

FA 25 6513-C BIG DATA FINAL PRESENTATION



**LLM DataPrep: Scalable Pipeline for Biomedical
Fine-Tuning**

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PROBLEM STATEMENT:

- Biomedical text (PubMed: **2.2M entries**) is **noisy, duplicated, and unstructured**
- Raw data **cannot** be used directly for LLM fine-tuning
- Need a **scalable pipeline** to transform big biomedical datasets into high-quality training data



DATA OVERVIEW

- Data Source Name: PubMed
- **Data Source Link:** <https://huggingface.co/datasets/MedRAG/pubmed>
- Dataset File Size: 2.78 GB (Parquet) & ~70GB(JSONL)
- Approximate Number of Records: 2.21 Million
- **Columns Include:** id, title, content, contents, PMID

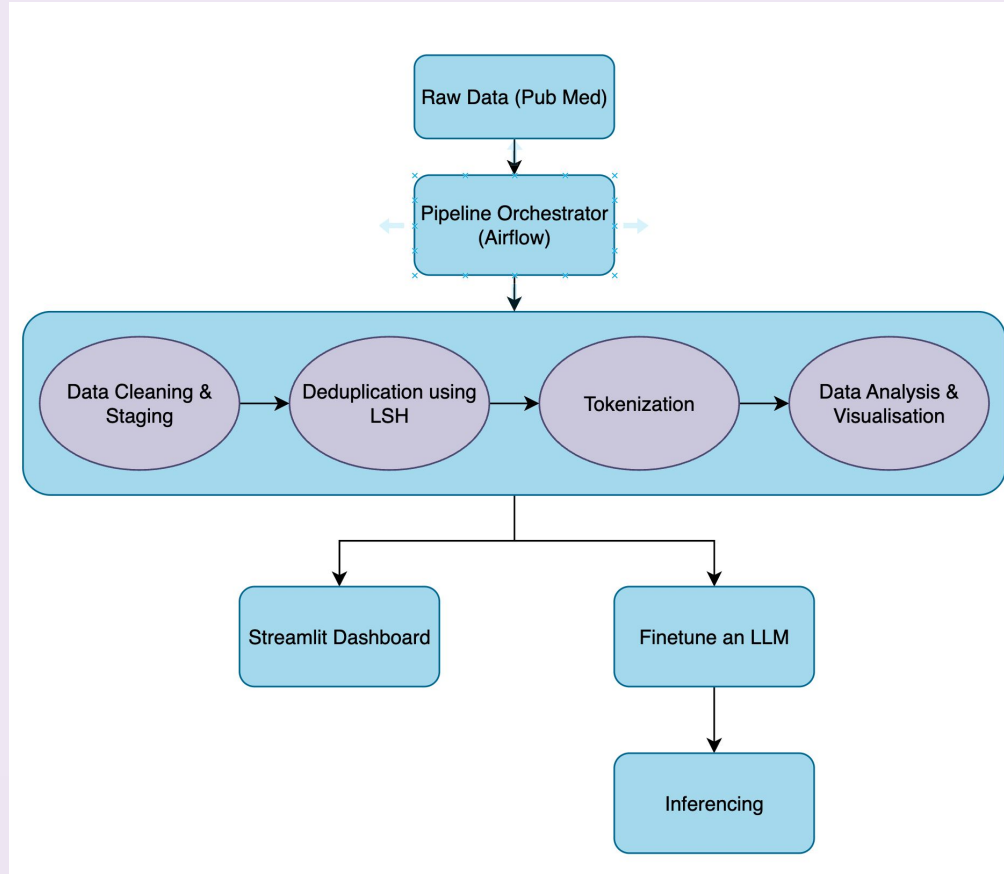
WHAT TECH STACK WE USED



PROPOSED SOLUTION

- Build a scalable end-to-end ETL pipeline to process millions of biomedical text records efficiently.
- Automatically clean, normalize, deduplicate, and tokenize PubMed data to produce high-quality training inputs.
- Orchestrate and automate all pipeline stages using Apache Airflow for reliability and repeatability.
- Generate a structured, LLM-ready dataset for domain-specific fine-tuning.

High Level Pipeline Architecture



Step 1 - Data Cleaning

```
--- Output of STEP 1: Data Cleaning & Staging ---  
STEP 1: Starting Data Cleaning and Staging...  
  Initial record count: 2209839  
  Cleaned records saved: 2209839  
  Stage 1 data written to hdfs:///user/gg3039_nyu_edu/LLM_DataPrep/cleaned/stage1_data
```

- **Loads the raw PubMed text and builds a clean main_text field by merging and normalizing the content.**
- **Removes noise such as citations, extra spaces, and short/invalid entries.**
- **Saves a cleaned, standardized dataset to HDFS for the next stage.**

Step 2: Deduplication Using MinHash LSH

```
--- Output of STEP 2: Near-Deduplication (LSH) ---  
STEP 2: Starting Near-Deduplication (LSH)...  
  Records removed by deduplication: 186606  
  Stage 2 data written to hdfs:///user/gg3039_nyu_edu/LLM_DataPrep/cleaned/stage2_data
```

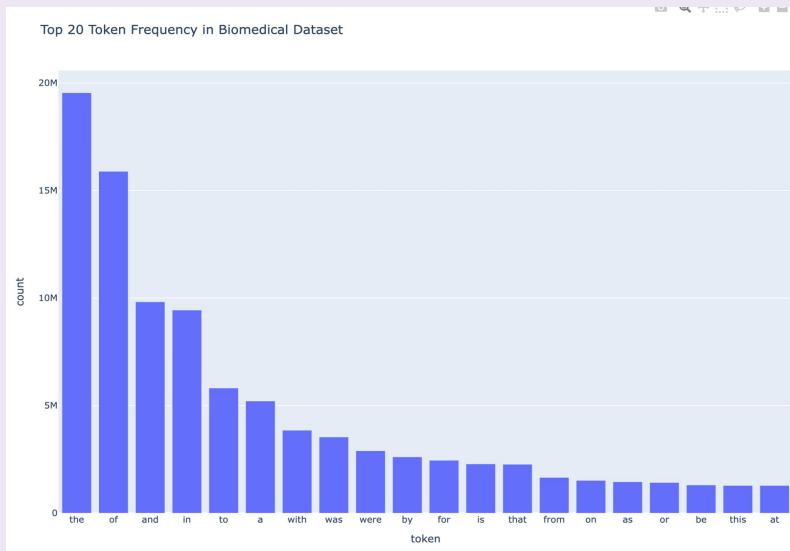
- **Tokenizes each document and converts it into a hashed feature vector using HashingTF, enabling efficient similarity checks.**
- **Uses MinHash LSH to group together texts that are highly similar and flags them as potential duplicates.**
- **Removes these near-duplicate records and saves a cleaned, deduplicated dataset to HDFS while reporting how many were dropped.**

Step 3: Distributed Tokenization

```
--- Output of STEP 3: Tokenization & Final Save ---  
STEP 3: Starting Tokenization and Final Save...  
Final records saved: 2023233  
Final LLM dataset written to hdfs:///user/gg3039_nyu_edu/LLM_DataPrep/final/llm_dataset
```

- Converts `main_text` and `title` into numeric token sequences that LLMs use for learning
- Standardizes the dataset to keep only the fields required for downstream LLM training: `id`, `PMID`, `title`, `main_text`, `tokens`
- Processes tokenization in parallel across the Spark cluster, enabling millions of records to be handled efficiently
- Writes the final structured dataset as Parquet to HDFS for fast retrieval during model fine-tuning
- Produces a terminal summary with the total number of tokenized records

Step 4: Data Analysis & Visualization



- Analyzes the cleaned and tokenized dataset to compute basic statistics like total records and average text length.
- Identifies the most common tokens in the corpus to understand vocabulary patterns.
- Generates an interactive Plotly chart and saves it for visualization and reporting.

Data Analysis - Hive Queries

```
-----  
VERTICES      MODE      STATUS TOTAL COMPLETED RUNNING PENDING FAILED KILLED  
-----  
Map 1 ..... container SUCCEEDED 52 52 0 0 0 0  
Reducer 2 ..... container SUCCEEDED 414 414 0 0 0 0  
Reducer 3 ..... container SUCCEEDED 207 207 0 0 0 0  
Reducer 4 ..... container SUCCEEDED 1 1 0 0 0 0  
-----  
VERTICES: 03/04 [=====] 100% ELAPSED TIME: 41.06 s  
-----  
INFO : Completed executing command(queryId=hive_20251210044813_2ccb8ee7-e83d-4f7b-a150-bf1b4f2ea9b0); Time taken: 41.358 seconds  
INFO : OK  
INFO : Concurrency mode is disabled, not creating a lock manager  
-----  
| token_word | token_count |  
-----  
| A. Very Short (<100 Chars) | 326 | 0.02 |  
| B. Standard Abstract (100-500 Chars) | 280822 | 13.88 |  
| C. Medium (501-1000 Chars) | 786033 | 38.85 |  
| D. Long (>1000 Chars) | 956052 | 47.25 |  
-----  
4 rows selected (41.501 seconds)  
0: jdbc:hive2://localhost:10000> |
```

Distribution of text lengths

```
-----  
VERTICES      MODE      STATUS TOTAL COMPLETED RUNNING PENDING FAILED KILLED  
-----  
Map 1 ..... container SUCCEEDED 52 52 0 0 0 0  
Reducer 2 ..... container SUCCEEDED 414 414 0 0 0 0  
Reducer 3 ..... container SUCCEEDED 1 1 0 0 0 0  
-----  
VERTICES: 03/03 [=====] 100% ELAPSED TIME: 34.86 s  
-----  
INFO : Completed executing command(queryId=hive_20251210045636_drd796f2-087a-4251-afdb-e5c93ca7b6be); Time taken: 35.002 seconds  
INFO : OK  
INFO : Concurrency mode is disabled, not creating a lock manager  
-----  
| title | duplicates |  
-----  
| Hypertension in the elderly. | 15 |  
| Laparoscopic cholecystectomy. | 13 |  
| Malignant hyperthermia. | 12 |  
| Lyme disease. | 12 |  
| Neuroleptic malignant syndrome. | 11 |  
-----  
5 rows selected (35.439 seconds)  
0: jdbc:hive2://localhost:10000> |
```

Top 5 Most repeated titles

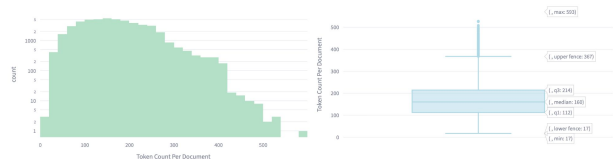
```
LATERAL VIEW EXPLODE(tokens) exploded_table AS token_word  
WHERE token_word NOT IN ('the', 'is', 'that', 'from', 'on', 'as', 'or', 'at', 'be', 'this')  
GROUP BY token_word  
ORDER BY token_count DESC  
LIMIT 10  
INFO : Query ID = hive_20251210044446_311cebac-0df0-4094-b726-lac7e8594de6  
INFO : Total jobs = 1  
INFO : Launching Job 1 out of 1  
INFO : Starting task [Stage=1:MAPRED] in serial mode  
INFO : Subscribed to counters: {} for queryid: hive_20251210044446_311cebac-0df0-4094-b726-lac7e8594de6  
INFO : Session is already open  
INFO : Dag name: SELECT  
token_word,  
COUNT(*) AS token_co...10 (Stage=1)  
INFO : Status: Running (Executing on YARN cluster with App id application_1756143132607_32901)  
-----  
VERTICES      MODE      STATUS TOTAL COMPLETED RUNNING PENDING FAILED KILLED  
-----  
Map 1 ..... container SUCCEEDED 52 52 0 0 0 0  
Reducer 2 ..... container SUCCEEDED 621 621 0 0 0 0  
Reducer 3 ..... container SUCCEEDED 1 1 0 0 0 0  
-----  
VERTICES: 03/03 [=====] 100% ELAPSED TIME: 77.05 s  
-----  
INFO : Completed executing command(queryId=hive_20251210044446_311cebac-0df0-4094-b726-lac7e8594de6); Time taken: 77.259 seconds  
INFO : OK  
INFO : Concurrency mode is disabled, not creating a lock manager  
-----  
| token_word | token_count |  
-----  
| of | 15325178 |  
| and | 9521785 |  
| in | 9090934 |  
| to | 5621679 |  
| a | 5025575 |  
| with | 3729374 |  
| was | 3428281 |  
| were | 2834538 |  
| by | 2505923 |  
| for | 2383933 |  
-----  
10 rows selected (77.978 seconds)
```

Most Common Non-stop word tokens

Visualization - Streamlit

Document Length Analysis

Token Count Histogram



3. Pipeline Transformation Flow

Comparing a small data sample (500 records) at each stage.

Raw Data (Input)	Stage 1: Cleaned & Filtered	Final Data (LLM Ready)
1000	850	750
2000	1700	1500
3000	2550	2250
4000	3400	3000
5000	4250	3750
6000	5100	4500
7000	5950	5250
8000	6800	6000
9000	7650	6750
10000	8500	7500

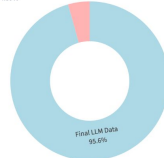
Cleaning removed citations, standardized content into 'main_text', and filtered short documents. (No records removed in this step, according to the log: 2,209,839 initial vs 2,209,839 cleaned)

id	title	match_text
pubmed230000_17327	Human human hydriodates secreted monoclonal antibodies to the H 395,000 Plasmodium	Human lymphoblastoid cell line, GM 672, and PB of Gambian adults immunized to
pubmed230000_17358	A suppressor lymphokine produced by human T leukemia cell lines. Partial characterization	Human T leukemia cell lines spontaneously release into their medium a suppressor lymph
pubmed230000_17359	Decay-accelerating factor is present on cultured human lymphocytes with endothelial cells	Decay-accelerating factor (DAF) has been previously described only in cells of bone marrow
pubmed230000_17360	Excitation of skinned muscle fibres by cultured human myofibrils. II. Influence of calcium and ionic gradients imposed by choline C replacement of K methasulphate on [Ca]i and [Mg]i	
pubmed230000_17361	BALB-b/3m2a-k mutation of the Na ⁺ /K ⁺ pump in the frog neural pigment epithelium	This paper presents electrophysiological evidence that small changes in [Na ⁺] _o modulate the
pubmed230000_17362	Binding of Borna's virus and monoclonal antibodies to defined regions of human neurone	Cleavage of cysteine and chymotrypsin digestion were applied to two [Na ⁺] _o fluctuations
pubmed230000_17363	Expression of myelin proteolipid protein and basic protein in normal and dysmyelinating C	Expression of myelin proteins was studied in the brains of 21-day-old normal mice and in
pubmed230000_17364	Schwann cell marker defined by a monoclonal antibody (224/50) with specific cytochrome X	A monoclonal antibody (mAb) designated 224/50 (light hatched) has been raised by fusion of
pubmed230000_17365	Purification and characterization of a bovine cerebral cortex cell surface sialoglycoprotein	A sialoglycoprotein from bovine cerebral cortex cells was purified to apparent homogeneity
pubmed230000_17366	Rat and mouse monoclonal antibodies to human myelin basic protein	BALB/c and Lewis cells were immunized with human myelin basic protein and the anti-

4. Deduplication and Cleaning Impact Summary

Initial Data Distribution (Total: 2,209,839)

nowed (Noise, Short, Duplicates)
4.33%



Final LLM Data
Records Removed (Noise, Short, Duplicates)

Pipeline Quality Assurance Report

- **Total Initial Records:** 2,209,839
- **Total Records Removed:** 96,995
- **Total Data Reduction Rate:** 4.39%

The removed records account for filtering out short or noisy documents (Stage 1) and removing near-duplicate documents (Stage 2: LSH). This ensures high-quality, non-redundant data for effective LLM fine-tuning.

2. LLM Fine-Tuning Metrics

Loaded Corolla Size

50,000 records

Mean Doc Token Count

167 tokens

Mean Char Length

1122 characters

Total Data Reduction

4.39%

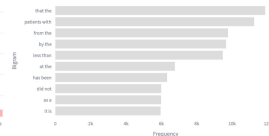
Token & Vocabulary Analysis

Top 20 Single Token Frequency



Top 10 Bigrams (Collocations)

Top 10 Bigrams (Collocations)



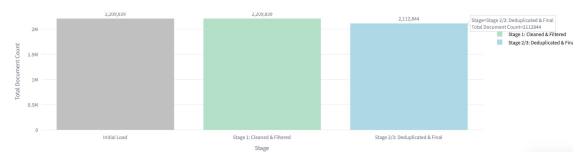
LLM DataPrep Pipeline: Biomedical Dataset Analysis

Showcasing Data Transformation and Quality Assurance

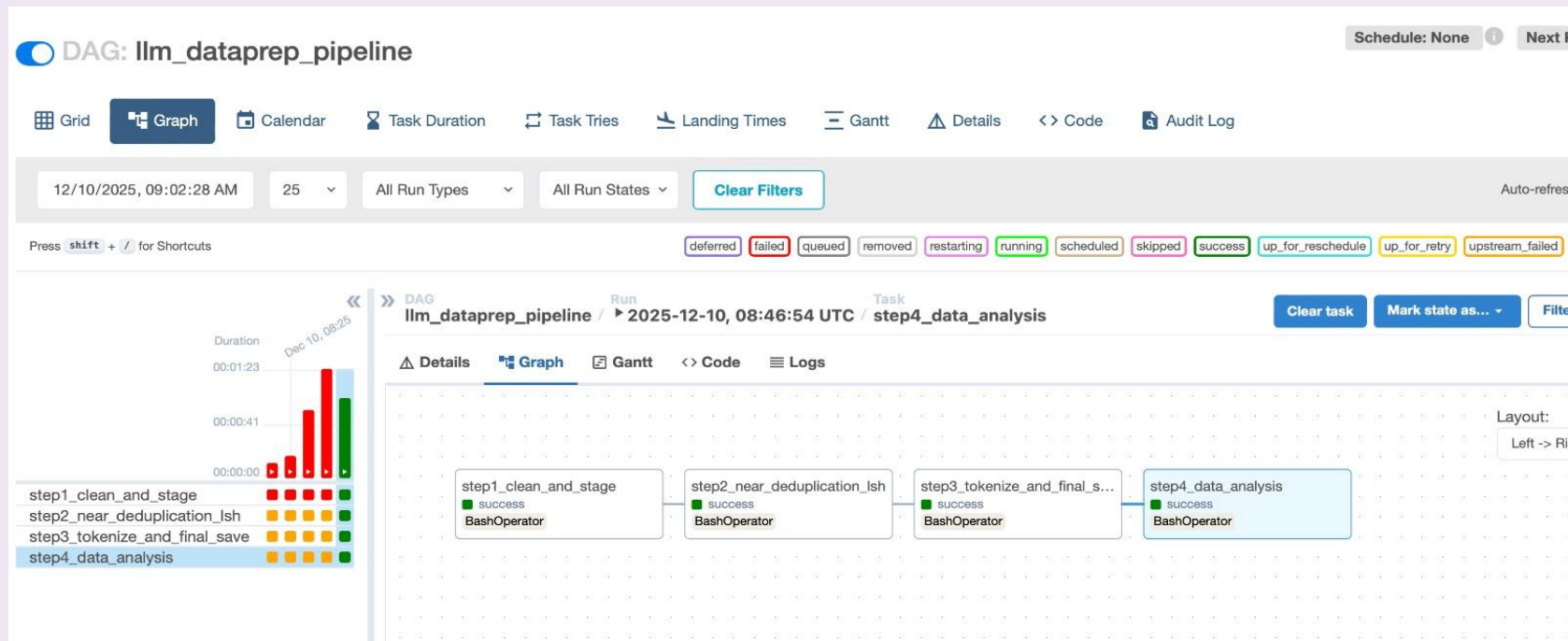
1. Document Count Flow and Reduction

Tracking record count through cleaning, filtering, and deduplication (Using Actual Pipeline Counts)

Records Flow Across Pipeline Stages



Pipeline orchestration through Airflow



Big Data Aspects We Focused On

- **Distributed processing:** Spark jobs across Dataproc cluster
- **Scalability:** Pipeline works on millions of biomedical records
- **Fault tolerance:** HDFS storage + Spark retry mechanisms
- **Optimized storage:** Parquet format for compression & speed
- **Parallel ETL stages:** Cleaning, dedupe, tokenization handled at scale
- **Workflow Orchestration at Scale (Airflow DAGs) :** Automated all pipeline stages using Apache Airflow, ensuring reproducibility, scheduling, and monitoring of large-scale ETL workflows.
- **Data Analysis:** Large-scale SQL analytics performed through Hive for dataset insights

Challenges faced

- **Setting up Airflow in NYU Dataproc**
- **Unavailability of GPU resources**
- **Preparing LLM fine-tuning-ready format**

Lessons Learned

- **Preprocessing quality drives LLM quality**
- **Distributed processing is essential at this scale**
- **Modular ETL design reduces debugging time**
- **Parquet + Spark = fast and scalable**

THANK YOU

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ANY QUESTIONS

