Please python scripts after reading the following README and Assignment in detail.

#### environment.yaml

```
name: msmarco-analysis
channels:
 - conda-forge
 defaults
dependencies:
  - python=3.9
 - pandas>=1.3.0
 - numpy > = 1.21.0
 - matplotlib>=3.4.0
 - seaborn>=0.11.0
 - tqdm>=4.65.0
 - requests>=2.26.0
  - datasets
  - pip
  - pip:
    - ipykernel # Optional: for Jupyter notebook support
```

### # MSMARCO Relevance Ranking Analysis

In MSMARCO, there are a few files as following,

```
Dataset({
    features: ['query_id', 'doc_id_a', 'doc_id_b'],
    num_rows: 39780811
})
```

### # MSMARCO Relevance Ranking Analysis

This project provides tools for analyzing the MSMARCO dataset for relevance ranking tasks. It includes comprehensive data analysis, statistics, and visualizations, with integration to Weights & Biases (wandb) for experiment tracking and visualization.

#### ## Features

- \*\*Data Analysis\*\*:
  - Query analysis (length, distribution)
  - Document analysis (length, distribution)
  - Relevance analysis (scores, distribution)
  - Query-document relationship analysis
- \*\*Visualization\*\*:
  - Interactive plots through wandb
  - Local PNG file generation
  - Statistical summaries and distributions
- \*\*Experiment Tracking\*\*:

- Track all analysis runs in wandb
- Compare different runs
- Monitor dataset statistics
- Share results with team members

## Setup

### Option 1: Using Conda (Recommended)

- 1. Install Miniconda or Anaconda if you haven't already:
  - [Miniconda](https://docs.conda.io/en/latest/miniconda.html)
  - [Anaconda](https://www.anaconda.com/products/distribution)
- 2. Create and activate the conda environment:
- ```bash
- # Create the environment from the environment.yml file conda env create -f environment.yml
- # Activate the environment conda activate msmarco-analysis

```
...
### Option 2: Using pip
1. Install the required dependencies:
```bash
pip install -r requirements.txt
...
## Downloading the Dataset
The MSMARCO dataset can be downloaded automatically using the
provided script:
```bash
python download_msmarco.py
```

This script will:

1. Create a `data` directory

2. Download the following files:
- Collection (documents)
- Queries
- Relevance judgments (qrels)
3. Extract and prepare the files
4. Verify the download
Alternatively, you can manually download and prepare the files:
1. Create a `data` directory in the project root
2. Download and place the following files in the `data` directory:
- `collection.tsv`: MSMARCO document collection
- `queries.tsv`: MSMARCO queries
- `qrels.tsv`: MSMARCO relevance judgments
## Usage
### Running the Analysis
1. Log in to wandb (if you haven't already):
```bash

```
wandb login
2. Run the analysis script:
```bash
python msmarco_analysis.py
The script will:
1. Load and process the MSMARCO data
2. Generate various statistics about queries, documents, and relevance
judgments
3. Create visualizations saved as PNG files
4. Upload all analysis results to wandb
### Viewing Results
1. **Local Output**:
  - Statistical summaries in the console
```

- Visualization plots saved as PNG files:

- Query length distribution
- Documents per query distribution
- Document length distribution
- Document length by relevance score

### 2. \*\*wandb Dashboard\*\*:

- Access your results at https://wandb.ai/your-username/msmarco-analysis
  - View interactive plots and statistics
  - Compare different analysis runs
  - Track dataset metrics over time

## ## Analysis Features

# ### Query Analysis

- Total number of queries
- Query length statistics
- Query length distribution visualization
- Interactive wandb plots

### ### Relevance Analysis

- Total number of relevance judgments
- Relevance score distribution
- Documents per query statistics
- Documents per query distribution visualization
- Interactive wandb tables and plots

### ### Document Analysis

- Total number of documents
- Document length statistics
- Document length distribution visualization
- Interactive wandb plots

# ### Query-Document Relationship Analysis

- Document length statistics by relevance score
- Visualization of document length distribution by relevance
- Interactive wandb plots and comparisons

### ## Environment Management

To manage the conda environment:

```
```bash
```

# Activate the environment

conda activate msmarco-analysis

# Deactivate the environment

conda deactivate

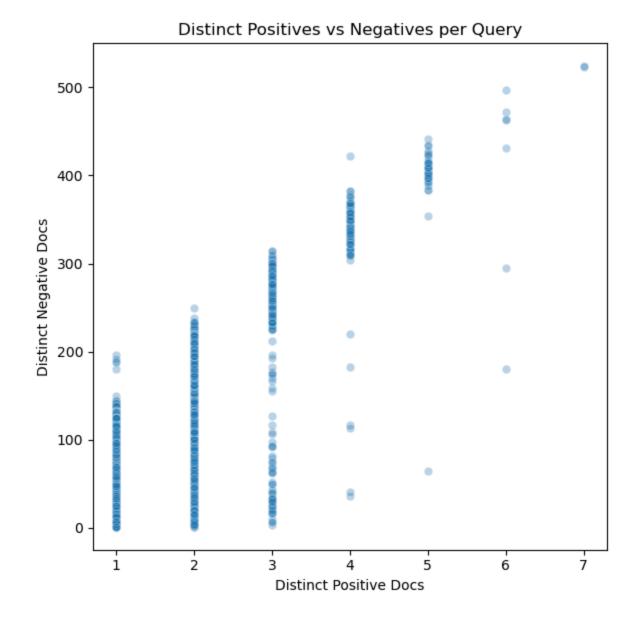
# Remove the environment

conda env remove -n msmarco-analysis

# Update the environment (if environment.yml changes)

conda env update -f environment.yml

...



# **Positives vs. Negatives Scatterplot**

### What it plots

Each point represents one query.

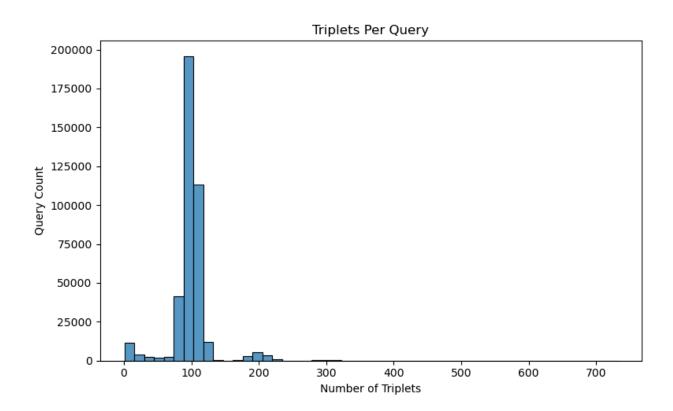
- The x-coordinate is the number of **distinct positive** passages for that query.
- The *y-coordinate* is the number of **distinct negative** passages for that query.

#### Why it matters

- Ideally, you want a good range of both positives and negatives per query so the model can learn to discriminate.
- If nearly every query has exactly one positive (x=1) but dozens of negatives (y»1), that's typical MS MARCO, but you might consider mining additional positives.
- Queries appearing near the diagonal (x≈y) have balanced supervision; points far from the diagonal show imbalance.

#### How to interpret

- A vertical line at x=1 shows "one relevant passage" per query.
- Spread along y shows negative sampling richness.
- Clusters of points with very low y (few negatives) may indicate queries with weak or missing negative supervision.



# **Triplets Per Query Histogram**

#### What it plots

On the *x-axis* is the number of triplets associated with a single query; on the *y-axis* is the count of queries that have exactly that many triplets.

#### · Why it matters

- If most queries have only a handful of triplets, the model sees fewer examples to learn per query.
- A long right-hand tail (some queries with hundreds or thousands of triplets) indicates a few "heavy" queries that could dominate training and skew the model.
- o A tight cluster around a single value means uniform coverage.

#### How to interpret

- A sharp peak at 1 or 2 suggests most queries have only one or two positive—negative pairs.
- A wide spread indicates diversity: some queries give you many negatives to sample from, which can help robustness.