Code Explaination

Documentation for Semantic Grouping of Clinical Studies

This document provides a detailed explanation of the code used for semantic grouping and retrieval of clinical studies. The code is designed to help researchers find similar historical clinical trials based on specific features such as study title, primary and secondary outcome measures, and eligibility criteria.

Environment Details

• **GPU**: RTX 3090 (24GB VRAM)

• **RAM**: 125GB

• **Template**: pytorch:2.1.0-py3.10-cuda11.8.0-devel-ubuntu22.04

Code Overview

The code is structured into several classes and functions, each serving a specific purpose. Below is a detailed breakdown of each major section.

1. Installation and Imports

The code begins with the installation of necessary libraries and importing required modules.

```
!pip install --no-cache-dir transformers==4.37.2 torch==2.1.0 scikit-
learn==1.3.2 pandas numpy tqdm spacy textblob gdown
!python -m spacy download en_core_web_sm
```

```
import os
import nltk
nltk.download(['punkt', 'stopwords'], quiet=True)
import spacy
import pandas as pd
import numpy as np
from transformers import AutoTokenizer, AutoModel
from sklearn.metrics.pairwise import cosine_similarity
from nltk.corpus import stopwords
import torch
from tqdm.auto import tqdm
import re
import warnings
from datetime import datetime
import gc
```

```
import gdown
from textblob import TextBlob
warnings.filterwarnings('ignore')

torch.backends.cuda.matmul.allow_tf32 = True
torch.backends.cudnn.allow_tf32 = True
```

2. DataLoader Class

The **DataLoader** class is responsible for loading and preprocessing the clinical trial data.

```
class DataLoader:
   def __init__(self, usecase_url, eligibilities_url):
        self.usecase_url = usecase_url.replace('/file/d/', '/uc?
id=').replace('/view?usp=sharing', '')
        self.eligibilities_url = eligibilities_url.replace('/file/d/', '/uc?
id=').replace('/view?usp=sharing', '')
 def download_and_load(self):
        usecase output = 'usecase 1.csv'
        eligibilities output = 'eligibilities.txt'
        try:
            gdown.download(self.usecase url, usecase output, guiet=False)
            gdown.download(self.eligibilities_url, eligibilities_output,
quiet=False)
            chunks = pd.read_csv(usecase_output, chunksize=10000)
            df = pd.concat(chunks)
            eligibilities = pd.read_csv(eligibilities_output, delimiter='|')
            print("\nColumns in original DataFrame:")
            print(df.columns.tolist())
            df = df[df['Funder Type'] == 'INDUSTRY']
            df = df.merge(eligibilities[['nct_id', 'criteria']],
                         left on='NCT Number',
                         right_on='nct_id',
                         how='left')
            start_date_col = next((col for col in df.columns if 'start' in
col.lower()), None)
            completion_date_col = next((col for col in df.columns if
'complet' in col.lower()), None)
```

3. TextProcessor Class

The **TextProcessor** class handles text cleaning and feature combination.

```
class TextProcessor:
   def __init__(self):
        self.stop words = set(stopwords.words('english'))
        self.text_columns = {
            'Study Title': 3.0,
            'Primary Outcome Measures': 2.5,
            'Secondary Outcome Measures': 2.0,
            'criteria': 2.5,
            'Conditions': 2.5,
            'Interventions': 2.0,
            'Phase': 1.5,
            'Brief Summary': 1.8
        }
        self.nlp = spacy.load('en_core_web_sm')
 def clean text(self, text):
        text = str(text).lower()
        text = re.sub(r'[^\w\s]', '', text)
       text = re.sub(r'\s+', ' ', text)
       words = text.split()
        text = ' '.join(word for word in words if word not in
self.stop words)
```

```
return text
def combine features(self, row):
        text parts = []
        for col, weight in self.text columns.items():
            if col in row.index and row[col]:
                cleaned text = self.clean text(row[col])
                text parts.extend([cleaned text] * int(weight * 5))
        return ' '.join(text_parts)
def process_batch(self, df, batch_size=1000):
        processed_texts = []
        for i in tqdm(range(0, len(df), batch_size), desc="Processing")
texts"):
            batch_df = df.iloc[i:i + batch_size]
            batch texts = []
            for _, row in batch_df.iterrows():
                processed text = self.combine features(row)
                batch_texts.append(processed_text)
            processed texts.extend(batch texts)
            if i % (batch size * 5) == 0:
                gc.collect()
        return processed_texts
```

4. BertSimilarityEngine Class

The BertSimilarityEngine class generates embeddings and computes similarity scores.

```
class BertSimilarityEngine:
    def init (self):
        self.device = torch.device('cuda' if torch.cuda.is_available() else
'cpu')
        self.tokenizer = AutoTokenizer.from pretrained('microsoft/BiomedNLP-
PubMedBERT-base-uncased-abstract-fulltext')
        self.model = AutoModel.from_pretrained('microsoft/BiomedNLP-
PubMedBERT-base-uncased-abstract-fulltext')
        self.model.to(self.device)
        self.model.eval()
        if self.device.type == 'cuda':
            self.model.half()
        print(f"Using device: {self.device}")
 def mean_pooling(self, model_output, attention_mask):
        token_embeddings = model_output[0]
        input mask expanded =
```

```
attention_mask.unsqueeze(-1).expand(token_embeddings.size()).float()
        return torch.sum(token_embeddings * input_mask_expanded, 1) /
torch.clamp(input mask expanded.sum(1), min=1e-9)
@torch.no grad()
    def encode_texts(self, texts, batch_size=32):
        embeddings = []
        for i in tqdm(range(0, len(texts), batch_size), desc="Encoding"):
            batch = texts[i:i + batch_size]
            encoded = self.tokenizer(batch, padding=True, truncation=True,
max length=512, return tensors='pt')
            encoded = {k: v.to(self.device) for k, v in encoded.items()}
            model output = self.model(**encoded)
            batch_embeddings = self.mean_pooling(model_output,
encoded['attention_mask'])
            embeddings.append(batch_embeddings.cpu().numpy())
            if i % (batch_size * 2) == 0:
                torch.cuda.empty cache()
        return np.vstack(embeddings)
 def compute_similarities(self, query_embedding, all_embeddings):
        return cosine_similarity(query_embedding.reshape(1, -1),
all_embeddings)[0]
```

5. TrialAnalyzer Class

The [TrialAnalyzer] class orchestrates the analysis and retrieval of similar trials.

```
class TrialAnalyzer:
    def __init__(self, usecase_url, eligibilities_url):
        self.data_loader = DataLoader(usecase_url, eligibilities_url)
        self.text_processor = TextProcessor()
        self.similarity_engine = BertSimilarityEngine()
        self.df = None
        self.embeddings = None

def calculate_trial_metrics(self, trial):
        metrics = {}
        try:
            metrics['enrollment_size'] = trial['Enrollment'] if
pd.notna(trial['Enrollment']) else 0
            metrics['has_results'] = 1 if pd.notna(trial.get('Study Results', '')) else 0
            metrics['completion_status'] = trial.get('Study Status', '')
```

```
metrics['duration_years'] = trial['duration_years'] if
pd.notna(trial.get('duration_years', '')) else 0
            text_length = len(str(trial.get('Brief Summary', '')))
            metrics['complexity_score'] = text_length / 100
            sentiment = TextBlob(str(trial.get('Brief Summary',
''))).sentiment.polarity
            metrics['sentiment_score'] = round(sentiment, 3)
        except Exception as e:
            print(f"Error calculating metrics: {str(e)}")
        return metrics
 def prepare_data(self):
        start time = datetime.now()
        print("Loading and preprocessing data...")
        self.df = self.data_loader.download_and_load()
        print(f"Total trials: {len(self.df)}")
        print("Processing text features...")
        processed_texts = self.text_processor.process_batch(self.df)
        print("Computing embeddings...")
        self.embeddings =
self.similarity_engine.encode_texts(processed_texts)
        del processed_texts
        gc.collect()
        end_time = datetime.now()
        print(f"Data preparation complete in {(end_time -
start_time).total_seconds():.2f} seconds")
 def analyze_trial_group(self, trials_df):
        analysis = {}
        try:
            analysis = {
                'total_trials': len(trials_df),
                'unique_conditions':
len(set(trials_df['Conditions'].str.split(',').sum())),
                'unique interventions':
len(set(trials_df['Interventions'].str.split(',').sum())),
                'phase distribution':
trials_df['Phase'].value_counts().to_dict(),
```

```
'avg_enrollment': trials_df['Enrollment'].mean(),
                'avg_duration': trials_df['duration_years'].mean(),
                'completion rate': (trials df['Study Status'].str.lower() ==
'completed').mean(),
                'has_results_rate': trials_df['Study
Results'].notna().mean()
            }
        except Exception as e:
            print(f"Error in group analysis: {str(e)}")
        return analysis
 def find_similar_trials(self, nct_id, n_similar=10):
       try:
            query_idx = self.df[self.df['NCT Number'] == nct_id].index[0]
            query_trial = self.df.iloc[query_idx]
        except IndexError:
            print(f"NCT ID {nct_id} not found")
            return None
        similarities = self.similarity_engine.compute_similarities(
            self.embeddings[query_idx],
            self.embeddings
        )
        similar_indices = np.argsort(similarities)[::-1][1:n_similar+1]
        similar_trials = self.df.iloc[similar_indices].copy()
        similar_trials['similarity_score'] = similarities[similar_indices]
        similar_trials['rank'] = range(1, n_similar + 1)
        query_metrics = self.calculate_trial_metrics(query_trial)
        group_analysis = self.analyze_trial_group(similar_trials)
        for idx, row in similar_trials.iterrows():
            metrics = self.calculate_trial_metrics(row)
            for key, value in metrics.items():
                similar_trials.at[idx, key] = value
        similar_trials['common_conditions'] = similar_trials.apply(
            lambda x: len(set(str(x['Conditions']).split(',')) &
                     set(str(query trial['Conditions']).split(','))),
axis=1)
        similar_trials['common_interventions'] = similar_trials.apply(
```

6. Main Function

The main function orchestrates the entire process.

```
def main():
   torch.backends.cudnn.benchmark = True
    torch.backends.cudnn.enabled = True
 if torch.cuda.is_available():
        torch.cuda.empty_cache()
        print qpu util()
    start_time = datetime.now()
   print(f"Analysis started at {start time.strftime('%H:%M:%S')}")
   usecase url =
"https://drive.google.com/file/d/1CLvAQeuxJCjE6CoiopXToHVDsN7CgQkg/view?
usp=sharing"
   eligibilities url = "https://drive.google.com/file/d/1-
bkkhqXlb5eDd3hmsDEIfrPHXbMtVHqj/view?usp=sharing"
    analyzer = TrialAnalyzer(usecase_url, eligibilities_url)
    analyzer.prepare_data()
   test_ncts = ['NCT00385736', 'NCT00386607', 'NCT03518073']
   for nct in test ncts:
        print(f"\nAnalyzing {nct}:")
        result = analyzer.find_similar_trials(nct)
        if result is not None:
            similar_trials, query_metrics, group_analysis = result
            print(f"\nQuery Trial Analysis for {nct}:")
            print("Metrics:", query_metrics)
            print("\nSimilar Trials Group Analysis:")
            for key, value in group_analysis.items():
                print(f"{key}: {value}")
```

```
output columns = [
                'rank', 'NCT Number', 'Study Title', 'Phase', 'Conditions',
                'Interventions', 'Primary Outcome Measures', 'Secondary
Outcome Measures',
                'Study Status', 'duration_years', 'enrollment_size',
'has_results',
                'completion_status', 'complexity_score', 'sentiment_score',
                'common_conditions', 'common_interventions',
'similarity score'
            1
            available columns = [col for col in output columns if col in
similar_trials.columns]
            print("\nTop 10 similar trials:")
            pd.set_option('display.max_columns', None)
            pd.set option('display.max colwidth', None)
            print(similar_trials[available_columns].to_string())
            detail file = f'trial details {nct}.csv'
            similar_trials.to_csv(detail_file, index=False)
            summary file = f'trial analysis {nct}.csv'
            summary_df = pd.DataFrame({
                'metric': list(query metrics.keys()) +
list(group_analysis.keys()),
                'value': list(query_metrics.values()) +
list(group_analysis.values())
            })
            summary_df.to_csv(summary_file, index=False)
            print(f"\nDetailed results saved to {detail file}")
            print(f"Analysis summary saved to {summary_file}")
            if torch.cuda.is_available():
                print("\nGPU Memory Status:")
                print_gpu_util()
                torch.cuda.empty_cache()
 end time = datetime.now()
    total_time = (end_time - start_time).total_seconds()
    print(f"\nTotal analysis completed in {total_time:.2f} seconds")
```

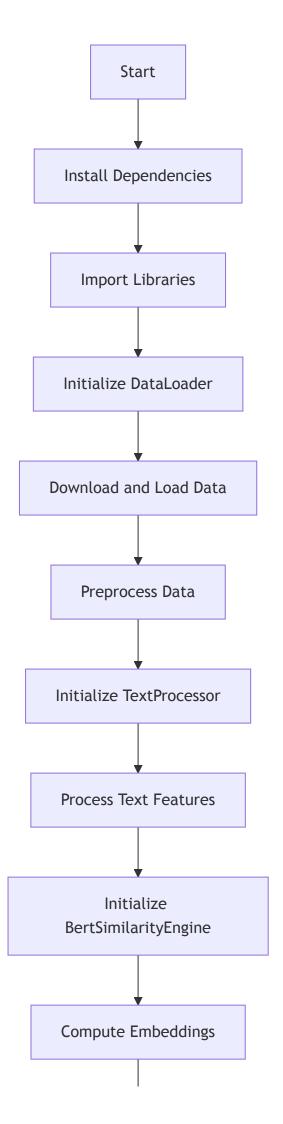
7. Helper Functions

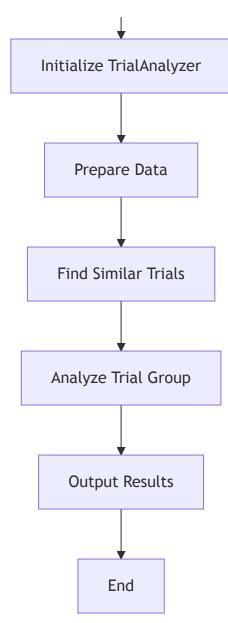
```
def print_gpu_util():
    if torch.cuda.is_available():
        print(f"GPU memory allocated:
        {torch.cuda.memory_allocated(0)/1e9:.2f} GB")
            print(f"GPU memory cached: {torch.cuda.memory_reserved(0)/1e9:.2f}
GB")
```

8. Visualizations

Below are some diagrams to visualize the workflow and class relationships.

Workflow Diagram





Class Relationship Diagram

pataLoader +init(usecase_url, eligibilities_url) +download_and_load() TextProcessor +init() +clean_text(text) +combine_features(row)

BertSimilarityEngine

+process_batch(df, batch_size=1000)

- +init()
- +mean_pooling(model_output, attention_mask)
- +encode_texts(texts, batch_size=32)
- +compute_similarities(query_embedding, all_embeddings)

TrialAnalyzer

- +init(usecase_url, eligibilities_url)
- +calculate_trial_metrics(trial)
- +prepare_data()
- +analyze_trial_group(trials_df)
- +find_similar_trials(nct_id, n_similar=10)