputs ranging from information extraction to cohort discovery.

| Natural Language User Input |  | Text2Cohort Generated Query  |
|-----------------------------|--|--|
| 1                           | How many different body parts and modalities are hosted on IDC?  | <code>SELECT COUNT(DISTINCT BodyPartExamined) as num_body_parts, COUNT(DISTINCT Modality) as num_modalities FROM bigquery-public-data.idc_current.dicom_all</code>   |
| 2                           | How many patients are on IDC?  | <code>SELECT COUNT(DISTINCT PatientID) AS num_patients FROM `bigquery-public-data.idc_current.dicom_all`</code>  |
| 3                           | How many male brain MRIs are hosted on IDC where the patient is older than 25 and acquired after 2005?                   | <code>SELECT COUNT(*) as num_of_scans FROM `bigquery-public-data.idc_current.dicom_all` WHERE Modality = 'MR' AND BodyPartExamined = 'BRAIN' AND PatientSex = 'M' AND CAST(REGEXP_EXTRACT(PatientAge, r'\d+') AS INT64) &gt; 25 AND CAST(EXTRACT(YEAR FROM StudyDate) AS INT64) &gt; 2005</code>   |
| 4                           | For the upenn_gbm collection, how many male and female patients?   | <code>SELECT PatientSex, COUNT(DISTINCT PatientID) FROM bigquery-public-data.idc_current.dicom_all WHERE collection_id = 'upenn_gbm' GROUP BY PatientSex</code>  |
| 5                           | For the upenn_gbm collection, how many patients under the age of 25 years, between 25 and 50, and greater than 50 years? | <code>SELECT CASE WHEN CAST(REGEXP_REPLACE(PatientAge, r'^0-9', '') AS INT64) &lt; 25 THEN 'under_25' WHEN CAST(REGEXP_REPLACE(PatientAge, r'^0-9', '') AS INT64) &gt;= 25 AND CAST(REGEXP_REPLACE(PatientAge, r'^0-9', '') AS INT64) &lt;= 50 THEN '25_to_50' WHEN CAST(REGEXP_REPLACE(PatientAge, r'^0-9', '') AS INT64) &gt; 50 THEN 'over_50' ELSE 'unknown_age' END AS age_group, COUNT(DISTINCT PatientID) AS num_patients FROM `bigquery-public-data.idc_current.dicom_all` WHERE collection_id='upenn_gbm' GROUP BY age_group</code> |
| 6                           | List all collection with at least 500 patients   | <code>SELECT collection_id, COUNT(DISTINCT PatientID) AS NumPatients FROM `bigquery-public-data.idc_current.dicom_all` GROUP BY collection_id HAVING NumPatients &gt;= 500</code>  |
| 7                           | List all the collections with at least 100000 images   | <code>SELECT collection_id, COUNT(*) AS num_images FROM `bigquery-public-data.idc_current.dicom_all` GROUP BY collection_id HAVING COUNT(*) &gt;= 100000</code>  |
| 8                           | List the collections with both PET and CT  | <code>SELECT DISTINCT collection_id FROM `bigquery-public-data.idc_current.dicom_all` WHERE modality IN ("CT", "PT") GROUP BY collection_id HAVING COUNT(DISTINCT modality) = 2</code>   |
| 9                           | For each collection on IDC, count the body parts, modalities, and series descriptions                                    | <code>SELECT DISTINCT collection_id, COUNT(DISTINCT SeriesDescription) AS NumSeries, COUNT(DISTINCT BodyPartExamined) AS NumBodyParts, COUNT(DISTINCT Modality) AS NumModalities FROM `bigquery-public-data.idc_current.dicom_all` GROUP BY collection_id</code>   |
| 10                          | For the upenn_gbm collection, download only male patient data for patients between 25 and 50 years of age                | <code>SELECT * FROM `bigquery-public-data.idc_current.dicom_all` WHERE collection_id = 'upenn_gbm' AND PatientSex = 'M' AND PatientAge LIKE '%Y' AND CAST(REGEXP_REPLACE(PatientAge, r'^\d+', '') AS INT64) BETWEEN 25 AND 50</code>   |

**Table 2.** Text2Cohort generated queries that failed to generate a correct response, corresponding to the natural language user input. Expert corrected generated queries are provided. Errors are highlighted in red, and corrections highlighted in blue.

|   | Natural Language User Input  | Text2Cohort Generated Query  | Expert Corrected Query   |
|---|--|--|--|
| 1 | List the collections with lung CT  | SELECT DISTINCT collection_id FROM `bigquery-public-data.idc_current.dicom_all` WHERE modality = 'CT' AND <b>BodyPartExamined LIKE '%Lung%'</b>  | SELECT DISTINCT collection_id FROM `bigquery-public-data.idc_current.dicom_all` WHERE modality = 'CT' AND <b>LOWER(BodyPartExamined) LIKE '%lung%'</b>   |
| 2 | What is the download size of each collection in GB   | SELECT collection_id, ROUND(SUM( <b>file_size</b> )/POWER(10,9),2) AS download_size_GB FROM `bigquery-public-data.idc_current.dicom_all` GROUP BY collection_id  | SELECT collection_id, ROUND(SUM( <b>instance_size</b> )/POWER(10,9),2) AS download_size_GB FROM `bigquery-public-data.idc_current.dicom_all` GROUP BY collection_id  |
| 3 | What collections are hosted on IDC that focus on glioblastoma?   | SELECT DISTINCT collection_id FROM `bigquery-public-data.idc_current.dicom_all` WHERE <b>StudyDescription</b> LIKE '%glioblastoma%'  | SELECT DISTINCT collection_id FROM `bigquery-public-data.idc_current.dicom_all` WHERE <b>LOWER(collection_cancerType)</b> LIKE '%glioblastoma%'  |
| 4 | How many collections have atleast 500 patients   | SELECT COUNT( <b>DISTINCT collection_id</b> ) FROM `bigquery-public-data.idc_current.dicom_all` GROUP BY collection_id HAVING COUNT(DISTINCT PatientID) >= 500   | SELECT COUNT( <b>collection_id</b> ) FROM (SELECT DISTINCT collection_id FROM `bigquery-public-data.idc_current.dicom_all` GROUP BY collection_id HAVING COUNT(DISTINCT PatientID) >= 500)   |
| 5 | How many collections on IDC have brain data  | SELECT COUNT(DISTINCT <b>StudyInstanceUID</b> ) FROM `bigquery-public-data.idc_current.dicom_all` WHERE Modality='MR' AND BodyPartExamined='BRAIN'   | SELECT COUNT(DISTINCT <b>collection_id</b> ) FROM `bigquery-public-data.idc_current.dicom_all` WHERE Modality='MR' AND BodyPartExamined='BRAIN'  |
| 6 | How many patients, images, modalities, body parts, sequences, and different scanners in the IDC upenn_gbm collection | SELECT COUNT(DISTINCT PatientID) AS num_patients, COUNT(*) AS num_images, COUNT(DISTINCT Modality) AS num_modalities, COUNT(DISTINCT BodyPartExamined) AS num_body_parts, COUNT(DISTINCT SequenceName) AS num_sequences, COUNT(DISTINCT <b>StationName</b> ) AS num_scanners FROM `bigquery-public-data.idc_current.dicom_all` WHERE collection_id = 'upenn_gbm' | SELECT COUNT(DISTINCT PatientID) AS num_patients, COUNT(*) AS num_images, COUNT(DISTINCT Modality) AS num_modalities, COUNT(DISTINCT BodyPartExamined) AS num_body_parts, COUNT(DISTINCT SequenceName) AS num_sequences, COUNT(DISTINCT <b>ManufacturerModelName</b> ) AS num_scanners FROM `bigquery-public-data.idc_current.dicom_all` WHERE collection_id = 'upenn_gbm' |

# Supplementary Materials

## Supplementary Results

**Table 1.** The complete list of curated natural language user inputs ( $N = 50$ ) with their corresponding Text2Cohort generated queries. Generated queries containing syntax or semantic errors are highlighted in red.

|    | Natural Language User Input                                       | Text2Cohort Generated Query   |
|----|---|---|
| 1  | How many collections are hosted on IDC                            | SELECT COUNT(DISTINCT collection_id) FROM `bigquery-public-data.idc_current.dicom_all`  |
| 2  | List all the collections  | SELECT DISTINCT collection_id FROM `bigquery-public-data.idc_current.dicom_all`   |
| 3  | How many body parts are present across all the collections on IDC | SELECT COUNT(DISTINCT BodyPartExamined) as num_body_parts FROM `bigquery-public-data.idc_current.dicom_all`   |
| 4  | List all the body parts   | SELECT DISTINCT BodyPartExamined FROM `bigquery-public-data.idc_current.dicom_all`  |
| 5  | How many modalities are present across all datasets on IDC        | SELECT COUNT(DISTINCT Modality) FROM bigquery-public-data.idc_current.dicom_all   |
| 6  | List all the modalities   | SELECT DISTINCT Modality FROM `bigquery-public-data.idc_current.dicom_all`  |
| 7  | How many different MRI sequences are present on IDC               | SELECT COUNT(DISTINCT SequenceName) FROM bigquery-public-data.idc_current.dicom_all WHERE modality = 'MR';  |
| 8  | List all the MRI sequences  | SELECT DISTINCT SeriesDescription FROM `bigquery-public-data.idc_current.dicom_all` WHERE Modality = 'MR'   |
| 9  | How many different body parts and modalities are hosted on IDC    | SELECT COUNT(DISTINCT BodyPartExamined) as num_body_parts, COUNT(DISTINCT Modality) as num_modalities FROM `bigquery-public-data.idc_current.dicom_all`           |
| 10 | How many images are hosted on IDC                                 | SELECT COUNT(*) FROM `bigquery-public-data.idc_current.dicom_all`   |
| 11 | How many patients are on IDC                                      | SELECT COUNT(DISTINCT PatientID) AS num_patients FROM `bigquery-public-data.idc_current.dicom_all`  |
| 12 | How many collections have at least 500 patients                   | SELECT COUNT(DISTINCT collection_id) FROM `bigquery-public-data.idc_current.dicom_all` GROUP BY collection_id HAVING COUNT(DISTINCT PatientID) >= 500             |
| 13 | List all collection with at least 500 patients                    | SELECT collection_id, COUNT(DISTINCT PatientID) AS NumPatients FROM `bigquery-public-data.idc_current.dicom_all` GROUP BY collection_id HAVING NumPatients >= 500 |
| 14 | List all the collections with at least 100000 images              | SELECT collection_id, COUNT(*) AS num_images FROM `bigquery-public-data.idc_current.dicom_all` GROUP BY collection_id HAVING COUNT(*) >= 100000                   |

|    |   |  |
|----|---|--|
| 15 | What are different MRI scanners used for datasets on IDC                              | SELECT DISTINCT Manufacturer, ManufacturerModelName FROM `bigquery-public-data.idc_current.dicom_all` WHERE Modality = 'MR'  |
| 16 | How many collections on IDC have brain data   | SELECT COUNT(DISTINCT StudyInstanceUID) FROM `bigquery-public-data.idc_current.dicom_all` WHERE Modality='MR' AND BodyPartExamined='BRAIN'   |
| 17 | Which IDC collections have brain images   | SELECT DISTINCT collection_id FROM `bigquery-public-data.idc_current.dicom_all` WHERE BodyPartExamined = 'BRAIN'   |
| 18 | How many collections have lung CT images hosted on IDC                                | SELECT COUNT(DISTINCT collection_id) FROM bigquery-public-data.idc_current.dicom_all WHERE modality = 'CT' AND LOWER(BodyPartExamined) LIKE '%lung%'   |
| 19 | List the collections with lung CT   | SELECT DISTINCT collection_id FROM `bigquery-public-data.idc_current.dicom_all` WHERE modality = 'CT' AND <b>BodyPartExamined LIKE '%Lung%'</b>  |
| 20 | List the collections with both PET and CT   | SELECT DISTINCT collection_id FROM `bigquery-public-data.idc_current.dicom_all` WHERE modality IN ("CT", "PT") GROUP BY collection_id HAVING COUNT(DISTINCT modality) = 2  |
| 21 | What is the download size of each collection in GB                                    | SELECT collection_id, ROUND(SUM(file_size)/POWER(10,9),2) AS download_size_GB FROM `bigquery-public-data.idc_current.dicom_all` GROUP BY collection_id   |
| 22 | For each collection on IDC, list the number of images                                 | SELECT collection_id as collection, COUNT(*) as num_images FROM `bigquery-public-data.idc_current.dicom_all` GROUP BY collection_id  |
| 23 | For each collection on IDC, list the number of patients                               | SELECT collection_id AS Collection, COUNT(DISTINCT PatientID) AS num_patients FROM `bigquery-public-data.idc_current.dicom_all` GROUP BY Collection  |
| 24 | For each collection on IDC, list all the body parts and modalities available          | SELECT collection_id, BodyPartExamined, modality FROM bigquery-public-data.idc_current.dicom_all GROUP BY collection_id, BodyPartExamined, modality ORDER BY collection_id, BodyPartExamined, modality   |
| 25 | Count the number of modalities for each collection on IDC                             | SELECT COUNT(DISTINCT Modality), collection_id FROM `bigquery-public-data.idc_current.dicom_all` GROUP BY collection_id  |
| 26 | For each collection on IDC, count the body parts and modalities                       | SELECT collection_id, COUNT(DISTINCT BodyPartExamined) AS num_body_parts, COUNT(DISTINCT Modality) AS num_modalities FROM `bigquery-public-data.idc_current.dicom_all` GROUP BY collection_id  |
| 27 | For each collection on IDC, count the body parts, modalities, and series descriptions | SELECT DISTINCT collection_id, COUNT(DISTINCT SeriesDescription) AS NumSeries, COUNT(DISTINCT BodyPartExamined) AS NumBodyParts, COUNT(DISTINCT Modality) AS NumModalities FROM `bigquery-public-data.idc_current.dicom_all` GROUP BY collection_id      |
| 28 | For each collection on IDC, list the body parts, modalities, and series descriptions  | SELECT collection_id, BodyPartExamined, Modality, SeriesDescription FROM `bigquery-public-data.idc_current.dicom_all` WHERE IFNULL(collection_id, "") != "" GROUP BY collection_id, BodyPartExamined, Modality, SeriesDescription ORDER BY collection_id |

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| 29 | For each collection hosted on IDC, what is the proportion of male and female patients?                            | <pre>WITH gender_counts AS ( SELECT collection_id, PatientSex, COUNT(DISTINCT PatientID) AS patient_count FROM `bigquery-public-data.idc_current.dicom_all` GROUP BY collection_id, PatientSex ), total_patients AS ( SELECT collection_id, COUNT(DISTINCT PatientID) AS total_count FROM `bigquery-public-data.idc_current.dicom_all` GROUP BY collection_id ) SELECT gender_counts.collection_id, total_patients.total_count, ROUND(gender_counts.patient_count / CAST(total_patients.total_count AS numeric), 2) AS male_proportion, ROUND((total_patients.total_count - gender_counts.patient_count) / CAST(total_patients.total_count AS numeric), 2) AS female_proportion FROM gender_counts JOIN total_patients ON gender_counts.collection_id = total_patients.collection_id ORDER BY gender_counts.collection_id;</pre> |
| 30 | How many male brain MRI images are hosted on IDC  | <pre>SELECT count(*) FROM bigquery-public-data.idc_current.dicom_all WHERE Modality = 'MR' AND BodyPartExamined = 'BRAIN' AND PatientSex = 'M'</pre>   |
| 31 | Give me patient id of all male brain MRI images hosted on IDC   | <pre>SELECT DISTINCT PatientID FROM `bigquery-public-data.idc_current.dicom_all` WHERE modality = 'MR' AND BodyPartExamined = 'BRAIN' AND PatientSex = 'M'</pre>   |
| 32 | I only want brain MRI DWI sequences   | <pre>SELECT * FROM bigquery-public-data.idc_current.dicom_all WHERE Modality = 'MR' AND BodyPartExamined = 'BRAIN' AND lower(SeriesDescription) LIKE '%dwi%'</pre>   |
| 33 | How many male brain MRIs are hosted on IDC where the patient is older than 25 and acquired after 2005?            | <pre>SELECT COUNT(*) as num_of_scans FROM `bigquery-public-data.idc_current.dicom_all` WHERE Modality = 'MR' AND BodyPartExamined = 'BRAIN' AND PatientSex = 'M' AND CAST(REGEXP_EXTRACT(PatientAge, r'\d+') AS INT64) &gt; 25 AND CAST(EXTRACT(YEAR FROM StudyDate) AS INT64) &gt; 2005</pre>   |
| 34 | Can you give me the patient id and study date for all pediatric studies hosted on IDC?                            | <pre>SELECT PatientID, StudyDate FROM bigquery-public-data.idc_current.dicom_all WHERE PatientAge LIKE '%Y' AND CAST(REGEXP_REPLACE(PatientAge, 'Y', '') AS NUMERIC) &lt; 18"</pre>  |
| 35 | How many images hosted on IDC have a transfer syntax uid of explicit VR little endian and explicit VR big endian? | <pre>SELECT TransferSyntaxUID, COUNT(*) AS image_count FROM `bigquery-public-data.idc_current.dicom_all` WHERE TransferSyntaxUID IN ('1.2.840.10008.1.2.1', '1.2.840.10008.1.2.2') GROUP BY 1</pre>  |
| 36 | How many images hosted on IDC where sourced from institutions in Maryland?  | <pre>SELECT COUNT(*) FROM `bigquery-public-data.idc_current.dicom_all` WHERE InstitutionAddress LIKE '%MD%' OR InstitutionAddress LIKE '%Md%' OR InstitutionAddress LIKE '%maryland%' OR InstitutionAddress LIKE '%Maryland%'</pre>  |
| 37 | What collections are hosted on IDC that focus on glioblastoma?  | <pre>SELECT DISTINCT collection_id FROM `bigquery-public-data.idc_current.dicom_all` WHERE <b>StudyDescription</b> LIKE '%glioblastoma%'</pre>   |
| 38 | I want images in the nslc_radiomics collection  | <pre>SELECT * FROM `bigquery-public-data.idc_current.dicom_all` WHERE collection_id = 'nslc_radiomics'</pre>   |
| 39 | I want all seg images in the nslc_radiomics collection  | <pre>SELECT * FROM `bigquery-public-data.idc_current.dicom_all` WHERE Modality = "SEG" AND StudyInstanceUID IN ( SELECT StudyInstanceUID FROM `bigquery-public-data.idc_current.dicom_all` WHERE collection_id = "nslc_radiomics" );</pre>   |

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| 40 | Download all brain MRI data on IDC  | SELECT * FROM `bigquery-public-data.idc_current.dicom_all` WHERE Modality = 'MR' AND BodyPartExamined = 'BRAIN'  |
| 41 | I want to download images in the IDC upenn_gbm collection   | SELECT * FROM `bigquery-public-data.idc_current.dicom_all` WHERE collection_id = 'upenn_gbm'   |
| 42 | How many patients, images, modalities, body parts, sequences, and different scanners in the IDC upenn_gbm collection    | SELECT COUNT(DISTINCT PatientID) AS num_patients, COUNT(*) AS num_images, COUNT(DISTINCT Modality) AS num_modalities, COUNT(DISTINCT BodyPartExamined) AS num_body_parts, COUNT(DISTINCT SequenceName) AS num_sequences, COUNT(DISTINCT <b>StationName</b> ) AS num_scanners FROM `bigquery-public-data.idc_current.dicom_all` WHERE collection_id = 'upenn_gbm'   |
| 43 | For the IDC upenn_gbm collection, list all modalities, body parts, sequences, and different scanners                    | SELECT DISTINCT Modality, BodyPartExamined, SeriesDescription, ManufacturerModelName FROM `bigquery-public-data.idc_current.dicom_all` WHERE collection_id='upenn_gbm'   |
| 44 | For the upenn_gbm collection, how many male and female patients   | SELECT PatientSex, COUNT(DISTINCT PatientID) FROM bigquery-public-data.idc_current.dicom_all WHERE collection_id = 'upenn_gbm' GROUP BY PatientSex   |
| 45 | For the upenn_gbm collection, how many teenagers  | SELECT COUNT(DISTINCT PatientID) AS num_teenagers FROM `bigquery-public-data.idc_current.dicom_all` WHERE collection_id = "upenn_gbm" AND CAST(SUBSTR(PatientAge, 1, LENGTH(PatientAge)-1) AS NUMERIC) >= 13 AND CAST(SUBSTR(PatientAge, 1, LENGTH(PatientAge)-1) AS NUMERIC) <= 19  |
| 46 | For the upenn_gbm collection, how many patients under the age of 25 years, between 25 and 50, and greater than 50 years | SELECT CASE WHEN CAST(REGEXP_REPLACE(PatientAge, r'^0-9', '') AS INT64) < 25 THEN 'under_25' WHEN CAST(REGEXP_REPLACE(PatientAge, r'^0-9', '') AS INT64) >= 25 AND CAST(REGEXP_REPLACE(PatientAge, r'^0-9', '') AS INT64) <=50 THEN '25_to_50' WHEN CAST(REGEXP_REPLACE(PatientAge, r'^0-9', '') AS INT64) > 50 THEN 'over_50' ELSE 'unknown_age' END AS age_group, COUNT(DISTINCT PatientID) AS num_patients FROM `bigquery-public-data.idc_current.dicom_all` WHERE collection_id='upenn_gbm' GROUP BY age_group |
| 47 | For the upenn_gbm collection, download only male patient data for patients between 25 and 50 years of age               | SELECT * FROM `bigquery-public-data.idc_current.dicom_all` WHERE collection_id = 'upenn_gbm' AND PatientSex = 'M' AND PatientAge LIKE '%Y' AND CAST(REGEXP_REPLACE(PatientAge, "[^\\d]", '') AS INT64) BETWEEN 25 AND 50   |
| 48 | For the upenn_gbm collection, how many patients corresponding to each scanner   | SELECT COUNT(DISTINCT PatientID), ManufacturerModelName FROM `bigquery-public-data.idc_current.dicom_all` WHERE collection_id = 'upenn_gbm' GROUP BY ManufacturerModelName   |
| 49 | For the upenn_gbm collection, download only T2 and FLAIR scans  | SELECT * FROM `bigquery-public-data.idc_current.dicom_all` WHERE collection_id = 'upenn_gbm' AND (REGEXP_CONTAINS(SeriesDescription, 'T2') OR REGEXP_CONTAINS(SeriesDescription, 'FLAIR'))   |
| 50 | List all collections that contain segmentation images   | SELECT DISTINCT collection_id FROM `bigquery-public-data.idc_current.dicom_all` WHERE regexp_contains(Modality, r"SEG")  |